Methods of Livestock Research on Smallholder Farms

Publication

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Project

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Abbreviations

ADG	Average daily gain
AIGR	American Institute for Goat Research of Langston University
Ani	Animal
ANOVA	Analysis of variance
ANOVA-ARR	GenStat® Analysis of Variance by ANOVA, REML, or Regression
Brd	Breed
BW	Body weight
CITI	Collaborative Institutional Training Initiative
CP	Crude protein
CRD	Completely randomized design
df	Degrees of freedom
DM	Dry matter
ESGPIP	Ethiopia Sheep and Goat Productivity Improvement Program
FCM_d	Fat-corrected milk arising from dietary energy
FRG	Farmer or Farming Research Group
GLIMMIX	General Linear Mixed Models
GLM	General Linear Models
IACUC	Institutional Animal Care and Use Committee
ISH	Individual smallholder household
KDA	Kebele development agent
lsd	Least significant difference
lsmeans	Least squares means
LU	Langston University
ME	Metabolizable energy
ME_{l-d}	Metabolizable energy from the diet used for lactation
ME_m	Metabolizable energy used for maintenance
MEI	Metabolizable energy intake
MIXED	Mixed effects model of SAS
MRT	Multiple range test
MS	Mean squares
n	Number of observations
N	Nitrogen
NDF	Neutral detergent fiber
NGO	Non-governmental organization
r	Coefficient of correlation
R^2	Coefficient of determination
RCR	Responsible Conduct of Research
RE	Recovered energy
SAS	Statistical Analysis System (SAS®)
SD	Standard deviation
SE	Standard error
SEM	Standard error of the mean
SS	Sums of squares
TB	Technical Bulletin
Trt	Treatment
USAID	United States Agency for International Development

Chapter 1. Introduction

There have been many excellent publications dealing with on-farm research, some of which are cited in this publication. However, efforts were made to minimize repetition of information available elsewhere. Rather, attention was directed at providing practical information considered important to conduct on-farm livestock research. However, a significant portion of this publication also is pertinent to livestock research regardless of where conducted. In this regard, a decision was made to include information on a variety of topics that might be useful to researchers working with livestock both on-farm and on-station.

Similar to the on-farm animal research manual of Amir and Knipscheer (1989), at least a Bachelor of Science degree may be necessary to derive maximal benefit from this publication. Likewise, the target audience is junior- to mid-level researchers and extension personnel, and hopefully it can be of value in training graduate students as well.

This publication covers many topics. In addition to animal science research, some aspects of related topics are addressed, including extension, statistics, and sociology. There was no intent to cover each area in great detail, such as in some of the references listed. Therefore, the publication should be viewed primarily as a 'bridge' connecting different topics for the concerted effort required in effective livestock research.

There is considerable attention directed to experimental design and statistical analysis. Examples are presented primarily with the Statistical Analysis System, or SAS®, because of greatest familiarity with this package. However, because other systems such as GenStat® are sometimes used, it was also given some attention as an example. For GenStat, because of limited experience and time constraints in development of the publication, there could be alternative or more appropriate methods available than those presented.

Throughout the publication, activities of a recent project in Ethiopia in which Langston University participated are addressed. Though developing countries are all different, these references to conditions in Ethiopia will generally be applicable to many other areas of the world.

There were only a limited number of hardcopies of this publication printed because of budget constraints. The primary mode of dissemination is free on-line access. Sometime in the future it is possible that another edition will be available. If so, this will be announced. Otherwise, only minor corrections will be made to this on-line publication, although it is conventional to include the access date in citations. Relatedly, parts of this publication may be reproduced with acknowledgement and citation.

Chapter 2. On-Station versus On-Farm Research

Purposes

On-farm livestock research is conducted on farms with producer participation rather than at locations such as universities, governmental institutions, or private entities. But, there is considerable variability in the nature of on-farm research (e.g., researcher- vs. farmer-controlled). Also, it is important that on-farm conditions be maintained to the maximum extent possible. That is, if farm conditions are modified so that they are similar to those on-station, then obviously the activity could not realistically be viewed as on-farm. Naturally some changes or additional activities are necessary for on-farm research compared with the normal production conditions and practices, but care should be exercised in their selection and implementation.

Some purposes of on-station and on-farm livestock research are common, whereas others are relatively unique. General purposes of on-farm livestock research can be highlighted as noted below.

- Original identification and comparison of useful technologies for livestock production
- Validation or evaluation of on-station livestock research findings, with attention to unique on-farm conditions
- Dissemination and transfer of useful livestock production technologies

Thus, the most appropriate method depends on the particular needs and setting. For example, Anderson and Lockeretz (1991) stated that when research is conducted on-farm only in response to specific funding source mandates, quality of the activities can be compromised if a more appropriate venue is on-station or if on-farm demonstrations would be more suitable.

Developmental or 'ground-work' activities often occur on-station before a technology is taken to the field. Hence, on-station research can be more risky, but preliminary studies minimize such concerns for later larger and more costly experimentation. Moreover, some techniques used on-station in developmental stages are not suitable on-farm. An example is small scale treatment of crop residues with different types and levels of chemicals to increase digestibility and(or) feed intake. Effectiveness is frequently assessed by an in vitro technique with substrate incubation in tubes containing buffer and ruminal fluid followed by digestion in a pepsin or detergent solution. After 'screening' a large number of treatments, then evaluation can proceed to feeding livestock treated residues and measuring variables such as voluntary feed intake and digestion. Eventually animal performance is determined on-station, after which on-farm research can occur (Devendra, 2013). However, Anderson and Lockeretz (1991) stated that exploratory on-farm research also can be valuable to identify the array of production practices being used, which can be followed by on-station research to explain why some practices are more effective and which ones are best suited for specific environmental conditions. But, prevalent production practices also could be addressed by means to identify topics for on-farm research, including surveys and other rural appraisal methods.

When livestock performance trials are conducted on-station, efforts are often made to simulate on-farm conditions. In fact, some research institutions use what are sometimes referred

to as 'branch' or 'field' stations, sites, or locations. Although this concept may be employed to address conditions different from those of the main site or 'campus,' in many cases farm conditions are closely matched. When field conditions are accurately simulated on-station, need for on-farm research is minimized, with the extent depending on factors such as effectiveness of extension or technology transfer programs in place, related cultural and social conditions, progressiveness or willingness of local farmers to adopt new technologies, etc. Also, as noted by Goetsch and Abebe (2009), even with strong evidence for benefit from a particular technology developed on-station, on-farm research and(or) demonstrations may still be required to convince farmers and obtain knowledge necessary for successful widespread implementation. Moreover, in some cases there are influencing conditions on-farm not previously realized or adequately considered on-station. Therefore, in terms of efficiency of utilization of resources and time, on-farm research offers many attributes.

The purpose of some on-farm research is to validate on-station experimentation. However, the utility of on-farm research need not be limited to this. That is, some on-farm research can substitute for or replace studies performed on-station. Relatedly, on-station research in that context is 'valid' regardless of agreement with on-farm findings. If results are disparate, then attention should be directed to the differing conditions responsible.

Advantages and Disadvantages

General advantages and disadvantages of on-station and on-farm livestock research are well known, although considerable variability in degrees exist for different settings. Relatedly, some considerations could be an advantage or disadvantage depending on how activities are implemented. Such factors should be carefully considered when deciding on most appropriate research approaches.

On-Station Research

Advantages

- Considerable potential control and monitoring of experimental conditions
- Relatively stable conditions to presumably minimize unexplained variability
  - □ Although, this would not be a significant attribute with some settings closely mimicking field conditions.
- Ability to impose treatments with unfavorable economic consequences unacceptable to smallholders without adequate compensation
- Capacity to maximize the number of replications and statistical power
- Minimal travel to study site(s)
- More appropriate for determining underlying factors responsible for treatment effects (St-Pierre and Jones, 1999)

Disadvantages

- Experimental conditions may not adequately simulate those on-farm.
- Regardless of how well field conditions are simulated, some livestock producers or groups may question applicability to their on-farm conditions.

- Use of a relatively narrow array of conditions compared with field settings to which findings may be applied
- Considerable investment in infrastructure and personnel regardless of level or efficiency of use in research
- Time constraints may limit direct, close involvement of researchers in day-to-day activities.

On-Farm Research

Advantages

- Findings are more likely to be adopted by other livestock producers.
  - Engstrom et al. (2010) stated that in some cases this is particularly facilitated when the technology being addressed requires a relatively large number of animals. Although, perhaps this is most relevant to the area of on-farm dairy trials in developed countries.
- No on-station infrastructure required
- Fewer on-station personnel needed due to input of producers and others such as extension and technology transfer personnel
- Opportunities to learn of other research area needs in the field
- Research conducted under real field conditions, typically with a wider range of conditions than on-station (St-Pierre and Jones, 1999)
- Generally considerable involvement of extension and technology transfer personnel
- Farmers learn best when actually conducting and being involved in activities themselves (Ponniah et al., 2008).
- Because of more variable conditions compared with on-station research, potentially a broader array of conditions to which findings can be extrapolated

Disadvantages

- Requires careful planning and close, continuous monitoring, generally more than needed for on-station research
- More variable conditions, increasing as researcher control decreases and that of farmers increases, thereby necessitating a greater number of experimental units and thorough characterization of conditions (Amir and Knipscheer, 1989)
- Detailed agreements, often containing financial considerations, may be required.
- Difficult to correct major procedural limitations once an activity is initiated
- Difficult to include treatments that have unfavorable economic effects
- Greater travel requirements

Researcher- vs. Farmer-Controlled On-Farm Research

Anderson and Lockeretz (1991) provided a thorough description of differences between researcher- and farmer-controlled on-farm research, pointing out the extremes of both approaches and intermediate positions as well. Similarly, Amir and Knipscheer (1989) described 'traditional' and 'innovative' approaches to on-farm research with animals, with the traditional approach including activities with and without farmer involvement. For this publication, emphasis is on researcher-controlled on-farm research, but naturally with producer involvement.

According to definitions of Amir and Knipscheer (1989), the traditional approach with smallholder participation is being addressed.

Researcher control is necessary so that experiments are designed that allow valid statistical analyses, with villages and farms rather than on-station sites chosen for the specific experimental conditions. In this regard, if data cannot be statistically analyzed, then only anecdotal differences can be casually viewed without any degree of certainty of repeatability in this or any other setting. But, it is obviously desirable and advantageous to have farmer involvement in all stages of the on-farm research process.

Responsible Conduct of Research

The same principles of Responsible Conduct of Research (**RCR**) for on-station research apply to research on-farm. Encompassed topics are plagiarism, fabrication, falsification, authorship, and other ethical issues such as intellectual property rights. An in-depth coverage of RCR is beyond the scope of this publication, and there are many excellent sources of information and training available, such as the Collaborative Institutional Training Initiative (CITI, 2013). The CITI (2013) also includes training resources for other related topics such as appropriate animal care procedures and Institutional Animal Care and Use Committees.

Chapter 3. Topic Identification

Introduction

There are numerous ways of identifying on-farm livestock research topics, with no single method most appropriate in all settings. Common means are listed below, some of which were addressed by Anderson and Lockeretz (1991) in a report of a workshop on "On-Farm Research Techniques."

- Surveys
- Tours
- Visits of smallholder farms
- Farmer advisory committees
- Focus groups
- Lead or progressive farmers
- Local or regional extension officers
- Non-governmental organizations
- Research organizations

However, topic identification frequently involves more than one of these mechanisms and occurs over a relatively long period of time. For example, the period of 1980-1982 was spent characterizing traditional farming systems to define objectives and goals of the Small Ruminant Collaborative Research Support Program to develop the Kenyan dual-purpose goat (Ponniah et al., 2008).

It is important that a participatory approach be included in the process of topic identification as well as other aspects of on-farm research, with respect given to and value realized from indigenous knowledge (Ponniah et al., 2008; Devendra, 2013). Research and extension personnel should be open to learning from farmers rather than only the converse (Ponniah et al., 2008; Devendra, 2013).

Surveys

Surveys can be useful to identify on-farm livestock research topics, but they are not commonly employed in this manner other than for determining general intervention needs, examples being early life health care and feed shortages in dry seasons. Chromy and Abeyasekera (2005) provided a thorough description of survey data analysis.

An important consideration for some surveys and questionnaires is that an incentive may be necessary for household participation. That is, farmers may feel that their information and input have value and, thus, compensation should be received. Relatedly, in some developing areas, a good example being Ethiopia, the number of graduate students has markedly risen in recent years, outpacing available faculty advisement time and on-station research resources. Consequently, surveys have become a common component of thesis projects either as the sole activity or to complement a relatively small amount of actual research with livestock.

Tours and Visits of Smallholder Farms

Although tours and smallholder farm visits have many commonalities and, thus, are grouped together here, there are notable differences. A primary one is a smaller number of people on visits than tours. Visits of individual farms and households by one or a small group of researchers may facilitate more meaningful interaction about most significant production constraints and possible means of addressing them. Also, it would be desirable for local extension personnel who smallholders are familiar with to participate in visits. Tours may be relatively more useful once a topic and desire for on-farm research have been established, such as to develop interest of a larger number of smallholders. However, tours of national and(or) foreign 'experts' are frequently used by governmental and non-governmental organizations (**NGO**) providing financial support to identify areas of on-farm research to be included in 'Requests for Applications' or 'Proposals' being developed.

Farmer Advisory Committees and Focus Groups

Anderson and Lockeretz (1991) in their workshop report mentioned both Farmer Advisor Committees and Focus Groups. Important points were that such entities may have limited interest in areas not of moderate to high relevance to their particular farms and, relatedly, different kinds of farmers should be included. Consideration should be given to producers from farms of various sizes and types as well as allied industries when appropriate. Moreover, working with entities providing 'advice' should not be allowed to transition into 'control' over on-farm or on-station research.

Members of committees or groups can be smallholder farmers participating in on-farm research. But, meetings with smallholders who will potentially take part in on-farm research, as well as later meetings with selected smallholders, should not involve the advisory 'group.' This is so that focus is maintained on the research activity and to allow participation of others, particularly local and(or) regional extension officers.

Lead, Progressive, or Contact Smallholder Farmers

Lead, Progressive, or Contact Farmers could have been addressed in the preceding section for Farmer Advisory Committees and Focus Groups, because inclusion of such producers is beneficial. However, frequently ideas for on-farm research arise from interaction between researchers and lead farmers, and such dialogue can help confirm the merit of topics for study. Thereafter, lead farmers can be of great assistance in recruiting other smallholders to participate in on-farm research and ensuring that the study is conducted properly on all farms.

Governmental, Non-Governmental, and Research Organizations

In some instances governmental organizations or NGO determine topics for on-farm livestock research. However, in most or all cases the areas arose from one or more of the aforementioned methods. An additional avenue used by some NGO is to observe on-farm research conducted by other entities. An example of this, though pertaining to on-farm demonstrations rather than research, occurred in the project "Ethiopia Sheep and Goat

Productivity Improvement Program (**ESGPIP**)" (2005 to 2011), supported by the U.S. Agency for International Development (**USAID**). The ESGPIP conducted a number of on-farm research activities involving ammoniation of crop residues via urea treatment. Field days were held at the end of these activities, which included demonstration of the treatment process, and similar demonstrations independent of on-farm research activities occurred as well. Other NGO with relatively small development programs in various areas of Ethiopia observed the success and impact of these ESGPIP demonstrations and, hence, initiated the same type of activity.

Large organizations, a notable example being USAID, provide funds to research organizations to identify topics of on-farm livestock research for smallholders. These organizations typically use one or more of the methods noted above. An example is a 2.5-week assessment visit to Liberia by personnel of Langston University (**LU**) in 2006. Funds were provided by USAID to develop a plan to revitalize the small ruminant industry. Methods used included tours, visits of smallholder farms, and dialogue with governmental officials, extension personnel, and university researchers and teachers. A similar assessment visit occurred in the early part of 2005 for the ESGPIP, generating an outline that resulted in the 'Request for Application' or 'Proposal' later that year.

Chapter 4. Protocols

Importance

Experimental protocols as addressed in this publication are detailed descriptions of research activities conducted in a defined period of time. They are key components of on-farm as well as on-station research, with the importance increasing as the number of people involved rises. Before protocols were required for review by Institutional Animal Care and Use Committees (**IACUC**), it was not uncommon for experiments to be conducted without a formal protocol if the number of participants was limited to a small group, such as to the lead researcher, a graduate student, and perhaps an animal care and(or) laboratory technician. Conversely, protocols are critical at sites like the American Institute for Goat Research (**AIGR**) of LU in part because of the participation of visiting scientists and students from many other countries and considerable diversity in research experience.

Protocols are very important for on-farm research because of the involvement of many individuals, some without extensive training in research, including smallholder farmers and households and usually one or more extension officers or agents. For example, in many on-farm research activities of the ESGPIP, one or more kebele development agents (**KDA**) that had previously worked directly with the participating households were involved. A kebele (often termed 'village') is the smallest administrative unit in Ethiopia, with ‘woreda’ being the next larger unit. Woreda extension officers were briefed and kept up to date on study progress and in some instances were active participants as well.

Development

When developing an experimental protocol, there should be input from and participation of most or all of the individuals and groups involved. Usually, however, participating smallholder farmers would not have been selected yet. Nonetheless, it would be beneficial to receive input from extension agents who will work directly with farmers in implementation of the activity or at least agents should be part of the selection process.

The first page of experimental protocols of the AIGR of LU is for use by the IACUC, addressing general questions pertaining to animal care and highlighting areas to receive special attention. Introduction and Rationale sections can be and are sometimes combined, and other headings can be used for such information as well. At least a brief literature review similar to the 'Introduction' section of a peer-reviewed journal article should be included to provide a justification for the study and bases for objectives. In some cases a description of literature searches that have been conducted may be necessary, which can also entail a power analysis addressing minimal and optimal numbers of observations. After a detailed description of procedures, sections can be included to address specific duties or responsibilities of different individuals or groups, which for the AIGR is the Research Farm and Central Laboratory. Finally, research findings are only of value if they are publicized; therefore, a section for communication or dissemination is included. Once the protocol is completed, it is circulated for signatures of all investigators as well as the lead person in support groups or divisions and pertinent administrators, which for the AIGR are the Research Leader and Director.

Procedures in protocols should be fairly detailed and may also include contingency plans. There will be much more information than required for recruiting participating smallholder farmers and households as well as for actual implementation of the activity at the farm level. For these purposes, a much simpler description may be developed. Responsibilities of the smallholder farms should be indicated, as well as any incentives. Because in most cases animals owned by smallholders are used, handling of animal health issues should be addressed. In this regard, including a statement of participation and activities of an animal health expert should be considered. This might also be an additional incentive for farmer participation. Although, as addressed in the Memorandum of Understanding of the publication "On-farm Research and Technology for Dual-purpose Goats" (1992), services and supplies to be provided to and by the smallholder households should be stated. Signatures of the smallholder farmers, research and extension personnel, and other participants can be included in protocols or Memorandums of Understanding.

Examples

Headings of protocols used at the AIGR are listed on the next two pages. Particularly for on-station research, information such as that given in a “Sample Animal Study Proposal” of OLAW (2014) should be addressed. This includes descriptions of housing facilities, transportation, restraint, veterinary care, hazardous agents, pain and distress, and certifications of activities like participation in pertinent training programs. As noted later, attention should also be given to animal numbers.

After headings of AIGR protocols, a description of a research activity of the AIGR used for recruiting farmers to participate is provided as an example. Then, a draft of a somewhat more official agreement that includes signatures of the producer as well as AIGR personnel is provided. However, this is a fairly informal agreement rather than a legally binding document, and would benefit from input of individuals or groups very knowledgeable about such issues. Relatedly, some farmers could be unwilling to participate in an activity if their signature is required.

Page 1

CRITERIA FOR ANIMAL CARE COMMITTEE
EVALUATION OF RESEARCH PROPOSALS

Protocol Title:

Investigators:

Answers to Questions:

1. Is there a computer model or in vitro system or another alternative that will accomplish the same objective?

2. Is there duplication of other research?

3. Is there another species more appropriate for this research?

4. Can this research be conducted adequately with fewer animals.

5. Is there pain or stress?

6. Are housing and care adequate?

7. Is there surgery?

8. Is there euthanasia?

9. Are personnel qualified?

10. Does the research utilize radioactive, biohazardous, or hazardous materials?

_____

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PROJECT NUMBER:

Experiment Number:

Title:

Principal Investigator (name, title, address, contact information):

Co-Investigators (name, title, address, contact information):

Page 3 and Subsequent Pages

INTRODUCTION:

RATIONALE:

OBJECTIVES:

EXPERIMENTAL PROCEDURES:

LABORATORY ANALYSES:

STATISTICAL ANALYSES:

PROJECT MILESTONES:

SCHEDULE FOR COMMUNICATING RESULTS:

COOPERATION REQUIRED:

PROJECT NEEDS:

SPECIAL REQUIREMENTS:

CONTACT INFORMATION:

REVIEWED BY:

Principal Investigator: _____ Date: _____

Co-Investigators: _____ Date: _____

Farm Manager: _____ Date: _____

Lab Coordinator _____ Date: _____

APPROVED BY:

Research Leader: _____ Date: _____

Director: _____ Date: _____

Example of Activity Description for Farmer Participation

Producer Requirements for Langston Parasite Resistance Project

General

- ☐ Accurate computer and/or handwritten records must be kept. Langston can provide assistance in this area if necessary.
- ☐ Feeding management can be as normal. However, a free-choice mineral supplement must be given. Langston can assist in selection of a mineral supplement if necessary.
- ☐ Initially, a minimum of 150 breeding females and 20 males are required. Thereafter, a minimum of 150 breeding females is required. The same females should be maintained to the extent possible. After the first year, the number of males will be adjusted according to the male testing criteria below. Body weight will be determined at weaning and breeding.
- ☐ Good management practices are necessary.
- ☐ Kidding/lambing will be in mid- to late spring. Breeding dates may have to be modified slightly in order for animals from each location to be at a similar age at the beginning of the buck/ram test mentioned below.
- ☐ There should be 6 fenced areas available for conduct of single sire pen breeding.
- ☐ Males, females, and lambs/kids must be identified; ear tags are acceptable but tattooing is preferred.
- ☐ Records must be kept regarding factors such as health care and reasons for culling.
- ☐ Langston will provide $3,000 annually to each producer for materials and supplies and other inputs. If necessary based on needs, a slightly greater amount could be agreed upon.

Initial male selection and testing

- ☐ 15 kids/lambs will be submitted to the Langston buck/ram test, with all males returned to the producer. There is no cost to the producer for the test, and the producer will receive all test data. The selection of males in year 1 (2013) will be random.
- ☐ Of the 15 males from a producer's herd/flock submitted to the ram/buck test, Langston will identify 5 candidate males with relatively high resistance and 5 candidate males with medium or moderate resistance based on data from the buck/ram test. Producers will be able to select 3 males from each candidate pool for breeding to selected females. Any of the remaining 9 males can be used for breeding with females not selected.

Initial female selection

- ☐ Langston will determine FAMACHA score 4 times annually and fecal egg count (FEC) of females once before and again at weaning, with producer assistance. One blood sample will be collected annually as well for DNA and other analyses.
- ☐ Langston will select 45-50 females with high resistance and 45-50 with medium resistance. Females not selected can be bred to any of the non-selected or other males.

Initial breeding

- ☐ Each of the 3 selected males with high resistance determined in the buck/ram test will be used to mate at least 15 females with high resistance. Likewise, each of the 3 selected males with medium resistance will be used to mate at least 15 females with medium resistance.

The selection of the specific 15 females within each group to be bred to specific males will be random.

- The producer and Langston will weigh lambs/kids at weaning at approximately 12 weeks of age.

Selection and breeding in years 2 and 3

- In years 2 and 3 (2014 and 2015, respectively), 4 male lambs/kids from each of the 3 resistant male bucks/rams will be randomly selected, and 2 male lamb/kid from each of the 3 median male bucks/rams will be randomly selected as well. These 18 males will be submitted to the Langston buck/ram test as noted above.
- Of the 18 males from a producer's herd/flock submitted to the ram/buck test, Langston will then identify 5 candidate males with relatively high resistance as noted above, and the 5 candidate males with medium or moderate resistance will be used as well. Producers will be able to select 3 males from each candidate pool for breeding to selected females as noted earlier.

PROJECT AGREEMENT

Project Title: Sustainable Small Ruminant Production through Selection for Resistance to Internal Parasites

Summary

Internal parasitism is an increasingly important constraint to small ruminant production. Sustainable and practical management practices to address internal parasitism are lacking. Selection of small ruminants for internal parasite resistance has not received adequate attention and offers a sustainable method of production. Project objectives are to determine early progress in selection of small ruminants for resistance to internal parasitism 'on- station' and 'on-farm'; characterize changes in performance due to selection; develop and implement a new second generation central sire performance test for small ruminants at Langston University; develop early-life indications of resistance and assess changes in physiological conditions affected by selection; evaluate economic and management considerations of whole herd/flock selection; disseminate potential benefits of selection and associated economic and management considerations for adoption by small ruminant producers. This project will provide small ruminant producers with a means to evaluate sires for resistance to internal parasites. Level and efficiency of small ruminant production, as well as profit, will be increased via change in animal performance, reduced mortality, and improved animal welfare, as well as decreased expenditures in animal health management supplies. It is projected that early life indicators of resistance of small ruminants to internal parasites will be developed. The demonstration of selection activities on-farm will increase technology adoption compared with activities only on-station.

Producer Responsibilities

1. Keep accurate records on animals being used in the project as well as those that may potentially enter later (e.g., doelings and ewe lambs that might be bred to kid/lamb at about 2 years of age but not as yearlings), as noted below. Langston will contact the producer for such information on a monthly basis.
   - Animal identification, gender, breed composition, parentage, age
   - Litter size, gender, birth date and weight
   - Weaning weight and female weight and body condition score at weaning
   - Any health treatments including deworming, products, dosages, estimated cost, dates, and reasons (e.g., if an animal is dewormed, the basis such as bottle-jaw or FAMACHA score(s) should be indicated)
   - Culling, including reasons and date
   - Provide as much information as possible on feeding practices, so as to allow for economics analysis
     - □ This could include the area grazed by a certain number of animals, rates of supplemental feeding and supplement feedstuff cost, etc.

2. Provide adequate management practices including feeding, with a free-choice mineral supplement and fresh clean water.

3. Maintain at least 150 breeding females that may be used. The same females should be maintained to the greatest extent possible.
4. Provide at least 15 bucks/rams selected by Langston with producer input in year 1 for the Langston Buck/Ram Test. These animals will be selected primarily based on FAMACHA score before weaning. This number will be increased to 18 in years 2 and 3, again with selection by Langston with producer input (i.e., 4 bucks/rams from each of the 3 sires used in the high resistance group and 2 bucks/rams from each of the 3 sires in the medium resistance group).
5. Select 3 of the 5 males with high resistance and 3 of the 5 males with medium resistance, as determined in the Langston Buck/Ram Test, to be bred to at least 15 females per male. These females (at least 45 per resistance group; i.e., high and medium) will be selected by Langston based on FAMACHA score and fecal egg count as noted below. Remaining females and males can be used as desired by the producer.
6. Provide cooperation/assistance to Langston in:
   - determining FAMACHA score of each animal at 4 and 8 weeks after kidding/lambing, at weaning, and 4 to 6 weeks post-weaning
   - collecting samples for fecal egg count and at eight 8 weeks after kidding/lambing and at weaning
   - setting up breeding groups in the fall and collect blood samples
   - determine body weight at weaning and breeding
7. Conduct breeding in 6 groups or pens for a 6 to 8 week season, with the groups noted below

Breeding group	Male	Female
A	High resistance #1	15-20 High resistance
B	High resistance #2	15-20 High resistance
C	High resistance #3	15-20 High resistance
D	Medium resistance #1	15-20 Medium resistance
E	Medium resistance #2	15-20 Medium resistance
F	Medium resistance #3	15-20 Medium resistance

Langston Responsibilities

1. Transport the bucks/rams to and from the Langston Buck/Ram Test
2. Provide all feed and care during the Langston Buck/Ram Test
3. Provide good care to the animals during the Langston Ram/Buck Test, overseen by our consulting veterinarian. However, if an animal dies, Langston will not replace it nor pay compensation, but will be responsible for disposal.
4. Provide the Langston Ram/Buck Test results of each herd/flock to the producer.
5. In Year 1, identify 5 candidate males with relatively high resistance and 5 candidate males with medium resistance based on data from the Langston Ram/Buck Test.
6. In Years 2 and 3, identify 4 bucks/rams from each of the 3 sires used in the high resistance group and 2 bucks/rams from each of the 3 sires in the medium resistance group, for a total of 18 animals, to be used in the Langston Buck/Ram Test with input of the producer.
7. Select 45-50 females with high resistance and 45-50 with medium resistance to internal parasites as noted above.
8. Visit the farms as noted above to perform the following, with producer assistance.

- determine FAMACHA score of each animal at 4 and 8 weeks after kidding/lambing, at weaning, and 4 to 6 weeks post-weaning
- collecting samples for fecal egg count 8 weeks after kidding/lambing and at weaning
- setting up breeding groups in the fall and collect blood samples
- determine body weight at weaning and breeding

9. Contact the producer monthly for information regarding production records.
10. Provide $1,500 at the end of each of the 3 weaning periods and $1,500 at the end of each of the 3 breeding seasons for materials and supplies.

Modification and Termination

This agreement may be cancelled or terminated without cause by either party by giving (30) calendar days advance written notice to the other party. Such notification shall state the effective date of termination or cancellation and include any final performance and/or payment invoicing instructions/requirements.

Agreement Period: March 15, 2013 to September 30, 2015.

Agreement Signatures:

_____	_____
Director American Institute for Goat Research Langston University	Producer
_____	_____
Date	Date

Chapter 5. Experimental Design

Introduction

The same considerations for experimental design are important to on-farm and on-station research. Kaps and Lamberson (2004) provided an excellent description of the concepts of experimental design for animal science research in a textbook entitled "Biostatistics for Animal Science," with key points following in different sections. This source as well as others can be consulted for greater detail.

- Steps of an experiment
  - □ Problem(s)
  - □ Hypothesis(es)
  - □ Experimental design
  - □ Data collection
  - □ Data analysis
  - □ Interpretation of results

- The experimental design indicates how data will be obtained.
  - □ Includes a set of rules to choose samples from populations
  - □ Describes how treatments are assigned to experimental units, or vice versa
  - □ Encompasses
    - Treatments (i.e., populations)
    - Sample size
    - Experimental units
    - Sample units
    - Replication
    - Experimental error
    - Restriction to reandomization or blocking

- Components of a statistical model
  - □ Means or expectations
  - □ Dispersion or variances and covariances
  - □ Distribution

- The method of data analysis is often determined before an experiment is initiated.
  - □ However, sometimes the most appropriate manner may not be discerned until later.
  - □ Relatedly, the method of means separation allowing clearest interpretation and presentation of findings should be used, which requires data to be available.

Experimental Units and Replication

General Considerations

- True replication is equally important on-farm and on-station.

- The lack of true replication can be viewed as a confounding issue (St-Pierre, 2007).
  - For example, if there are three treatments and one group of animals per treatment, then group is confounded with treatment and a valid statistical analysis is not possible.
  - In other words, there may have been differences among groups not apparent to the researcher that prevented attributing any group difference to treatment.

- Though seemingly a straight-forward and simple concept, lack of true replication continues to be a very common limitation in livestock research conducted around the world and, correspondingly, a reason for rejection of manuscripts submitted to peer-reviewed journals.

- The experimental unit is the smallest unit to which a treatment is applied.
  - Experimental units must be independent of each other, or the correlation between experimental units must be accounted for.

- Treatment effects are measured on sample units.
  - Sample units may or may not be the same as the experimental unit.
    - For example, if animals are managed as groups with measures made on individual animals, then group is the experimental unit and animal is the sample unit.
  - All sample units within an experimental unit (e.g., animals within a group or pen) need not necessarily be used (e.g., measurements made or samples collected). An example would be variables measured in only five of ten animals per group or pen.
    - St-Pierre (2007) provides more information about determining appropriate numbers of sample units in experimental units.

- Variance among experimental units generally decreases with an increasing number of sample units (St-Pierre and Jones, 1999; St-Pierre, 2007).

- There must be at least two experimental units per treatment, in which case the experiment is replicated.
  - Repetitions or repeated measures on the same experimental unit are not replications, since they are not independent.
  - Experiments may be replicated in different years as well as at different locations to broaden the environmental conditions and populations to which the findings may be applied.

- Repeated measures on experimental units, or the frequency of data collection, can affect variation among experimental units and, thus, the power of the test (St-Pierre and Jones, 1999).

- That is, with a constant number of experimental units, more frequent or a greater number of repeated measurements can decrease P values or lessen the number of observations required to detect a difference at a particular P value.

Other Considerations

In some studies, different treatments are imposed on animals in one or more groups. Examples of replication with one animal group are studies of Patra et al. (2008a,b). All animals resided in the same pasture, although other pastures were used when available forage became low. One-half of the animals were free to move throughout the pasture and the other half were tethered and allowed to graze only within defined circular areas. The locations of tethered animals were changed daily in the morning to maintain available forage above a threshold level. Free-moving animals could graze in the same circular areas as tethered animals, which frequently occurred, or in other areas. The reason why this approach was chosen rather than using two pastures and two groups of animals on each treatment (i.e., four total pastures and animal groups) was to ensure that all animals had access to the same forage at the beginning of the daily grazing period when tethered animals were moved to achieve an unbiased assessment of selection and other measurements. The only other way to accomplish this would have been to place non-experimental or 'grazer' free-moving animals with experimental tethered animals in their minimum of two pastures as well as 'grazer' tethered animals in the minimum of two pastures with experimental free-moving animals. This would have been logistically challenging and probably not resulted in forage conditions as similar as with the approach taken.

There are instances in which it is difficult to discern if animals are managed individually or in groups, as can be evidenced by grazing experiments of Berhan et al. (2005), Tovar-Luna et al. (2011), and Keli et al. (2012). The Berhan et al. (2005) study was similar to those of Patra et al. (2008a,b) in that animals on different treatments were in the same pasture while grazing. Treatments were pasture access for 4, 8, or 24 hours. Therefore, animals given 4 and 8 hours of pasture access resided in a nearby confinement facility when not grazing, with separate pens for each treatment to avoid the need for sorting the next day. Data were analyzed with animal as the experimental unit, although animals on 4- and 8-hour treatments were not truly independent. But, if animals on these treatments had been confined at night in two pens per treatment, then it would be unclear how animals with 24 hours of pasture access could have been similarly managed. Probably the only way to achieve this would have been to have at least two groups of animals per treatment and two pastures for grazing by replicate animal groups of each treatment. This approach was not used because of logistical considerations, such as a necessity to utilize 'grazer' animals to maintain desired levels of available forage, which would have complicated animal removal for those with limited pasture access.

Considerations for the study of Tovar-Luna et al. (2011) in which goats had continuous pasture access or were confined at night are essentially the same as for the study of Berhan et al. (2005). The is also true for the experiment of Keli et al. (2012) in which animals had access to pasture continuously, for 8 hours between milking in the morning and afternoon, or when the leaf surface moisture level (i.e., dew) was below a threshold between milking in the morning and afternoon only or until dark. These studies entailed repeated measurements in different physiological states and fairly large numbers of animals to evaluate performance. This

necessitated use of pastures with different types of forage for grazing at different times of the year. Hence, it would have been very difficult to have animals grazing two or more pastures simultaneously. This might have been achieved by decreasing pasture size, although the existing area already was somewhat small relative to that of typical production settings.

Another issue in of the aforementioned studies of Berhan et al. (2005), Tovar-Luna et al. (2011), and Keli et al. (2012) is the likely small magnitude of variation among animals due to effects of confinement relative to impacts of the grazing treatments. That is, animals were placed in the same or adjacent pens with little difference in conditions between or among pens. Furthermore, no feed was dispensed when confined, other than limited amounts of alfalfa hay when pasture access was very short in the study of Keli et al. (2012).

There are instances in which means of achieving true replication exist but at first may not be readily apparent. An example is the Merera et al. (2010) study with 18 treatments, although six did not involve feeding, with slaughter soon after arrival at the abattoir. The 12 feeding treatments were arranged in a 2 × 2 × 3 factorial, with two sheep origins in Ethiopia (Highland and Lowland areas), two levels of vitamin E in supplemental concentrate, and three lengths of feeding (2, 4, and 6 weeks). A feeding facility with 12 pens was rented for the study. Initially the 12 treatments were to be imposed on animal groups in each of the pens. Hence, pen or animal group would be confounded with treatment, there would not be true replication, and a valid statistical analysis could not have been performed. But, after further thought, a split-plot design was adopted, with animal origin and vitamin E supplement treatment as main plots and feeding length as a subplot. Therefore, there were three pens and animal groups for each of the four main plot treatments, with animals removed from each pen after 2, 4, and 6 weeks. The assignment of the four main plot treatments to pens was random, depicted in Table 1. As noted by St-Pierre (2007), error terms have an identity. As shown in Table 2, in this case animal group or pen within main plot treatment was the experimental unit for main plots, with the error term of pen within origin × vitamin E level. For the effect of feeding period length and interactions involving this variable, individual animal was the experimental unit, with residual error used to test subplot effects.

Table 1

Treatment arrangement for the experiment of Merera et al. (2010), with a 2 ×2 × 3 factorial arrangement of treatments and split-plot design

	Pen											
Treatment[1]	1	2	3	4	5	6	7	8	9	10	11	12
Animal origin	Highland	Lowland	Highland	Highland	Lowland	Lowland	Highland	Lowland	Highland	Lowland	Lowland	Highland
Vitamin E	No	Yes	Yes	Yes	Yes	No	No	No	No	Yes	No	Yes
Feeding period length												
2 wk	3 lambs	3 lambs	3 lambs	3 lambs	3 lambs	3 lambs	3 lambs	3 lambs	3 lambs	3 lambs	3 lambs	3 lambs
4 wk	3 lambs	3 lambs	3 lambs	3 lambs	3 lambs	3 lambs	3 lambs	3 lambs	3 lambs	3 lambs	3 lambs	3 lambs
6 wk	3 lambs	3 lambs	3 lambs	3 lambs	3 lambs	3 lambs	3 lambs	3 lambs	3 lambs	3 lambs	3 lambs	3 lambs

[1]Animal origin and dietary supplementation with vitamin E were main plots and feeding period length was a subplot.

Table 2
Sources of variation and degrees of freedom (**df**) in the study of Merera et al. (2010)[1]

Source of variation	df
Origin	1
VE[2]	1
Origin × VE	1
Pen within origin × VE (main plot error term)	8
Length	2
Length × origin	2
Length × VE	2
Length × origin × VE	2
Residual	88

[1]Assuming 9 animals per pen and on each of the 12 treatments.
[2]Vitamin E.

Statements of SAS for General Linear Models (**GLM**) and mixed effects model (**MIXED**) analyses, as well as analysis of variance by GenStat (Analysis of Variance by ANOVA, REML, or Regression; **ANOVA-ARR**), are provided in Appendix 1 page 167, with results the same for each method (Appendix 2 Tables 69, 70, and 71, respectively). The simulated data set is presented in Appendix 3 Table 163. There were no significant effects of, or interactions involving, vitamin E. Therefore, those sources of variation were removed from the model. Table 63 in Chapter 10 - Dissemination provides an example of how these data could be presented in tabular form, with means separation by non-orthogonal contrasts.

The analyses above contained balanced data with no missing observations. However, often some data are missing. In such cases, mixed effects models can have advantages compared with GLM, although other relevant considerations regarding use of SAS GLM vs. MIXED procedures are addressed later. According to Howell (2013), if missing data are not completely random, results with GLM will be biased. Conversely, with mixed effects models, only an assumption of 'random missing data' is necessary. As an example, 11 observations were removed from the data set in Appendix 3 Table 163 without regard to treatments (Appendix 3 Table 164). As shown in Appendix 2 Tables 72, 73, and 74, results are very similar for SAS GLM, SAS MIXED, and GenStat ANOVA-ARR analyses, respectively, with only small differences among the methods in P values. Appendix 3 Table 165 has 10 values removed in a nonrandom manner. All 10 missing values were for the 6-week period, 7 of the 10 were of animals from origin 1, and 6 were for the VE 1 level. As shown in Appendix 2 Tables 75, 76, and 77 for SAS GLM, SAS MIXED, and GenStat ANOVA-ARR analyses, respectively, differences among methods in P values were slightly greater than when missing observations were random.

Experimental Error (most from Kaps and Lamberson, 2004)

- Experimental error consists of explained and unexplained causes.
  - ☐ Unexplained variability is that between or among experimental units of a treatment and, thus, is termed experimental error.

- There are two components of experimental error, one is systematic (e.g., can be assigned to one source and produces bias if impacting treatments unequally) and one is random.
  - If systematic error is recognized, then it should be corrected for, if possible.
  - Random error presumably will cancel out, or sum to 0, with an adequate number of experimental units. Rounding is one source of random error.

- Treatments should be randomly applied to experimental units, or vice versa, to avoid bias.
  - However, there may be some exceptions.
    - For example, if the spread among animals in body weight is relatively large, it may be possible after animals are randomly assigned to treatments or replications within treatments (even if this is done within body weight groups or 'blocks') to increase the similarity among treatments or replications within treatments in means and an index of variability such as the standard deviation (**SD**) by exchanging a small number of animals.

- Animals selected for an experiment should be representative of the population of interest.
  - For example, findings with one breed or subgroup within a breed, such as an ecotype, may not be necessarily applicable to other subgroups or breeds.
  - Likewise, results with one type of a farm might not be pertinent to another.

Accuracy and Precision (most from Kaps and Lamberson, 2004)

- Known sources of variability should be accounted for in the design and analysis.

- Determining the minimum number of experimental units requires knowledge of expected variability, such as from previous similar experiments or the literature.

- Accuracy relates to how close an estimated mean is to the true value.

- Precision pertains to repeatability, or how close estimates are to one another regardless of distance from the true mean.
  - Random error affects precision much more than accuracy.

Conducting power analyses, though always and obviously meritorious, has become much more common than in the past. One reason for this is review by IACUC to ensure any research with animals has a reasonable expectation of detecting differences and, hence, achieving stated objectives, which is naturally also the desire of researchers. Likewise, it is undesirable to use a greater number of animals on a study than necessary for a host of reasons. In addition to protocols, many grant programs now require that results of a power analysis be included in proposals.

Power analyses are addressed in various statistics references, including Kaps and Lamberson (2004), and for various analytical methods. As an example, the following statements of SAS can be used to determine the required number of observations per treatment for 1-sided and 2-sided tests.

```
1)  data a;
2)  do n = 2 to 100;
3)  alpha = 0.05;
4)  mi0 = 60.3;
5)  mi1 = 38.7;
6)  stdev = 17.28;
7)  df = n - 1;
8)  lambda = (abs(mi1-mi0)/stdev)*sqrt(n);
9)  tcrit_one_tail = TINV(1-alpha,df);
10) tcrit_low = TINV(alpha/2,df);
11) tcrit_up = TINV(1-alpha/2,df);
12) power_one_tail = 1-CDF('t',tcrit_one_tail,df,lambda);
13) power_two_tail = CDF('t',tcrit_low,df,lambda) + 1-CDF('t',tcrit_up,df,lambda);
14) output;
15) end;
16) proc print data = a (obs=1);
17) title 'one-tailed';
18) WHERE power_one_tail>.80;
19) VAR alpha n df power_one_tail;
20) run;
21) proc print data = a(obs=1);
22) title 'two-tailed';
23) where power_two_tail>.80;
24) var alpha n df power_two_tail;
25) run;
```

These statements allow the number of observations (**n**) to vary from 2 to 100 (statement 2), specify a P value of 0.05 (statement 3), indicate treatment means of 60.3 and 38.7 (statements 4 and 5, respectively), and a SD of 17.28 (statement 6). From these statements, the resulting two sets of output are shown in Tables 3 and 4.

Table 3
Example SAS output for a one-tail power test for the minimum number of observations

obs	alpha	N	df	power_one_tail
5	0.05	6	5	0.83478

Table 4
Example SAS output for a two-tail power test for the minimum number of observations

obs	alpha	N	df	power_two_tail
7	0.05	8	7	0.85644

Hence, at least eight observations per treatment would be required to detect a difference (i.e., less than or greater) between treatment means with the variability specified. This number of observations refers to that of experimental units rather than sample units. It is important that the appropriate SD of experimental units (e.g., groups of animals) be entered rather than the SD for

individual sample units or animals. Further examples from two LU experiments are given in Table 5, depicting how the number of experimental units required increases with increasing SD and decreases with an increasing magnitude of difference between means.

Table 5
Example power analyses for a level of significance of 0.05

Study	k[1]	Treatments[2]	Means (%)	SD (%)	Sample size	
					1-sided test	2-sided test
Tovar-Luna et al. (2007)	k_g	C & F	60.3 & 38.7	17.28	6	8
Tovar-Luna et al. (2010)	k_{md}	EL & ML	66.7 & 71.4	6.09	12	16
Tovar-Luna et al. (2010)	k_{md}	ML & LL	71.4 & 60.7	6.09	4	5
Tovar-Luna et al. (2010)	k_{md}	EL & LL	66.7 & 60.7	6.09	8	11
Tovar-Luna et al. (2010)	k_{ld}	EL & ML	59.5 & 51.9	16.39	30	39
Tovar-Luna et al. (2010)	k_{ld}	ML & LL	51.9 & 65.4	16.39	11	14
Tovar-Luna et al. (2010)	k_{ld}	EL & LL	59.5 & 65.4	16.39	49	62
Tovar-Luna et al. (2010)	k_l	C & F	64.3 & 60.9	5.56	18	23

[1]k = efficiency of metabolizable energy utilization; k_g = k for tissue accretion; k_{md} = k for dietary energy used for maintenance; k_{ld} = k for dietary energy used for lactation; k_l = dietary energy used for maintenance and lactation.
[2]C = concentrate-based diet; F = forage-based diet; EL = early lactation; ML = mid-lactation; LL = late lactation.

Blocking, Randomized Complete Block Design, and Randomized Block Design

- Experiments with a completely randomized design (**CRD**) entail animals randomly selected from a population exposed to each treatment (Kaps and Lamberson, 2004). Simple examples of CRD are given in Figures 1 and 2.

Figure 1. Completely randomized design with four treatments (EU = experimental unit).

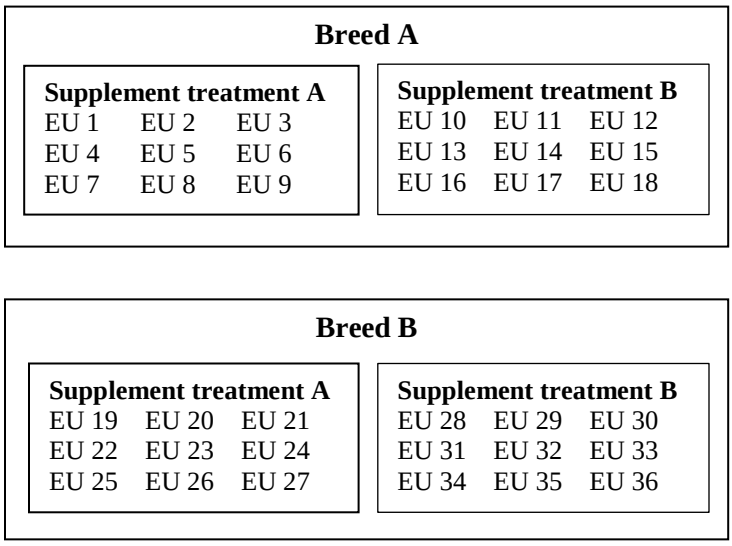
Treatment 1		
EU 1	EU 2	EU 3
EU 4	EU 5	EU 6
EU 7	EU 8	EU 9

Treatment 2		
EU 10	EU 11	EU 12
EU 13	EU 14	EU 15
EU 16	EU 17	EU 18

Treatment 3		
EU 19	EU 20	EU 21
EU 22	EU 23	EU 24
EU 25	EU 26	EU 27

Treatment 4		
EU 28	EU 29	EU 30
EU 31	EU 32	EU 33
EU 34	EU 35	EU 36

Figure 2. Completely randomized design with a 2 × 2 factorial arrangement of treatments (EU = experimental unit).



Blocking is common in livestock research both on-station and on-farm, with highlights from Kaps and Lamberson (2004) given below.

- Blocking reduces unexplained variability by accounting for a known source.
  - Common blocking factors in livestock research are body weight, age, location or environment, etc.
  - In some cases breed could also be considered a blocking factor but in other instances serves as a treatment, often one of two or more main effect treatments.

- When there is one experimental unit from each treatment per block, the design is termed 'randomized complete block.' In this case the treatment × block interaction cannot be tested and serves as the error term for treatment.

- If there are at least two experimental units per treatment in each block, then the design is a 'randomized block' and the treatment × block interaction can be tested.
  - This design is preferable when there is a reasonable expectation that the treatment effect differs among blocks.

- The number of blocking factors is not limited to one.
  - Examples are breed, gender, and body weight. That is, both males and females of two breeds could be used in a study, or there might be blocking by body weight within more than one breed or gender.

- Blocking factors may be fixed or random.
  - Kaps and Lamberson (2004) state that blocks are fixed if there is a relatively small number that represent distinct populations chosen in some nonrandom process.

    - Examples from those provided above would be breed, age, and location or environment.
    - Village would be a common fixed blocking factor in on-farm research, although as will be noted later, factors such as village may be assumed random in some cases.
  - If the blocking factor is random, so is the treatment × block interaction, which is then the error term for testing the effect of treatment.

- Figures 3 and 4 depict simple randomized complete block and randomized block designs, respectively.
  - The randomized complete block design example has three blocks and three treatments, with one experimental unit of each treatment per block.
  - The example for a randomized block design has two blocks, two treatments, and two experimental units of each treatment per block.

Figure 3. Randomized Complete Block Design
(EU = experimental unit; Trt = treatment)

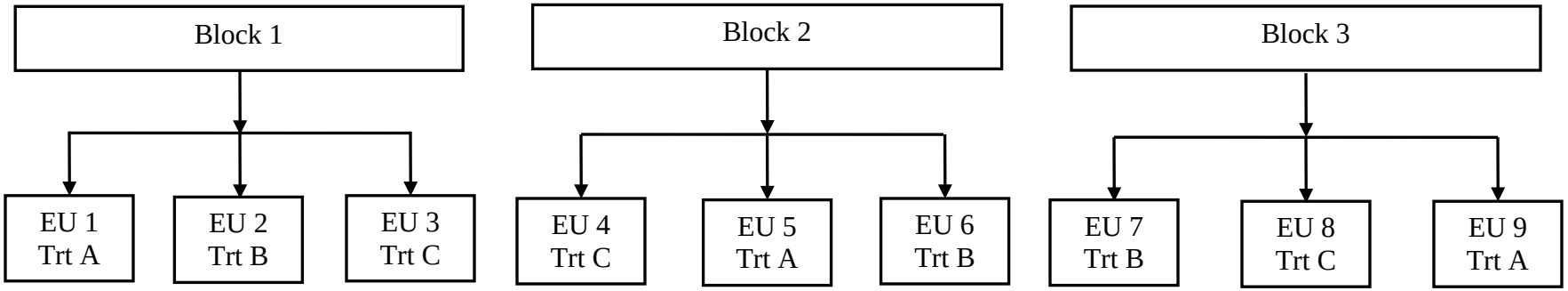
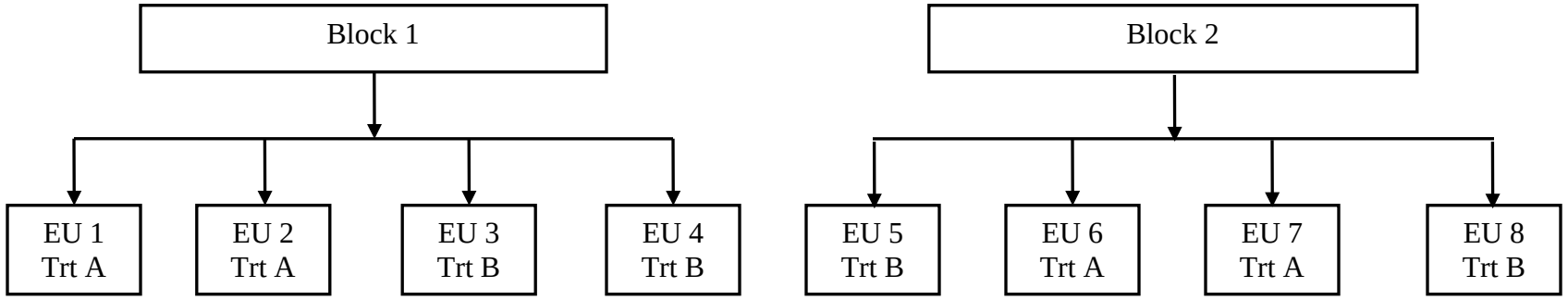


Figure 4. Randomized Block Design
(EU = experimental unit; Trt = treatment)



Crossovers, Switchbacks, and Latin Squares

- Crossovers and Latin squares are useful designs for livestock research; however, they are more common in on-station than on-farm research.
  - □ But, because the number of animals required is fewer than with other designs in which animals are exposed to only one treatment, there may be some on-farm experiments with limited numbers of animals and(or) households for which such designs are appropriate.

- A crossover consists of two periods and treatments, with animals exposed to one treatment in the first period and the second treatment in the subsequent period.
  - □ Some on-farm dairy production trials in developed countries have used crossovers with paired farms (Engstrom et al., 2010).

- Latin squares consist of more treatments and periods than crossovers, although those with more than six treatments and periods are rare.

- A challenge of crossover and Latin square experiments is to ensure minimal or preferably no carryover effects of one treatment in a period on the response to another treatment in a subsequent period.
  - □ Care should be taken to minimize the number of times a treatment imposed on a particular animal or group of animals follows the same treatment.
    - For example, with a 4 × 4 Latin square the assignment can be such that a treatment does not follow another particular treatment more than once.
  - □ The strength of the test also can be increased by use of simultaneous Latin squares.
  - □ Moreover, in some studies one main effect treatment will be applied to one Latin square with a set of animals and a second main effect treatment will be employed with a second animal set. The same treatments will be applied within each square.
    - An example of such a study is two simultaneous 5 × 5 Latin squares, one with forage A and a second with forage B.
    - Different levels of a concentrate supplement could be applied within each square (e.g., 0, 10, 20, 30, and 40%).

- Model components of simple crossovers and Latin squares are animal, period, and treatment.
  - □ These experiments have the implicit assumption of no interactions between treatment and animal or period.
  - □ A notable strength of these designs is that each animal serves as its own control.

- The primary purpose of a switchback design is to control variation among animals and time.
  - □ With a switchback design, at least three periods are involved. If there are two treatments (i.e., A and B), then some animals would be subjected to treatment A, B, and A in periods 1, 2, and 3, and others would be subjected to treatment B, A, and B in periods 1, 2, and 3, respectively.
  - □ The same would be true for three or more treatments, although in such cases every animal would not be exposed to each treatment.
  - □ Moreover, in some situations it might be desirable for a switchback to entail four periods, such as for lactating animals.

- In this case, animals would be subjected to two treatments twice in the four periods (i.e., A, C, A, and C in periods 1, 2, 3, and 4, respectively).

□ An attribute of a switchback is that fewer animals are required for the same statistical power compared with other designs such as a CRD.

- However, limitations are that it assumes treatment differences are the same regardless of period of time (i.e., nonsignificant treatment × time interaction) and that the relatively small number of animals employed adequately represent the population of interest.

Tables 6 and 7 provide simple examples of crossover and switchback designs. Table 7 illustrates how switchback experiments can involve more than two treatments. Moreover some switchback designs may have four periods, for which period effects can be evaluated with two treatments (St-Pierre and Jones, 1999).

Table 8 is a 4 × 4 Latin square. As noted above, with four treatments an arrangement is possible in which no treatment imposed on an animal, group, or pen follows another treatment more than once during the study.

Table 9 is an example of four simultaneous 4 × 4 Latin squares. Two squares are with low quality forage and two are with forage of higher quality. Within each square there are four drinking water treatments.

A consideration for studies with multiple periods such as crossovers, switchbacks, and Latin squares is inclusion of what is commonly referred to as a 'washout' or 'interval' period. This entails exposing all experimental units to the same conditions between periods rather than immediately beginning a new period with a different treatment. Purposes are to minimize potential carryover effects of a treatment in the subsequent period as well as overall period differences. Without a washout period, it may be necessary to consider the effect of treatment sequence, such as in the study of Goetsch and Johnson (1999) as recommended by Milliken and Johnson (1984). But, there can be studies for which no washout treatment can be identified to eliminate period differences (e.g., Tsukahara et al., 2013). In such instances, an experimental design with treatments imposed in one period without a repeated measure would be required.

Experiments with multiple periods of short to moderate lengths can be the best or only option in some instances of achieving true replication by exposing small numbers of households and animals to different treatments in the periods. There may also be situations where this type of design is an option, although houseolds and animals could be continuously exposed to one treatment the entire experiment as well. An example is a growth study with meat goats of 5 months of age and 1 month after weaning. The production phase of interest is from then until the time of typical sale and(or) slaughter, assumed 10 to 12 months depending on prevailing market conditions. Therefore, this growing/finishing period is 4 to 6 months long. Imposing the same treatments on housholds and animals throughout the experiment would allow evaluation of potential treatment × time interactions. But, if there is a limitation such as in the number of households, animals, or pens, a repeated measures design could be employed, an example being a 4 × 4 Latin square with four periods and treatments. However, a meaningful assessment of growth performance requires a feeding period of a minimum length. With relatively short

periods, the value in body weight (**BW**) change as a variable is limited by fluctuations in conditions such as gastrointestinal tract digesta mass. In fact, with a very short performanc experiment BW gain might even be greater for a diet high in low quality forage compared with one higher in digestibility and concentrate level because of a greater increase in digesta mass with the former diet depending on the nature of that fed before the trial. Though minimums are

Table 6
Example of a crossover design (treatments are shown in the body of the table)

	Period	
Animal, group, or pen	1	2
1	A	B
2	B	A
3	B	A
4	A	B
5	A	B
6	A	B
7	B	A
8	A	B
9	B	A
10	A	B
11	B	A
12	B	A

Table 7
Example of a switchback design (treatments are shown in the body of the table)

	Period		
Animal, group, or pen	1	2	3
1	A	B	A
2	B	A	B
3	C	B	C
4	B	C	B
5	C	A	C
6	A	B	A
7	C	B	C
8	A	C	A
9	B	C	B
10	A	B	A
11	C	A	C
12	B	C	B
13	B	A	B
14	A	C	A
15	C	B	C
16	C	A	C
17	B	A	B
18	A	C	A

Table 8
Example of a 4 × 4 Latin square (treatments are shown in the body of the table)

	Period			
Animal, group, or pen	1	2	3	4
1	A	D	B	C
2	B	A	C	D
3	C	B	D	A
4	D	C	A	B

Table 9
Example of four simultaneous 4 × 4 Latin squares (water treatments are shown in the body of the table in period columns)

			Period[1]			
Animal, group, or pen	Latin square	Forage quality	1	2	3	4
1	1	Low	A	D	B	C
2	1	Low	B	A	C	D
3	1	Low	C	B	D	A
4	1	Low	D	C	A	B
5	2	Low	D	B	C	A
6	2	Low	C	D	A	B
7	2	Low	A	C	B	D
8	2	Low	B	A	D	C
9	3	High	A	C	D	B
10	3	High	D	A	B	C
11	3	High	B	D	C	A
12	3	High	C	B	A	D
13	4	High	C	A	B	D
14	4	High	B	C	D	A
15	4	High	D	B	A	C
16	4	High	A	D	C	B

[1]A = fresh water; B, C, and D = different sources of brackish or saline groundwater.

debatable and naturally depend on the nature of measures and expected treatment differences, probably most ruminant livestock researchers could agree on at least 42 days for BW change. And if treatment effects are appreciable, then a washout period, such as of at least 2 weeks, would be required. The length of such an experiment is described below.

- 4 periods × 42 days = 168 days
- 3 washout periods × 14 days = 42 days

The total experiment length is 210 days or 7 months, hence running from 5 to 12 months of age.

In some cases experiments do not encompass the entire phase of production of interest, such as soon after weaning until harvest at 10 to 12 months in the example above. Rather, a smaller segment is addressed, with the assumption that similar effects would occur in other parts

of the phase as well. For example, a recent experiment with meat goats began at 285 ± days of age (i.e., 9.5 months) and lasted 70 days (2.33 months in five 2-week periods). Five treatments were imposed on the same animals throughout the experiment. When the article on this study was being evaluated for publication, a reviewer asked why animals were not randomly assigned to the treatments at the beginning of each period. Because BW gain was the most important variable, such a practice or experimental design was not considered because a 2-wk period is much shorter than necessary for accurate estimation to reflect true change in empty BW or tissue mass. Relatedly, substantial treatment effects on average daily gain (**ADG**) were anticipated, creating considerable potential for treatment carryover effects with such short periods and without any potential for addressing by use of a washout period.

Split-Plot

- Split-plot designs are frequently used in livestock research and may involve CRD, randomized block designs, or Latin squares (Kaps and Lamberson, 2004).
  - □ With split-plots, main plots require a greater number of observations than subplots.
    - However, this statement of Kaps and Lamberson (2004) perhaps should be clarified in that the error term for testing main effects has fewer df than that or those used to test subplots. In accordance, less variability would be expected among main plot vs. subplot experimental units and, thus, the strength of the test is stronger for the main plots than subplots.
  - □ Subplot treatments are applied to all main plot treatments.
    - An example (Askar et al., 2013) is a grazing study with eight 0.4-ha pastures, four exposed to a low stocking rate and four to a high stocking rate (Table 10).
    - Low stocking rate pastures contained one lactating doe, one yearling wether, and one growing wether, whereas there were two animals per type in each pasture for the high stocking rate.
    - The main plot treatment was stocking rate and the subplot was physiological state of the animal. The treatment arrangement was a 2 × 3 factorial, but also could be considered a 2 × 3 × 4 factorial with data in the four periods of the experiment analyzed as a repeated measure.

Table 10
Example of a split-plot design with a 2 × 3 factorial arrangement of treatments

		Animal		
Pasture	Stocking rate	Number	Physiological state	Use[1]
1	Low	1	Growing wether	EU
1	Low	2	Yearling wether	EU
1	Low	3	Lactating doe	EU
2	High	4	Growing wether	EU
2	High	5	Yearling wether	EU
2	High	6	Lactating doe	EU
2	High	7	Growing wether	Grazer
2	High	8	Yearling wether	Grazer
2	High	9	Lactating doe	Grazer
3	High	10	Growing wether	EU
3	High	11	Yearling wether	EU
3	High	12	Lactating doe	EU
3	High	13	Growing wether	Grazer
3	High	14	Yearling wether	Grazer
3	High	15	Lactating doe	Grazer
4	Low	16	Growing wether	EU
4	Low	17	Yearling wether	EU
4	Low	18	Lactating doe	EU
5	Low	19	Growing wether	EU
5	Low	20	Yearling wether	EU
5	Low	21	Lactating doe	EU
6	High	22	Growing wether	EU
6	High	23	Yearling wether	EU
6	High	24	Lactating doe	EU
6	High	25	Growing wether	Grazer
6	High	26	Yearling wether	Grazer
6	High	27	Lactating doe	Grazer
7	High	28	Growing wether	EU
7	High	29	Yearling wether	EU
7	High	30	Lactating doe	EU
7	High	31	Growing wether	Grazer
7	High	32	Yearling wether	Grazer
7	High	33	Lactating doe	Grazer
8	Low	34	Growing wether	EU
8	Low	35	Yearling wether	EU
8	Low	36	Lactating doe	EU

[1]EU = experimental unit; Grazer = animal included for the different stocking rate treatments but from which data were not collected.

Chapter 6. Treatment Considerations

Ideas, Questions, and Hypotheses

Appropriate Methods

When an original and novel idea, question, and(or) hypothesis is developed, it must be accompanied by a feasible means of study. That is, the hypothesis must be testable with available and appropriate methods, which can be difficult to achieve in some instances. An example is determining effects of acclimatization (i.e., adaptation to temperature and humidity) on nutrient needs of livestock. Environmentally controlled chambers can be used, with measurement of heat energy via respiration calorimetry. But, differences between such conditions and those outside with free movement, such as the activity energy cost, would limit potential to extrapolate findings to practical production settings. Thus, Patra et al. (2009) measured heart rate to predict heat energy of animals housed in indoor pens but with free movement. Heart rate was multiplied by the quantity of heat energy per heart beat determined for each animal at multiple times. The facility where animals were housed had no insulating materials, no artificial cooling, and only minimal external heat was supplied when temperature was very low. As a result, temperature inside the facility was similar to that outside as desired. However, even this approach has limitations, such as different exposure to wind and sunlight compared with normal production settings.

Another challenging area for study is metabolism by splanchnic tissues (primarily the gastrointestinal tract and liver) in grazing livestock, albeit an area not likely to be addressed in on-farm research. Interest in this topic relates to the strong relationship between heat energy production by these tissues and the whole body (Goetsch, 1998b). Thus, gaining a better understanding of factors influencing splanchnic energy use could contribute to development of means of predicting the grazing activity energy cost. The most common means of determining energy use by and nutrient flux across the gastrointestinal tract and liver has been continuous infusion of a blood flow marker in a mesenteric vein and frequent sampling of arterial, portal venous, and hepatic venous blood. This method would be very difficult to use in free-movement conditions, which led to experiments by Patra et al. (2008a,b) to ascertain if a tethered animal, with minimal restraint, could serve as a model to study metabolism by one allowed free movement within a pasture.

Because of the considerable amount of energy that can be used in the act of grazing (Lachica and Aguilera, 2003), there have been efforts to characterize factors influencing this cost. Some findings have suggested a relationship between available forage mass and grazing time. Hence, experiments with cattle and goats have employed different stocking rates. However, most of these studies entailed only two stocking rates, and in some cases because of weather conditions, differences in forage mass were relatively small and total time spent grazing was fairly short. Therefore, methods to predict change in grazing time or the grazing activity energy cost from differences in available forage mass have not resulted from this research. To characterize such relationships, more than two stocking rates or levels of available forage mass yielding a wide range in grazing time would be beneficial, which would be challenging to achieve while maintaining an adequate number of replications.

The nature of the procedures required has contributed to the limited knowledge about the grazing activity energy cost of ruminants. In this regard, Goetsch et al. (2010) addressed the three general methods that have been employed recently. One used with cattle is based on differences in heat energy expended when animals are lying compared with periods while eating, standing, and walking, with multiplication of these values by total time spent in the various activities (Brosh et al., 2006). However, an implicit assumption of this technique is that heat energy while lying is constant regardless of specific conditions, including grazing vs. confinement settings. That heat energy was greater for unrestrained than for tethered goats throughout all hours of the day (Patra et al., 2008a,b) casts doubt on this premise and suggests that values so derived would be underestimates. A second approach for comparing heat energy by grazing animals with confined animals (Lachica et al., 2007) would avoid this issue, but the confounding of different dietary and other environmental conditions makes interpretation challenging. The third approach is to subtract the various components of measured total heat energy to derive the grazing activity energy cost by difference (Beker et al., 2009, 2010; Tovar-Luna et al., 2011). But, this method also relies on many assumptions, such as energy requirements for maintenance and production, efficiencies of energy utilization, etc., which has resulted in relatively high variability. Although each of these methods has limitations, those of the third at least can be addressed, such as through a high number of observations.

Appropriate Treatments and Conditions

In addition to considerations noted above pertaining to experimentation methods, the treatments selected and all other experimental conditions imposed should be appropriate. An article published in an animal science journal provides an example of how this may not always be achieved. The experiment was conducted with growing lambs fed a high concentrate diet. The treatment arrangement was a 2 × 2 factorial, with two types (e.g., A and B) of a class of feed additive and two levels of a second class of additive (e.g., 0 and 0.3%). Objectives of the study as originally stated when the article was submitted were to determine effects of 1) dietary inclusion of the first additive class, 2) type of the first class of additive (i.e., A vs. B), and 3) inclusion of the second class of additive in diets consumed by growing lambs incurring subacute or subclinical ruminal acidosis. However, the first objective was unachievable because the study lacked a control diet without additive A or B. This shortcoming could have been addressed with a 2 × 2 + 1 factorial treatment arrangement. Also, sorghum grain was the primary cereal grain in the diet, 50% of which was in the whole, unprocessed form. As a result, ruminal pH was above that reflecting subacute or subclinical ruminal acidosis, and therefore the third objective could not be achieved. Rather, it could only be addressed in the context of high concentrate diets without subclinical ruminal acidosis and with dietary inclusion of the additive of the first class. That is, effects of the additive of the second class were not assessed in the absence of additive A and B and would not necessarily be the same. This could have been accomplished with a 3 × 2 factorial arrangement of treatments rather than a 2 × 2. In light of these issues, the objectives were modified to evaluate effects of the second additive class with lambs fed high grain finishing diets containing either additive A or B.

Another example of conditions perhaps not optimal to achieve stated objectives is an experiment to evaluate secondary productivity (i.e., animal production) on native rangeland

compared with that on transformed or previously degraded land. Secondary productivity was assessed by change in BW of 200 goats grazing each area of land for 1 month. However, it was stated that normal utilization would involve fewer goats (typically 12) grazing continuously throughout the year. Therefore, in addition to the lack of true replication, applicability of the findings to normal production settings assumes that grazing 200 goats for 1 month is an appropriate model for grazing 12 goats for 12 months. Moreover, change in BW was unexpectedly greater for goats on degraded vs. native rangeland. This was explained by greater accumulation of thorns and other plant particles in fiber of goats on degraded land because of greater presence of forbs and browse plant species compared with more grasses in the rangeland area. Thus, under such conditions shearing and determining clean fiber yield would be a consideration.

Control Treatments

Experiments should have adequate control treatments to gauge the magnitude of effects of treatments of greatest interest, which in some instances necessitates more than one control. Without such treatments, too many questionable assumptions may be required. An obvious example is experiments comparing different types of supplemental feedstuffs. Without an unsupplemented control, differences among supplemental treatments can be scrutinized, but the magnitude of effect of each is unknown. Another example involves treatments for adverse health conditions, such as internal parasitism. If a study is conducted to evaluate efficacy of one or more anthelmintic treatment regimes, there should be a control group not being treated unless a serious health concern would exist. That is, even if samples from treated animals are collected before as well as after treatment, there is no way of knowing if any differences in variables between times are due to treatment or change in one or more other conditions having no relevance to treatment.

Inclusion of negative control treatments in on-farm research is important but can be difficult to implement. For example, if there is one treatment per household with the individual smallholder household (**ISH**) approach, then naturally smallholders will prefer to have their animals on a treatment expected to improve performance and economic return. Therefore, an incentive would be required for smallholders with animals exposed to a negative control treatment. However, care must be exercised with this approach. For example, in one ESGPIP activity, households with animals on a negative control treatment were given the same supplement fed by other households, but with a stipulation that the experimental animals not receive the supplement. Technically this did occur as was agreed upon. However, after observing the improved performance of animals of other households, at least one household started providing its negative control animals with a different type of supplemental feedstuff. Conversely, if animals of all households are exposed to each treatment, either with the farmer or farming research group (**FRG**) or ISH approach, then reluctance to subject one or a small number of animals to a negative control treatment is less of an issue. A somewhat related problem that occurred in another on-farm research activity of the ESGPIP involved competitiveness in animal performance among households. There was at least one instance when it was learned via a night visit that a farmer was providing his/her animals with additional supplemental feedstuffs so that they would grow at the same or a faster rate than those of other households.

Multiple Objectives

Even though people frequently refer to the hypothesis being studied, in most cases there is more than one of interest and(or) there may be a primary hypothesis and one or more secondary hypotheses. An example of a secondary objective is in studies of Patra et al. (2008a,b). The primary objective was to determine if a tethered goat could be used as a means of investigating the physiology of grazing by free-moving animals. But, characterizing tethering as a production practice, common in many areas of the world, compared with free movement was also of interest. However, emphasis given to secondary objectives may vary among journals. For example, less attention was placed on the secondary objective noted above in an article published in the Journal of Animal Science, because tethering is not common in the U.S., than in an article published in the Asian-Australian Journal of Animal Science.

Depending on the nature of treatments, what might be termed as 'default' treatments or a default treatment scheme can be beneficial. For example, if some risky treatments are employed that in the end do not elicit the hypothesized effects, publication might be difficult, since nonsignificant differences are often not highly valued by reviewers. An example of this is the study of Goetsch et al. (2000). The two treatments initially of greatest interest, switching diets with different concentrate levels in early lactation (i.e., from 20 to 60% and 60 to 20%), were based on a somewhat speculative framework of logic. These treatments did not elicit expected effects. However, three other treatments, continuous feeding of diets with 60, 40, or 20% concentrate, were included as control treatments and for a hypothesis originally deemed as secondary (i.e., determining effects of continuous feeding of diets varying in levels of forage and concentrate). Because these control treatments yielded interesting new information, they were used in the manuscript to address the new primary hypothesis and the other two treatments contributed to a secondary, less important hypothesis. Similar considerations exist for inclusion of a wide array of variables.

Nonsignificant or Unexpected Results

Although some reviewers may not see great merit in nonsignificant or unexpected results, there may be situations where nonsignificant differences are postulated and preferred. An example of this is the tethering experiments of Patra et al. (2008a,b). Forage intake, selectivity, digestibility, and grazing behaviors were similar between tethered and free-moving goats. Hence, if appropriately conducted a tethered goat could be used to study many characteristics of free-moving goats on pasture. Conversely, heat energy production was greater for free-moving vs. tethered goats during all hours of the day. Thus, a tethered goat would not be an acceptable model to study energy metabolism by free-moving goats, such as energy use by the gastrointestinal tract and liver. However, because the different treatments associated with tethering vs. free movement had similar effect on heat energy throughout the day regardless of the specific activities of goats, there may be potential to study factors such as energy use by and nutrient flux across splanchnic tissues through short-term restraint of free-moving goats on pasture during different periods of the day, preferably on different days. While restrained, a blood flow marker could be infused and blood samples collected. In fact, results of Patra et al. (2008a,b) provide some support for use of this approach in previous studies with grazing cattle (Hersom et al., 2003) and sheep (Goetsch, 1998a).

New Knowledge

It is very important to be cognizant of potential new knowledge that may be generated from treatments of an experiment. Generation of new knowledge is a major criterion for evaluation of manuscripts by peers. For example, some reviewers first read through 'Introduction' and 'Materials and Methods' sections and then predict findings based on this information and other knowledge. If findings can be projected reasonably well, it can be deduced that adequate knowledge in this area already existed and there was insufficient justification for the experiment. An example of such a consideration relates to experimentation with goats based on research with other ruminant species. Some authors have stated that even though a certain condition or treatment response is known to occur with cattle and(or) sheep, similar experimentation should be conducted with goats. Greater justification for experiments with goats may be required, since reviewers could argue that unless authors clearly explain why responses with goats might be unique and not comparable, adequate new knowledge could not be generated.

Confounding

Many factors should be contemplated when devising a treatment strategy, one of the most important being confounding. Confounding occurs when more than one condition varies between or among treatments, thereby preventing identification of the true cause of treatment differences. It can be quite difficult to totally avoid confounding; therefore, in many cases the best that can be done is to minimize and(or) restrict it to conditions with known impacts. Occasionally there are dilemmas concerning whether to accept some confounding to adequately represent practical field applications. Such choices will depend primarily on specific objectives of the experimentation, which should be clearly discussed in the resultant scientific manuscript. The study of Prieto et al. (2000) provides a relevant example. The experiment, as designed in the original grant proposal, entailed different dietary levels of soybean meal to yield levels of crude protein ranging from less than 10% to above 20%. This design would have minimal confounding, with simple substitution of soybean meal for ground corn to increase the crude protein concentration. However, in developing the detailed protocol for the experiment, it was realized that few if any livestock producers would feed diets with high levels of soybean meal to achieve a dietary crude protein concentration of 20% or more. Because soybean meal protein is fairly extensively degraded in the rumen, much of the nitrogen from the high crude protein diets would be excreted in urine. Hence, treatments with inherent confounding were used, in order to have treatments relevant to field conditions. Soybean meal provided supplemental nitrogen for the lower crude protein diets, and additional protein was provided to high protein diets with a mixture of blood, feather, and fish meals, each high in rumen undegraded protein. Besides the greater practical relevance of these diets compared with the original soybean meal diets, it was felt that animal responses to dietary crude protein level would better reflect effects on amino acid absorption, in that amino acid absorption would increase more and presumably linearly with increasing dietary level of crude protein.

The study of Puchala et al. (2005) provides another example of confounding. Ruminal methane emission by goats consuming Sericea lespedeza (*Lespedeza cuneata*) vs. sorghum-sudangrass (*Sorghum bicolor*) was determined. Sericea lespedeza served as a forage high in

condensed tannins, which were postulated to decrease ruminal methane emission based on previous studies. Sorghum-sudangrass was used as a forage very low in condensed tannins. However, Sericea lespedeza is a legume and sorghum-sudangrass is, of course, a grass. Therefore, any difference in ruminal methane emission or other measures could not be necessarily attributed to level of condensed tannins. That is, level of condensed tannins was confounded with forage type, legume vs. grass. Nonetheless, in the manuscript considerable effort was made to thoroughly review and summarize available literature that indicated little to no effect of forage type on ruminal methane emission. Furthermore, since polyethylene glycol binds condensed tannins in the rumen and is thought to have little or no effects on other conditions, including a period in which polyethylene glycol was added to the diet could have been considered, as was empoloyed in a subsequent experiment (Animut et al., 2008). Moreover, other experiments included comparisons with alfalfa, a legume with very little condensed tannins, to avoid or lessen this confounding.

It is desirable to conduct research at different sites both on-station and on-farm. Use of only one site restricts conditions to which findings can be applied. An important consideration for on-farm research is whether to subject different sites, such as villages, to different treatments or to impose different treatments on animals or groups of animals within each village. For the former approach, obviously for true replication there should be at least two villages per treatment. However, if differences in conditions among villages are appreciable, then the relatively high number of villages per treatment required to detect significant differences would make management of such a large study very difficult. For example, as addressed by Goetsch and Abebe (2009), in one on-farm research activity of the ESGPIP, villages to which all dietary treatments were applied were located at different positions on the downslope of a hill. Internal parasitism was evident early in the experiment, with the severity varying among villages. The level of parasitism increased as position on the hill became lower, corresponding to increasing wetness. Although animals were treated with anthelmintics to address the problem, applying all treatments to each village minimized the effect of this and other factors differing among sites. But, if village had been the experimental unit and the number of observations (i.e., villages) per treatment was limited, the probability of confounding would be relatively high.

Applied Treatments and Measures for Basic or Fundamental Questions

Another item for treatment considerations is the type of question to be answered. First, long-term research progress is most rapid when reasons why treatment responses occur are thoroughly understood rather than merely noting if performance is significantly affected. By understanding underlying physiological processes responsible for treatment effects, other scenarios to which results are applicable can be best projected. Likewise, new treatments for responses greater than from the present experiment can be devised. In this regard, careful and insightful treatment designs (often, however, with a large number of treatments) can yield basic or fundamental information from simple production responses such as live weight gain, feed intake, and efficiency of feed conversion. For example, it is possible to supplement with a cereal grain (e.g., corn) and a feedstuff high in ruminally degraded fiber (e.g., soybean hulls) to similarly alter ruminal microbial protein synthesis and total energy absorption, although absorption of glucose and glucose precursors (e.g., propionate) would be greater for corn (Galloway et al., 1993; Goetsch et al., 1994; Heird et al., 1994). Likewise, a single feedstuff or a

mixture of high in rumen undegraded protein can elicit amino acid absorption comparable to that with supplemental corn or soybean hulls but without markedly impacting energy absorption (Galloway et al., 1996; Goetsch, 1999). Assuming an unsupplemented control treatment, differences in performance responses should allow differentiation among effects of levels of absorbed energy, amino acids, and glucose availability. These points are highlighted below.

- Control – forage alone
- Corn – affects volatile fatty acids for energy, glucose, and amino acids
- Soybean hulls – affects volatile fatty acids and amino acids
- Rumen undegraded protein sources – affects amino acids

To determine influences, treatment differences are examined.

- Glucose – corn vs. soybean hulls
- Volatile fatty acids for energy – soybean hulls vs. rumen undegraded protein sources
- Glucose and volatile fatty acids – corn vs. rumen undegraded protein sources
- Amino acids – control vs. rumen undegraded protein sources

A final treatment consideration is an approach sometimes termed 'stacking.' Although, it is rarely used because it requires considerable prior experimentation to facilitate accurate prediction of treatment effects. Hence, such studies might be termed 'culmination.' This is because effects of specific treatments or treatment components depend on others to which they have been added. The best way to describe the method is by an example study in which it was used (Hardin et al., 1989). Six supplementation treatments used in experiments with confined and grazing cattle are listed below.

1) Control – no supplement, forage alone
2) LC – low level of supplemental corn
3) HC – high level of corn
4) HCF – HC plus vegetable oil and calcium carbonate
5) HCFU – HCF plus urea
6) HCFUGB – HCFU plus corn gluten and blood meals

Again, effects of each feedstuff added to the supplement depend on the presence of the other component(s). That is, any effects of vegetable oil might not be the same if given without corn or with the low level, effects of urea depend on presence of the high level of corn and vegetable oil, and so forth. Moreover, effects of supplement components already present might change when others are added.

Interactions

One of the most challenging aspects of treatment design, data interpretation, and manuscript preparation is handling of interactions. An interaction occurs when the effect of one factor varies with or depends on one or more others.

When an interaction is significant, interaction means must be addressed and it is generally not appropriate to consider only main effect means. But, exceptions exist, depending on the nature of the interaction. If the interaction occurs because of a difference in the magnitude of change, then if this justification is clearly stated, main effect means can be presented and discussed. Conversely, if the interaction is due to a different direction of change or effect, main effect means cannot be presented and interaction means must be discussed.

Table 11 provides examples of interactions. The scenarios could be thought of as different variables or the same variable in multiple experiments. The treatment arrangement is a 2 × 2 factorial. For each scenario, the overall treatment and interaction effects were significant. Hence, interaction means are presented and there is at least one difference among individual interaction means. Relevant analyses by SAS and GenStat are described in Appendix 1 page 168.

Table 11
Examples of interactions involving livestock breed and supplementation in ADG (g)

	Breed A		Breed B	
Scenario	No supplement	Supplement	No supplement	Supplement
1	50[a]	75[b]	75[b]	125[c]
2	50[a]	75[b]	75[b]	50[a]
3	50[a]	50[a]	75[b]	125[c]

[a,b,c]Means in a row without a common superscript letter differ ($P < 0.05$).

Scenario 1 has the same direction of change for both breeds but a different magnitude. Supplementation increased ADG of breed B by 50 g but only by 25 g for breed A. Thus, if the author(s) so desired, data could be addressed in the context of main effect means after the nature of the interaction is appropriately described. Conversely, in scenario 2 supplementation increased ADG by breed A and decreased ADG by breed B. Therefore, the direction of effect or change differed and only interaction means can be discussed. Scenario 3 is different than the other two scenarios in that supplementation had no effect with breed A and increased ADG by breed B. Nonetheless, because change occurred with only one of the breeds, it is only appropriate to address interaction means, without presentation of main effect means.

The P values for differences among individual interaction means and corresponding superscripts or letters to denote interaction mean differences are only relevant if the interaction is significant. Therefore, if the interaction is nonsignificant yet one or more main effects is significant, then main effect mean differences should be described, which in nearly all cases cannot be achieved by use of superscripts or letters situated on interaction means. Chapter 10 – Dissemination has a number of example table structures to clearly and efficiently identify differences among both interaction and main effect means while minimizing table size.

Time

For variables that are measured with the same animal at different times, the statistical analysis needs to consider the main effect (main plot) of treatment(s), effects of time (subplot), and the treatment × time interaction(s). As implied, this can be done as a split-plot in time with

the GLM procedure but most appropriately by repeated measures analysis with a mixed effects model.

An example experiment consists of four treatments, four animals per treatment, and four sampling times, as shown in Table 12. Sources of variation and df are listed below. The number of observations for the main plot is 16 and the total number of observations is 64. Relevant analyses by SAS and GenStat are described in Appendix 1 page 169.

Table 12
Sources of variation and df with four treatments, animals per treatment, and sampling times

Source of variation	df
Treatment	3
Animal within treatment (error term for treatment or the main plot)	12
Time	3
Treatment × time	9
Residual error	36

First, a P value must be selected to establish significance of the treatment × time interaction (e.g., 0.05), as is necessary for main effect interactions. If the P value for the treatment × time interaction is less than 0.05, it is generally not valid or acceptable to present or discuss main effect treatment means. Main effect treatments would thus generally have to be addressed in terms of effects at the different times. However, main effect means (i.e., averaged over time) can sometimes be discussed if adequately justified. An example would be average or total feed intake over a number of weeks. There may be an impetus to present total feed cost for the whole experiment, which depends on intake in the different periods or weeks. However, this should be stated in the manuscript. The other exception involves the nature of the interaction, similar to that addressed above for main effects. If clearly stated that the interaction was due to differences in magnitude rather than direction, then main effect means can be the focus. An example of this situation is an experiment with treatments of different levels of a feed additive, different weeks of a feeding trial, and a variable of feed intake. If feed intake increased with increasing additive level in all weeks, but in some weeks the rate of change was greater than in others, main effects could be discussed. However, the nature of the interaction and assumptions must be stated. On the other hand, if intake increased with increasing level of additive in some weeks but decreased in others, then treatment effects should be presented and addressed by week.

In some cases, possibly for simplicity, authors average values over time if the interaction with treatment is nonsignificant, and then the analysis is re-run without inclusion of variation sources involving time (i.e., time and treatment × time). Resulting sources of variation and df for this example study are given in Table 13, with relevant analyses also described in Appendix 1 page 170.

Table 13
Sources of variation and df with four treatments, animals per treatment, and sampling times with a nonsignificant treatment × time interaction and averaging of values across times for each animal before analysis

Source of variation	df
Treatment	3
Residual error	12

The *F* value for treatment would be the same as derived with the earlier split-plot analysis.

If the treatment × time interaction is significant, then there are essentially two options. One is to present means for treatment-time combinations (i.e., interaction means) with one pooled standard error (**SE**), assuming homogeneous variation. Differences among means can be determined by least significant difference (**lsd**) procedures. However, there are very large numbers of such means in many instances (e.g., 16 with the preceding example). To handle the data in this way entails a very liberal approach, in that there is a relatively high probability of noting a significant difference between two means regardless of a real difference (i.e., Type I error). Therefore, in many instances the analysis is conducted separately for each time, assuming that treatment differences at the same time are of primary interest rather than comparisons of treatments at different times. In this case, the treatment means for each time has a separate pooled SE. Differences among means at each time can be determined by lsd, orthogonal contrasts, etc. One may also be interested in time effects. If the treatment × time interaction is nonsignificant, then means for the different times can be averaged over treatment and discussed accordingly. If an interaction exists, then the same considerations hold true for discussing time effects as were mentioned for treatment.

When presenting such data in the 'Results' or 'Results and Discussion' section, as noted earlier the presence or absence of treatment × time interactions needs to be established before discussing treatment effects. For example, if authors begin discussing main effects and do not list time effects in tables or mention them in the text, reviewers should and will almost always question whether or not there was a significant treatment × time interaction. If an interaction exists, it is of value to characterize what was primarily responsible, rather than merely listing the specific significant differences among treatments for each time. The means and their differences can be described in general in the text, with the reader free to more closely view the time-treatment means in tables if of interest.

Chapter 7. Experiment Implementation

Cultural and Social Considerations

Cultural and social considerations vary markedly among smallholder communities in developing countries around the world. Hence, it is beyond the scope of this publication to thoroughly address them. However, Vernooy (2005) provided a list of questions that should be contemplated when designing and before initiating on-farm research, which are overviewed below.

- Appropriate stakeholders should be involved. Some who have been excluded could act to lessen chances for success of the activity.

- Involvement of an individual or household could create a security or livelihood risk due to the empowering nature of the activity that might put another group or entity in a subordinate position.

- Because of the participatory nature of on-farm research, the activity could be viewed as a threat to the local establishment.

- There should be consideration for who will benefit and how and whether others will be disadvantaged.

- Potential adverse effects in the community should be addressed, including the creation or worsening of existing conflicts. This might occur by affecting power relations or directing benefits toward particular individuals or groups; marginalizing certain groups; or further increasing the stature or status of individuals or groups already of a relatively high position.

Other areas for attention are gender and various socially disadvantaged groups. Fajber (2005) indicated that most marginalized groups (e.g., poor, socially or politically outcast, and ethnic minorities) have relatively limited decision-making power concerning how resources are managed and that some traditional research and development activities have not adequately engaged such groups. Therefore, there should be a detailed analysis of social and gender issues before such activities are undertaken.

Selecting Implementing Partners, Villages, Extension Personnel, and Smallholder Households

One aspect of on-farm research pertinent to the group(s) (e.g., ESGPIP and LU) working with the partner implementing the research on-farm (e.g., universities, colleges, governmental research institutes), as well as the ultimate funding source (e.g., USAID), is how the implementing partner is selected. The first step is to communicate topics to be addressed and requirements for the activity (Goetsch and Abebe, 2009). Activities supported by the ESGPIP entailed involvement of extension personnel, information dissemination (e.g., via field days), a design appropriate for valid statistical analyses, characterization of conditions, and conduct in accordance with a previously agreed upon timetable that included reporting and publication. Initially, topic communication was attempted through distribution of a short activity description to potential partners, similar to a 'Request for Proposals' or ‘Applications’ of granting agencies, but less detailed. This approach was not particularly successful, with only a few responses received, and ultimately transitioned into greater solicitation and assistance efforts. First, one or

more visits were made to possible partners to introduce the activity, followed by multiple phone calls and E-mail messages. The implementing partner then submitted a proposal or activity description including a budget, which was modified to varying degrees during review by the ESGPIP regarding both procedures and the budget request. Eventually, a cooperative agreement was formed and the activity commenced.

Most important considerations in selecting implementing partners, villages, extension personnel, and smallholder households are common sense ones. Individuals, groups, and(or) organizations most familiar with the potential villages should be involved and, concomitantly, well informed about the particular on-farm research to be conducted. The importance of education and training for the successful adoption of new technologies cannot be overstated. An example of this was given by Amir and Knipscheer (1989) regarding the introduction of exotic cattle in Asia and a lack of adequate attention to changes in management inputs necessary. A similar situation existed for the introduction of Boer goats and Dorper sheep in Ethiopia by the ESGPIP. Relative to local breeds, greater management inputs are required for breeds with high production potential that may not be well adapted to local conditions if greater economic returns are to be realized.

Using the ESGPIP as an example, selection of villages for on-farm research can be best achieved at the extension level one or two steps above agents/officers working directly with smallholder households. In Ethiopia, this level equates to woreda extension officers. Woreda extension officers chose KDA they felt were most appropriate and villages with characteristics closely matching needs of the on-farm research. Attributes of KDA are obvious, including knowledge, enthusiasm, work ethic, willingness to follow a research protocol, honesty, integrity, communication skills, etc.

Some areas and communities are referred to as ‘technology resistant.’ Certainly reasons for this should be contemplated and addressed if possible. However, assuming that this issue cannot be adequately dealt with in the timeframe available, other locations should be selected for on-farm research.

In some settings appropriate individuals or groups in the community (e.g., chief or elders) should be consulted before interaction with smallholder households. Obviously, village leaders and their beliefs must be respected and efforts made to gain their trust.

Smallholder households selected should be representative of those to which the technology for adoption is targeted. In one sense it would be preferable to select the most progressive or ‘lead’ households. Certainly some households can be from this category, but less progressive households should be represented as well. Otherwise, a potential scenario may be created in which a beneficial intervention might be readily adopted by progressive but not average households. In some cases technology adoption by a lead farmer results in many other households following suit. However, households with a low likelihood of adopting the technology after the research activity should be excluded. Amir and Knipscheer (1989) described traditional farmers as cautious and conservative in adopting new technologies compared with more progressive farmers. Nonetheless, appropriate use of incentives and reimbursement to compensate for potential decreased economic returns often can create

willingness to participate in on-farm research. But, care should be taken to minimize potential for adverse economic effects. Involving at least one literate family member can be important for record-keeping, but as mentioned later use of the FRG approach lessens this concern.

Working With Implementing Partners, Extension Personnel, Graduate Students, and Smallholders

A critical aspect of working with smallholder households in on-farm research is training, which should be primarily conducted by extension agents/officers with which households are familiar and comfortable. In some cases, training can be provided by previously trained progressive smallholder farmers. Also, there are gender considerations that vary among countries, regions, and cultures.

Amir and Knipscheer (1989) mentioned the desirability of involving farmer associations, if existent, in on-farm research activities. This can be of value in providing infrastructure and other inputs, advertisement, information regarding most significant constraints, technologies likely to be adopted, etc.

An activity of the ESGPIP very beneficial to on-farm research was a complementary training program for KDA. Numerous KDA in six regions of Ethiopia received training in all or most aspects of small ruminant production. As a part of this activity, the Ethiopia Sheep and Goat Production Handbook was developed by Ethiopians located throughout the country. Other training aids were also developed for KDA, including 48 Technical Bulletins (available at www.esgpip.org), video clips, and flip charts. Most topics of KDA training were directly related to on-farm research. Notable examples include ammoniation of crop residues via urea treatment, multi-nutrient supplement blocks, and appropriate use of such feedstuffs as well as regionally and locally available byproducts.

Extension agents/officers working directly with smallholders, including KDA of Ethiopia, are usually very busy and do not focus solely on livestock production. Hence, there may not be adequate time available for on-farm livestock research in seasons with intensive crop production activities. In some cases on-farm research activities requiring close attention of extension agents/officers may have to be planned around busy periods. Also, available resources (including transportation) are often scarce, and salaries may be limited as well. Furthermore, other responsibilities of KDA were not decreased when working on ESGPIP on-farm livestock research. Hence, it may be necessary to provide supportive funds such as a stipend incentive included in a per diem allocation, particularly when considerable travel is required.

The frequency of visits to participating smallholders depends on the nature of the activity. Amir and Knipscheer (1989) suggested frequencies of 15 days, 1 month, and 1 day for on-farm research pertaining to feeding practices, animal health, and disease control, respectively. Moreover, the frequency depends on the specific activities being performed by the smallholders. For example, in one activity of the ESGPIP KDA visited each participating household weekly. Households fed different crop residue treatments daily from a large burlap bag after placing refusals in a separate bag. At the end of the week, the KDA weighed bags with daily refusals,

unused feed, and fresh residue for the next week, facilitating a weekly measure of crop residue intake.

Graduate students can be very useful in conducting on-farm research with smallholders in developing countries. A number of the early on-farm research activities of the ESGPIP were conducted directly by university faculty receiving ESGPIP support funds. However, as is true in many developing countries, faculty members were quite busy with teaching, administration, and other duties. Consequently, as the ESGPIP progressed on-farm research conducted with universities shifted to direct support of graduate student programs for their M.Sc. thesis or Ph.D. dissertation. Although university faculty participated in such programs through academic advisement, this approach did require considerable time and attention of ESGPIP staff and LU researchers.

Regardless of the implementing partner, it is important that the entity managing the research impart close attention to ensure adherence to the approved protocol exactly as agreed upon and to communicate frequently with the supervising organization providing support funds if any changes are contemplated. In a small number of cases very detrimental procedural changes were made during the study without knowledge of the ESGPIP, perhaps because of inadequate training, as many implementing research partners of the ESGPIP had B.S. or M.Sc. degrees. Tools such as this publication may be of value in this regard.

Adaptation

Livestock should be adapted to experimental conditions before measurements are initiated so that effects of treatments typical of field or practical settings are realized. For example, if animals are gathered in a new area for a study, they should be acclimatized to these conditions before BW is measured to assess ADG. However, one aspect of adaptation for which there is some disagreement among researchers is whether or not there should be adaptation to specific treatments. Although some exceptions exist, in general this would not be beneficial. For example, consider two treatments imposed for 14 weeks, with the first 2 weeks serving as an adaptation period. Presumably animals would have been randomly allocated to treatments before the adaptation period or assigned to achieve similar mean BW and variability. If a difference in ADG occurred among treatments each week, but was not necessarily similar in magnitude among weeks, then BW at the end of the adaptation period could have significantly differed between treatments, thereby potentially underestimating the treatment effect that use of BW after adaptation as a covariate would not appropriately address. In practical production settings, effects of treatments over the entire period of exposure would be of greater interest than those from a particular portion of the study.

Data Collection and Handling

Conditions

With more variable conditions on-farm vs. on-station, a greater number of experimental units is required for the same statistical power (Amir and Knipscheer, 1989). Furthermore, it is important to thoroughly characterize experimental conditions. If not, then findings cannot be extrapolated to other settings and are pertinent only to a specific site and period of time. For example, at minimum, forage composition (e.g., ash, crude protein, and neutral detergent fiber)

should be determined in grazing experiments. Similarly, botanical composition (e.g., Guru et al., 2008) is a useful measure. Other examples include byproduct feedstuffs (e.g., poulty litter, dried ruminal digesta from abattoirs) that can vary considerably in nutritional characteristics. Thus, a thorough description of production conditions and assessments such as chemical composition are needed to ascertain the applicability of results to other settings. Collecting weather data at the sites is desirable; however, many developing countries have excellent meteorological agencies. For example, the National Meteorological Agency of Ethiopia has more than 1,200 conventional stations and 25 automatic stations, and the Kenya Meteorological Department operates more than 1,200 conventional rainfall/temperature stations and 39 automatic stations.

Investigator Notes

The American Society of Animal Science website has a very useful set of information sources regarding preparation of scientific manuscripts, entitled ASAS Writing Workshop (Galyean and Lewis, 2013). One of the key points is the importance of investigator or researcher notes. Accurate records must be kept, which is required by some entities such as the U.S. Food and Drug Administration. Researchers should not assume that they will remember everything about an experiment. In accordance, notes should be made as events occur rather than later.

Data Recording in the Field

For most important measures such as change in BW, the primary researcher or a delegate thereof should be present to conduct, assist, or monitor the activity. The format of data collection or record sheets should be developed or approved by the researcher. Raw data collection records should include the name of the person recording. Data sheets should be constructed in a manner to minimize recording time, but also to minimize time required later to merge with previously collected data. For example, if data are collected from animals as they are released from pens of a FRG barn, the order on data sheets should be by pen or group followed by animal identification number, presumably designated by ear tags. Table 14 provides an example of this structure. Conversely, if data are recorded when all animals are together, the order should be by animal identification number without a designation for pen or group (shown in Table 15), which can easily be accomplished in spreadsheets later by sorting.

Table 14
Example data collection sheet with ordering by group or pen then animal number

FRG	Group or pen	Animal number	Variable 1	Variable 2
A	1	1	85	45
A	1	4	45	56
A	1	12	62	43
A	1	14	23	94
A	1	19	44	72
A	1	20	62	99
A	1	28	57	22
A	1	29	98	87
A	1	35	33	77
A	1	36	56	49
A	2	3	77	58
A	2	9	43	23
A	2	10	55	55
A	2	13	77	55
A	2	16	90	46
A	2	25	56	88
A	2	27	11	17
A	2	30	34	62
A	2	33	87	66
A	2	40	80	85
A	3	2	99	82
A	3	7	55	43
A	3	11	85	66
A	3	18	49	88
A	3	21	58	55
A	3	22	94	90
A	3	26	17	22
A	3	34	22	35
A	3	37	72	93
A	3	38	45	67
A	4	5	76	28
A	4	6	23	33
A	4	8	66	89
A	4	15	46	74
A	4	17	76	94
A	4	23	95	76
A	4	24	88	56
A	4	31	62	89
A	4	32	62	67
A	4	39	56	44

Table 15
Example data collection sheet with ordering by animal identification number

FRG	Group or pen	Animal number	Variable 1	Variable 2
A	1	1	85	45
A	3	2	99	82
A	2	3	77	58
A	1	4	45	56
A	4	5	76	28
A	4	6	23	33
A	3	7	55	43
A	4	8	66	89
A	2	9	43	23
A	2	10	55	55
A	3	11	85	66
A	1	12	62	43
A	2	13	77	55
A	1	14	23	94
A	4	15	46	74
A	2	16	90	46
A	4	17	76	94
A	3	18	49	88
A	1	19	44	72
A	1	20	62	99
A	3	21	58	55
A	3	22	94	90
A	4	23	95	76
A	4	24	88	56
A	2	25	56	88
A	3	26	17	22
A	2	27	11	17
A	1	28	57	22
A	1	29	98	87
A	2	30	34	62
A	4	31	62	89
A	4	32	62	67
A	2	33	87	66
A	3	34	22	35
A	1	35	33	77
A	1	36	56	49
A	3	37	72	93
A	3	38	45	67
A	4	39	56	44
A	2	40	80	85

Usually with limited numbers of animals on smallholder farms, the method of animal identification, if existent, is not complex (e.g., a number on an ear or neck tag of one color). However, with many animals, tags of different colors might be used, each with a different meaning. Thus, it is possible for the same numbers to be on tags of different colors. To address such a scenario on some farms collaborating with the AIGR on a project dealing with selection for resistance to internal parasites, a letter preceding numbers was used to designate tag color (e.g., W = white, Y = yellow, O = orange, R = red, and so forth). Initially, at each data collection time a new set of recording sheets was used and the animal identification code was entered in the order animals were handled to avoid the need for multiple animal number lists. Although this did minimize time required for data collection, appreciable problems occurred later when data from different times and sets of recording sheets were combined. Errors occurred in discerning tag color perhaps due to fading, tags were occasionally lost, animals were sometimes missed, duplicate identifiers existed because of tag color errors or use of improper replacement tags, etc. Therefore, in subsequent years data sheets with alphanumeric animal identification information from previous times were available for checking. Moreover, when samples were collected for laboratory analyses, a sequential number was included to reduce problems with mis-labeling of samples and sample loss or inadvertent discarding before analysis.

In contrast to examples noted above, data can be collected vertically for animals or animal groups. An example is supplement consumption by a treatment group of animals of a FRG, or animals of a household on one treatment, over a number of days. Table 16 provides an example of this.

Table 16
Example of a data collection sheet with vertical data entry[1]

		Household									
Weekday	Day	A	B	C	D	E	F	G	H	I	J
Monday	1	4.3	5.6	3.2	1.2	5.4	3.2	4.5	5.3	2.3	1.9
Tuesday	2	6.2	2.3	1.4	5.2	3.3	3.9	3.5	3.6.	2.5	2.9
Wednesday	3	4.5	3.3	2.5	4.3	3.3	1.0	5.7	5.0	3.5	2.8
Thursday	4	6.2	4.1	3.5	5.4	3.2	4.5	5.3	2.3	1.9	3.2
Friday	5	4.4	2.0	2.9	3.2	4.9	6.0	1.1	3.2	2.9	2.2
Saturday	6	3.2	3.3	2.6	1.9	5.2	5.6	3.2	1.2	5.4	3.2
Sunday	7	2.9	2.6	4.0	2.7	3.2	2.3	1.4	5.2	3.3	3.9
Monday	8	1.9	4.9	2.7	3.3	3.0	3.3	2.5	4.3	3.3	1.0
Tuesday	9	8.4	1.0	0.9	2.5	3.2	4.1	3.5	5.4	3.2	4.5
Wednesday	10	4.2	3.2	4.5	5.3	2.3	1.9	3.7	7.0	3.7	3.6
Thursday	11	3.2	3.9	3.5	3.6.	2.5	2.3	1.4	5.2	3.3	3.9
Friday	12	4.2	1.0	5.7	5.0	3.5	3.3	2.5	4.3	3.3	1.0
Saturday	13	2.8	4.5	5.3	2.3	1.9	4.1	3.5	5.4	3.2	4.5
Sunday	14	9.0	4.4	4.1	2.2	4.8	7.4	2.5	5.2	3.3	5.5

[1]Example data under household columns could be for a variable such as supplement consumption by groups of animals (kg).

Changing Vertical Listings of Data to Horizontal

After data are collected, preferably periodically rather than waiting until the end of the study, rearrangement may be necessary for statistical analysis. For analysis via SAS, data for each sampling and(or) experimental unit, or repeated measure, are typically arranged horizontally. This structure is opposed to the vertical arrangement noted in Table 16 that may be more convenient for data recording in the field. Data can be transposed in spreadsheets such as Excel for use in SAS by copying and pasting into an Editor file or moving that and other files into the Editor file as is addressed later. Table 17 contains data from Table 16 transposed for use in SAS.

Splitting Horizontal Listings of Data Into Different Time Periods

If data are arranged as in Table 17 and it is of interest to investigate effects of day, then SAS statements below can be used. Acronyms such as sadi (daily supplement intake on an as fed basis) are used to denote variables and are not SAS commands.

```
data adisecond; set data adifirst;
sadi = s1; day = 1; output;
sadi = s2; day = 2; output;
sadi = s3; day = 3; output;
sadi = s4; day = 4; output;
and so forth
```

Some people find working with data in SAS initially in a horizontal presentation, as in Table 17, advantageous compared with the vertical approach of Table 16. Although both can be used and preference varies among individuals, the horizontal method permits fairly simple actions such as specifying initial values as covariates before ‘output’ statements to create values for different times. With an initial vertical listing, covariates can be created by deleting all other times, renaming variables at the remaining time, and then merging that data set with the original one with all times.

Averaging Over Periods of Time

It is common to average daily values to derive means for one or more weeks, often corresponding with the frequency of determining BW. This can be done with spreadsheets; however, many researchers prefer to have as much raw data as is reasonable in SAS Editor files for greatest flexibility and ease of viewing of calculations. A number of SAS statements to derive weekly means are below.

```
data adsifirst; input village household treatment s1 s2 s3 s4 and so forth;
sadiwk1 = mean(s1,s2,s3,s4,s5,s6,s7);
sadiwk2 = mean(s8,s9,s10,s11,s12,s13,s14);
and so forth
```

Table 17
Example of transposing data collected in a vertical manner to be in rows for use in SAS[1]

Village	Household	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11	S12	S13	S14
A	A	4.3	6.2	4.5	6.2	4.4	3.2	2.9	1.9	8.4	4.2	3.2	4.2	2.8	9.0
A	B	5.6	2.3	3.3	4.1	2.0	3.3	2.6	4.9	1.0	3.2	3.9	1.0	4.5	4.4
A	C	3.2	1.4	2.5	3.5	2.9	2.6	4.0	2.7	0.9	4.5	3.5	5.7	5.3	4.1
A	D	1.2	5.2	4.3	5.4	3.2	1.9	2.7	3.3	2.5	5.3	3.6.	5.0	2.3	2.2
A	E	5.4	3.3	3.3	3.2	4.9	5.2	3.2	3.0	3.2	2.3	2.5	3.5	1.9	4.8
A	F	3.2	3.9	1.0	4.5	6.0	5.6	2.3	3.3	4.1	1.9	2.3	3.3	4.1	7.4
A	G	4.5	3.5	5.7	5.3	1.1	3.2	1.4	2.5	3.5	3.7	1.4	2.5	3.5	2.5
A	H	5.3	3.6.	5.0	2.3	3.2	1.2	5.2	4.3	5.4	7.0	5.2	4.3	5.4	5.2
A	I	2.3	2.5	3.5	1.9	2.9	5.4	3.3	3.3	3.2	3.7	3.3	3.3	3.2	3.3
A	J	1.9	2.9	2.8	3.2	2.2	3.2	3.9	1.0	4.5	3.6	3.9	1.0	4.5	5.5

[1]S1 = supplement intake on day 1; S2 = supplement intake on day 2; S3 = supplement intake on day 3, and so on (kg).

```
data adsithird; set adsisecond;
if day = 1 then wk = 1; if day = 2 then wk = 1; if day = 3 then wk = 1; if day = 4 then wk = 1;
if day = 5 then wk = 1; if day = 6 then wk = 1; if day = 7 then wk = 1;
if day = 8 then wk = 2; if day = 16 then wk = 2; if day = 17 then wk = 2; if day = 18 then wk = 2;
if day = 19 then wk = 2; if day = 20 then wk = 2; if day = 21 then wk = 2;
and so forth
```

Or, the following statements could be used:

```
if day < 8 then wk = 1;
if day > 7 and < 15 then wk = 2;
if day > 14 and < 22 then wk = 3;
and so forth
```

However, more efficient programming is shown below.

```
data adithird; set adifirst;
array s{14} s1-s14;
do i = 1 to 14;
sadi = s{i};
day = i;
keep village household treatment sadi day;
output;
end;

if day <= 7 then wk = 1;
else if 8 <= day <= 14 then wk = 2;
else if 15 <= day <= 21 then wk = 3;
else wk = 4;
```

Then statements such as these can be used to average over day for weekly means.

```
proc sort data = adsithird; by village household wk;
proc means noprint; by village household wk;
var adsi; id treatment; output out = adsifourth mean = adsi;
```

ADG by Regression

An important measure in many livestock experiments is change in BW, commonly assessed as ADG. This variable can be derived by dividing the magnitude of change from the beginning to end of the study, or any period within, by the number of days. However, if BW is measured fairly frequently, such as weekly, and if conditions are constant throughout the study, then it may be preferable to determine ADG by regressing BW against time or day of the study. This is particularly beneficial when an animal has an unusually low or high value at a particular time, especially at the end of the study. As an example, SAS Editor file statements below are for an 84-day experiment with BW measured weekly.

```
data bw1; input animal treatment $ bw0 bw1 bw2 bw3 bw4 bw5 bw6 bw7 bw8 bw9 bw10 bw11
bw12;
cards;
1 A 20.0 21.0 21.5 21.9 22.9 23.6 24.2 25.7 26.1 26.8 28.1 28.5 29.2
2 B 20.6 21.1 22.4 22.7 22.9 23.5 24.3 25.0 25.7 26.4 27.2 27.9 28.4
and so on
;
data bw2; set bw1;
bw = bw0; day = 0; output;
bw = bw1; day = 7; output;
bw = bw2; day = 14; output;
bw = bw3; day = 21; output;
bw = bw4; day = 28; output;
bw = bw5; day = 35; output;
bw = bw6; day = 42; output;
bw = bw7; day = 49; output;
bw = bw8; day = 56; output;
bw = bw9; day = 63; output;
bw = bw10; day = 70; output;
bw = bw11; day = 77; output;
bw = bw12; day = 84; output;

proc sort; by animal;
proc reg outest = adgreg noprint; by animal; model bw = day;
proc print data = adgreg;
```

The output file for this 'print' statement is shown in Table 18.

Table 18
Example SAS output file for determination of ADG by regression

obs	Animal	_MODEL_	_TYPE_	_DEPVAR_	_RMSE_	intercept	day	bw
1	1	MODEL1	PARMS	bw	0.25642	19.8857	0.11170	-1
2	2	MODEL1	PARMS	bw	0.23406	20.5725	0.09278	-1

A more efficient manner of programming is given below.

```
data bw1; input animal treatment $ b1-b12;
datalines;
1 A 20.0 21.0 21.5 21.9 22.9 23.6 24.2 25.7 26.1 26.8 28.1 28.5 29.2
2 B 20.6 21.1 22.4 22.7 22.9 23.5 24.3 25.0 25.7 26.4 27.2 27.9 28.4
and so on
;
data bw2; set bw1;
array b{12} b1-b12;
do i = 1 to 12;
bw = b{i};
adg = i;
keep animal treatment bw adg;
output;
end;

proc sort data = bw2; by animal;
proc reg outest = adgreg noprint; by animal;
model bw = adg;
proc print data = adgreg;
```

The 'day' variable is ADG determined by regression in kg/day. These values are very similar to those derived simply by dividing BW change by 84 days (i.e., 0.10952 and 0.09286 kg/day for animal 1 and 2, respectively.

Merging Data Sets

A common data handling activity for livestock research is merging data sets. If different data sets have the same categories, then merging in SAS is very simple, with an example shown below.

```
data aniset1; input animal period treatment anivar1 anivar2;
data aniset2; input animal period treatment anivar3 anivar4;
proc sort data = aniset1; by animal period;
proc sort data = aniset2; by animal period;
data aniset3; merge aniset1 aniset2; by animal period;
```

In many livestock experiments, conditions in different time periods apply to all animals regardless of treatments (e.g., composition of the basal diet). Thus, it may be necessary to combine animal and feed data sets by period, as shown below.

```
data feedset1; input period feedvar1 feedvar2;
proc sort data = aniset3; by period; proc sort data = feedset1; by period;
data anifeedset1; merge feedset1 aniset3; by period;
```

Also, frequently variables have values that differ among treatments as well as periods, such as studies with different supplements, an example of which is given below.

```
data suppset1; input period treatment suppvar1 suppvar2;
proc sort data = anifeedset1; by period treatment;
proc sort data = suppset1; by period treatment;
data anifeedsuppset1; merge anifeedset1 suppset1; by period treatment;
```

Another method in SAS of including data relevant to more than one experimental and(or) sample unit is to use 'if-then' statements. For example, statements below list levels of crude protein (**CP**) and neutral detergent fiber (**NDF**) in forage consumed by all animals in a period and in different types of supplement.

```
data aniset4; input animal period treatment anivar1 anivar2;
if period = 1 then foragecp = 10;
if period = 2 then foragecp = 9;
if period = 3 then foragecp = 11;
if period = 4 then foragecp = 10;
if period = 1 then foragendf = 62;
if period = 2 then foragendf = 64;
if period = 3 then foragendf = 61;
if period = 4 then foragendf = 67;
if period = 1 and treatment = 1 then supplementcp = 31;
if period = 2 and treatment = 1 then supplementcp = 29;
if period = 3 and treatment = 1 then supplementcp = 33;
if period = 4 and treatment = 1 then supplementcp = 28;
if period = 1 and treatment = 2 then supplementcp = 41;
if period = 2 and treatment = 2 then supplementcp = 40;
if period = 3 and treatment = 2 then supplementcp = 36;
if period = 4 and treatment = 2 then supplementcp = 39;
if period = 1 and treatment = 1 then supplementndf = 20;
if period = 2 and treatment = 1 then supplementndf = 18;
if period = 3 and treatment = 1 then supplementndf = 19;
if period = 4 and treatment = 1 then supplementndf = 21;
if period = 1 and treatment = 2 then supplementndf = 16;
if period = 2 and treatment = 2 then supplementndf = 15;
if period = 3 and treatment = 2 then supplementndf = 14;
if period = 4 and treatment = 2 then supplementndf = 19;
```

Calculations

Calculations can be made in spreadsheets and in statistical programs such as SAS. An increasing popularity of menu-driven approaches for statistical analyses has contributed to a shift towards more reliance on spreadsheets. However, in many cases both spreadsheets and SAS are used for calculations. Furthermore, some graduate student advisors and senior scientists assisting junior researchers find it much easier to develop and check complex calculations if

variable abbreviations are viewed rather than cell locations. A very simple example of the use of SAS syntax for calculations in an intake and digestion experiment are given below. Variables in the input statement would have been previously calculated, most likely with spreadsheets.

```
data dig1;
input ptaiad ptaiaf ptomf ptomd ptcpf ptcpd ptndff ptndfd ptadff ptadfd encfmjkg encdmjkg
fecdm;

/*
ptaiad = percentage of acid insoluble ash in the diet actually consumed on a dry matter basis
ptaiaf = percentage of acid insoluble ash in feces on a dry matter basis
ptomf = percentage of organic matter in feces on a dry matter basis
ptomd = percentage of organic matter in the diet actually consumed on a dry matter basis
ptcpf = percentage of crude protein in feces on a dry matter basis
ptcpd = percentage of crude protein in the diet actually consumed on a dry matter basis
ptndff = percentage of neutral detergent fiber in feces on a dry matter basis
ptndfd = percentage of neutral detergent fiber in the diet actually consumed on a dry matter basis
ptadff = percentage of acid detergent fiber in feces on a dry matter basis
ptadfd = percentage of acid detergent fiber in the diet actually consumed on a dry matter basis
encfmjkg = concentration of energy in feces in MJ/kg on a dry matter basis
encdmjkg = concentration of energy in the diet actually consumed in MJ/kg on a dry matter basis
fecdm = fecal excretion of dry matter in g/day
*/

dmdig = 100 - (100 * ptaiad / ptaiaf);
omdig = 100 - (100 * ptaiad / ptaiaf * ptomf / ptomd);
cpdig = 100 - (100 * ptaiad / ptaiaf * ptcpf / ptcpd);
ndfdig = 100 - (100 * ptaiad / ptaiaf * ptndff / ptndfd);
adfdig = 100 - (100 * ptaiad / ptaiaf * ptadff / ptadfd);
endig = 100 - (100 * ptaiad / ptaiaf * encfmjkg / encdmjkg);

fecom = fecdm * (ptomf / 100);
feccp = fecdm * (ptcpf / 100);
fecndf = fecdm * (ptndff / 100);
fecadf = fecdm * (ptadff / 100);
fecen = fecdm / 1000 * (encfmjkg / 100);

dmint = fecdm / ((100 - dmdig) / 100);
omint = fecom / ((100 - omdig) / 100);
cpint = feccp / ((100 - cpdig) / 100);
ndfint = fecndf / ((100 - ndfdig) / 100);
adfint = fecadf / ((100 - adfdig) / 100);
enint = fecen / ((100 - endig) / 100);

ddmi = dmint - fecdm;
domi = omint - fecom;
```

```
dcpi = cpint - feccp;
dndfi = ndfint - fecndf;
dadfi = adfint - fecadf;
dei = enint - fecen;
mei = dei * 0.82;
mec = mei / (dmint / 1000);

meimbw = (mei * 1000) / mbw;

/*
dmdig = total tract digestibility of dry matter as a percentage
omdig = total tract digestibility of organic matter as a percentage
cpdig = total tract digestibility of crude protein as a percentage
ndfdig = total tract digestibility of neutral detergent fiber as a percentage
adfdig = total tract digestibility of acid detergent fiber as a percentage
endig = total tract digestibility of energy as a percentage

fecom = fecal excretion of organic matter in g/day
feccp = fecal excretion of crude protein in g/day
fecndf = fecal excretion of neutral detergent fiber in g/day
fecadf = fecal excretion of acid detergent fiber in g/day
fecen = fecal excretion of energy in MJ/day

dmint = intake of dry mater in g/day
omint = intake of organic matter in g/day
cpint = intake of crude protein in g/day
ndfint = intake of neutral detergent fiber in g/day
adfint = intake of acid detergent fiber in g/day
enint = intake of energy in MJ/day

ddmi = intake of digested dry matter in g/day
domi = intake of digested organic matter in g/day
dcpi = intake of digested crude protein in g/day
dndfi = intake of digested neutral detergent fiber in g/day
dadfi = intake of digested acid detergent fiber in g/day
dei = intake of digested energy in MJ/day
mei = intake of metabolizable energy in MJ/day (assuming a concentration of 82% of digestible
energy)
mec = concentration of metabolizable energy in MJ/kg on a dry matter basis

meimbw = intake of metabolizable energy as kJ/kg BW^0.75
*/
```

Economic Analysis

On-farm research activities should include an economic analysis, although in many cases the potential complexity may be limited. In this regard, partial budgeting is most frequently used for economic analysis of on-farm research. As addressed by Ibrahim and Olaloku (2000), with partial budgeting fixed costs are assumed constant and only net changes in costs and benefits, or gains and losses, receive attention. Partial budgeting is most appropriate for evaluation of single rather than multiple interventions. If a technology increases profit, then the marginal rate of return, or net income per unit of additional expenditure, should be evaluated, which brings out the importance of considering factors such as available capital. Furthermore, Ibrahim and Olaloku (2000) recommended caution when interpreting partial budgeting results concerning areas such as limited resources, time and management skills required for implementation, secondary as well as primary objectives of farmers, and risk associated with some technologies.

The study of Guru et al. (2008) provides an example of partial budgeting. The experiment entailed supplementation with three different concentrate mixtures, which were 50% wheat bran and 1% salt plus 49% noug cake, noug cake treated with formaldehyde, or linseed meal. Local feedstuff prices were used along with total feedstuff intake during the study to estimate cost of supplementation. Change in animal value was based on live weight gain, a historical average dressing percentage of this breed of goat under similar production conditions, and a local price per unit of carcass weight. The difference between gross returns and the total cost of supplementation was determined as a reflection of profit. Although this approach was useful for comparing the three treatments, there are a number of limitations. For example, the experiment did not include a negative control treatment. Thus, there is an implied assumption that not providing a supplement was impractical or unsound management. The same applies to use of a positive control treatment that would have entailed a supplement with only wheat bran and salt. Moreover, other expenses were not considered, such as the basal diet, labor, etc. Hence, it was also necessary to assume that such costs were similar among treatments. Another important aspect for experiments such as this is cultural considerations. In this situation, participating smallholders were not familiar with formaldehyde or particularly excited about its use as a feedstuff treatment, perhaps because of the odor or general fear of chemicals. Therefore, it is doubtful that this supplement would be used in the future regardless of results of this on-farm study.

Chapter 8. Statistical Analyses

Introduction

As mentioned earlier, this publication is not intended to provide considerable detail about all areas, such as statistical analyses. However, notes regarding practical considerations of statistical analyses for livestock research are offered.

Data Entry

For all software programs, data must be entered in a pre-defined format. There are several methods of entering data for analysis by SAS that can be categorized as internal reads, external reads, and imported data. With the first method, data are embedded within the SAS Editor file. An advantage of this approach is simplicity because there is only one file, minimizing potential for errors due to changes made in others. Such files can be cumbersome to work with if numbers of observations and(or) variables are large, although a 'hide' function of SAS Editor files is useful in this regard.

There are several methods for external reads. The INFILE statement can be used to input data from different types of files, including prn (print, space delimited), txt (text, tab delimited), csv (comma separated value, comma delimited), and xls or xlsx (Excel). For example, the following statements specify the physical location of a csv file and list its variables.

```
FILENAME IN1 'C:\Documents and Settings\AIGR\My Documents\My SAS
Files\V8\YK-12-04\Data\data4.csv';
data study1;
INFILE IN1 DLM=',' FIRSTOBS=2 MISSOVER;
INPUT ani prd trt var1 var2 and so forth;
```

The DLM statement specifies comma as the delimiter, which is the character separating values of the variables. The default delimiter in SAS is a blank space. The FIRSTOBS=2 syntax indicates that the first line is not data. This line typically contains variable definitions or acronyms and, thus, should be ignored. The MISSOVER statement indicates that if the end of line is encountered before all variables in the INPUT statement have received a value, then a "missing value" should be assigned to those variables, which is a . (period) by default in SAS.

The advantage of an external read directly from an Excel file is that many researchers gather data in spreadsheets. Alternatively, with an internal read selected cells of a spreadsheet are copied and pasted into the SAS Editor file. For an external read, prn, txt, or csv files are created using the "Save As" option in Excel. If a mistake has been made in data entry (Excel), with an internal read both SAS and Excel files must be corrected. Otherwise, confusion can occur later if the researcher compares data and is unsure which file is correct. If a researcher is using prn, txt, or csv files for external reads, then the Excel file must be corrected and the output file re-created. Conversely, if an Excel file is being used in a direct external read, then a change in Excel is automatically made in the SAS file. But, direct external reads with Excel files are more complicated than the other methods noted above, and it is simple to save Excel files in

these other formats. Nonetheless, example SAS statements and notes regarding direct external reads with Excel files are given below.

```
FILENAME IN DDE 'Excel|C:\Users\GIGR-TG\Documents\SAS
Training\(data1.xlsx)data1|R2C1:R15C4' NOTAB;
data studyb;
INFILE IN DLM='09'X NOTAB DSD MISSOVER;
```

The DDE denotes Dynamic Data Exchange, which is a property of many Windows programs. The Excel file and particular worksheet with data of interest must be open. To derive the physical location to paste between tick marks in the FILENAME statement, data are highlighted and copied to the clipboard. Then in SAS ACCESSORIES, DDE TRIPLET is selected under the SOLUTIONS menu. Pressing Ctrl-Insert copies the address to the clipboard and replaces data in the buffer. After clicking the OK icon, the address is pasted. For other terms in the INFILE statement, NOTAB indicates that tabs in the data are ignored, as they are now delimiters. DLM='09'X indicates that tabs are delimiters rather than spaces. The DSD statement indicates a missing value if there are two consecutive delimiters in a row.

For importation, SAS recognizes various forms of data. The only disadvantage of direct importation using SAS is that row headers (first row in Excel) are used as variable names and sometimes non-allowable SAS variable name characters are in the Excel header row. However, this can be easily overcome by avoiding the offending characters in the header row. Another disadvantage is that if there are several worksheets in an Excel workbook, importing all worksheets or sometimes even the desired worksheet can be difficult.

Whatever the data entry method used, once read into SAS a permanent SAS data set can be created. A permanent SAS data set is the most efficient read if the data do not change and the data set will be accessed repeatedly for analysis. Data must be first read into SAS and then saved using a SAS two-level name. This two-level name is designated by a period between the first and second level, such as sasuser.mydata. A LIBNAME must reference the physical location, usually a sub-directory, where the permanent SAS data set is stored. Several libraries are automatically created by SAS, and SASUSER is a convenient oine. Files can be imported into the WORK library; however, these files are temporary and will be deleted once SAS is exited. Therefore, it is advisable to create personalized libraries with specific meanings.

Distribution of Data and Transformation

Parametric statistical tests on data that are not normally distributed can yield misleading results (McDonald, 2009a). Data transformation can, in many instances, improve analyses. A typical way to evaluate normality is with the Shapiro-Wilk statistic of the Univariate procedure of SAS. A statement for this test is given below.

- proc univariate normal plot; var variablename;

This procedure also provides other tests for normality of residuals (Kolmogorov-Smirov, Cramer-von Mises, and Anderson-Darling). Typically, P values less than 0.05 indicate a non-

normal distribution. The GenStat 'W-test for Normality' of 'Summary Statistics' under 'Stats' also can be used to perform a Shapiro-Wilk test for normality.

Various transformations can be used to normalize data and(or) stabilize variance, including log, square root, arcsine, and inverse. Back-transformed means and SE are usually reported in tables and figures, although in some cases analyzed transformed values are presented as well. Each transformation has specific types of data for which it is most appropriate. McDonald (2009a) stated that it is best to use a transformation that is common for a particular type of data and field, assuming that an adequate defense can be provided as well. An example is the log transformation of fecal egg count data after addition of a value such as 1 because of the potential raw count of 0. However, other values can be added to identify one that yields a normal distribution (e.g., Vanimisetti et al., 2004). Moreover, in some cases a number of transformations for different variables are employed in an experiment. For example, Rodríguez-De Lara et al. (2010) stated:

- "Analyses of variance were done with transformed and original data, variables in percentage were transformed to arc sine, reaction time, sperm concentration per ejaculate, normal alive motile sperm and number of semen doses were log 10 transformed, semen pH was transformed to square root."

Transformations and back transformations can be made in spreadsheets and with statistical software packages such as SAS.

Although normal distribution of data is important, there may be variables for which no transformation is adequate, examples being in studies of Goetsch et al. (2012) and Tsukahara et al. (2013), which may involve considering categorical variables as continuous. In support of analyses conducted with non-normal data, the following was stated by Goetsch et al. (2012):

- "Snedecor and Cochran (1978) stated 'many results that are useful in statistical work, although strictly true only when the population is normal, hold well enough for rough-and-ready use when samples come from non-normal populations'."
- "Furthermore, Bradley (1978) in his treatise on robustness cites various statistical studies supporting that the *t*-test and *F*-test are extremely robust and fairly immune to deviations from normality."

Moreover, the central limit theorem is that the distribution of means will become more normal as the number of samples or observations increases.

Non-parametric Tests

According to McDonald (2009b), there are other methods of analyzing non-normally distributed data without assumptions concerning distribution. However, such methods can incur appreciable data loss and are less powerful than parametric analyses. Non-parametric analyses are most common for ranked data. Some analyses for non-parametric data are the Wilcoxon T Test, Mann-Whitney U Test, and Spearman's correlation.

Homogeneity of Variance

Parametric tests such as ANOVA assume similar within group variation (McDonald, 2009b). This is a reason to allocate animals with similar mean BW and variability to groups and treatments, as well as giving attention to other factors depending on the particular experiment. Another consideration for within group variation is presentation of SE in tables. Most journals prefer one pooled SE for treatments to minimize table cluttter, assuming that the number of observations is the same or similar. Presentation of pooled SE implies that within group variation is not different. An example for which individual treatment SE should be reported is in Table 19. In this study, the number of animals per pen and automated feeding unit differed markedly, ranging from 2 to 12. Separate columns are used for the SE, although in some articles individual treatment SE are listed as "mean ± SE." Although it is assumed that SE is for the mean, some journals require SEM for clear differentiation from SE of the difference (i.e., **SED**).

A common method of evaluating homogeneity of variance is Bartlett's test. However, according to McDonald (2009b) the Bartlett test is sensitive to departures from normality. Levene's test is less sensitive to departures from normality but less powerful than the Bartlett test if data are approximately normal (McDonald, 2009b). Welch's ANOVA can be used when group variance is not assumed to be equal (SAS, 2013).

Examples of evaluating homogeneity of variance can be illustrated with data in Appendix 3 Table 166 and analysis utilizing SAS. First, the following SAS statements can be used to evaluate variation within treatments without considering FRG or household.

```
proc glm;
classes treatment;
model variable = treatment;
means treatment / hovtest = bartlett;
means treatment / hovtest = levene welch;
```

Means of 7.050, 7.450, 7.223, and 6.925 and SD of 3.530, 4.898, 4.599, and 3.437 result for treatments 1, 2, 3, and 4, respectively. The P value for the Bartlett test is 0.058, indicating that within treatment variation nearly differed significantly among treatments. However, the P value for Levene's test (0.514) was much greater. The P value for a difference among treatments with Welch's test was 0.952, similar to that for the GLM analysis (0.949).

Because treatments were equally represented in the four FRG, it may also be of interest to evaluate variation within FRG with SAS statements noted below.

```
proc glm;
classes frg;
model variable = frg;
means frg / hovtest = bartlett;
means frg / hovtest = levene welch;
```

Table 19. Effects of the number of animals per automated feeding system and length and time of feeder access on feed intake, growth performance, and behavior of Boer goat wethers

	Cont-6[1]		Cont-12[1]		Day-2[1]		Day-4[1]		Night-4[1]		Night-8[1]		
Item[2]	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Mean	SE	Contrast[3]
Feed intake and growth performance													
DMI, kg/d	2.04	0.118	2.01	0.083	1.45	0.204	1.50	0.144	1.92	0.144	1.76	0.102	R,T
ADG, g	237	14.6	252	10.3	174	25.3	207	17.9	247	17.9	211	12.6	R,t,itl
ADG:DMI, g/kg	116	5.5	126	3.9	120	9.5	138	6.7	130	6.7	121	4.7	itl
RFI, g/d	49	45.3	-25	32.0	-167	78.4	-257	55.4	-81	55.4	-112	39.2	R
Feeding behavior													
Feeder occupancy, h/d	1.83	0.21	1.55	0.15	1.23	0.37	1.34	0.26	1.51	0.26	1.25	0.18	r
DMI rate, g/min	20.7	2.95	24.1	2.09	19.7	5.11	21.2	3.62	22.6	3.62	24.1	2.56	
Intra-meal interval, min	35.0	3.01	28.2	2.13	25.7	5.21	18.3	3.68	19.9	3.68	21.5	2.61	R
Meals/d	9.5	0.69	11.3	0.49	5.7	1.20	7.5	0.85	8.5	0.85	9.5	0.60	R,T,L
DMI, g/meal	213	18.8	178	13.3	257	32.5	233	23.0	223	23.0	186	16.3	r,l
Time, min/meal	11.3	1.47	8.1	1.04	13.1	2.54	12.6	1.80	10.7	1.80	7.9	1.27	t
Visits/d	25.5	2.96	25.8	2.09	31.4	5.12	29.9	3.62	20.0	3.62	22.6	2.56	T
DMI, g/visit	82.3	8.26	83.5	5.84	46.3	14.3	54.5	10.1	97.1	10.1	80.0	7.15	r,T
Time, min/visit	4.2	0.32	3.6	0.23	2.4	0.56	2.9	0.39	4.4	0.39	3.4	0.28	R,T,itl
Position and movement behavior													
Active, % day	8.0	0.77	6.2	0.54	6.8	1.33	5.0	0.94	5.2	0.94	6.5	0.66	r
Lying, % day	48.2	5.40	57.1	3.82	70.2	9.35	57.6	6.61	67.1	6.61	54.6	4.67	r, IRL
Standing, % day	43.8	4.91	36.7	3.47	23.0	8.50	37.4	6.01	27.7	6.01	38.9	4.25	r, IRL
Steps/h	450	45.5	344	32.2	398	78.8	289	55.7	292	55.7	372	39.4	ǂ
Energy measures													
HR, beats/min	114	3.3	116	2.4	103	5.8	103	4.1	114	4.1	108	2.9	R,t
HE, kJ/kg $BW^{0.75}$	631	18.5	639	13.1	593	32.0	535	22.7	646	22.7	574	16.0	R,t,L,IRL
Waiting and aggression[4]													
Waiting, min/h	6.5	1.09	7.7	0.77	5.5	1.88	5.2	1.33	4.8	1.33	8.1	0.94	
Intra-aggressive behaviors/h	1.8	1.12	2.5	0.79	4.3	1.94	2.4	1.37	2.1	1.37	9.8	0.97	R,t,l,ITL
Inter-aggressive behaviors/h	1.3	0.70	1.4	0.49	6.5	1.21	0.7	0.86	1.9	0.86	2.7	0.61	R,L,irl, ITL
Total aggressive behaviors/h	3.1	1.36	3.9	0.96	10.8	2.36	3.1	1.67	3.9	1.67	12.5	1.18	R,ITL

[1]Cont-6 and Cont-12 = 6 and 12 wethers per pen and feeder with continuous access, respectively; Day-2 and Day-4 = 2 and 4 wethers per feeder with 8 h/d access during daytime; Night-4 and Night-8 = 4 and 8 wethers per feeder with 16 h/d access at night.

[2]RFI = residual feed intake, HR = heart rate, HE = heat energy.

[3]R and r = restricted feeder access (mean of Cont-6 and Cont-12 vs. the mean of Day-2, Day-4, Night-4, and Night-8; $P < 0.05$ and 0.10, respectively); L and l = maximum potential feeder occupancy per animal (mean of Cont-12, Day-4, and Night-8 vs. Cont-6, Day-2, and Night-4; $P < 0.05$ and 0.10, respectively); T and t = time of restricted feeder access (mean of Day-2 and Day-4 vs. mean of Night-4 and Night-8; ; $P < 0.05$ and 0.10, respectively); IRL = interaction between restricted feeder access and maximum potential feeder occupancy per animal ($P < 0.05$); ITL and itl = interaction between time of restricted feeder access and maximum potential feeder occupancy per animal ($P < 0.05$ and 0.10, respectively).

[4]h refers observation hours (0700 to 1900 h for Cont-6 and Cont-12, 0800 to 1600 h for Day-2 and Day-4, and 0700 to 0800 h and 1600 to 1900 h for Night-4 and Night-8).

The Bartlett test can be determined with GenStat with 'Test for Homogeneity' of 'Statistical Tests' under 'Stats.' The P values for GLM analysis and the Welch test were similar (0.719 and 0.732, respectively). The P values for differences in variation within FRG were 0.075 and 0.473 for Bartlett and Levene tests, respectively.

Variation within treatment × FRG units can be tested with data averaged by treatment and FRG, such as with SAS statements noted below.

```
proc sort data = table30; by treatment frg;
proc means noprint; var variable; by treatment frg;
output out = table30avg mean = variable;

proc glm;
classes treatment;
model variable = treatment;
means treatment / hovtest = bartlett;
means treatment / hovtest = levene welch;
```

Variation within treatments was similar for Bartlett, Levene, and Welch tests (0.372, 0.384, and 0.909, respectively). Hence, based on these findings with this simulated data set, homogeneous variation could be assumed.

Correlation

The coefficient of correlation (**r**) is a very useful measure for most fields of science. It often provides an initial assessment of specific aspects that should receive greatest and(or) future attention. But, correlation coefficients are rarely if ever the only statistical test of an experiment, at least with livestock, because coefficients of correlation measure the strength of the linear relationship between two variables but provide no indication of cause and effect (Kaps and Lamberson, 2004). In fact, there may be no direct relationship, with two variables simply being influenced positively or negatively by another factor. The proportion or percentage of variability in one factor explained by another, or coefficient of determination ($\mathbf{R^2}$), is equal to r^2.

Simple Linear Regression

Simple linear regression is similar to correlation analysis, although a decision is made concerning which variable is dependent upon another. An example of a common use of simple linear regression was given earlier in Chapter 5 - Experiment Implementation in the 'ADG by Regression' section. This example utilized SAS, although similar procedures are available with other statistical packages.

A consideration for simple linear regression is whether to use a no-intercept model, in which y (the dependent or predicted variable) equals 0 when x (the independent or predictor variable) is 0. It is generally assumed that a no-intercept model should not be used if x is never equal (or at least close) to 0. An example for which it would be inappropriate to use a no-

intercept model is regression of the percentage of digestible CP (**DCP**) against the percentage of total CP in the diet on a dry matter (**DM**) basis as shown in Figure 5.

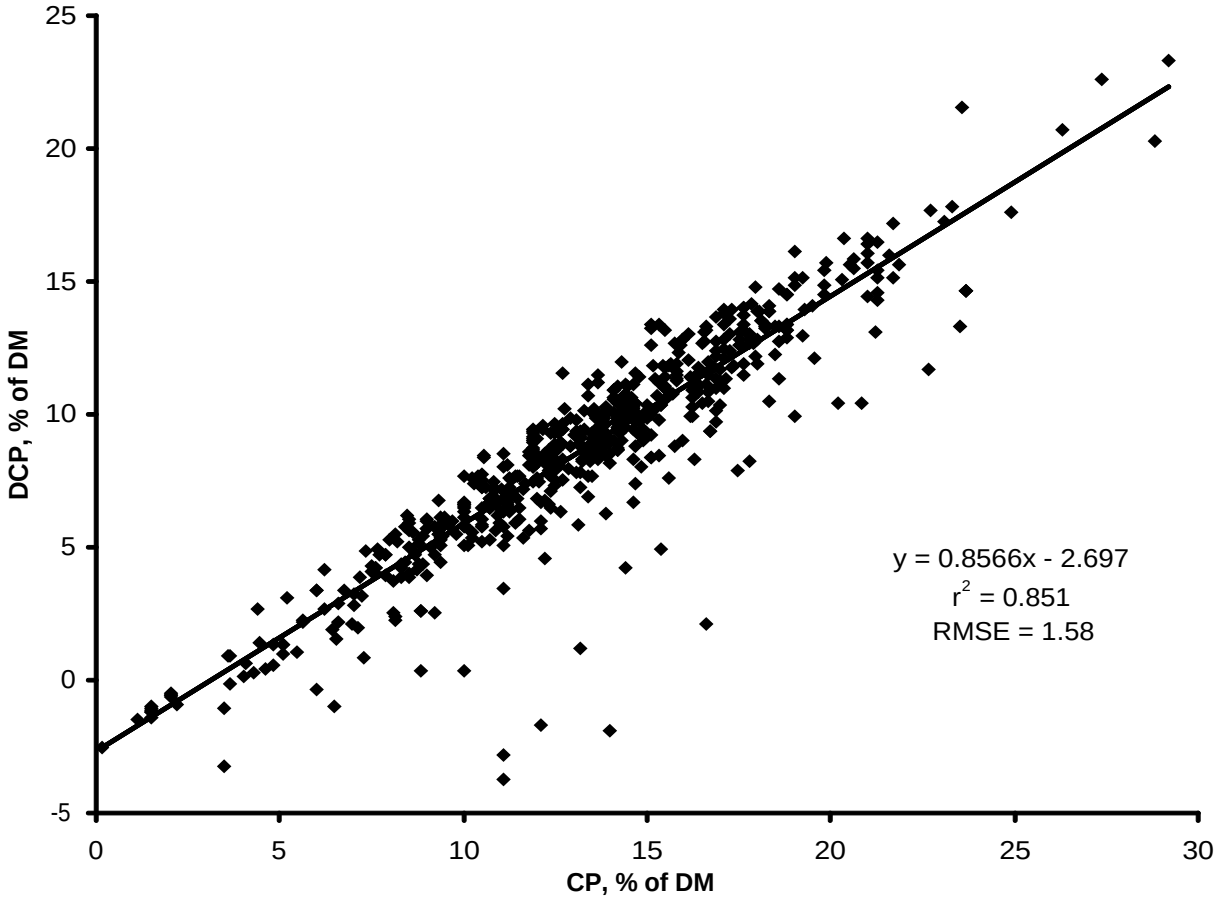


Figure 5. Regression of DCP on dietary CP concentration; all data, n = 622; RMSE = root mean square error.

The study of Nsahlai et al. (2004) provides an example of when it could be considered appropriate to use a no-intercept model. In this study treatment mean observations from the literature were used to study the dietary metabolizable energy (**ME**) requirement for milk production ($\mathbf{ME_{l\text{-}d}}$) by goats. Assumptions were used to partition $ME_{l\text{-}d}$ and fat-corrected milk, or milk energy, derived from $ME_{l\text{-}d}$ ($\mathbf{FCM_d}$). Thus, dietary ME used for maintenance ($\mathbf{ME_m}$) and that used for tissue gain were estimated, as well as milk energy arising from mobilized tissue. Regressions were also conducted with and without correction for energy lost from excess nitrogen (**N**) excretion. A moderate number of observations had very low $ME_{l\text{-}d}$ and FCM_d and, in fact, a few estimates of $ME_{l\text{-}d}$ were negative. Intercepts of regressions of $ME_{l\text{-}d}$ against FCM_d were very small but significantly different from 0. However, for several reasons a no-intercept model was used, as shown in Figure 6: 1) small magnitude of the intercepts, 2) numerous

assumptions employed, 3) the fact that physiologically FCM_d should be 0 with 0 $ME_{l\text{-}d}$, 4) the relatively small impact on the magnitude of the regression coefficient, and 5) the slight decrease in the regression coefficient SE.

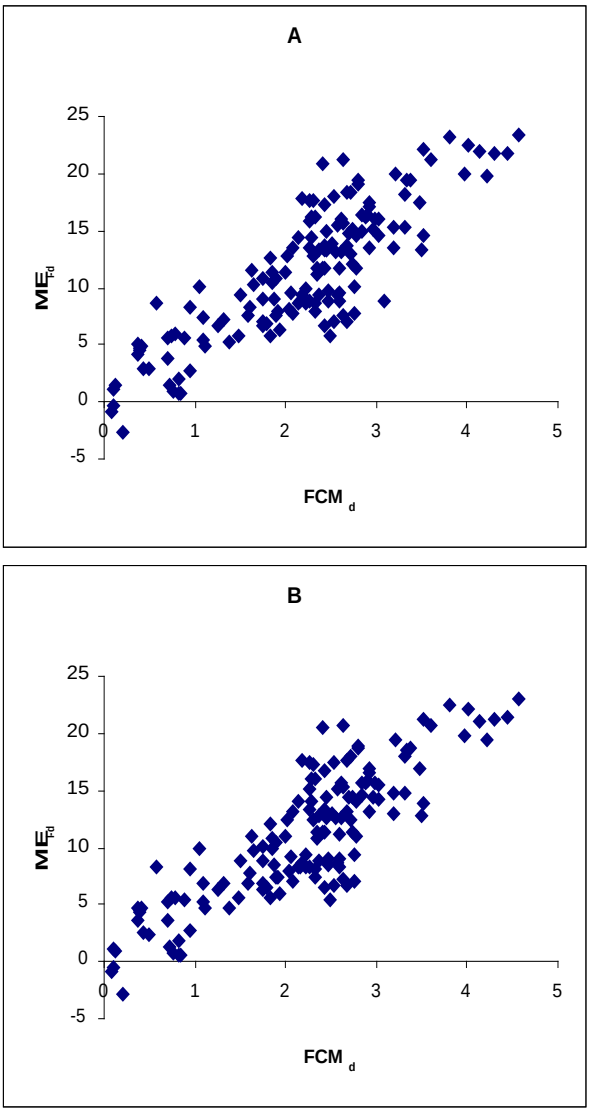


Figure 6. Relationships between 4% fat-corrected milk (FCM; kg/d) and $ME_{l\text{-}d}$ (MJ/d) without (A) and with (B) correction for loss of energy in excretion of excess N.

An example of SAS statements to specify a no-intercept model is below.

```
proc reg;
model variable1 = variable2 / noint;
```

In some instances, such as regressions with treatment mean observations from the literature, it is desirable to weight by the number of experimental units contributing to the mean (St-Pierre, 2001). Example SAS statements to do so are below.

```
proc reg;
weight n;
model variable1 = variable2;
```

Multiple Regression

Multiple regressions are used to assess the relationship between a dependent variable and two or more independent factors. For an example, Luo et al. (2004) first used analysis of covariance (Snedecor and Cochran, 1978) to determine differences among intercepts and slopes of simple linear regression equations for different goat biotypes. SAS statements similar to those used in the study of Luo et al. (2004) for the relationship between ME intake (**MEI**) and ADG of different biotypes or breeds of goats are below.

```
proc glm;
classes breed;
model mei = breed adg breed*adg / solution;
```

The output consists of the intercept and slope for the last or reference breed listed unless a dummy variable is included. Probability values are given for differences between that intercept and slope and 0, which obviously would be less than 0.05. Differences in intercepts and slopes between other breeds and the reference are given along with corresponding P values. If P values are nonsignificant, then breed may be omitted from the model and one equation can be used for all breeds and observations. If three or more breeds are used, it is possible that some differ in the intercept but not slope, and vice versa. After the initial regression with each breed individually, breeds can be grouped and differences examined with dummy variables in a systematic, sequential approach. An example of this process appears in Figure 7, with two meat goat breeds (Boer and indigenous as biotypes 1 and 3, respectively) differing from a third (dairy as biotype 2) in ME_m and two of the biotypes (dairy and Boer) differing from the other (indigenous) in the ME requirement for ADG. Examples of simple SAS statements to generate and employ dummy variables are below.

```
if biotype = 1 then d1 = '1';
if biotype = 2 then d1 = '2';
if biotype = 3 then d1 = '1';
if biotype = 1 then d2 = '2';
if biotype = 2 then d2 = '2';
if biotype = 3 then d2 = '1';

proc glm;
classes d1 d2;
model variable1 = d1 variable2 d2*variable2 / solution;
```

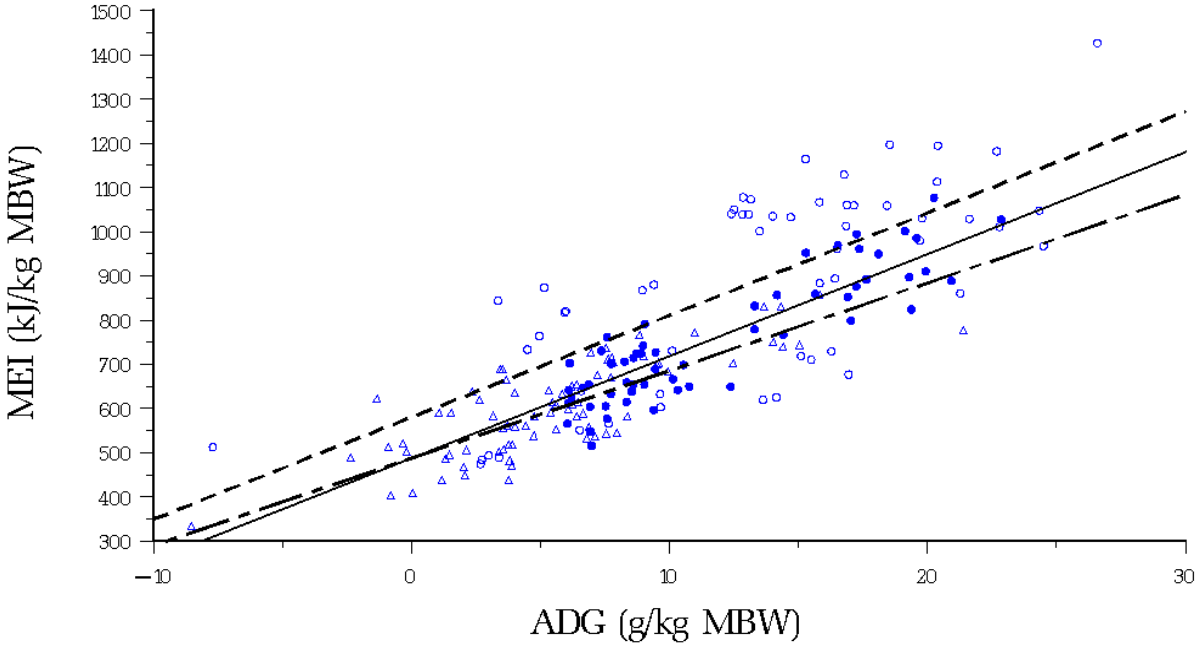


Figure 7. The relationship between MEI and ADG of growing goats. Circles (○), dots (●), and triangles (△) are observations for growing dairy, meat (≥ 50% Boer) and indigenous goats, respectively. The dotted line is for dairy goats, the solid line is for meat goats, and the mixed line is for indigenous goats. The multiple regression equation is: MEI = 488.5 (SE = 14.41) + (91.5 (SE = 18.69) × D1) + (23.09 (SE = 1.24) × ADG) – (3.28 (SE = 1.98) × D2 × ADG) [n = 189; R^2 = 0.74]. D1 = 0 and D2 = 0 for meat goats; D1 = 1 and D2 = 0 for dairy goats; and D1 = 0 and D2 = 1 for indigenous goats. MBW = kg $BW^{0.75}$. Source: Luo et al. (2004).

A simple method to determine the proportion of total variability explained by each independent variable is with 'standardized estimates,' with an example of relevant SAS statements below.

```
proc reg;
model variable1 = variable2 variable3 / stb;
```

The two standardized estimates are summed, and proportions of variation attributable to the independent variables are obtained by dividing their estimates by the total.

Polynomial Regression

Polynomial regressions differ from simple linear and multiple regressions in that one or more curvilinear relationships exist. For example, as an animal grows, feed intake generally rises fairly rapidly relative to BW, followed by a decreasing rate of increase and, eventually, constant intake assuming a continuous adequate plane of nutrition. However, changes in factors such as the nature of the diet can impact this pattern. Nonetheless, in simplest terms such a curvilinear relationship can be evaluated via SAS statements like those shown below, with BW2 equal to BW × BW.

```
proc glm;
model feedintake = bw bw2 / solution;
"or" model feedintake = BW BW*BW / solution;
```

As mentioned earlier, fixed effects such as breed can be included in models as noted below.

```
proc glm;
classes breed;
model feedintake = breed bw bw2 breed*bw breed*bw2;
```

It is genberally agreed that sequential sums of squares (**SS**) should be used when evaluating model development for polynomial regression, that is, determining the order of the polynomial. Sequential SS are calculated for each independent variable in the sequence that they appear in the model. For example, a cubic model could be of interest when investigating effects of time after ingestion of different levels of a feed additive on disappearance in the digestive tract. The model would include level of the additive as the dependent variable and linear, quadratic, and cubic effects of time as independent variables. The sequential SS would be SS(linear | intercept), SS(quadratic | intercept, linear), and SS(cubic | intercept, linear, quadratic). Using the last SS as an example, this sequence of calculation reads the SS for the cubic effect given that SS for intercept, linear, and quadratic effects have already been calculated. This is the additional SS attributable to the cubic effect. If the cubic effect is nonsignificant and the quadratic effect is significant, then the resulting model would include the intercept and linear and quadratic effects. Moreover, if linear and quadratic effects are nonsignificant and the cubic effect is significant, then the model would include linear, quadratic, and cubic effects. This approach using sequential SS ensures that the lower order terms are always included in the model.

Nonlinear Regression

Nonlinear regressions are beyond the scope of this publication. Sources such as Kaps and Lamberson (2004) can be consulted in this regard. Suffice it to say that nonlinear regressions are very important in livestock research. For example, grafted polynomial analyses have been proposed to model many biological functions (Fuller, 1960). Grafted polynomials are segmented polynomials that are continuous and have a continuous first derivative(s) at the join point, at which the nature of the function changes. Grafted polynomials are only nonlinear if the join points are assumed to be unknown. An example is the study of Asmare et al. (2007) that employed grafted polynomial analysis to determine when urea N infused into a jugular vein had equilibrated with body water of goats to predict body composition via the urea space technique previously used with sheep and cattle, as shown in Figure 8.

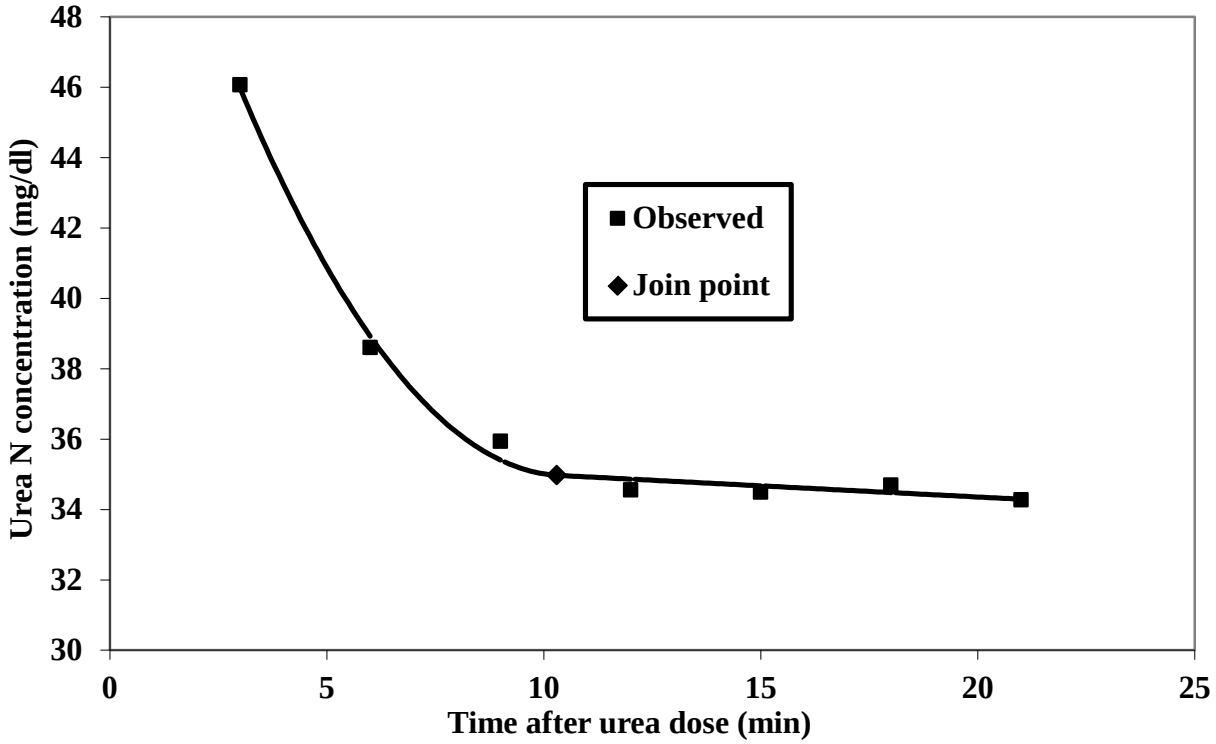


Figure 8. Fit of a quadratic-linear grafted polynomial model for one example observation of Asmare et al. (2007).

Mixed Effects Models

Mixed effects models are appropriate when some effects are fixed and others are random (Kaps and Lamberson, 2004). One advantage of mixed effects models of SAS compared with SAS GLM, in addition to providing correct prediction of random effects and estimates of SE (Kaps and Lamberson, 2004), is that the most appropriate covariance structure for random factors can be used. This decision is often based on the Schwartz Bayesian Criterion (BIC), Akaike's Information Criterion (AIC), and(or) the Corrected Akaike's Information Criterion (AICC). Common structures that were evaluated by Goetsch et al. (2012) were Ante-dependence ([ANTE(1)], Autoregressive ([AR(1)], Compound Symmetry (CS), Heterogeneous Compound Symmetry (CSH), Huynh-Feldt (HF), Unstructured (UN), and Variance Components (VC). An example of the specification of a particular covariance structure in SAS is shown below.

```
proc mixed covtest cl;
classes pen breed animalgroup;
model variablename = pen breed pen*breed;
random animalgroup breed(animalgroup) / type = cs;
lsmeans pen breed / pdiff;
```

Evaluation of Regression Equations for Prediction

As alluded to in previous sections, regression analyses are often used to develop methods of prediction. Prediction equations should be evaluated with one or more independent data sets rather than the one used for development. Evaluation can be also performed by regressing observed against predicted values or residuals (St-Pierre, 2003), with examples shown below in Figure 9 from Nsahlai et al. (2004) for residuals and later in Figure 17 for observed values from Beker et al. (2009). If the former observed value approach is used, lack of bias is indicated by an intercept not different from 0 and slope not different from 1. Examples of other studies cited elsewhere in the publication using such methods are Luo et al. (2004), Moore et al. (2004), and Beker et al. (2010).

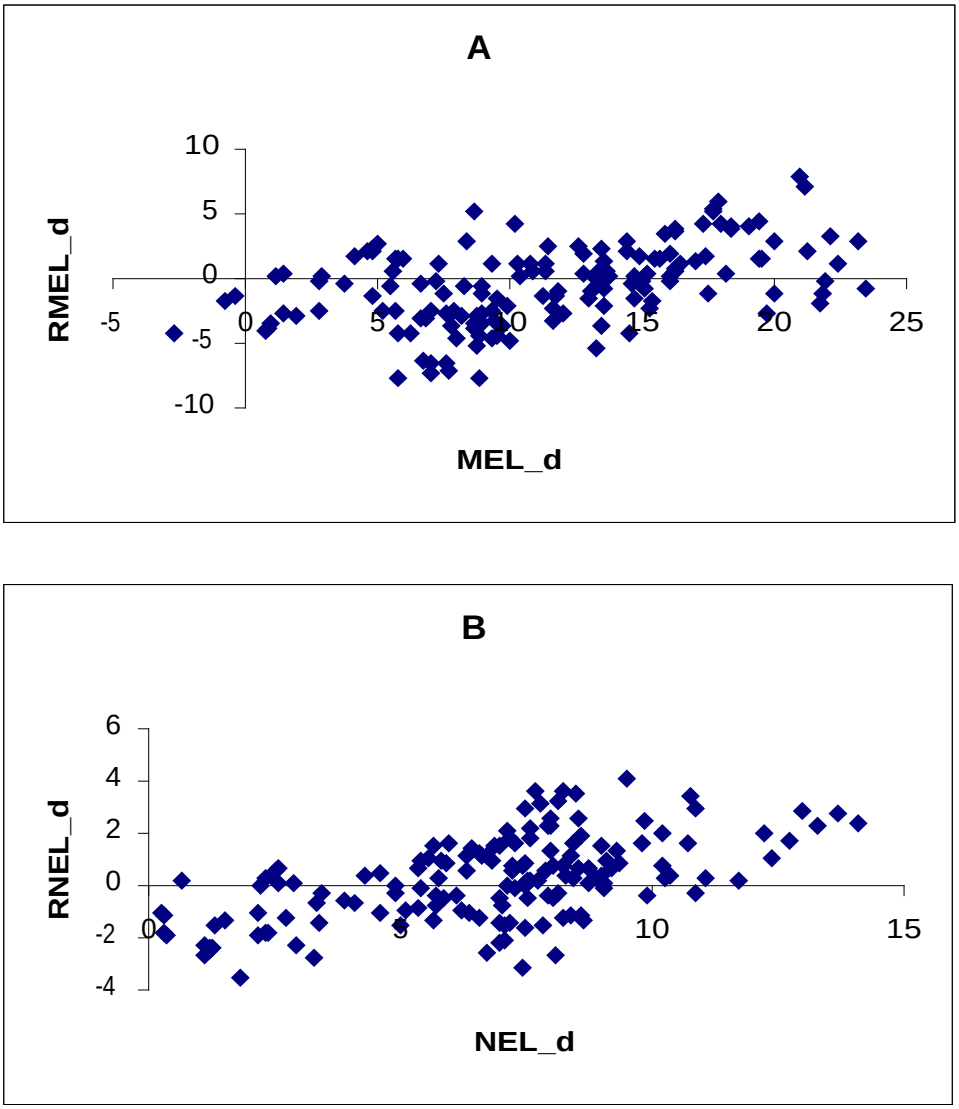


Figure 9. Relationship between (A) dietary ME for lactation (MEL_d; MJ/day) and residual MEL_d (RMEL_d; MJ/day) and (B) dietary net energy for lactation between (NEL_d; MJ/day) and and residual (NEL_d; MJ/day) without correcting for excess urinary N.

Covariates

Covariates are commonly employed in livestock research, frequently to adjust for variability among experimental units in conditions not adequately addressed in the allocation to treatments. For example, it is normal for animals to be assigned to groups and treatments for similar BW and variability in BW, as BW can be readily measured. The allocation may also consider one or more other factors, an example being milk yield in lactation studies, but there are limits to the number that can be used. Furthermore, in some cases it may not be clear if and(or) how initial values will relate to later measurements and(or) the determination of initial values might not occur until after the experiment (e.g., blood metabolite concentrations).

It is conventional to exclude a covariate, such as initial BW, if the effect is nonsignificant. This is usually the case if the number of experimental units is high, variability in initial BW is low to moderate, and the initial animal allocation was appropriate. Alternatively, high variability can be addressed by blocking as noted before.

An example situation in which inclusion of a covariate such as initial BW is avoided or at least employed and interpreted carefully is with breeds that naturally differ in BW, such as Boer and Spanish goats. In this case, initial BW and breed are confounded, and inclusion of initial BW as a covariate adjusts BW of all animals to one mean value irrespective of breed. Greater ADG naturally would be expected for the larger breed, depending of course on adequacy of the nutritional plane. Initial BW can be used as a covariate to determine if it is responsible for a difference in ADG, or ADG could be scaled by initial BW or mature size without covariate analysis. But, when addressing other variables such as slaughter and carcass weights that are influenced both by conditions before and during an experiment, in order for appropriate consideration of all responsible factors, both initial BW and unadjusted ADG and BW should be presented as such.

The 2012 guidelines of the Journal of Dairy Science (ADSA, 2012) list some recommendations regarding covariate use, with a relevant quote below.

- "Most statistical procedures are based on the assumption that experimental units have been assigned to treatments at random. If animals are stratified by ancestry or weight or if some other initial measurement should be accounted for, the model should include a blocking factor, or the initial measurement should be included as a covariate."

There certainly are experiments in which it is possible to adequately allocate animals to treatments simply randomly. But often this is not the case, with animals first ranked in order by a variable such as initial BW and then randomly allocated within subgroups, with the number of animals per subgroup equal to the number of animal groups or treatments. Once all animals are allocated, then group and treatment means and SE or SD are examined, and some animals may be switched to achieve more uniform means and variation. In such instances, the ranking and grouping by BW is a facet of the allocation rather than true blocking, unless there is some reason to suspect that treatment effects would vary with BW. If so, then the interaction between treatment and BW should be considered, which would probably be most appropriate with BW

treated as a continuous rather than a discrete variable that could also allow testing of polynomial effects (e.g., treatment × BW and treatment × BW^2).

Means Separation

In order to address different methods of means separation, it is necessary to understand Type I and II errors.

- Type I – The hypothesis that there is not a treatment difference is rejected (i.e., the test indicates that at least one difference exists among treatment means, but actually there are no differences). Type I errors are also known as α.

- Type II – There is a treatment difference, but the test performed indicates that there is not a difference. Type II errors are also known as β.

Multiple range tests (**MRT**) such as Duncan's are more conservative than the lsd method, but they detect fewer real differences (Snedecor and Cochran, 1978). Based on the definitions above, this sentence can be rewritten as: "The lsd method has more Type I but fewer Type II errors than MRT." For both lsd and Tukey tests, a significant *F*-test must precede examination of differences among specific treatment means to minimize the probability of Type I errors. The lsd method also has more Type I but fewer Type II errors than the Tukey test (Kaps and Lamberson, 2004).

Only one method of means separation should be employed. For example, it is almost never acceptable to separate means via orthogonal contrasts and another method such as lsd or a MRT. Some journals have fairly rigid guidelines and authors must provide adequate justification if an alternative method is used. For example, a statement of the Journal of Dairy Science 2012 guidelines (ADSA, 2012) is given below.

- "Contrasts (preferably orthogonal) are used to answer specific questions for which the experiment was designed; they should form the basis for comparing treatment means. Multiple-range tests are not appropriate when treatments are orthogonally arranged. Fixed-range, pairwise, multiple comparison tests should be used only to compare means of treatments that are unstructured or not related."

Orthogonal contrasts are preferred and most appropriate in many situations, examples of which are given later in the Peer-Reviewed Journal Article section of Chapter 10 - Dissemination. Essentially they allow partitioning of variability due to treatment (e.g., five treatments with four df) into that attributable to 'sub-treatments' (e.g., four). But such contrasts do not entail a comparison of all treatment means with one another, which does occur with methods such as lsd with a protected *F*-test and MRT. An example of SAS statements for orthogonal contrasts is at the Appendix 1 page 166 for data described in Table 64 of Chapter 10 – Dissemination. Immediately preceding those SAS statements are ones for non-orthogonal contrasts at Appendix 1 page 164-165 for data described in Table 63 of Chapter 10. Moreover, the 'estimate' SAS statement can be used to determine the difference between means or groupings of means being contrasted, along with the SE of the difference, which is shown on Appendix 1 page 166.

As noted elsewhere, students are sometimes taught that statistical analyses and treatment comparisons should be pre-planned, as recommended by the ASAS Writing Workshop (Galyean and Lewis, 2013). Certainly statistical analyses should be carefully considered when an experiment is planned. However, in many instances data may be analyzed differently than initially expected, for example when a journal insists on its preferred method of means separation. It is, nonetheless, fairly common for more than one method of means separation to be evaluated after an experiment to select the method facilitating the clearest presentation of results and data interpretation. For example, with an experiment having treatments of 0, 2.5, 5.0, 7.5, and 10.0% of a feed additive, contrasts for linear, quadratic, and possibly cubic and quartic effects of additive level (including the 0% level) would not allow for a direct test of the different between 0 and 10% levels, which might be of interest. Moreover, with such treatments another factor to be considered and justified is how the 0% level is handled. One option is for a contrast of the 0% diet vs. the mean of the other four treatments and then contrasts for effects of level (i.e., linear, quadratic, and perhaps cubic) with only the additive-containing diets (i.e., 2.5, 5.0, 7.5, and 10%).

Parsad (2013) addressed the issue of planned and unplanned treatment comparisons, with the latter termed 'data snooping.' Other comments of Parsad (2013) regarding different methods of means separation are given below.

- The most appropriate method of means separation depends on factors such as the number and specific contrasts of interest and desirability of comparing individual vs. groups of treatments.

- Means separation by lsd, Duncan's MRT, and the Tukey test can be used for both planned and unplanned comparisons.

    □ Conversely, the Bonferroni method should only be used for pre-planned comparisons.

    □ When the number of confidence intervals or contrasts of groups is high, resulting in wide simultaneous confidence intervals, Scheffe or Tukey methods are more appropriate than Bonferroni.

- The Tukey method can be used for all potential treatment comparisons, with adjustment for multiple testing.

- The Dunnett method is appropriate for pre-planned comparisons of treatments of interest to one control treatment.

- The Hsu method is appropriate for multiple comparisons with the 'best' treatment, which is identified after data collection.

For the lsd method of SAS GLM and MIXED procedures, P values for differences between treatments are examined to determine placement of superscripts or letters with means to denote significant differences in tables and figures. Examples are given for both procedures in

the tables below since the format of P values in SAS Output files differs slightly. Table 20 containing percentage of protein in milk is from Table 65 of Chapter 10 - Dissemination.

Table 20
Analysis of the percentage of milk protein by the SAS GLM procedure for a study investigating effects of dietary concentrate level on ADG, DM intake, change in body condition score, and milk composition by Alpine does at 1 to 2, 3 to 4, and 5 to 6 months of lactation (Table 65 of Chapter 10 – Dissemination)

Source of variation	df	Type III SS	MS	P > *F*
Diet	1	0.021	0.021	0.505
Phase	2	1.029	0.514	< 0.001[1]
Diet × phase	2	0.407	0.203	0.021

[1]P = 0.0002.

The significant interaction indicates that interaction means should be evaluated; Table 21 presents P values for differences between these means.

Table 21
P values from SAS GLM analysis of interaction means for percentage of milk protein in a study investigating effects of dietary concentrate level on ADG, DM intake, change in body condition score, and milk composition by Alpine does at 1 to 2, 3 to 4, and 5 to 6 months of lactation (Table 65 of Chapter 10 – Dissemination)

	Mean number[1]					
Mean number	1 (C-1)	2 (C-2)	3 (C-3)	4 (F-1)	5 (F-2)	6 (F-3)
1 (C-1)		0.0010	0.0117	0.0494	<0.0001	0.4801
2 (C-2)	0.0010		0.3433	0.1204	0.3847	0.0064
3 (C-3)	0.0117	0.3433		0.5299	0.0490	0.0583
4 (F-1)	0.0494	0.1204	0.5299		0.0116	0.1924
5 (F-2)	<0.0001	0.3847	0.0490	0.0116		0.0004
6 (F-3)	0.4801	0.0064	0.0583	0.1924	0.0004	

[1]C = concentrate; F = forage; 1 = 1 to 2 months; 2 = 3 to 4 months; 3 = 5 to 6 months.

The most common way to determine superscripts or letters from P values is to first rank the means from least to greatest or vice versa, with the former method used below. Then P values for adjacent means are viewed, starting with the two lowest. If the value is greater than that chosen as significant, most commonly 0.05, a line is placed by the two similar means. Thereafter, the same assessment is performed for the next greatest mean below these. If a difference exists, then the line is discontinued and the P value between the next adjacement means is inspected. Table 22 provides an example of this based on P values in Table 21.

Table 22
Example of determining superscript or letter positions to denote differences between interaction means for the study described in the preceding tables and investigating effects of dietary concentrate level on ADG, dry matter intake, change in body condition score, and milk composition by Alpine does at 1 to 2, 3 to 4, and 5 to 6 months of lactation (Table 65 of Chapter 10 – Dissemination)

Mean number	Diet[1]	Phase[2]	Mean (%)	Lines and letters to denote differences			
5	F	2	2.25[a]	a			
2	C	2	2.39[ab]		b		
3	C	3	2.51[bc]			c	
6	F	1	2.59[bc]				
4	F	3	2.75[cd]				d
1	C	1	2.84[d]				

[1]C = concentrate; F = forage.
[2]1 = 1 to 2 months; 2 = 3 to 4 months; 3 = 5 to 6 months.

Tables 23, 24, and 25 provide a similar example using the SAS MIXED procedure for analyzing small intestinal disappearance of essential amino acids in a study consisting of two simultaneous 6 × 6 Latin squares, with two dietary levels of CP (13 and 19%) and six mixtures of feedstuffs high in CP (A, B, C, D, E, and F).

Table 23
Analysis of small intestinal essential amino acid disappearance by the SAS MIXED procedure in a study consisting of two simultaneous 6 × 6 Latin squares, with two dietary levels of CP (13 and 19%) and six mixtures of feedstuffs high in CP (A, B, C, D, E, and F)

Source of variation	df	P > *F*
CP level	1	0.005
Period	5	0.283
CP mixture	5	0.019
CP level × mixture	5	0.094

With the nonsignificant interaction, main effect means can be evaluated, as shown below for CP mixtures.

Table 24
P values from an analysis by the SAS MIXED procedure for differences between main effect means of small intestinal disappearance in a study with two simultaneous 6 × 6 Latin squares, two dietary levels of CP (13 and 19%) and six mixtures of feedstuffs high in CP (A, B, C, D, E, and F)

CP mixture		
First	Second	P > *F*
A	B	0.0007
A	C	0.0151
A	D	0.0142
A	E	0.1099
A	F	0.0165
B	C	0.2628
B	D	0.2739
B	E	0.0484
B	F	0.2481
C	D	0.9791
C	E	0.3754
C	F	0.9713
D	E	0.3616
D	F	0.9504
E	F	0.3948

Table 25
Example of determining superscript or letter positions to denote differences between main effect means of small intestinal essential amino acid disappearance in a study consisting of two simultaneous 6 × 6 Latin squares, with two dietary levels of CP (13 and 19%) and six mixtures of feedstuffs high in CP (A, B, C, D, E, and F)

Mean number	CP mixture	Mean (%)	Lines and letters to denote differences		
1	A	20.5[a]	a		
5	E	28.7[ab]		b	
6	F	33.1[bc]			c
3	C	33.3[bc]			
4	D	33.4[bc]			
2	B	39.0[c]			

In experiments with different treatment levels, such as the aforementioned diets with 0.0, 2.5, 5.0, 7.5, and 10.0% of an additive, the treatments are discrete and should be treated as such. Nonetheless, in some cases authors have analyzed data with level or perhaps dietary intake (mass) as a continuous variable or variables (e.g., linear and quadratic effects). This may be allowable as an additional analysis if there is interest, for example, in predicting effects of additive levels between those employed (e.g., 4 or 6%). But predictions should not extend beyond the bounds of the levels. Another consideration with such treatments and use of contrasts to address level effects is that it is not possible to discern significant differences

between any two treatments. That is, the presentation of results must be confined to phrases such as ones below.

- Variable 1 increased linearly ($P < 0.05$) as dietary level of the additive increased.
- Variable 1 decreased linearly ($P < 0.05$) as dietary level of the additive increased.
- Variable 1 increased at a decreasing rate (linear and quadratic; $P < 0.05$) as dietary level of the additive increased.
- Variable 1 increased at an increasing rate (linear and quadratic; $P < 0.05$) as dietary level of the additive increased.
- Variable 1 decreased at a decreasing rate (linear and quadratic; $P < 0.05$) as dietary level of the additive increased.
- Variable 1 decreased at an increasing rate (linear and quadratic; $P < 0.05$) as dietary level of the additive increased.
- Variable 1 increased and then decreased (quadratic; $P < 0.05$) as dietary level of the additive increased.
- Variable 1 decreased and then increased (quadratic; $P < 0.05$) as dietary level of the additive increased.

Sometimes treatment levels are not equally spaced, in which case it is necessary to generate appropriate polynomials to assess linear, quadratic, and cubic effects (and beyond). This can be done with the IML procedure of SAS. Editor statements are below and the Output is in Table 26 for an experiment in which one type of forage was fed daily or on the second, fourth, or eighth day.

```
proc iml;
x = {1 2 4 8};
xp = orpol (x,3);
print xp;
```

Table 26
Example SAS output file for determination of orthogonal polynomials with levels of 1, 2, 4, and 8

0.5	-0.512878	0.5296271	-0.454369
0.5	-0.326377	-0.105925	0.7951466
0.5	0.0466252	-0.767959	-0.397573
0.5	0.7926291	0.3442576	0.0567962

Thus, the appropriate SAS statements for contrasts to assess linear, quadratic, and cubic effects appear below.

```
contrast 'lin' treatment -0.512878 -0.326377 0.0466252 0.7926291;
contrast 'qua' treatment 0.5296271 -0.105925 -0.767959 0.3442576;
contrast 'cub' treatment -0.454369 0.7951466 -0.397573 0.0567962;
```

Another example is shown in Table 27 for an experiment with treatment levels of 0, 1, 5, 10, and 20.

```
proc iml;
x = {0 1 5 10 20};
xp = orpol (x,4);
print xp;
```

Table 27
Example SAS output file for determination of orthogonal polynomials with levels of 0, 1, 5, 10, and 20

0.4472136	-0.440798	0.4226911	-0.389441	0.5247522
0.4472136	-0.379576	0.2159914	0.1438822	-0.767182
0.4472136	-0.134688	-0.393349	0.7104586	0.3498348
0.4472136	0.1714214	-0.665742	-0.560182	-0.116612
0.4472136	0.7836408	0.4204089	0.095282	0.0092062

```
contrast 'lin' treatment -0.440798 -0.379576 -0.134688 0.1714214 0.7836408;
contrast 'qua' treatment 0.4226911 0.2159914 -0.393349 -0.665742 0.4204089;
contrast 'cub' treatment -0.389441 0.1438822 0.7104586 -0.560182 0.095282;
contrast 'qrt' treatment 0.5247522 -0.767182 0.3498348 -0.116612 0.0092062;
```

Chi-Square and GENMOD and GLIMMIX of SAS

Chi-Square

Some data are categorical, e.g., many reproduction variables. An example is litter size, commonly 1, 2, or 3 in small ruminants (i.e., discrete numbers). Appendix 3 Table 160 has a simulated data set consisting of 160 observations, two treatments, two groups per treatment, 40 animals per group, and various ages. Litter size was limited to 1 or 2, and 10 females did not conceive. First, a simple overall view of the results can be achieved with the following SAS statements for a Chi-square analysis considering litter size only.

```
proc freq;
tables littersize / chisq fisher;
```

The null hypothesis of this test is simply that the probability of a litter size of 1 is equal to that of a litter size of 2. Frequencies were 98 and 52 for litter sizes 1 and 2, respectively. The P value of 0.0002 is smaller than the preselected value (e.g., 0.05), indicating the null hypothesis should be rejected and the probability of a litter size of 1 is greater than of a litter size of 2.

The test above does not consider treatment, group, or animal age. A next step might be to test for differences between treatments and among groups and groups within treatments with the following SAS statements.

```
proc freq;
tables littersize*treatment littersize*group littersize*treatment*group / chisq fisher;
```

The first null hypothesis is that frequencies of litter sizes for one treatment are independent of those for the other treatment, with independence declared if the P value is greater than a predetermined value (i.e., 0.05), and the null hypothesis for the second term of "littersize*group" would be comparably structured. Chi-square P values were both < 0.001, indicating dependency of litter sizes of one treatment on those of the other and at least one group on those of one or more other groups. Similarly, Chi-square P values for "littersize*treatment*group" were 0.0011 and 0.0269 with controlling for litter size of 1 and 2, respectively.

A limitation exists with use of Chi-square analysis in scenarios such as this, in that the most appropriate error term is group within treatment. In accordance, Rutledge and Sunsett (1982) stated that in some cases Chi-square analysis has been used excessively, without adequate attention to such considerations as well as interactions. Nonetheless, further Chi-square analyses can be conducted to determine for which groups differences in litter size exist as well as for which groups treatment differences in litter size were present. The following SAS statements could be used in this regard.

```
proc sort; by group;

proc freq;
tables littersize / chisq fisher;
by group;

proc freq;
tables littersize*treatment / chisq fisher;
by group;
```

Chi-square P values for the first frequency procedure were <0.0001, 0.5271, 1.0000, and 0.0016 for groups 1, 2, 3, and 4, respectively. Hence, there were differences in frequencies of litter size for groups 1 and 4 but not for groups 2 and 3 (i.e., litter size 1 was independent of litter size 2 for groups 2 and 3 but not groups 1 and 4).

Chi-square P values for the second frequency procedure were 0.9113, <0.0001, <0.0001, and 0.4652 for littersize*treatment with groups 1, 2, 3, and 4, respectively. Hence, litter size for the treatments was independent of one another in groups 1 and 4 but dependent in groups 2 and 3. That these treatment differences were not consistent among replicate groups suggests that data should be scrutinized as to why inconsistencies occurred and that perhaps a blocking analysis should be considered.

SAS GENMOD

The GENMOD procedure of SAS might be used with this example data set, but group would be termed a repeated measure. The first set of SAS statements below is for inclusion of an intercept and the second set is for a no-intercept model. Results are given in Table 28.

```
proc genmod;
classes treatment group;
```

```
model littersize = treatment age treatment*age / d = poisson type3;
repeated subject = group(treatment) / type = ech modelse covb corrw;

proc genmod;
classes treatment group;
model littersize = treatment age treatment*age / d = poisson type3 noint;
repeated subject = group(treatment) / type = ech modelse covb corrw;
```

Even though litter size is categorical, for comparison purposes the SAS GLM procedure was used with litter size considered continuous, with the following statements and results are in Table 28. The comparison of results with GENMOD and GLM analyses shows a considerable effect of classifying group within treatment as a repeated measure with the former procedure and considering litter size to be continuous with the latter. A more appropriate method of analysis with the General Linear Mixed Models procedure (**GLIMMIX**) of SAS is addressed immediately below as well as in a number of scenarios in Chapter 9 – On-Farm Research Examples.

```
proc glm;
classes treatment group;
model littersize = treatment group(treatment) age treatment*age;
test h = treatment e = group(treatment);
```

Table 28
P values for analysis of litter size data by SAS GENMOD and GLM procedures[1]

	P value		
Procedure/model	Treatment	Age	Treatment × age
GENMOD			
With intercept	0.142	0.783	0.727
No intercept	0.170	0.784	0.726
GLM	0.635	0.721	0.818

[1]Data set given in Appendix 3 Table 160.

SAS GLIMMIX

Categorical data can be analyzed with the SAS GLIMMIX procedure. With GLIMMIX, totals for each animal group or experimental unit are entered as such unless it is simply a 'yes-no' variable. For litter size (shown in Appendix 3 Table 161), numbers of females per group with a litter size of 1 and 2 are entered (LSone and LStwo, respectively), along with the total number giving birth (Total). Moreover, if the potential effect of age and its interaction with treatment are of interest, then the average of age of animals in the group should be included. If variability in age is high or differences exist among groups, then the SD of age might be included as well.

Without considering age, the following SAS statements can be used.

```
proc glimmix;
class treatment;
model lsone / total = treatment;
lsmeans treatment / odds or cl ilink diff;
```

Statements are not included for litter size of 2 because the treatment P value is the same as for litter size of 1 with values limited to 1 and 2. Some of the results of this analysis are below.

- Treatment P value = 0.102
- Means of 0.811 and 0.671 for treatment 1 and 2, respectively
- SEM = 0.0455 and 0.0539 for treatment 1 and 2, respectively

Although the results are not listed here, SAS® 9.3 Help and Documentation describes these lsmeans statement options below.

- diff – requests differences of lsmeans
- ilink – applies the inverse link transform to the lsmeans (not differences) and produces the SE on the inverse linked scale
- cl – constructs confidence limits for means and or mean differences
- odds – reports odds of levels of fixed effects if permissible by the link function
- or (odds ratios) – reports (simple) differences of lsmeans in terms of odds ratios if permissible by the link function

The following SAS statements can be used to address the potential effect of age and its interaction with treatment.

```
proc glimmix;
class treatment;
model lsone / total = treatment age treatment*age;
lsmeans treatment / odds or cl ilink diff;
```

Results of this analysis are shown below.

- P values
  - Treatment = 0.218
  - Age = 0.096
  - Age*treatment = 0.262
- Means = 0.818 and 0.660 for treatment 1 and 2, respectively
- SEM = 0.0465 and 0.0572 for treatment 1 and 2, respectively

Hence, because neither the effect of age nor the age × treatment interaction was significant, their inclusion in the model had little impact on findings and omission could be considered. In this regard, the treatment P value is much greater when age and the interaction are included in the model because of the limited number of groups or experimental units and, thus, substantial effect

on the denominator df. If there were more than two treatments, contrasts could be used to partition effects, 'diff' be used as an option for the lsmeans statement, and(or) '/ solution' could be inserted at the end of the model statement to evaluate relationships between individual treatments and age if the interaction was significant.

Another consideration for analysis of categorical data is blocking or appropriately addressing the experimental unit. The analysis with SAS GLIMMIX is very similar to that with the SAS MIXED procedure in this regard. As an example, a simulated data set in Appendix 3 Table 162 has four villages, 12 households per village, three treatments imposed on animals of four households per village, and five animals per household. Variables are the same as in the preceding example.

With the following SAS statements, village and treatment*village are considered random effects (age not addressed); the denominator df for treatment is 6.

```
proc glimmix;
classes treatment village;
model lsone / total = treatment;
random village treatment*village;
lsmeans treatment / odds or cl ilink diff;
contrast '1 vs 23' treatment -2 1 1;
contrast '2 vs 3' treatment 0 -1 1;
```

- Treatment P value = 0.005
- Means = 0.474, 0.243, and 0.701 for treatment 1, 2, and 3, respectively
- SEM = 0.0573, 0.0499, and 0.0522 for treatment 1, 2, and 3, respectively

The subsequent statements also consider random effects of village and treatment*village, but with age included in the model as a continuous covariate, as well as treatment*age.

```
proc glimmix;
classes treatment village;
model lsone / total = treatment age treatment*age / solution;
random village treatment*village;
lsmeans treatment / odds or cl ilink diff;
contrast '1 vs 23' treatment -2 1 1;
contrast '2 vs 3' treatment 0 -1 1;
```

- P values = 0.329, 0.0004, and 0.235 for treatment, age, and treatment*age, respectively
- Means = 0.520, 0.242, and 0.686 for treatment 1, 2, and 3, respectively
- SEM = 0.0690, 0.0540, and 0.0597 for treatment 1, 2, and 3, respectively

In some cases village might be considered a fixed rather than random effect, such as with analysis of continuous variables via SAS GLM vs. SAS MIXED and ANOVA-ARR of GenStat. The following SAS statements also yield a denominator df for treatment of 6, similar to GLM

analysis of continuous variables with treatment*village as the error term to test the effect of treatment.

```
proc glimmix;
classes treatment village;
model lsone / total = treatment village;
random treatment*village;
lsmeans treatment / odds or cl ilink diff;
contrast '1 vs 23' treatment -2 1 1;
contrast '2 vs 3' treatment 0 -1 1;
```

- P value = 0.005 and 0.537 for treatment and village, respectively
- Means = 0.473, 0.240, and 0.705 for treatment 1, 2, and 3, respectively
- SEM = 0.0576, 0.0498, and 0.0522, respectively

Inclusion of age in this model also resulted in a nonsignificant effect of treatment.

Even though including age in the model precluded a significant effect of treatment, age did not differ among treatments with SAS GLM analysis and a treatment error term of treatment*village; the overall age P value was 0.243 (1.95, 1.98, and 2.05 yr for treatments 1, 2, and 3, respectively; SEM = 0.038). However, the correlation between age and the percentage of litters with a litter size of 1 was 0.42 (P = 0.003). This example, although with simulated data, illustrates the importance of addressing factors in the allocation process that may affect variables of greatest interest.

Chapter 9. On-Farm Research Examples

Introduction

Goetsch and Abebe (2009) addressed the two general approaches used in on-farm research by the ESGPIP: working with organized groups of smallholders in FRG or ISH. The most appropriate method depends on factors such as the nature of the intervention, variability in production practices among households within a site, cultural conditions, cohesiveness of smallholders in an area, proximity of households within a community, trust, ability to work effectively together, animal theft concern, availability of implementing personnel including extension agents/officers, etc. Regardless of the approach, it was necessary to characterize production conditions and practices, perform an economic analysis, involve extension agents/officers working directly with smallholders, and disseminate findings. In addition, personnel of the ESGPIP assured that the design was conducive to a valid statistical analysis through the proposal review process. The activities also were participatory, with smallholders making contributions such as labor, animals, and other cost-sharing functions. Funds of the ESGPIP provided to implementing partners (e.g., university, college, regional research institute) for allocation to smallholders were restricted to 'extras,' including feedstuffs, forage seed, fertilizer, other supplies, etc. Other funds were used for student and technician support, per diem for researchers and extension personnel, laboratory analyses, office supplies, field days, etc.

Ponniah et al. (2008) contrasted FRG with severeal other types of producer groups. It was stated that FRG can be established specifically for a research activity (i.e., research-induced), or the activity can be conducted with an existing group originally formed for a different purpose (i.e., producer-based). Most FRG of the ESGPIP were research-induced. However, some had been involved in on-farm research before the ESGPIP and a small number participated in more than one ESGPIP study. Moreover, there were FRG developed primarily from smallholder households that had previously participated in projects that included establishment of women groups and a goat distribution development program similar to that of Heifer Project International. Those projects also encompassed relevant technology interventions such as training in goat production and management and introduction of improved forages and multi-purpose tree legumes.

In ESGPIP on-farm research with FRG, there were typically three to five villages per activity. It is desirable to start with as many as logistically possible in case problems arise resulting in the need to discard data from one or more FRG. Each FRG consisted of nine or ten smallholder households. Except for the lead household, others contributed the same number of animals as the number of treatments, normally three or four. The lead household sometimes provided twice that number, in which case nine households were involved, yielding 40 animals per FRG with four treatments. Most of the ESGPIP on-farm research activities entailed various feeding management practices, such as the examples below.

- Ammoniation of crop residues via urea treatment
- Supplement blocks (e.g., urea-molasses as well as other locally available byproducts)
- Byproducts
  - Khat (*Catha edulis*) residue

  - Poultry litter
  - Sweet potato vine
  - Pigeon pea
- Cactus
- Browse

A simple barn was constructed at the lead smallholder household site of each FRG, usually consisting of the same number of pens as treatments. The ESGPIP provided funds for most materials, with smallholders supplying labor and items such as metal and plastic sheeting for the roof and(or) doors. In late afternoon or early evening when animals returned from grazing, one animal per household was placed in each pen where the feeding management treatment was imposed. Animals usually resided in the pen until the treatment period ended (i.e., feedstuff consumption was complete) or when grazing began the next morning. During the daytime, households rotated management of animals grazing as a group.

The ISH approach has a small advantage over FRG in terms of maintaining normal production conditions. The primary difference is grouping of animals from different households within a FRG at the lead household site and most or all animals placed in pens according to the treatments during part or all of the evening period. For example, with one unsupplemented control treatment and three other treatments involving different levels or types of supplemental feedstuffs, the barn at the lead household site might have three pens if used only for feeding or four if all animals were confined at night. Otherwise, animals with both methods were managed similarly. Less variation among households is expected with FRG than ISH, which would be advantageous in terms of statistical power, but perhaps unfavorable for extrapolating findings to other settings. There may also be greater participation by more smallholders for the ISH vs. FRG approach. With FRG there is naturally a high degree of involvement of the lead household, but with the EGPIP on-farm activities other participating smallholders also spent considerable time assisting at the lead household site and managing animals as a group during the daytime.

Monitoring and supervision by the researcher is much easier for FRG vs. ISH studies. For example, with five FRG each with nine households, the researcher has five sites to visit routinely rather than 45 smallholder households. Extension agents/officers should be involved in on-farm research irrespective of the approach; however, it is probably more important for ISH than FRG. Another attribute of studies with FRG is a stronger statistical analysis compared with ISH experiments because each treatment is subjected to animals of each household rather than one treatment per household as is most common with the ISH approach (addressed in greater detail later). Fewer households can be used with FRG to achieve the same statistical power as an experiment with ISH.

The ‘group’ aspect of FRG provides an advantage in information dissemination. Working with groups has become the norm in many developing countries to maximize the number of households that can be reached and minimize cost (Ponniah et al., 2008). Farmer Field Schools have been effectively used as well, although there are differences compared with FRG involved in on-farm research. Nonetheless, Farmer Field Schools certainly could employ interventions previously evaluated in on-farm research conducted either with FRG or ISH.

Chapter 9. On-Farm Research Examples

Examples of on-farm research activities for eight categories, types, or families are highlighted in Table 29. SAS analyses are described for each example in the subsequent text and Appendices 1 and 2, and the menu approach of GenStat is also employed for some examples. Appendix 3 contains the simulated data sets. Moreover, after the last example in this chapter, Table 52 provides a brief summary of comparisons of P values via the different analyses.

Table 29
Overview of on-farm research examples

Example family[1]	Description in text	Appendix 2 tables	Appendix 3 table	Description
A	Tables 1 and 2	69, 70, 71, 72, 73, 74, 75, 76, 77	163	Split-plot analysis; all treatment effects fixed
B	Figure 10 and Table 30	78, 79, 80, 81, 82, 83, 84, 85, 86, 87	166	FRG; one animal/ISH on each treatment; data set 1
B	Figure 10 and Table 30	88, 89, 90, 91	169	FRG; one animal/ISH on each treatment; data set 2
C	Figure 11 and Table 31	92, 93, 94, 95	170	ISH; considering woreda and village; one treatment per ISH; data set 1
C	Figure 11 and Table 32	96, 97, 98, 99, 100, 101, 102, 103	170	ISH; considering village and not woreda; one treatment per ISH; data set 1
C	Figure 11 and Table 32	104, 105, 106, 107	171	ISH; considering village and not woreda; one treatment per ISH; data set 2
C	Figure 12 and Table 33	108, 109, 110, 111, 112, 113, 114, 115	173	ISH; considering village and not woreda; one animal of each ISH per treatment
C	Figure 13 and Table 34	116, 117, 118, 119, 120, 121, 122, 123, 124	175	ISH; split-plot analysis; four villages; two breeds per household; one treatment per ISH; village as fixed and random; continuous and categorical variables
D	Figure 14 and Table 35	125, 126, 127	176	Different seasons; different villages in each season; one treatment per ISH; village as random
D	Figure 15 and Table 36	128, 129, 130, 131	177	Different seasons; same villages in each season; one treatment per ISH; village as random; household as random or fixed
D	Figure 15 and Table 37	132, 133, 134	177	Different seasons; same villages in each season; one treatment per ISH; village as fixed; household as random or fixed
E	Table 39	137, 138	178	Monthly measures; one village and one breed; continuous variable
E	Table 40	139, 140	179	Monthly measures; two villages and one breed; continuous variable
E	Table 41	141, 142	180	Monthly measures; one village and two breeds; continuous variable
E	Table 42	143, 144	181	Monthly measures; two villages and two breeds; continuous variable
F	Table 43	145	182	Monthly measures; one village and one breed; categorical variable
F	Table 44	146	183	Monthly measures; two villages and one breeds; categorical variable
F	Table 45	147	184	Monthly measures; one village and two breeds; categorical variable
F	Table 46	148	185	Monthly measures; two villages and two breeds; categorical variable
G	Figure 16 and Table 47	149, 150	186	One treatment per village; two treatments and six villages; continuous variable
H	Table 48	151, 152, 153	187	Switchback; one village
H	Table 49	154, 155	188	Switchback; two villages
H	Table 50	156, 157	189	Latin square; one village
H	Table 51	158, 159	190	Simultaneous Latin squares; four villages

[1]A in Chapter 5 – Experimental Design; B-H in Chapter 9 – On-Farm Research Examples.

Farmer Research Groups

No Missing Data

A typical FRG activity of the ESGPIP is depicted in Figure 10, and Table 30 describes an analysis by the SAS GLM procedure. There are four feeding management treatments, four villages, ten smallholder households per village, and four animals per household. The design can be considered a randomized block, with FRG as a fixed block (fixed vs. random assumptions discussed in greater detail later). In such instances when FRG or village is assumed to be fixed, inferences about the populations are based on random differences among observations within the groups (Kaps and Lamberson, 2004). SAS statements are in Appendix 1 page 171, results of analyses are in Appendix 2 Table 78, and Appendix 3 Table 166 contains the simulated data set.

Table 30
Example SAS GLM analysis for a FRG study[1]

Source of variation	Error term	df
Treatment	Treatment × FRG	3
FRG	Treatment × FRG	3
Treatment × FRG	Household(FRG)	9
Household(FRG)	Residual	36
Residual		108

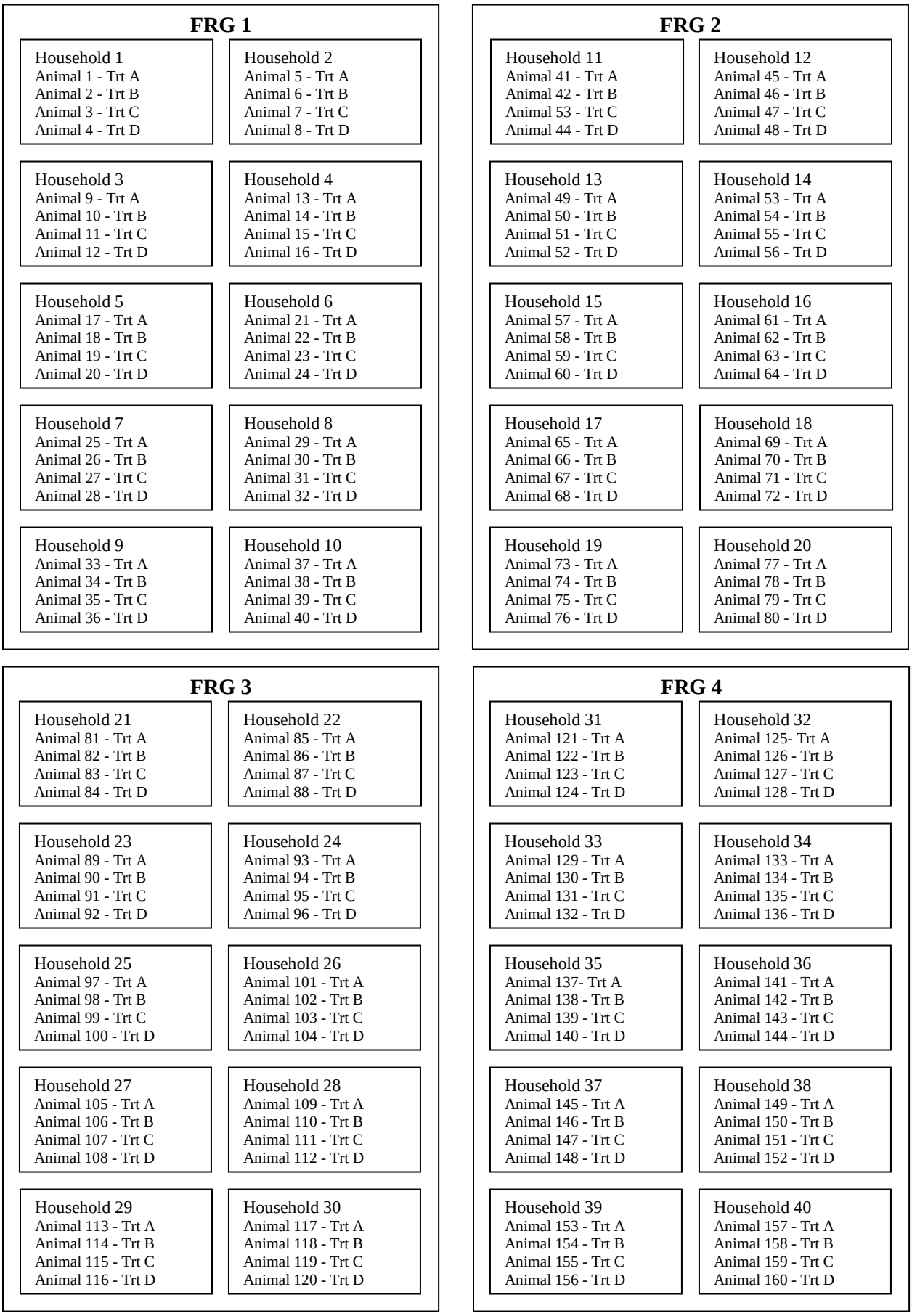
[1]Total of 40 households, 160 animals, and 40 animals per FRG.

If a mixed effects model of SAS is used, then the denominator df to test the effect of treatment is 9 for the interaction between treatment and FRG as for GLM analysis, but with random effects of FRG, treatment × FRG, and household within FRG. However, with a mixed effects model and assuming these random effects, differences among FRG and the interaction between treatment and FRG are not evaluated. Furthermore, it could be beneficial to view differences among households for purposes such as selection or exclusion from future studies, but this also is not addressed with the SAS MIXED analysis. In this regard, a mixed effects model with FRG assumed fixed was also used, with statements for SAS MIXED analysis in Appendix 1 page 171 and results in Appendix 2 Table 79. For this and other analyses with the SAS MIXED procedure, the least complex default covariance structure of 'Variance Components' was used, which assumes independence of factors considered random.

Use of analysis of variance (**ANOVA**) via GenStat (ANOVA by ANOVA, REML, or Regression; **ANOVA-ARR**) is similar to the SAS MIXED analysis, in that the interaction between treatment and FRG is not evaluated, which is also true for the effect of FRG if considered a random blocking factor. Inputs for analyses by GenStat are in Appendix 1 page 171, along with results in Appendix 2 Tables 80 and 81 for FRG considered random and fixed, respectively.

The classification of FRG as fixed vs. random (or village for the ISH approach to be addressed later) may not be an easy one. In this regard, Kaps and Lamberson (2004) provided comments quoted below.

Figure 10. Example of a FRG study (Trt = treatment).



- "An effect is defined as fixed if:
  - there is a small (finite) number of groups or treatments;
  - groups represent distinct populations, each with its own mean;
  - and the variability between groups is not explained by some distribution.

- The effect can be defined as random if:
  - there exists a large (even infinite) number of groups or treatments;
  - the groups investigated are a random sample drawn from a single population of groups;
  - and the effect of a particular group is a random variable with some probability or density distribution."

St-Pierre and Jones (1999) recommended that blocks, such as pens of dairy cattle, be assumed random rather than fixed, which is in accordance with the aforementioned conditions of Kaps and Lamberson (2004). Similarly, St-Pierre (2001) noted how study or experiment in meta-analyses should be classed as random because assumptions of fixed effects would limit inference of findings to only those particular groups, pens, or studies at the specific points in time when research was conducted. However, St-Pierre (2001) also stated that inferences from analyses of multiple studies can be made, even if study is presumed fixed, as long as extrapolation is restricted to conditions similar to studies in the database. But, determining what constitutes similar vs. dissimilar conditions could be difficult. Nonetheless, relevance of assumptions regarding groups or pens of animals or experiments to FRG as noted above, and villages as discussed later, is questionable. Perhaps in part based on the aforementioned view of Kaps and Lamberson (2004) concerning random differences among observations within groups, there is not ample rationale to support the contention that categorizing FRG or village as fixed restricts applicability or inference of results only to those specific locations, conditions, and times. Furthermore, FRG and village might be considerd fixed blocks, somewhat comparable to crop experiments with blocks of land differing in fertility, slope, moisture level, etc. That is, differences among FRG or villages may exist that influence results independent of, or dependent upon, treatments imposed. It would seem of value to address such effects, requiring a thorough characterization of differing conditions in order to explain effects and interactions, rather than merely assessing the overall treatment impact.

In articles such as St-Pierre and Jones (1996) and St-Pierre (2001, 2007), it is pointed out that in previous studies factors such as animal pen or study in meta-analyses were considered fixed rather than random because adequate statistical programs for use of mixed effect models were not available. But, it is also possible that with the availability of such programs today, as well as seemingly strong conclusions of limited scopes of inference if all but treatment effects are considered random, in some cases factors considered random could just as appropriately (perhaps even moreso) be categorized as fixed. For example, it is conceivable that with a relatively small number of FRG or villages of an on-farm research activity, their selection might be purposely to achieve an array of conditions adequate to represent the population of interest. It may have been concluded that the likelihood of achieving this diversity would be limited if somehow selection could be performed in a truly random manner. This is in line with considerations addressed earlier in Chapter 7 – Experiment Implementation in the section 'Selection of Implementing Partners, Villages, Extension Personnel, and Smallholder Households.'

Missing Data

An additional consideration for analysis of data with the FRG approach is missing data. As noted before for the experiment of Merera et al. (2010) addressed in Tables 1 and 2 of Chapter 5 – Experimental Design, the nature of the missing data can influence the outcome. As an example, the data set in Appendix 3 Table 167 was derived by removing 9 observations without regard to treatment or FRG (i.e., completely random) from the simulated data set in Appendix 3 Table 166. The data set in Appendix 3 Table 168 also has 10 missing observations, but 7 are of treatment 1 and 3 are of treatment 2. Appendix 2 Tables 82 and 85 (results of SAS GLM analysis) and Appendix 2 Tables 83 and 86 (results of SAS MIXED) depict similarity between analysis methods with random missing values but a substantial difference with non-random missing data. Hence, in such instances a mixed effects model could be preferable, although due attention should be given to reasons for non-random missing data and validity or usefulness of remaining data. Appendix 2 Tables 84 and 87 contain results from GenStat ANOVA-ARR for data sets with observations removed at random and non-randomly, respectively (Appendix 3 Tables 167 and 168, respectively). The treatment P value was similar to those for SAS GLM and MIXED analyses with random missing observations. The treatment P value for the data set with non-random missing data was similar to that for SAS MIXED analysis and, likewise, was considerably different from that of SAS GLM.

Nature of the Data

The nature of a data set also influences P values from analyses with factors such as FRG or village considered fixed vs. random. For example, with the data set in Appendix 3 Table 166, the treatment P value for SAS GLM analysis with FRG considered fixed (Appendix 2 Table 78) is not greatly different than that for SAS MIXED analysis with FRG as random (Appendix 2 Table 79). Furthermore, P values rounded to three decimal places for treatment and FRG are the same for GLM and MIXED procedures if with MIXED FRG also is considered fixed (Appendix 2 Table 79). But, with another simulated data set given in Appendix 3 Table 169, the P value for treatment from SAS GLM and MIXED analyses is different with FRG assumed fixed for GLM and random for MIXED. Moreover, P values for treatment and FRG are different for both analyses with FRG as fixed for MIXED (GLM results in Appendix 2 Table 88; MIXED results in Appendix 2 Table 89). Results of comparable GenStat analyses appear in Appendix 2 Tables 90 and 91.

Individual Smallholder Households

Household Animals on One Treatment

The ESGPIP had more on-farm research activities with ISH than FRG, mainly for three reasons: concern about animal theft when animals were located at the lead household at night, relatively long distances between farms within villages, and lack of need for construction of a barn at a lead household site with the ISH approach. There was considerable variability in the structure of on-farm research activities with ISH. For some activities, similar to the FRG approach, each ISH had the same number of animals as treatments, with one animal per treatment. However, because of the difficulty for ISH to impose different treatments without use

of a barn at the lead household, all animals of an ISH were usually subjected to the same treatment.

An early on-farm ESGPIP research activity entailed two woredas (administrative area or unit one step above villages or kebeles), two villages per woreda, nine households per village, and three animals per household. There were three treatments, with three households per treatment in each village as shown in Figure 11.

The statistical analysis with the GLM procedure of SAS in Table 31 considers woreda. The design can be considered a randomized block as for the FRG approach noted above, with fixed blocks of woreda and village.

Table 31
Example SAS GLM analysis for an ISH study with woreda considered and one treatment per household[1]

Source of variation	Error term	df
Treatment	Treatment × woreda	2
Woreda	Treatment × woreda	1
Treatment × woreda	Village(woreda)	2
Village(woreda)	Household(treatment × village × woreda)	2
Treatment × village(woreda)	Household(treatment × village × woreda)	4
Household(treatment × village × woreda)	Residual	24
Residual		72

[1]Total of 36 households, 108 animals, and 27 animals per village.

If a mixed effects model of SAS is used, the denominator df to test the effect of treatment is also 2 based on the treatment × woreda interaction, with random effects of all sources of variation other than treatment. Statements for SAS GLM, SAS MIXED, and GenStat ANOVA-ARR analyses for data set 1 appear in Appendix 1 page 172-173, results are in Appendix 2 Tables 92, 93, 94, and 95, and the simulated data set is in Appendix 3 Table 170.

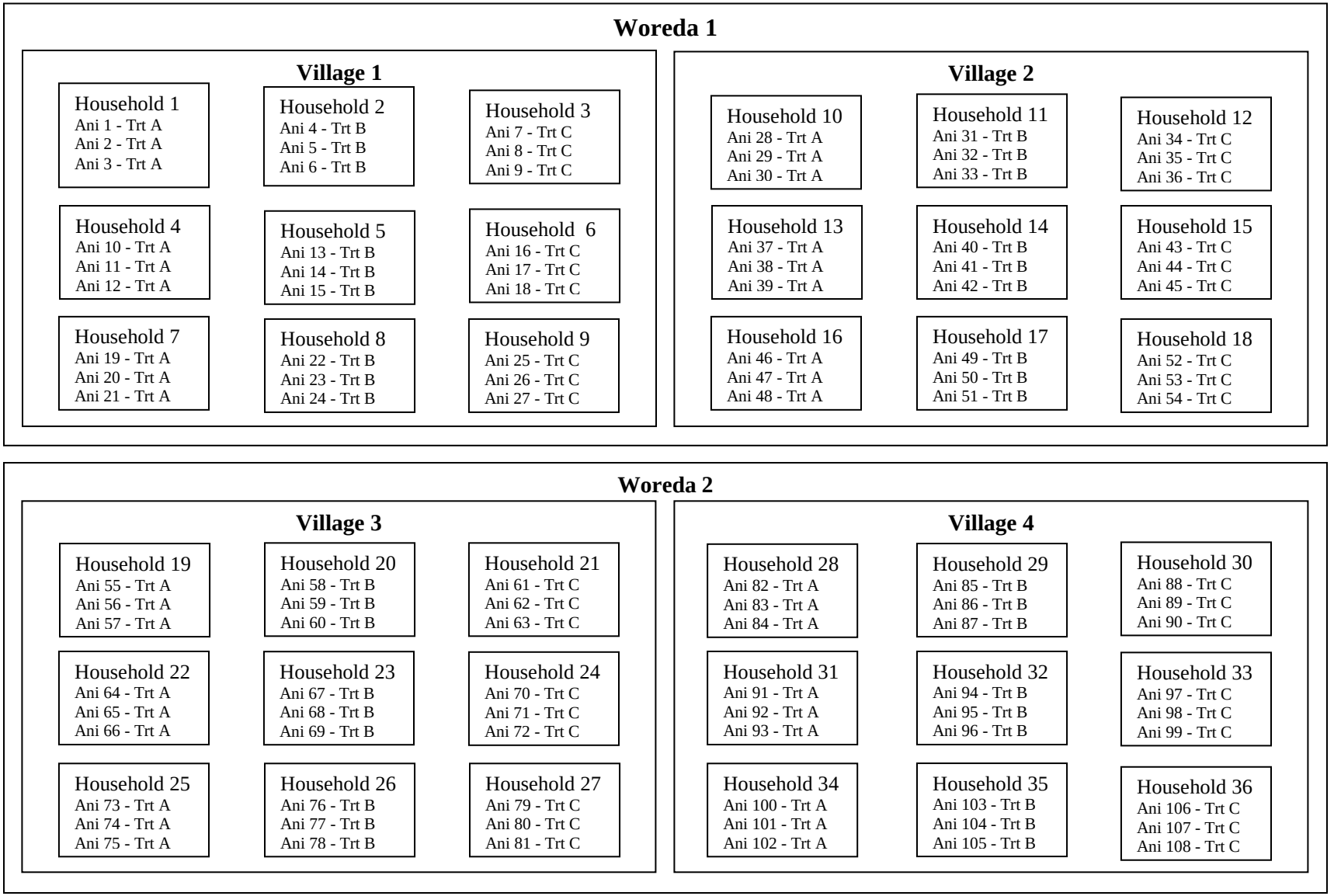
If there is inadequate reason to consider woreda as a significant source of variation (e.g., nonsignificant effects of woreda and treatment × woreda in above analyses), it can be dropped from the model as shown in Table 32 with analysis by the GLM procedure of SAS.

Table 32
Example SAS GLM analysis for the ISH approach with all animals from a household on one treatment without considering woreda[1]

Source of variation	Error term	df
Treatment	Treatment × village	2
Village	Treatment × village	3
Treatment × village	Household(treatment × village)	6
Household(treatment × village)	Residual	24
Residual		72

[1]Total of 36 households, 108 animals, and 27 animals per village.

Figure 11. Example of an ISH study with animals of each household subjected to one treatment in villages in two woredas (Ani = animal; Trt = treatment).



The denominator df is 6 for treatment × village when random effects of village, treatment × village, and household(treatment × village) are assumed with a mixed effects model of SAS. Statements for SAS GLM, SAS MIXED, and GenStat ANOVA-ARR analyses are in Appendix 1 page 174, results for data set 1 are in Appendix 2 Tables 96, 97, 98, and 99, and the simulated data set 1 is in Appendix 3 Table 170.

This analysis is somewhat similar to those addressed by St-Pierre and Jones (1999) for non-regulatory on-farm feeding trials with dairy cattle. However, village may not be comparable to a pen or group of animals at a specific research site. Regardless, St-Pierre and Jones (1999) stated that if the treatment × pen interaction is nonsignificant, it can be pooled with the animal within pen × treatment effect and used to test treatment. This is not recommended for on-farm livestock research addressed in this publication because village or FRG is an integral part of the experimental design. Fewer villages or FRG than pens or groups of animals in those dairy experiments may be an important difference in this regard.

As noted earlier regarding the FRG approach, the nature of a data set influences P values from analyses with village considered fixed vs. random. For example, with data set 1 the treatment P value differed between the GLM analysis and the mixed effect model with only treatment considered fixed (Appendix 2 Tables 96 and 97). But, treatment and village P values were the same for GLM and MIXED analyses with FRG considered fixed. Somewhat different findings were noted, however, with analysis of a different data set (i.e., data set 2 in Appendix 3 Table 171). Results are in Appendix 2 Table 104 for SAS GLM, Appendix 2 Table 105 for SAS MIXED, and Appendix 2 Tables 106 and 107 for GenStat ANOVA-ARR. With this data set, the treatment P value was the same for SAS GLM and MIXED analyses regardless of whether village was considered fixed or random, and the P value for village if considered fixed for SAS MIXED analysis was the same as well. The GenStat P values were also the same as for the SAS analyses.

Household Animals on Each Treatment

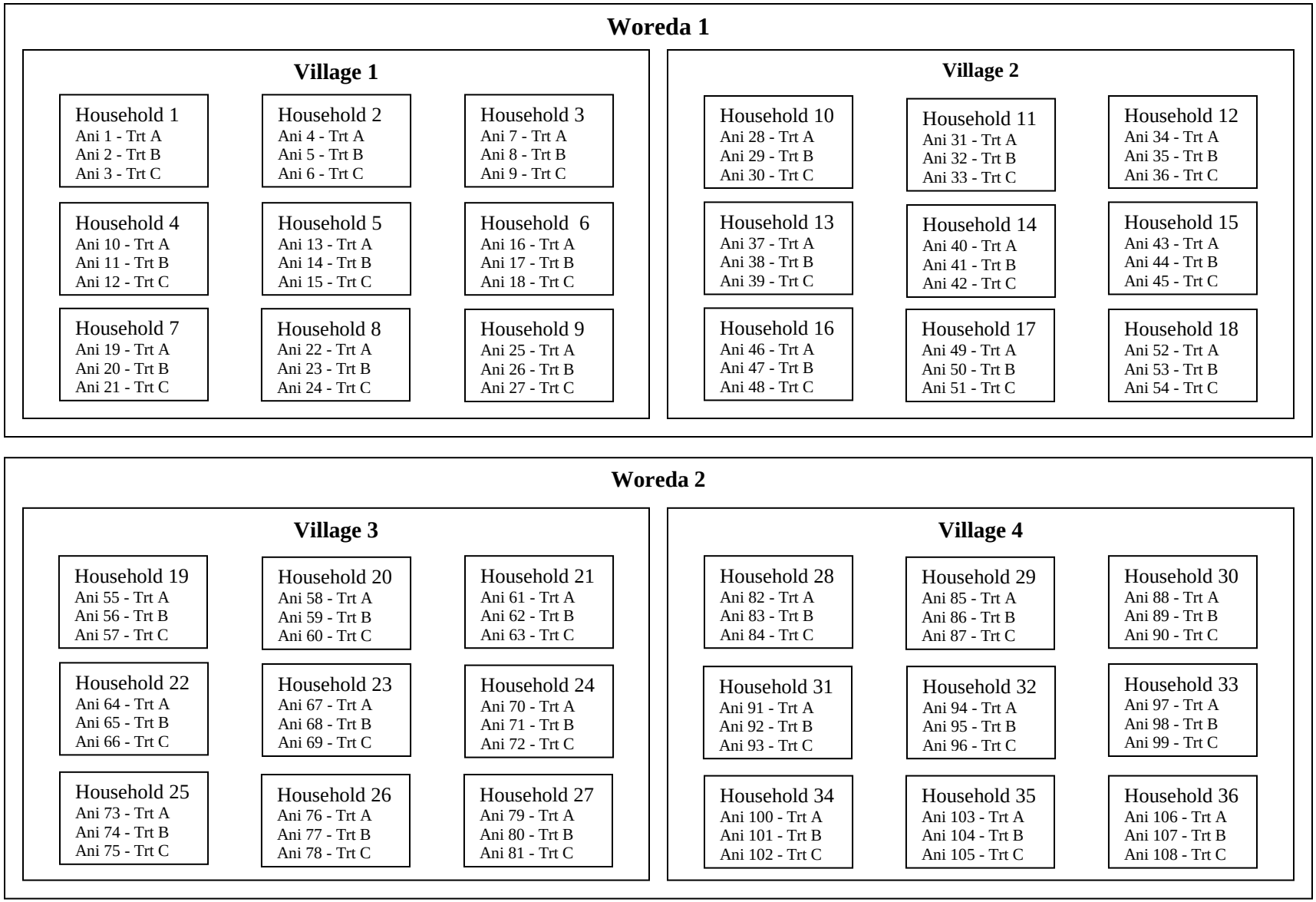
A similar study as noted above but with an animal from each household subjected to every treatment is depicted in Figure 12, and the SAS GLM analysis without considering woreda as a source of variation is described in Table 33.

Table 33
Example SAS GLM analysis for the ISH approach with animals from each household subjected to each treatment without considering woreda[1]

Source of variation	Error term	df
Treatment	Treatment × village	2
Village	Treatment × village	3
Treatment × village	Household(village)	6
Household(village)	Residual	32
Residual		64

[1]Total of 36 households, 108 animals, and 27 animals per village.

Figure 12. Example of an ISH study with animals in each household subjected to each treatment in villages in two woredas (Ani = animal; Trt = treatment).



A difference between this scenario (Table 33) and that in Table 32 with one treatment per household is more df for testing treatment × village. Another assumed benefit is lower household(village) variability because of even distribution of treatments across households. Furthermore, this design is somewhat different than the FRG approach in that management or production practices would probably be more variable among households. Again, the denominator df is 6 for treatment × village with random effects of village, treatment × village, and household(treatment × village) for the SAS MIXED analysis. Analysis of variance via GenStat ANOVA-ARR is similar to the above example with SAS MIXED and the earlier FRG example in Table 30. That is, the potential interaction between treatment and village is not evaluated, as is also true for the effect of village if considered a random blocking factor. Statements for SAS GLM, SAS MIXED, and GenStat ANOVA-ARR analyses are presented in Appendix 1 page 175, results are in Appendix 2 Tables 108, 109, 110, and 111, and the simulated data set is in Appendix 3 Table 173.

Missing Data and Household Animals on One vs. Each Treatment

If possible, the probability, number, and nature of missing observations expected should be considered when deciding if animals of a household will be subjected to one or all treatments. Data sets in Appendix 3 Tables 172 and 174 provide an example of this situation, with 7 observations removed from data sets in Appendix 3 Tables 170 and 173, respectively. These observations were removed without regard to treatment, village, or household (i.e., random). Differences in P values for SAS GLM analysis due to deletion of observations are relatively greater when animals of a household are assigned to all treatments (i.e., Figure 12 and Table 33) vs. only one (i.e., Figure 11 and Table 32; i.e., greater difference in P values of Appendix 2 Table 112 vs. 108 compared with the difference in P values of Appendix 2 Table 100 vs. 96). The same is true for analysis by SAS MIXED (i.e., greater difference in P values of Appendix 2 Table 113 vs. 109 compared with Appendix 2 Table 101 vs. 97) and GenStat ANOVA-ARR (i.e., greater difference in P values of Appendix 2 Table 114 vs. 110 and 115 vs. 111 than for P values of Appendix 2 Table 102 vs. 98 and 103 vs. 99). This is because if all animals of a household are on one treatment, missing observations affect the accuracy but not number of household observations (unless of course all observations of a household are missing).

Households with Subplots

There may be instances in which there are subplot factors for households. An example involving two breeds at each household is depicted in Figure 13. Appendix 3 Table 175 has a simulated data set for the design in Figure 13. Variables listed are numbers of animals for the two breeds at each household with a litter size of 1 and 2 and the total number giving birth. Thus, the variables are categorical. Nonetheless, for illustrative purposes the same simulated data set was used for analysis by SAS GLM and MIXED procedures with the litter size 1 variable considered to be continuous. For this scenario, Table 34 describes the GLM analysis, SAS statements are in Appendix 1 page 176, and results are in Appendix 2 Table 116.

Figure 13. Example of an ISH study with a split-plot treatment arrangement, entailing four villages, 12 households per village, two breeds of animals present at each household, and five animals per breed and household (Brd = breed; Ani = animal; Trt = treatment).

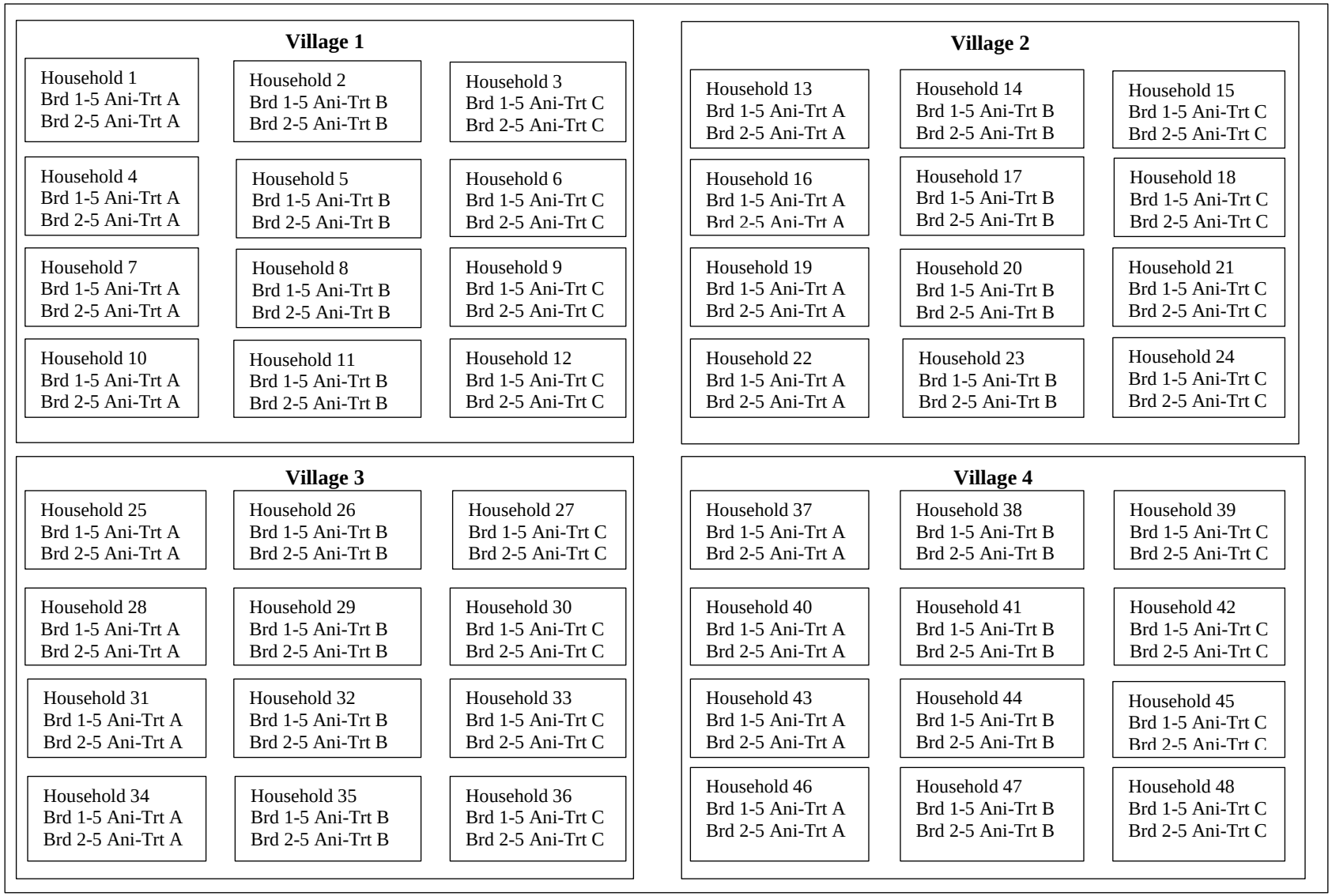


Table 34
Example SAS GLM analysis for an ISH study with a split-plot treatment arrangement, entailing four villages, 12 households per village, two breeds at each household, and five animals per breed and household, with the variable considered continuous[1]

Source of variation	Error term	df
Treatment	Treatment × village	2
Village	Treatment × village	3
Treatment × village	Household(treatment × village)	6
Household(treatment × village)	Residual	36
Breed	Residual	1
Treatment × breed	Residual	2
Village × breed	Residual	3
Treatment × village × breed	Residual	6
Residual		36

[1]Total of 48 households and 96 observations with two breeds per household.

For analysis by the SAS MIXED procedure, as in other examples, village could either be considered random or fixed, with SAS statements in Appendix 1 page 176 and results in Appendix 2 Tables 117 and 118, respectively. With both approaches, the random term to test for effects of treatment and village is treatment × village, with a denominator df of 6. Therefore, the three-way interaction, treatment × village × breed, is not be included in the model as a fixed effect. Hence, the denominator df for testing effects of the subplot factors of breed, treatment × breed, and village × breed is 45 if village is considered random and 42 if fixed (vs. 36 for the SAS GLM analysis). The P values for these effects differ slightly between SAS GLM and MIXED analyses, as is also true for those of treatment and village. Again, the potential effect of treatment × village is not tested with the SAS MIXED analysis.

Appendix 2 Tables 119 and 120 contain results of the SAS MIXED analysis with the effect of the subplot of breed and interactions involving breed omitted, with village considered random and fixed, respectively. In contrast to results of the analysis by SAS GLM, this results in small changes in main effect P values.

The analysis of the number of animals per household and breed with a litter size of 1 as a categorical variable by the SAS GLIMMIX procedure as noted in Appendix 1 page 176 is very similar to that by the SAS MIXED procedure. Village is considered random in Appendix 2 Table 121 and fixed in Appendix 2 Table 122, again with the effect of treatment × village used to test effects of treatment and village. The three-way interaction is not included in the models, resulting in 45 and 42 df with village as random and fixed, respectively, for residual variation used to test effects of breed and its interactions with treatment and village. Appendix 2 Tables 123 and 124 contain results with the subplot of breed omitted, considering village as random and fixed, respectively. As occurred for the SAS MIXED analysis, omission of the subplot factors from the model influenced P values for treatment and village. Moreover, the results are the same if the data set consists of values on a household basis rather than breed within household.

Studies in Different Seasons or Years

Some ESGPIP on-farm research was conducted in more than one season, such as a study with different levels of sweet potato vine and pigeon pea. This activity was conducted in a different village in two seasons. However, the first example in Figure 14 depicts two different villages in each season, which would be preferable for extrapolation to a wider array of conditions than possible with only one village. The design is a randomized block with season and village as fixed blocks. The experiment has nine smallholder households per village, three treatments, two sheep per household, and one treatment per household. The analysis with the GLM procedure of SAS is described in Table 35.

Table 35
Example SAS GLM analysis for the ISH approach with one treatment per household, two seasons, and four villages (two per season)[1]

Source of variation	Error term	Df
Treatment	Village(treatment × season)	2
Season	Village(treatment × season)	1
Treatment × season	Village(treatment × season)	2
Village(treatment × season)	Household(treatment × village × season)	6
Household(village × treatment × season)		24
Residual		36

[1]Total of 36 households, 72 animals, and 18 animals per village and season.

A mixed effects model with random effects of village(treatment × season) and household(village × treatment × season) results in a denominator df of 6 based on village(treatment × season) to test effects of treatment, season, and treatment × season. Statements for SAS GLM, SAS MIXED, and GenStat ANOVA-ARR analyses are in Appendix 1 page 178, results are in Appendix 2 Tables 125, 126, and 127, and the simulated data set is in Appendix 3 Table 176.

If the same villages and households are used in both seasons as shown in Figure 15, then season is a repeated measure and the analysis should be conducted with a mixed effects model, although the design remains a randomized block. For repeated measures analysis, values in the simulated data set in Appendix 3 Table 177 are averages across animals within households and seasons. The analysis described in Table 36 assumes only treatment, season, and treatment × season to be fixed effects and village is considered random. With village random, then probably in most cases household would also be random. However, if there is a reason to consider household fixed even though village is random, the household(treatment × village) term is removed from the 'random' statement, with P values for treatment, season, and treatment × season affected by this change. Statements for these analyses by the SAS MIXED procedure are in Appendix 1 page 179, and results are in Appendix 2 Tables 128 and 129 for considering household random and fixed, respectively.

Figure 14. Example of an ISH study with households in different villages used in two seasons (Ani = animal; Trt = treatment).

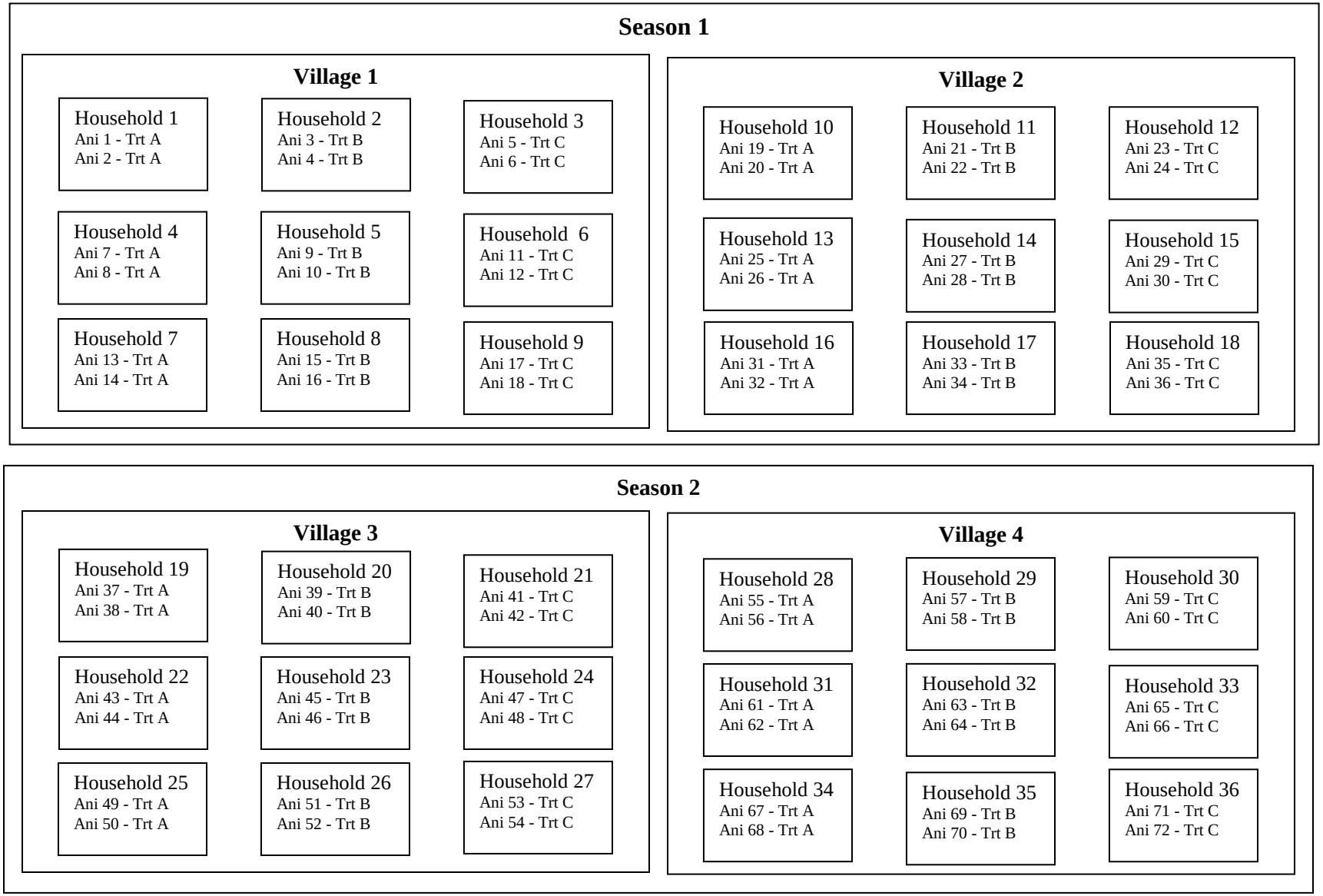


Figure 15. Example of an ISH study with households in the same villages in two seasons (Ani = animal; Trt = treatment).

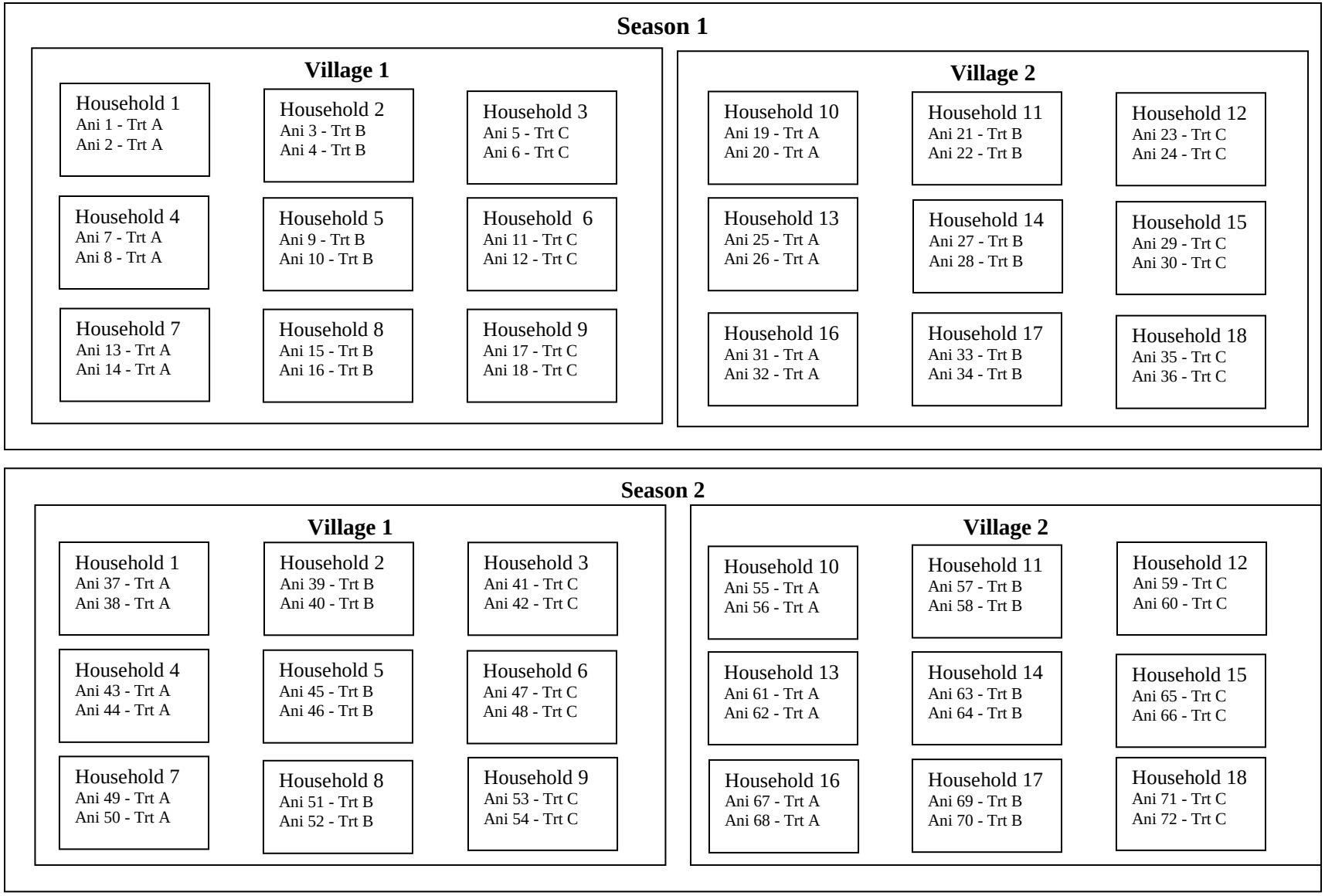


Table 36
Example SAS MIXED analysis for the ISH approach with one treatment per household, two seasons, and the same two villages and smallholder households in each season, with treatment, season, and treatment × season considered fixed effects[1]

Source of variation	Error term	df
Treatment – fixed	Treatment × village	2
Village – random		1
Treatment × village – random		2
Season - fixed and repeated measure	Village(treatment × season)	1
Treatment × season – fixed	Village(treatment × season)	2
Village(treatment × season) – random		3
Household(treatment × village) – subject and random or fixed		12
Residual		12

[1]Total of 18 households, 9 households per village, and a repeated measure of season. The df are for values averaged across animals (i.e., one observation per household).

With the 'Repeated Measures' option of 'Mixed Models (REML)' of GenStat, an analysis fairly similar to that with SAS MIXED in Table 36 can be conducted, but without input of 'village(treatment × season)' as a random effect. As shown in Appendix 1 page 179, inputs are household as the subject, season for the time point, and fixed effects of treatment, season, and treatment × season. However, with the 'Linear Mixed Models' option of 'Mixed Models (REML)' of GenStat, an analysis could be conducted with a Random Model of 'village/household' (i.e., 'village + village.household'). Results of the analyses are in Appendix 2 Tables 130 and 131.

A mixed effects model analysis also could be conducted considering village to be fixed, as noted in Table 37. Here treatment × village is not used as the error term for treatment and village since it is being considered fixed and, thus, the error term for treatment, village, and treatment × village is household(treatment*village). Statements for analyses by the SAS MIXED procedure and GenStat with the 'Repeated Measurements' option of 'Mixed Models (REML)' and 'Linear Mixed Models' are in Appendix 1 page 180; results are in Appendix 2 Tables 132 (SAS MIXED; household as random) and 134 (GenStat). The P values are the same with each method, as is also true as shown below with household considered fixed.

Table 37
Example SAS MIXED analysis for the ISH approach with one treatment per household, two seasons, and the same two villages and smallholder households in each season, considering fixed effects of main effects and interactions of treatment, season, and village[1]

Source of variation	Error term	df
Treatment – fixed	Household(treatment × village)	2
Village – fixed	Household(treatment × village)	1
Treatment × village – fixed	Household(treatment × village)	2
Household(treatment × village) – subject and random or fixed		12
Season – fixed and repeated measure	Residual	1
Treatment × season – fixed	Residual	2
Village × season – fixed	Residual	1
Treatment × village × season fixed	Residual	2
Residual		12

[1]Total of 18 households, 9 households per village, and a repeated measure of season. The df are for values averaged across animals (i.e., one observation per household).

Considering treatment × village random would not seem logical if treatment and village are being treated as fixed. Doing so for use as the error term for treatment and village would preclude testing of the interaction, which would be desirable with village considered fixed. As noted for the analysis addressed above for Table 36, one potentially could consider household random, in which case the 'random' statement would be removed. Relevant SAS statements are in Appendix 1 page 180 and results of the analysis are in Appendix 2 Table 133.

Although the most appropriate analysis is with a mixed model because of the repeated measure of season, a GLM analysis with SAS is, nonetheless, described in Table 38. The same analysis can be conducted with ANOVA-ARR of GenStat. Statements for SAS GLM and GenStat ANOVA-ARR analyses appear in Appendix 1 page 181 and results are in Appendix 2 Tables 135 and 136, respectively.

Table 38
Example SAS GLM analysis for the ISH approach with one treatment per household, two seasons, and the same two villages and smallholder households in each season[1]

Source of variation	Error term	df
Treatment	Treatment × village	2
Village	Treatment × village	1
Treatment × village	Household(treatment × village)	2
Household(treatment × village)	Residual	12
Season	Residual	1
Treatment × season	Residual	2
Village × season	Residual	1
Treatment × village × season	Residual	2
Residual		12

[1]Total of 18 households, 9 households per village, and a repeated measure of season. The df are for values averaged across animals (i.e., one observation per household).

Year-Round Performance Monitoring

Continuous Variables

In some cases it is of interest to monitor animal performance over relatively long periods of time; e.g., a year or more. The purpose of lengthy monitoring could be to simply characterize baseline conditions before implementing an intervention at one or more locations. Subsequent performance would be monitored; an ESGPIP example is the introduction of crossbreds of improver breeds of Dorper sheep and Boer goats. The analysis of this type of data is similar to that described above in Tables 36 and 37, depending on the number of study sites (e.g., villages) and, if there are multiple areas, whether location is considered random or fixed. Example simulated data sets for different scenarios are addressed below, with village considered fixed when more than one.

- Appendix 3 Table 178: one village, one breed, ten households per village, continuous variable, observations averaged across multiple animals of each household, and monthly measures

- Appendix 3 Table 179: two villages, one breed, ten households per village, continuous variable, observations averaged across multiple animals of each household, and monthly measures
- Appendix 3 Table 180: one village, two breeds, ten households per village, continuous variable, observations averaged across multiple animals of each household, and monthly measures
- Appendix 3 Table 181: two villages, two breeds, ten households per village, continuous variable, observations averaged across multiple animals of each household, and monthly measures

Tables 39, 40, 41, and 42 describe analyses of data in Appendix 3 Tables 178, 179, 180, and 181, respectively. Statements for SAS MIXED and GenStat by the 'Repeated Measurements' option of 'Mixed Models (REML)' and 'Linear Mixed Models' are in Appendix 1 pages 182-185 with results in Appendix 2 Tables 137 and 138 for the analysis in Table 39; 139 and 140 for Table 40; 141 and 142 for Table 41; and 143 and 144 for Table 42.

Table 39
Example SAS MIXED analysis of year-round monthly monitoring of a continuous performance variable of animals of ten households in one village

Source of variation	Error term	df[1]
Month – repeated	Residual	11
Household – random and subject		9
Residual		99

[1]The df are for values averaged across animals (i.e., one observation per household).

Table 40
Example SAS MIXED analysis of year-round monthly monitoring of a continuous performance variables of animals of two villages with ten households per village

Source of variation	Error term	df[1]
Village	Household(village)	1
Month – repeated	Residual	11
Village × month	Residual	11
Household(village) – random and subject		18
Residual		198

[1]The df are for values averaged across animals (i.e., one observation per household).

Table 41
Example SAS MIXED analysis of year-round monthly monitoring of a continuous performance variable of animals of ten households and two breeds in one village

Source of variation	Error term	df[1]
Breed	Household(breed)	1
Month – repeated	Residual	11
Breed × month	Residual	11
Household(breed) – random and subject		8
Residual		88

[1]The df are for values averaged across animals (i.e., one observation per household).

Table 42
Example SAS MIXED analysis of year-round monthly monitoring of a continuous performance variable of animals of two villages with ten households per village and two breeds

Source of variation	Error term	df[1]
Breed	Household(breed × village)	1
Village	Household(breed × village)	1
Breed × village	Household(breed × village)	1
Household(breed × village) – random and subject		16
Month – repeated	Residual	11
Breed × month	Residual	11
Village × month	Residual	11
Breed × village × month	Residual	11
Residual		176

[1]The df are for values averaged across animals (i.e., one observation per household).

Categorical Variables

Simulated data in Appendix 3 Tables 182, 183, 184, and 185 are for activities similar to those described in Tables 39, 40, 41, and 42, respectively, but with categorical variables for litter size (i.e., 1 or 2). The GLIMMIX procedure of SAS was used to analyze these data as described in Tables 43, 44, 45, and 46 for data in Appendix 3 Tables 182, 183, 184, and 185, along with SAS statements in Appendix 1 page 186-187 and results in Appendix 2 Tables 145, 146, 147, and 148, respectively.

Table 43
Example SAS GLIMMIX analysis of year-round monthly monitoring of a categorical performance variable of animals of ten households in one village

Source of variation	Error term	df
Month	Household × month	11
Household × month		99

Table 44
Example SAS GLIMMIX analysis of year-round monthly monitoring of a categorical performance variable of animals of two villages with ten households per village

Source of variation	Error term	df
Village	Household(village)	1
Household(village)		18
Month	Residual	11
Village × month	Residual	11
Residual		198

Table 45
Example SAS GLIMMIX analysis of year-round monthly monitoring of a categorical performance variable of animals of two breeds in one village with ten households

Source of variation	Error term	df
Breed	Household(village)	1
Household(breed)		8
Month	Residual	11
Breed × month	Residual	11
Residual		88

Table 46
Example SAS GLIMMIX analysis of year-round monthly monitoring of a categorical performance variable of animals of two villages with ten households per village and two breeds

Source of variation	Error term	df
Village	Household(breed × village)	1
Breed	Household(breed × village)	1
Village × breed	Household(breed × village)	1
Household(breed × village)		16
Month	Residual	11
Village × month	Residual	11
Breed × month	Residual	11
Village × breed × month	Residual	22
Residual		176

One Treatment Per Village

There are many advantages to subjecting all treatments to households and animals within each village or FRG compared with the assignment of villages and all of their households and animals to different treatments. Important ones are the ability to address effects of village or group independent of treatment and potential interaction between treatment and village. Another attribute is existence of high variability among villages that would necessitate a larger number of villages and households. But, there may be instances where the one treatment per village approach can be considered and perhaps is the only logistically feasible approach. One such scenario might be implementation of a number of improved management practices, such as internal parasite control, mineral supplementation, vaccinations, and other health care activities. That is, allowing some households within a village to receive benefit from such interventions could promote issues with others not involved, as addressed early in Chapter 7 – Experiment Implementation in the section concerning Cultural and Social Considerations. Nonetheless, in order to assess the magnitude of improvements in animal performance and economic returns, a basis of comparison is needed. Because of confounding with time, characterizing conditions before treatment imposition would not be desirable as a control to assess the magnitude of impact. Hence, having some villages not receiving assistance in the improved practices as a control treatment could be a consideration, although still an incentive or means of compensation may be required because of benefits received in other villages.

Because of likely relatively higher variability among villages than households within villages, perhaps three villages per treatment could be a minimum. Naturally this is more realistic with a small number of treatments, which would most likely be the case for a treatment consisting of a series of interventions, such as preferred management practices noted above. In this regard, Figure 16 depicts such a study with six villages and two treatments, with a corresponding example simulated data set in Appendix 3 Table 186. An analysis with the SAS GLM procedure is described in Table 47, with results in Appendix 2 Table 149. Results for a relevant analysis with the SAS MIXED procedure is in Appendix 2 Table 150. SAS statements are in Appendix 1 page 187. Because of the fairly simiple nature of these analyses and the examples given earlier addressing factors such as repeated measures, subplots, and categorical variables, such considerations are not addressed for this setting of imposing one treatment to each village with a continuous variable.

Figure 16. Example of a study with six villages, two treatments, six households per village, and three animals per household, with villages subjected to different treatments

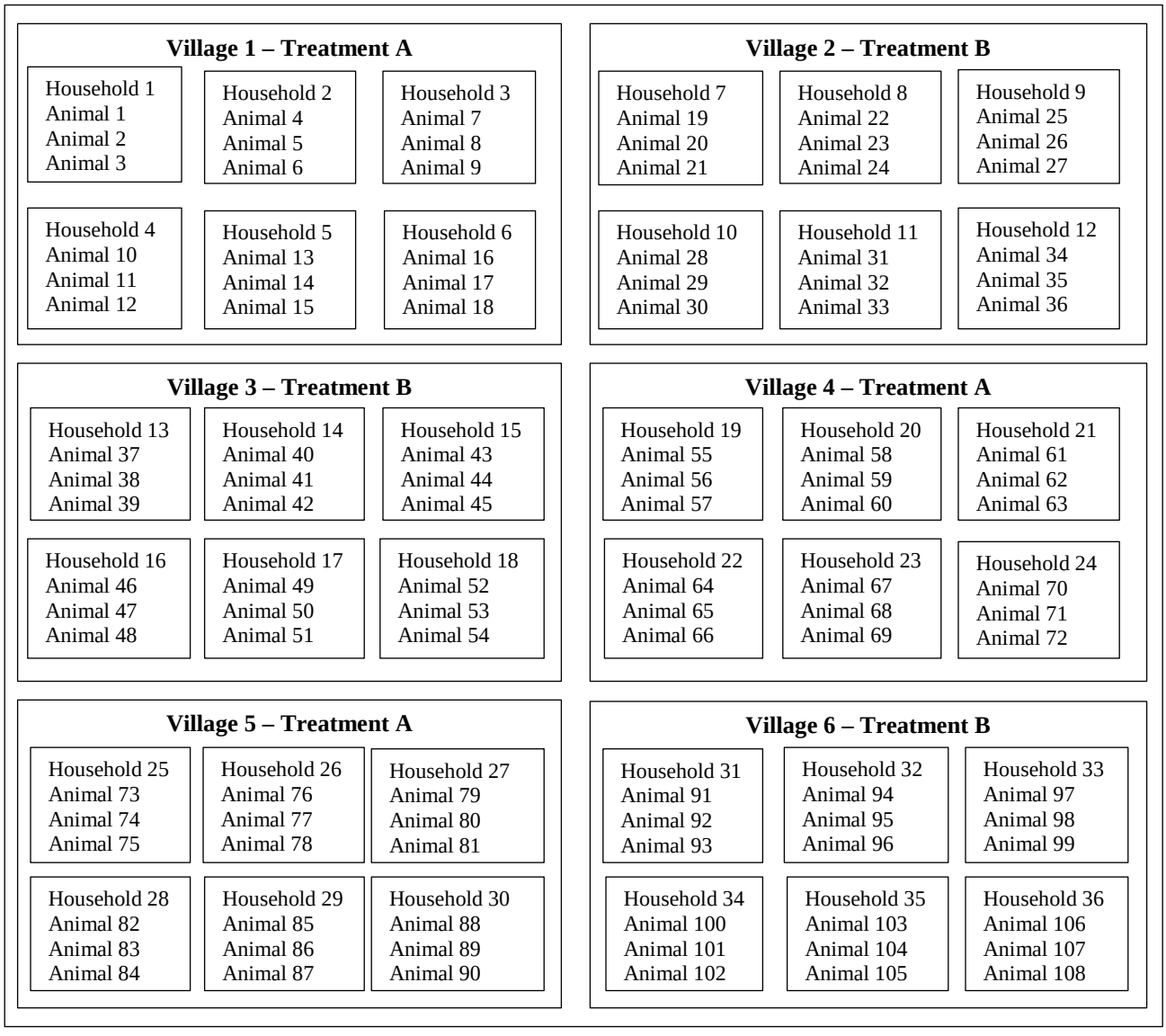


Table 47
Example SAS GLM analysis for the ISH approach with one treatment per village, six villages, two treatments, six households per village, and three animals per household

Source of variation	Error term	df
Treatment	Village(treatment)	1
Village(treatment)	Household(treatment × village)	4
Household(treatment × village)	Residual	30
Residual		72

Crossovers, Switchbacks, and Latin squares

As noted previously, in some instances experimental designs in which the same animals are exposed to different treatments in different periods are used when the number of animals or households is limited, such as might occur in on-farm studies with lactating dairy goats. Therefore, examples are given for switchback and Latin square experiments; the analysis for crossovers and Latin squares is the same.

Table 48 describes the analysis for a switchback experiment with three periods, 12 households, two treatments, and two sequential orders of imposing treatments. Animal might be in the model rather than household if there is one animal per household or all animals are from the same farm. The analysis in Table 49 is similar to that in Table 48, except that two villages or locations are used rather than one, with village considered fixed. Analyses are described in Appendix 1 pages 188-189. Results of SAS MIXED and GenStat by the 'Repeated Measurements' option of 'Mixed Models (REML)' and 'Linear Mixed Models' are given in Appendix 2 Tables 151, 152, and 153 for the analysis described in Table 48 and in Appendix 2 Tables 154 and 155 for the analysis described in Table 49, and simulated data sets appear in Appendix 3 Tables 187 and 188, respectively.

Table 48
Example SAS MIXED analysis for a switchback design with one village, three periods, 12 households, and two treatments

Source of variation	Error term	df
Order	Household(order)	1
Household(order)		10
Period	Residual	2
Treatment	Residual	1
Residual		21

Table 49
Example SAS MIXED analysis for a switchback design with two villages, three periods, 12 households, and two treatments

Source of variation	Error term	df
Village	Household(village × order)	1
Order	Household(village × order)	1
Village × order	Household(village × order)	1
Household(village × order)		20
Period	Residual	2
Treatment	Residual	1
Treatment × village	Residual	1
Residual		44

Table 50 describes the analysis for a 4 × 4 Latin square with four households, four treatments, and four periods. Again, in some instances animal might be used rather than household if there is one animal per household or if all animals are from one farm. The analysis described in Table 51 is similar to that in Table 50, except that there are four villages or locations rather than one, again with village considered fixed. Analyses are described in Appendix 1 pages 190-191. Results of SAS MIXED and GenStat by the 'Repeated Measurements' option of 'Mixed Models (REML)' and 'Linear Mixed Models' are given in Appendix 2 Tables 156 and 157 for the analysis described in Table 50 and in Appendix 2 Tables 158 and 159 for the analysis described in Table 51, and simulated data sets appear in Appendix 3 Tables 189 and 190, respectively.

Table 50
Example SAS MIXED analysis for a 4 × 4 Latin square with one village

Source of variation	Error term	df
Treatment	Residual	3
Household	Residual	3
Period	Residual	3
Residual		6

Table 51
Example SAS MIXED analysis for four simultaneous 4 × 4 Latin squares with four villages

Source of variation	Error term	df
Village	Household(village)	3
Household(village)		12
Period	Residual	3
Treatment	Residual	3
Treatment*village	Residual	9
Residual		33

There may also be instances in which measures are repeated in periods of Latin squares or switchbacks. Similarly, variables could be recorded more than once within months as noted before. In such cases, the SAS MIXED repeated measures statement would include both time descriptors in one term, such as noted below.

```
repeated period*time / subject = household(village);
repeated period*day / subject = household(village);
repeated month*time / subject = household(village);
repeated month*day / subject = household(village);
```

Comparison of Analysis P values

Table 52 summarizes comparisons of P values derived from SAS and GenStat analyses. In many instances P values are the same, but differences sometimes occur, as is also true in a small number of cases for df. A detailed description of the statistical procedures of the packages or systems would be required to address these issues, which is beyond the scope of this publication.

Table 52
Comparison of P values of analyses of on-farm research examples via SAS and GenStat

Example family	Description	Appendix 2 tables	Appendix 3 table	SAS GLM vs. MIXED[1]	SAS GLM vs. GenStat	SAS MIXED vs. GenStat	GenStat Repeated vs. Linear Mixed
A	Tables 1 and 2	69, 70, 71, 72, 73, 74, 75, 76, 77	163	Same	Same	Same	
B	Figure 10 and Table 30	78, 79, 80, 81, 82, 83, 84, 85, 86, 87	166	Trt different if FRG random; Trt and FRG same if FRG fixed	Trt same if FRG random and fixed; FRG same if fixed		
B	Figure 10 and Table 30	88, 89, 90, 91	169	Trt different if FRG random and fixed; FRG different if fixed	Trt same if FRG random and fixed; FRG same if fixed		
C	Figure 11 and Table 31	92, 93, 94, 95	170	Trt different if woreda random and fixed; woreda different if fixed	Trt same if village random and fixed; village same if fixed		
C	Figure 11 and Table 32	96, 97, 98, 99, 100, 101, 102, 103	170	Trt different if village random; Trt and village same if village fixed	Trt same if village random and fixed; village same if fixed		
C	Figure 11 and Table 32	104, 105, 106, 107	171	Same	Same		
C	Figure 12 and Table 33	108, 109, 110, 111, 112, 113, 114, 115	173	Trt different if village random and fixed; village different if fixed	Trt same if village random and fixed; village same if fixed		
C	Figure 13 and Table 34	116, 117, 118, 119, 120, 121, 122, 123, 124	175	All different with village random and fixed			
D	Figure 14 and Table 35	125, 126, 127	176	Trt different if village random and fixed	Trt same if village random and fixed		
D	Figure 15 and Table 36	128, 129, 130, 131	177			Different	Trt different; season and Trt.season same
D	Figure 15 and Table 37	132, 133, 134	177			Same	Same
E	Table 39	137, 138	178			Different	Same
E	Table 40	139, 140	179			Different	Same
E	Table 41	141, 142	180			Different	Same
E	Table 42	143, 144	181			Different	Same
G	Figure 16 and Table 47	149, 150	186	Trt different			
H	Table 48	151, 152, 153	187			Very similar but not exactly the same	Very similar but not exactly the same
H	Table 49	154, 155	188			Same except for order	Same
H	Table 50	156, 157	189			Different	Same
H	Table 51	158, 159	190			Different	Same

[1]Trt = treatment; FRG = Farmer Research Group.

Chapter 10. Dissemination

Peer-Reviewed Journal Article

Introduction

Research is conducted to learn and transfer knowledge gained to others, including scientists, extension personnel, producers, industries, etc. Publication of manuscripts in peer-reviewed journals is an important method of dissemination. The ASAS Writing Workshop (Galyean and Lewis, 2013) provides excellent guidelines for all aspects of scientific manuscripts. The "Suggested Sequence of Events for Building the Journal Article" is quoted below.

1. Review the literature related to the hypothesis
2. Statistical models and treatment comparisons should be defined before you start the experiment
3. Conduct the experiment using data collection and record keeping guidelines discussed previously
4. Analyze the data using planned models and comparisons
5. Develop an outline for the manuscript
6. Write the Introduction (use the literature review - update as needed)
7. Write the Materials and Methods (use the investigator notes)
8. Create the tables and figures (may be done after data analysis)
9. Write the Results and Discussion
10. Create the Literature Cited - verify citations with text
11. Write the Abstract

Skills in preparation of manuscripts for peer-reviewed journals are gained primarily through experience, both in actual writing and studying work of others. The manner in which articles are constructed varies among authors, and sometimes an individual uses different approaches with some articles. For many authors a daily or 2-day stepwise section-by-section approach is more effective than a marathon effort. Relatedly, it is unlikely that productive researchers can devote full attention to one activity for a prolonged period of time. Allowing at least a short period of contemplation before working on the Discussion section can be beneficial. Also, some authors construct the Abstract last, and others may delay finalizing the Introduction until the full interpretation in the Discussion is complete. Prior preparation of abstracts and oral or poster presentations at scientific society meetings can be quite helpful in developing interpretation and clarity of presentation in manuscripts.

Articles should be prepared soon after an experiment is completed and all data are available. As time elapses, interest in the topic and perhaps adequate recollection of logic and procedures may decline. Investigator or researcher notes are very important in this regard. Furthermore, usually findings in a particular area are needed quickly to plan future studies. If more than 1 or 2 years after study completion is taken to fully interpret data and prepare the scientific report, it may be necessary to work in a number of different areas, each with relatively slow progress, to avoid experiment conduct with inadequate supportive information from past

research. Without this knowledge, efficiency of experimentation and rate of long-term research progress are restricted.

General Considerations

A crucial quality of scientific manuscripts is clarity of presentation. If clarity is inadequate, readers may not complete the article and reviewers cannot adequately evaluate the manuscript. Frequently an author can readily understand his/her own writing, but it can be quite unclear to others. Hence, the article must be very, very clear to the writer in order for there to be a reasonable expectation of sufficient clarity for a large fraction of readers. Having others read the manuscript even before internal and external review is useful to identify areas in need of enhanced clarity.

Each paragraph of an article should be logically arranged, and every sentence should be appropriately situated within paragraphs. Use of outlines is advisable, with much prior thought given before actual writing commences. However, some authors on occasion may need to reorganize the manuscript during or after construction of the initial draft, a practice made easier by today's word-processing programs, perhaps feeling that a very detailed outline could be too constraining in regards to an integrative interpretation in the Discussion. A list of short phrases less than one line long for each paragraph can aid in rearrangement and ensure that all sentences belong in a paragraph. Every sentence and paragraph should be essential to the manuscript. Also, after constructing a fairly good rough draft, setting the paper down for a few days or longer can be beneficial; upon return thoughts that seemed clear earlier may be less so in a fresh viewing and interpretation not readily apparent before could be more be evident now.

It is imperative that the required format and guidelines of journals be carefully followed. This is probably of greatest relevance to section or associate editors rather than reviewers, since editors typically have at least some charge for style and format. Most editors wish to focus on the science, and poor compliance with journal style and format can be distracting and in some cases might make the difference in a borderline editorial decision.

When constructing a manuscript, the attentiveness of reviewers and readers needs to be kept in mind at all times. Some researchers view manuscript preparation as telling a story, albeit a true one. The story must be interesting for readers to spend adequate time in its study, given the probability of significant time constraints.

An obvious decision during publication of a manuscript is to identify the most appropriate journal. This selection has marked impact on reviewer recommendations, and is often one of the factors reviewers consider. The journal with the most appropriate audience for the subject should be chosen. As an example, articles about feeding a byproduct not found in a particular region or country of the majority of the readership of a journal should be submitted elsewhere, and the same applies to region-specific production practices. Articles on goats might represent a similar scenario. Many reviewers for some journals focus on cattle, sheep, and swine and have little regard for the importance of goats world-wide. However, choosing a journal before writing an article is not imperative, as current word-processing programs allow format changes to be made fairly quickly.

Publication costs can be important. Many research programs are not well funded, and for productive scientists publication in free or low-cost journals is a mechanism to maximize use of resources for actual experimentation. Relatedly, for promotions and recognition in certain circles, evaluation committees and peers often favorably view journals perceived as prestigious, such as those with a high impact factor. Personal and professional goals are important considerations in such instances.

One factor somewhat related to journal selection is how findings of large studies are parsed into manuscripts. Pressure for high numbers of publications can lead to relatively small packages of data in several articles. This relates to the term known as 'least publishable unit.' However, many researchers feel that data should be packaged in the manner easiest for readers to quickly comprehend and utilize, regardless of the number of articles. For example, it can be difficult and time-consuming to go back and forth between a number of companion papers. In addition, often reviewers and editors recommend short papers with little data be combined or long papers be split up.

Sections

Views on which manuscript section is most important vary, but people generally agree that the abstract is at least among the most important. Journals differ appreciably in abstract style, including length, use of statistical inferences, abbreviations, etc. However, in common is that the primary hypothesis(es) needs to be briefly, clearly, and concisely stated. A general overview of procedures is required, but only for an adequate understanding of the results and their meaning. Most significant findings must be presented. It is advisable to restrict findings to those of greatest significance, which were derived from the study and are comprehensively addressed in the main body of the paper. A summary and(or) concluding sentence(s) based on findings presented in the abstract is critical. Moreover, new information provided should be highlighted.

The Introduction should provide an adequate background and supporting information for the hypothesis(es). Each treatment or condition affected by treatments must be addressed. Relatedly, the information should be specifically relevant to the treatments. As an example, if an experiment deals with different levels of a particular supplement, then the reasoning for studying different levels should be addressed rather than simply discussing merits of this supplement. The Introduction should establish why the study and its findings are important, rather than allowing the reader to make this determination without appropriate guidance and direction from the author(s).

In most cases the Introduction section should be somewhat detailed rather than superficial. However, due to word or character limitations imposed by some journals it can be quite difficult to cover all areas in need of attention. It should be clear that the authors are familiar with the literature, both recent and past. It is preferable that citations be easily accessible to most readers and peer-reviewed rather than abstracts and other non-refereed reports. Lastly, although citations are necessary, most journals discourage excessive referencing, and often limit number of citations for a particular point to a maximum of three.

The Materials and Methods section should provide sufficient information to allow other researchers to conduct a comparable experiment with a reasonable degree of accuracy. Hence, every procedure and practice that might affect results, before and during the experiment, must be described. It is advantageous, if possible, to present procedures in the same order as the results. With multiple experiments in an article, if results are addressed by experiment, then the Materials and Methods section should be structured accordingly. Citations for standard procedures are typically used, although modifications must be described. Most journals allow a previous article by an author containing a detailed description of procedures to be cited. Although, in many instances reviewers request that procedures also be described in the current submission, perhaps with brevity, so that it is not absolutely necessary for readers to view all such references. When reading the Results section, how each result was derived should be readily apparent. Furthermore, no result can be addressed for which its derivation was not previously described.

As mentioned elsewhere, it is often stated that statistical procedures should be set before initiating experimentation. Tentative plans for statistical methods to evaluate results should be made. However, in many instances there are different options such as for means separation. For example, in some studies treatment means can be separated by lsd or orthogonal contrasts. It is acceptable and advantageous to evaluate these possibilities in order to choose the method that allows the clearest interpretation and presentation of data. This may not be possible before data are collected. That is, if the method to most appropriately present the findings is known prior to an experiment, knowledge of the outcomes is inferred and justification for the study might not be obvious.

In the Results section, the text should not contain redundant information in tables or figures. The Results section should clearly and briefly address the findings in the same order as data appear in tables and figures. The description of statistical procedures must closely coincide with the presentation of information in the Results section. An example involves interactions, such as between time and treatment. Either it should be stated from the outset that interactions did not occur, or interactions must be addressed for each variable. If interactions exist but still main effects are addressed, clear justification is required (e.g., interactions were due to differences of magnitude rather than direction).

Results and Discussion sections can be combined or separate for many journals. This decision is primarily determined by personal preferences of authors as well as the nature of the findings. The Discussion should include more than a simple comparison of values with previous findings. Although, such information can be important to establish validity of results and reader confidence and are meaningful when explaining differences between findings. In cases where there is minimal actual interpretation, combining Results and Discussion sections is a consideration. However, when the Discussion is integrative and ties together a large number of measures, possibly placing results in a new conceptual framework, then a separate Discussion section is preferable.

Relevance of all measures should be established in the Discussion section. If variables are not discussed, it is likely that deletion of of those data will be recommended by reviewers and

editors. This is common for research groups that examine a standard set of variables regardless of specific objectives and true pertinence. For retention of these variables in the manuscript, authors are typically required to add relevant interpretation or defend their value; e.g., future database construction.

The Discussion should be based on the specific measures and their differences or similarities to other treatments in the study and other relevant literature. The nature of measures can place limits or bounds on the scope of interpretation presented. For example, in a performance experiment with determinations of live weight gain, feed intake, and efficiency of feed utilization, it would be difficult to address cellular, tissue, or organ metabolism unless the treatments are specifically designed for this or adequate supporting citations are given. But, it may not be possible to provide such justification with acceptable brevity. Also, conditions to which results and interpretation can be applied must be readily apparent, which is set by FRG and villages selected as well as characteristics of smallholder households of each.

The degree or extent of speculation allowed varies among journals, reviewers, editors, etc. In most cases some speculation is permitted, since it is difficult in one experiment to adequately address all factors contributing to differences or similarities and conclusively identify the factor(s) primarily responsible. Appreciable speculation generally will be permitted as long as the basis and entailed assumptions are given. Some speculation seems appropriate given that the authors are most capable of extending the results beyond a particular experiment or to extrapolate to field conditions. Science and knowledge advance through presentation of new ideas.

Few or no livestock experiments are perfect, devoid of problems or flaws. But, if a manuscript is submitted for publication, then it has been decided that any problems were not so severe as to render the findings of no value. Many authors struggle with how best to present experimentation problems in the initial submission. The issue should be presented if it is thought that results could have been influenced or perhaps to help others avoid similar situations. However, fully addressing the limitation may force reviewers to recommend rejection rather than ask for further comment, discussion, or clarification in a revision. Thus, it is common to briefly describe the issue in the initial submission, but wait to provide a full explanation of limitations until asked to do so by a reviewer or editor.

Some experienced and well respected researchers believe that only one, two, or at the most three major findings or important points should be presented in an article; i.e., this is the most one can expect readers to retain. Although this is somewhat debatable, these key findings should be the focus of the Summary and(or) Conclusions section. Relatedly, limitations of findings should be addressed in this section and in the Discussion, particularly regarding conditions to which these results can or should not be applied.

Review

Two common, general reasons for rejection are serious experimental design or conduct problems and inadequate new knowledge to justify publication. Regarding the first issue, an initial step for many reviewers is to look for 'fatal flaws.' These are serious problems in the

design or implementation of an experiment that preclude achievement of objectives. From a practical standpoint, in terms of the reviewer's time, this is a reasonable initial activity. However, if such a concern is found, reviewers should provide a clear description of the limitation in a constructive fashion, which may help authors in future experimentation.

The second reason for rejection, generation of inadequate new knowledge to justify publication, is much more subjective. As stated earlier, a quick assessment method is to read the Introduction and Materials and Methods sections and then predict the results. Because the reviewer's knowledge of the subject presumably arose from previous published research, if the results can be predicted reasonably accurately, then it may be assumed that adequate knowledge in this area existed and insufficient new knowledge was derived. However, such assertions must be made carefully, since there is value in research to confirm previous findings and determine if similar responses occur under other experimental settings, as it is not possible to perfectly replicate or simulate all conditions of an earlier study.

Additional reasons for rejection are extremely poor data interpretation and technical preparation of the article. These are considerations that could possibly be rectified with revision, in contrast to the first two situations. If the revision required is so extensive that a second full-scale review would be required, likely recommendations are rejection with the opportunity for revision and resubmission as a new paper or revise and resubmit for a full review. Some editors opt for the first decision, so as to insure that authors seriously consider all comments. If a clear reason for rejection is not apparent, then the reviewer should focus on possible means of enhancing the manuscript, regarding both interpretation and data presentation.

Some articles require considerable language and technical editing, even though these author responsibilities are clearly stated in journal guidelines. It can be difficult for reviewers to decide how much of the editorial burden is their responsibility. In this regard, because editors realize these conditions detract from the focus of reviewers on the science, it is typically advised that reviewers only change wording and phrasing to enhance understanding of the science presented, with remaining major responsibilities falling to editors or other editorial services.

Reviewers have a key responsibility in making sure interpretation is sound. If deemed unsound, reviewers should justify their contention, providing citations when something is not well known. Reviewers can offer justifiable alternative explanations, but should not attempt to force change to an equally plausible rationale simply because of personal preference. Again, unsound interpretation can result in rejection, but before such a recommendation authors should be given ample opportunity to adopt interpretation supported by the data and other published findings.

Revision

A general recommendation for revising scientific manuscripts is to make the task of the associate or section editor in assessing merit of the revision as easy as possible. Authors should be complete and thorough so that it is not necessary to send the revision packet back to original reviewers. This step unnecessarily inconveniences the editor and reviewers and interferes with the desire of journals to minimize time from initial submission to publication. Relating to the

former, some editors and reviewers prefer to read new submissions rather than re-reading previous submissions.

Authors should be complimentary regarding improvements in the manuscript resulting from the review, in part because of the time and effort required, reinforced by the fact that in most instances there is no monetary incentive for reviewing. And, authors should exercise caution to avoid inadvertently offending or insulting reviewers or editors, and refrain from commenting on inadequate knowledge or poor judgment of reviewers. Moreover, to criticize a reviewer may imply poor selection by the editor, which is also not constructive.

Revising manuscripts promptly helps project an attitude that the authors consider publishing in this journal a high priority. A lengthy revision time also may require the editor and reviewers evaluate the entire manuscript again in more detail than necessary with a prompt return. Rapid response will be appreciated and could also prevent detection of further concerns.

A critical step with most journals is for authors to provide line-by-line responses to each reviewer comment. In some cases when authors simply state that the manuscript has been revised in accordance with review comments without specifically describing changes or reasons for non-compliance, the editor may simply return the revision packet. Without specific responses, it would place too great of a demand on the editor's time. Similarly, it is a major concern if the editor determines that review comments have been inadequately addressed in the revised manuscript in contrast to general line-by-line author responses to the contrary. Likewise, if it is felt that authors did not make a reasonable attempt to consider reviewer comments, the editor alone or with input of original reviewers may reject without further opportunity to revise.

Authors should fully comply with as many reviewer comments as possible. This allows the opportunity for authors to disagree with comments they feel strongly about and argue successfully against such changes. Authors should thoroughly address reviewer comments. It should be perfectly clear that comments were seriously considered and contemplated. It is preferable to say too much vs. not enough in the responses to reviewer comments. However, additions to the manuscript in response to reviewer comments should be brief but adequate to handle the concern. Also, modifications should be limited to those directed by reviewers and editors, with other unsolicited changes increasing chances of re-evaluation by original reviewers and renewed scrutinty. Any changes or additions to discussion in the text should be specified in the responses to reviewer comments as well. It is good to remember that in the responses to reviewer comments, authors are communicating with the editor and perhaps reviewers, whereas in the manuscript readers are the target audience and only require information adequate to understand conduct of the experiment and appropriate interpretation. Authors should attempt to carefully incorporate added information into the text such that it flows naturally as if in the initial submission. Often this is not the case and experienced readers can easily identify sentences and sections inserted during the revision process.

When reviewers comment on limitations in the experimental design or an implementation problem, as noted earlier in regard to manuscript preparation, it is desirable to add additional discussion, ideally with supportive citations. It is generally not sufficient to simply repeat contentions in revision comments already present in the manuscript text. Another issue in

revising is that sometimes a review comment is unclear. In addition to stating that authors are unsure of the intent, they should provide their interpretation of the comment, fully address it, and state a willingness for make further change is there was misunderstanding.

After all reviewer comments have been addressed through responses and changes in the manuscript itself, the entire manuscript should be carefully reviewed again to search for other improvements, which should also be added to the responses to reviewer comments or in the cover letter to the editor. This effort may prevent the editor or reviewers from finding minor errors, and potentially avoid a second revision.

Tables and Figures

Data repetition in the text and tables and(or) figures should be avoided. Although, it is common to provide additional information in the text beyond that presented in tables if so warranted and justified by the statistical analysis and results.

With interactions involving time, as well as for factorial arrangements of treatments, table construction requires careful consideration and planning. Arrangements are simplest if only discussing main effects. However, in order to facilitate possible use of data by future researchers combining data from several experiments, means for individual treatment combinations should be presented regardless of significance of the interaction. This can be done in tables in the main body of the paper, or in an appendix. A number of examples of possible table layouts from AIGR experiments follow.

The study from which DM intake shown below in Table 53 was derived entailed four 4-week periods. After stating in the manuscript that most treatment × period interactions were significant, a statistical analysis by period was conducted. However, because total feed intake over the entire 16-week experiment was important, average values for the whole experiment, reflective of total feed intake, were presented regardless of significance of the interaction. Means were separated by lsd when the overall treatment effect was significant at $P < 0.05$ (i.e., Fisher's protected *F*-test).

Table 53
Effects of separate offering of forage and concentrate on DM intake by Alpine doelings

		Treatment[1]					
Item	Period[2]	A-25C	A-50C	A-75C	AC-AF	LC-AF	SE
DM intake (g/day)							
Concentrate	1	163^{a}	316^{b}	504^{c}	471^{c}	332^{b}	21.4
	2	152^{a}	316^{b}	487^{d}	512^{d}	392^{c}	16.4
	3	162^{a}	338^{b}	467^{c}	618^{d}	414^{bc}	22.7
	4	181^{a}	393^{b}	530^{c}	753^{d}	443^{b}	16.2
	Mean	165^{a}	341^{b}	497^{c}	588^{d}	395^{b}	15.8
Forage	1	446^{d}	260^{bc}	124^{a}	177^{ab}	335^{cd}	37.2
	2	430^{c}	286^{b}	129^{a}	116^{a}	249^{b}	21.5
	3	455^{d}	301^{c}	107^{ab}	56^{a}	196^{b}	26.7
	4	514^{c}	355^{b}	143^{a}	130^{a}	253^{b}	29.8
	Mean	461^{c}	300^{b}	126^{a}	115^{a}	258^{b}	27.7
Total	1	609	576	628	648	667	49.9
	2	582	602	616	628	640	28.6
	3	618	638	575	674	610	45.1
	4	694	748	673	866	696	43.6
	Mean	626	641	623	704	653	38.6

[1]A-25C = ad libitum consumption of a mixed 25% concentrate, 75% forage diet; A-50C = ad libitum consumption of a mixed 50% concentrate, 50% forage diet; A-75C = ad libitum consumption of a mixed 75% concentrate, 25% forage diet; AC-AF = ad libitum consumption of concentrate and forage offered separately; LC-AF = limited consumption of concentrate (approximately 2% body weight) and ad libitum consumption of forage.
[2]Periods were 4 weeks in length.
[a,b,c,d,e]Means within a row without a common superscript letter differ ($P < 0.05$).

The experiment with ADG data shown in Table 54 involved a comparison of growth performance by four goat breeds subjected to two dietary treatments, with change in diet quality at the beginning of Phase 2 as one of the treatments. Thus, phases were analyzed separately. No dietary treatment × breed interactions were significant, allowing presentation of main effect means. However, again, in order for researchers to potentially use these data later, interaction means were listed regardless of the significance of the interaction. Means were separated by lsd when the overall treatment effect was significant at $P < 0.05$.

Table 54
Effects of dietary concentrate level on ADG by growing Alpine, Angora, Boer, and Spanish wether goats

			Breed					Diet[1]		
Item	Phase[2]	Diet	Alpine	Angora	Boer	Spanish	SE	75	50	SE
ADG (g)	1	75	68	72	91	62	10.9			
		50	50	46	90	36				
		Mean	59[a]	59[a]	90[b]	49[a]	7.7	73[b]	55[a]	5.5
	2	75	59	50	64	22	13.9			
		50	57	75	100	28				
		Mean	58[b]	63[b]	82[b]	25[a]	9.6	49	65	6.8
	1-2	75	54	61	95	32	8.1			
		50	54	61	95	32				
		Mean	59[b]	61[b]	86[c]	37[a]	6.1	61	60	4.1

[1]75 = 75% concentrate; 50 = 50% concentrate.
[2]Phases were 12 weeks in length; wethers on both diets received the 75% concentrate diet in phase 2.
[a,b,c,d]Main effect means without a common superscript letter differ ($P < 0.05$).

The studies from which data in Tables 55 and 56 were derived are similar in all but one respect. Both entailed factorial arrangements of treatments. Data in Table 55 are presented separately for four 4-week periods, since treatments consisted of different lengths of nutrient restriction and realimentation. The "a,b,c" footnote in Table 55 and footnote "2" in Table 56 describe how differences among main effect and interaction means were denoted. In brief, main effect means were presented only when the interaction between main effects was nonsignificant, with superscript letters placed by means to reflect differences where appropriate. Differences among means for the main effect of dietary treatment and interaction means in Table 56 were handled similarly, although mean differences for the main effect of genotype were addressed in the text rather than table. Hence, from these tables reviewers and readers can easily discern significance of the main and interaction effects.

Table 55
Effects of urea treatment of wheat straw and supplementation with soybean meal or different levels of broiler litter on N and NDF intake and digestibility in yearling Spanish goats

		Supplement[1]					Straw[2]		
Item[3]	Straw[2]	C	S	LL	HL	SE	U	T	SE
N									
Intake (g/d)	U	3.6	9.2	11.4	15.7	0.70	10.0[a]	18.5[b]	0.87
	T	12.4	17.9	20.2	23.4				
	Mean	8.0[a]	13.6[b]	15.8[c]	19.6[d]	0.50			
Digestion (%)	U	44.6	70.1	48.4	43.9	5.10	51.7	56.8	5.14
	T	58.4	65.6	54.3	49.0				
	Mean	51.5[a]	67.8[b]	51.4[a]	46.4[a]	3.60			
Digestion (g/d)	U	1.6	6.4	5.5	7.0	1.15	5.1[a]	10.4[b]	0.63
	T	7.2	11.8	10.8	11.8				
	Mean	4.4[a]	9.1[b]	8.1[b]	9.4[b]	0.81			
NDF									
Intake (g/d)	U	203	255	316	369	20.9	285	400	52.8
	T	352	354	429	466				
	Mean	278[a]	304[a]	373[b]	416[b]	14.8			
Digestion (%)	U	54.7[a]	57.3[ab]	53.2[a]	66.0[c]	2.63			
	T	69.9[c]	64.5[bc]	66.2[c]	64.1[bc]				
Digestion (g/d)	U	103[a]	136[ab]	163[b]	232[cd]	13.4			
	T	242[cd]	227[c]	281[de]	299[e]				

[1]C = corn-based supplement fed at 0.64% BW (DM basis); S = C plus 0.25% BW of soybean meal; LL = C plus 0.5% BW of broiler litter; HL = C plus 1.0% BW of broiler litter.
[2]U = untreated wheat straw; T = wheat straw ammoniated with urea; mean = main effect means for supplement.
[3]d = day.
[a,b,c,d]Means within straw-supplement, supplement, and straw treatments without a common superscript letter differ ($P < 0.05$); superscripts for straw-supplement treatments are presented when the interaction between straw type and supplement was significant ($P < 0.05$); main effect means for straw and supplement treatments appear when the interaction between straw and supplement was nonsignificant ($P > 0.05$).

Table 56

Effects of length of feed restriction and realimentation and level of supplementation during realimentation on ADG by yearling Boer × Spanish and Spanish doelings

			Dietary treatment[1,2]					
Item	Day	Breed[3]	C	H-28	L-28	H-56	L-56	SE
ADG (g)	1-28	BS	59	11	-20	20	-27	20.3
		S	26	23	28	46	14	
	29-56	BS	24^{ef}	34^{ef}	41^{f}	-63^{ab}	-96^{a}	16.0
		S	6^{de}	13^{ef}	-5^{cd}	-40^{bc}	-36^{bcd}	
	57-84	BS	85^{cd}	-9^{a}	0^{a}	123^{d}	112^{cd}	17.3
		S	26^{ab}	32^{ab}	34^{ab}	64^{bc}	68^{bc}	
	85-112	BS	61	78	84	104	99	12.3
		S	16	28	58	70	71	
		Mean	39^{a}	53^{ab}	71^{bc}	87^{c}	85^{c}	8.6

[1]C = control, daily supplementation with 0.75% BW of concentrate mixture; H-28 = sequential 28-day periods of no supplementation and daily supplementation with 1.50% BW of concentrate mixture; L-28 = sequential 28-day periods of no supplementation and daily supplementation with 0.75% BW of concentrate mixture; H-56 = sequential 56-day periods of no supplementation and daily supplementation with 1.50% BW of concentrate mixture; L-56 = sequential 56-day periods of no supplementation and daily supplementation with 0.75% BW of concentrate mixture.

[2]Main effect means are presented when different ($P < 0.05$) and with a nonsignificant ($P > 0.10$) dietary treatment × breed interaction.

[3]BS = Boer × Spanish; S = Spanish.

[a,b,c,d,e,f]Means within breed × dietary treatment or mean dietary treatment grouping without a common superscript letter differ ($P < 0.05$).

Table 57 displays another useful way to address address treatment effects. In this experiment, the treatment main effect was partitioned by orthogonal contrasts. Letters in the "Effect" column provide a simple mode of indicating contrast significance. Orthogonal contrasts are most appropriate for many experiments, though sometimes with interactions their use may become cumbersome.

Table 57
Effects of level of broiler litter in diets containing wheat straw on intake and apparent total tract digestibility of DM and N in growing Alpine doelings

	Treatment[1]					
Item	U	S	LL	HL	SE	Effect[2]
DM						
Intake (g/day)	420	380	517	544	48.3	T
Digestibility						
%	67.0	76.5	66.5	66.3	3.30	T
g/day	262	286	343	362	29.5	s,t
N						
Intake (g/day)	7.4	8.9	7.8	10.2	0.82	L
Digestibility						
%	54.4	80.4	49.5	47.6	2.98	T
g/day	3.7	7.1	3.9	4.9	0.46	S,T

[1]U = concentrate fed with urea-treated wheat straw; S = concentrate containing soybean meal fed with untreated wheat straw; LL = concentrate containing a low level of broiler litter fed with untreated wheat straw; HL = concentrate containing a high level of broiler litter fed with untreated wheat straw.
[2]Effect: S and s = type of straw or nitrogen supplementation (U vs. mean of S, LL, and HL; $P < 0.05$ and 0.10, respectively); T and t = type of nitrogen supplement (S vs. mean of LL and HL; $P < 0.05$ and 0.10, respectively); L = level of broiler litter (LL vs. HL; $P < 0.05$).

Journals annually update style and format guidelines for tables as well as other components of articles. Although as addressed in previous examples (e.g., Tables 54, 55, and 56), tables can be designed such that the reader knows the significance (e.g., $P < 0.05$) of main effects and interactions without the specific P values being listed. Some journals that previously preferred this structure now require presentation of the exact main effect and interaction P values. Table 58 provides an example of such a table. In addition to presence of superscript letters denoting a treatment P value below 0.05, the actual overall treatment P value is presented.

Table 58
Effects of dietary forages on BW and DM intake and digestion[1]

		Treatment[2]					
Experiment		SER	SER-PEG	ALF	GRASS	SE	P value
1, fresh forage	BW (kg)	35.5	36.2	36.8	36.2	1.27	0.911
	DM						
	Intake (g/day)	907[b]	858[a]	785[b]	740[b]	22.4	< 0.001
	Digestibility (%)	49.4[b]	51.7[b]	60.3[a]	65.0[a]	2.03	< 0.001
	Digestibility (g/day)	449	443	474	480	21.5	0.636
2, hay	BW (kg)	37.7	37.9	37.8	37.3	1.20	0.979
	DM						
	Intake (g/day)	859[ab]	943[a]	741[bc]	666[c]	50.6	0.005
	Digestibility (%)	56.1[b]	61.3[a]	63.6[a]	63.3[a]	1.27	0.002
	Digestibility (g/day)	482[ab]	579[a]	475[ab]	421[b]	36.6	0.040

[1]n = 6 per treatment.
[2]SER = Sericea lespedeza; SER-PEG = SER plus polyethylene glycol; ALF = alfalfa; GRASS = sorghum-sudangrass.
[a,b,c,d]Means in a row without a common superscript letter differ ($P < 0.05$).

The experiment with data shown in Table 59 was more complex than that shown in Table 58, with a 3 × 2 factorial arrangement of treatments involving three breeds and two dietary treatments. Dietary treatments entailed different levels of feeding in two 10-week phases. The table initially submitted to the journal did not include main effect or interaction P values, but rather listed breed main effect means when the interaction was nonsignificant. But when presentation of P values was mandated, this alternate method of denoting differences among breed means was substituted to limit the width and number of columns of an already wide table.

Table 59
Effects of feed intake restriction on BW, body condition score, and ADG

	P value[1]				Angora		Boer		Spanish			
Item	Trt	Brd	Int	Phase	CONT	REST	CONT	REST	CONT	REST	SE	Breed[2]
BW (kg)												
Initial	0.92	< 0.01	0.89		13.7	13.9	21.4	21.5	19.5	19.0	0.82	Angora < Spanish < Boer
End of phase 1	< 0.01	< 0.01	0.34		16.5	12.8	22.7	16.9	20.1	16.4	0.78	Angora < Boer, Spanish
End of phase 2	< 0.01	< 0.01	0.39		18.6	15.9	26.5	21.3	22.5	18.8	0.86	Angora < Spanish < Boer
BCS[3]												
Initial, week 0	0.57	< 0.01	0.50		2.66	2.71	3.12	3.05	3.07	3.02	0.055	Angora < Boer, Spanish
End of phase 1	< 0.01	0.79	0.05		2.78^{b}	2.25^{a}	3.16^{c}	2.04^{a}	3.03^{bc}	2.04^{a}	0.119	
End of phase 2	< 0.01	0.12	< 0.01		2.66^{a}	2.50^{a}	3.22^{b}	2.39^{a}	3.16^{b}	2.39^{a}	0.115	
ADG (g)	< 0.01	< 0.01	< 0.01	1	43^{e}	-20^{c}	16^{d}	-76^{a}	8^{d}	-48^{b}	5.0	
	< 0.01	< 0.01	0.15	2	26	44	50	65	27	32	3.5	

[a,b,c,d,e]Means in a row without a common superscript letter differ (P < 0.05).
[1]Trt = treatment (CONT = intake for moderate energy accretion in 10-week phases 1 and 2; REST = 50% of CONT intake in phase 1 relative to initial BW, followed by the greater level of feeding in phase 2 based on initial or actual BW when greater); Brd = breed; Int = interaction between treatment and breed.
[2]< indicates P < 0.05 for breed mean effect means when the interaction was nonsignificant (P > 0.05).
[3]BCS = body condition score; 1 to 5, with 1 and 5 = extremely thin and obese, respectively.

Table 60 is similar to Tables 58 and 59, although significant ($P < 0.05$) differences were simply denoted with asterisks.

Table 60
Effects of tethering on grazing behavior, heart rate, and energy expenditure of Boer × Spanish goats

	Treatment[1]		Period[2]			Effect[3]	
Item	Free	Tethered	1	2	SE	Treatment	Period
Grazing behavior (min/day)							
Ruminating	360	362	361	361	27.4		
Grazing	405	366	398	374	325		
Idle	675	711	682	705	35.9		
Heart rate (beats/min)	102	83	95	90	1.5	*	*
Energy expenditure							
MJ/day	12.30	9.47	11.28	10.49	0.77	*	
kJ/kg $BW^{0.75}$	633	512	589	557	27.4	*	

[1]Free = free movement in 0.72-ha paddocks; tethered = attachment to a 3-m tether for access to an area of 28.3 m^2 that was moved daily; 8 observations per treatment.
[2]Consecutive 2-week periods of the crossover experiment.
[3]* = $P < 0.05$.

Data in Table 61 provide an example of a study in which three factors were addressed. The treatment arrangement was a 2 × 2 × 3 factorial, with two breeds, two diets, and three levels of feeding in a split-plot design. There were a number of significant two-way interactions. The three-way interaction was not significant for any variable, although the table structure was conducive to presentation of three-way interaction means.

Table 61
Effects of level of feed intake and breed of growing meat goats on heart rate (HR) and energy expenditure (EE)

				Level of feed intake			
Item	Breed[1]	Diet[2]	Mean[3]	Fasting	Maintenance	Ad libitum	SE
HR (beats/min)	BS	Mean		54.7[a]	70.8[b]	91.9[c]	2.02
	S	Mean		51.9[a]	71.5[b]	99.7[c]	
	BS	CON	72.4[a]				2.21
		FOR	72.5[a]				
	S	CON	69.0[a]				
		FOR	79.7[b]				
EE (kJ/kg $BW^{0.75}$)	Mean	Mean		270[a]	390[b]	500[c]	8.7

[a,b,c]Means in a row, breed × amount feed intake grouping, or breed × diet grouping without a common superscript letter differ ($P < 0.05$).
[1]BS = Boer (75%) × Spanish; S = Spanish; Mean = average of values for all goats.
[2]CON = concentrate-based diet (65% concentrate); FOR = forage (alfalfa hay); Mean = average of values for all goats or for goats of each breed.
[3]Mean = average of values for goats on each breed × diet treatment.

But, Table 62 does include presentation of some three-way interaction means. This experiment had a 2 × 2 × 3 factorial arrangement of treatments, with two species (goats and sheep), two origins (highland and lowland areas of Ethiopia), and three lengths of rest (0, 1, and 2 days). The structure of Table 62 is somewhat different than Table 61, with a more horizontal and wider presentation.

Table 62
Effects of days of rest, species (goats and sheep), and origin (Highland and Lowland areas) on BW, carcass weight, and mass of non-carcass tissues

		Rest (days)				Highland			Lowland				Goats		Sheep			
Item	Species	0	1	2	SE	0 day[1]	1 day[1]	2 days[1]	0 day	1 day	2 days	SE	H[2]	L[2]	H	L	SE	Effect[3]
Harvest BW (kg)						20.3^{ab}	21.6^{bc}	20.9^{abc}	21.1^{abc}	19.3^{a}	22.0^{c}	0.47						
Empty BW (kg)	Goats					15.7^{bc}	15.9^{c}	15.5^{abc}	14.4^{ab}	15.7^{bc}	15.8^{bc}	0.55						
	Sheep					14.0^{a}	15.7^{bc}	14.9^{abc}	15.1^{abc}	14.0^{a}	15.0^{abc}							
Carcass weight																		
kg						7.86^{ab}	8.37^{bc}	7.97^{ab}	8.07^{abc}	7.64^{a}	8.45^{b}	0.204	8.35	8.16	7.77	7.94	0.167	SP
% live weight													40.2^{c}	38.7^{b}	37.0^{a}	38.2^{b}	0.56	
% empty BW													53.2	54.0	52.3	54.0	0.60	OR
Feet (g)	Goats	630^{b}	585^{b}	615^{b}	17.3													
	Sheep	468^{a}	515^{a}	505^{a}														
Liver (g)		324^{a}	356^{b}	349^{b}	7.4													

[1]Days of rest before harvest.
[2]H = Highland; L = Lowland.
[3]SP = species, OR = origin ($P < 0.05$); abbreviations are shown when interactions involving these main effects were nonsignificant ($P > 0.05$).
[a,b,c]Means within rest, species × rest, origin × rest, or species × origin groupings without a common superscript letter differ ($P < 0.05$).

Table 63 provides an example of a study with a complex array and large number of treatments. Six of the 12 treatments involved different lengths of rest before harvest and six different feeding period lengths. The sheep originated from highland or lowland areas of Ethiopia. Means were separated by 12 non-orthogonal contrasts. Because of the large number of columns required for presentation of treatment means, numbers were used to denote the significance of contrasts. SAS statements are at Appendix 1 page 164-165.

Contrasts were also used for means separation with data of the 6 × 6 Latin square experiment shown in Table 64, with SAS statements in Appendix 1 page 166, although with the 2 × 3 factorial arrangement of treatments contrasts were included for interactions. Hence, rather than one column with letter abbreviations or numbers to denote significance as in Tables 57, 62, and 63, one column for each contrast contains the exact P values. Currently it is probably more common to present P values with three rather than two decimal places. Relatedly, with more complex factorial designs and need to present main effect and interaction means for different variables, in some cases it is necessary to have a table for P values and another for means and SE.

Table 65 presents data from an experiment with lactating dairy goats consuming two different diets with measures in three periods. Interaction means are presented regardless of significance of the interaction, and main effect means for period are given when the interaction was nonsignificant and at least one significant difference was detected between periods. However, with just these values, it is not clear if the main effect of diet was significant when the interaction was nonsignificant. Hence, the table includes a column for presenting the P value for diet. And again, some journals could require P values with three decimal places.

Table 63
Effects and interactions of sheep origin, feeding, and linear and quadratic effects of rest and feeding period lengths on BW, linear measures, and carcass composition

	Rest treatments[1]						Feeding treatments[2]									
Item	H-R1	H-R2	H-R3	L-R1	L-R2	L-R3	H-F2	H-F4	H-F6	L-F2	L-F4	L-F6	SE[3]	SE[4]	SE[5]	Effect[6]
BW																
Initial (kg)							20.4	21.1	20.6	20.7	20.2	20.6		0.57		
Gain (g/day)							209	120	125	118	90	113		15.1		8,9,10,11
Empty (kg)	18.5	18.4	17.3	16.5	16.3	16.2	19.0	19.7	21.0	17.6	17.7	20.0	0.51	0.46	0.48	1,3,6,8,9
Body length (cm)	54.1	54.2	54.8	48.7	53.0	50.6	56.0	56.0	56.3	52.4	53.1	52.5	0.77	0.59	0.68	1,3,5,7,8
Paunch girth (cm)	75.8	74.7	72.4	77.0	78.7	78.9	74.3	78.3	79.1	78.4	77.4	81.3	1.01	0.98	1.07	1,3,6,8,9,12
Lean (kg)	4.59	5.27	5.15	4.30	4.43	4.37	4.86	4.44	5.60	4.08	4.04	4.73	0.139	0.210	0.220	3,4,8,9,10
Intermuscular fat (g)	131	138	117	105	65	91	153	151	113	162	211	223	28.7	25.0	28.3	1,2,8,11

[1]H and L = Highland and Lowland sheep, respectively; R1, R2, and R3 = rest for 1, 2, and 3 days, respectively.
[2]F2, F4, and F6 = feeding for 2, 4, or 6 weeks, respectively.
[3]SE for the analysis of rest treatments.
[4]SE for the analysis of feeding treatments.
[5]SE for the analysis of all treatments.
[6]1 = rest vs. feeding; 2 = origin × rest vs. feeding; 3 = effect of origin with rest treatments; 4 = linear effect of rest length; 5 = quadratic effect of rest length; 6 = origin × linear effect of rest length; 7 = origin × quadratic effect of rest length; 8 = effect of origin with feeding treatments; 9 = linear effect of feeding length; 10 = quadratic effect of feeding length; 11 = origin × linear effect of feeding length; 12 = origin × quadratic effect of rest length; listing of contrast numbers indicates $P < 0.05$.

Table 64
Effects of dietary CP level and supplemental ruminally undegraded intake protein from different ratios of fish and blood meals on site and extent of organic matter (OM) digestion and ruminal fluid characteristics in Boer × Spanish wethers

	12% CP (DM basis)[1]			15% CP (DM basis)[1]				Effect[2] (P <)				
Item	100F	67F	33F	100F	67F	33F	SE	CP	L	Q	CP×L	CP×Q
OM												
Intake (g/day)	1,001	938	979	979	958	935	2.6	0.01	0.01	0.01	0.01	0.01
Duodenum (g/day)												
Total	428	501	517	495	566	647	28.4	0.01	0.01	0.66	0.30	0.54
Microbial	151	162	169	159	196	203	11.7	0.01	0.01	0.38	0.24	0.54
Non-microbial	278	332	357	333	372	435	22.9	0.01	0.01	0.97	0.66	0.55
Ileum (g/day)	207	260	282	263	294	345	20.7	0.01	0.01	0.88	0.88	0.49
Feces (g/day)	190	253	247	240	268	295	17.8	0.01	0.01	0.15	0.92	0.22
Digestion (% intake)												
Apparent ruminal	58.4	47.1	48.4	50.2	41.5	32.0	2.89	0.01	0.01	0.26	0.19	0.24
True ruminal	72.9	65.0	64.5	66.6	61.8	54.7	2.28	0.01	0.01	0.55	0.50	0.29
Small intestine	21.5	25.3	23.4	22.9	28.2	31.1	2.42	0.06	0.05	0.35	0.23	0.72
Hindgut	1.6	0.4	3.7	2.6	2.7	5.3	1.57	0.23	0.13	0.21	0.88	0.76
Total tract	81.4	73.0	75.3	75.7	72.3	68.5	1.77	0.01	0.01	0.03	0.71	0.04

[1]100F, 67F, and 33F = 100, 67, and 33% of supplemental ruminally undegraded intake protein from fish meal and 0, 33, and 67% from blood meal, respectively.
[2]CP = dietary CP level; L and Q = linear and quadratic effects of levels of supplemental ruminally undegraded intake protein from fish and blood meals, respectively; CP × L and CP × Q = interaction between CP level and linear and quadratic effects of levels of fish and blood meals, respectively.

Table 65
Effects of dietary concentrate level on ADG, DM intake, change in body condition score, and milk composition by Alpine does at 1 to 2, 3 to 4, and 5 to 6 mo of lactation

	40% forage			60% forage				Month of lactation				
Item	1 to 2 mo	3 to 4 mo	5 to 6 mo	1 to 2 mo	3 to 4 mo	5 to 6 mo	SE	1 to 2	3 to 4	5 to 6	SE	Diet, P <
ADG (g/day)	-136	24	121	-61	46	4.17	25.2	-90[a]	35[b]	97[c]	17.8	0.42
BCS[1] change	-0.56	0.55	0.39	-0.14	0.42	0.33	0.127	-0.35[a]	0.49[b]	0.36[b]	0.090	0.48
DM intake (kg/day)	2.23	2.14	2.10	2.42	2.81	2.55	0.130					0.01
Milk composition (%)												
Fat	3.84	2.87	3.26	2.99	2.40	3.17	0.188	3.42[b]	2.63[a]	3.21[b]	0.133	0.01
Protein	2.84[d]	2.39[ab]	2.51[bc]	2.59[bc]	2.25[a]	2.75[cd]	0.888					
Lactose	4.23[bc]	4.24[bc]	4.17[ab]	4.33[c]	4.06[a]	4.16[ab]	0.050					
Solids-non-fat	7.98[c]	7.52[b]	7.57[b]	7.79[bc]	7.20[a]	7.80[bc]	0.103					
Total solids	11.82	10.39	10.83	10.77	9.60	10.96	0.264	11.30[b]	9.99[a]	10.90[b]	0.187	0.02

[1]BCS = body condition score; 1 to 5, with 1 = extremely thin and 5 = extremely obese.

In addition to determining effects of treatments, it is also often of value to study relationships between various factors. As addressed earlier, correlation analysis is useful in this regard. Correlation coefficients can be presented in the text, but if a large number are of interest, a table can be used, an example of which is given in Table 66.

Table 66
Relationships between variables for yearling meat goats[1]

	Item[2]							
Item	BCS (1-5)	US (%)	US (kg)	Water (%)	Fat (%)	Protein (%)	Ash (%)	Energy (MJ/kg)
SBW (kg)	0.80	0.06	0.65	-0.44	0.58	0.01	-0.30	0.58
	0.01	0.70	0.01	0.01	0.01	0.93	0.02	0.01
BCS (1-5)		0.00	0.48	-0.54	0.78	0.12	-0.45	0.78
		0.99	0.01	0.01	0.01	0.46	0.01	0.01
US (%)			0.79	0.21	0.00	-0.51	-0.19	-0.05
			0.01	0.20	1.00	0.01	0.24	0.78
US (kg)				-0.08	0.32	-0.36	-0.37	0.29
				0.64	0.05	0.03	0.03	0.08
Water (%)					-0.83	-0.14	0.40	-0.84
					0.01	0.38	0.02	0.01
Fat (%)						0.08	-0.49	1.00
						0.62	0.01	0.01
Protein (%)							0.34	0.17
							0.04	0.30
Ash (%)								-0.45
								0.01

[1]P values are given below the correlation coefficients; concentrations are on a shrunk body weight (SBW) basis.
[2]BCS = body condition score, 1 and 5 = extremely thin and obese, respectively; US = urea space.

Rather than use of footnote 1, a column could be inserted to include row headings specifying correlation coefficient, or r, and the P value for each variable. However, such a table would be quite wide with a large number of variables.

Equations are sometimes developed either to help understand relationships between or among various factors or to predict responses. Equations can be presented in the text as noted below, tables (e.g., Tables 67 and 68), or figures (e.g., Figure 7 and 17).

- Equation 1 - time grazing/eating (hours): EE_a%, observed = 3.73 (SE = 7.034) + (0.716 (SE = 0.1683) × EE_a%, predicted) (R^2 = 0.24; mean bias = 7.4).

Or, the ± symbol could be used in place of SE.

- Equation 1 - time grazing/eating (hours): EE_a%, observed = (3.73 ± 7.034) + ((0.716 ± 0.1683) × EE_a%, predicted) (R^2 = 0.24; mean bias = 7.4).

Table 67
Equations for regressions of heat energy (HE) by different goat breeds expressed as a percentage of HE in wk 0 for animals subjected to restricted feed intake, corrected for HE of corresponding animals on a constant plane of nutrition adequate for maintenance and moderate energy accretion, against length of restriction (week) in phase 1 (HEMBW%CH, kJ/kg $BW^{0.75}$)

		HEMBW%CH			
Phase and breed	Intercept or independent variable	Parameter estimate	SE	P value	Model R^2
Phase 1					
Angora	Intercept	95.8	2.43	0.01	0.58
	Week	-8.18	1.144	0.01	
	$Week^2$	0.655	0.1098	0.01	
Boer	Intercept	95.3	2.63	0.01	0.41
	Week	-4.34	1.237	0.01	
	$Week^2$	0.271	0.1187	0.03	
Spanish	Intercept	97.4	2.21	0.01	0.53
	Week	-4.69	1.068	0.01	
	$Week^2$	0.282	0.1021	0.01	

Table 68
Summary of regression parameters for Lucas test equations (DCP = b_0 + b_1 × CP; DCP = apparently digestible CP) used to estimate DCP in goats

Database	Residual deleted	n	R^2	RMSE[1]	b_0 = MFCP[2]	b_1 = true CPD[3]
Entire	None	622	0.851	1.58	2.697 ± 0.202	85.66 ± 1.44
Subset 1	≤ 1.58, > 1.58	515	0.965	0.71	2.635 ± 0.099	86.89 ± 0.73
Subset 2	≤ 1.58	562	0.952	0.86	2.670 ± 0.116	88.31 ± 0.84
Subset 3	≤ 3.16	601	0.927	1.06	2.620 ± 0.138	86.63 ± 0.99

[1]Root mean square error.
[2]Metabolic fecal CP.
[3]True CP digestibility.

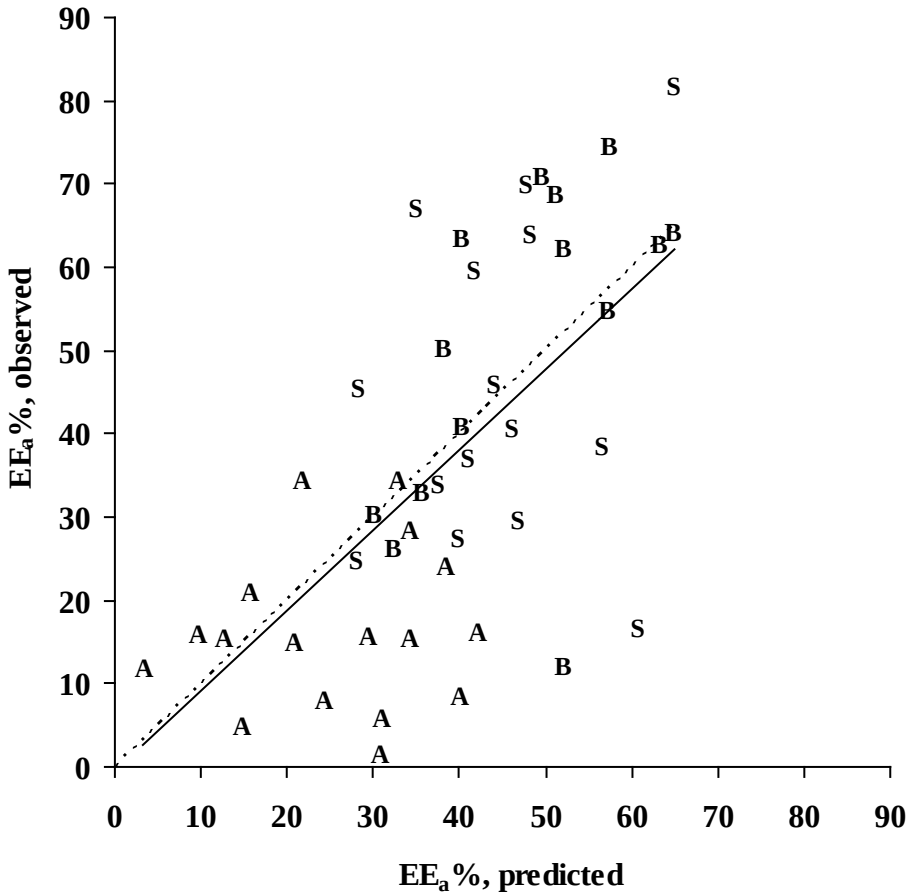


Figure 17. The relationship between observed energy expenditure by goats due to activity (EE_a%, % of the ME requirement for maintenance plus activity of a goat in confinement) and that predicted from time spent grazing/eating based on data of Beker et al. (2009). A, B, and S = Angora, Boer, and Spanish goats, respectively. The solid line depicts Equation 5: EE_a%, observed = -0.35 (SE = 7.220) + 0.963 (SE = 0.1759) × EE_a%, predicted (R^2 = 0.40; mean bias = 1.8). The dashed line depicts EE_a%, observed = EE_a%, predicted.

Although SE were not included in Figure 5 or 17 because of the nature of the data and specific purpose of the equations, in most cases figures contain an index of variability. Figures 18 and 19 below provide examples, with SE bars included above but not below points to minimize figure clutter.

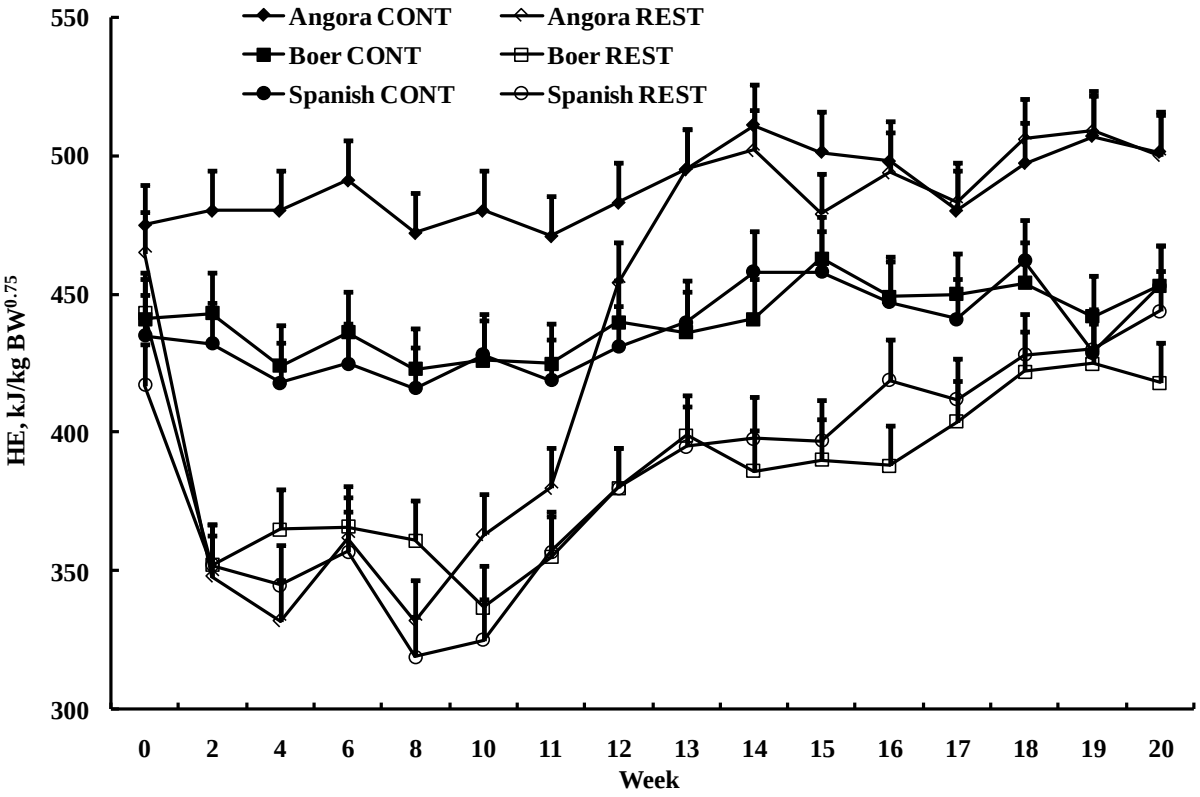


Figure 18. Heat energy (HE) relative to kg $BW^{0.75}$ of different breeds of goats with restricted (REST) or unrestricted (CONT) feed availability in weeks 1 to 10 and unrestricted feed availability in weeks 11 to 20.

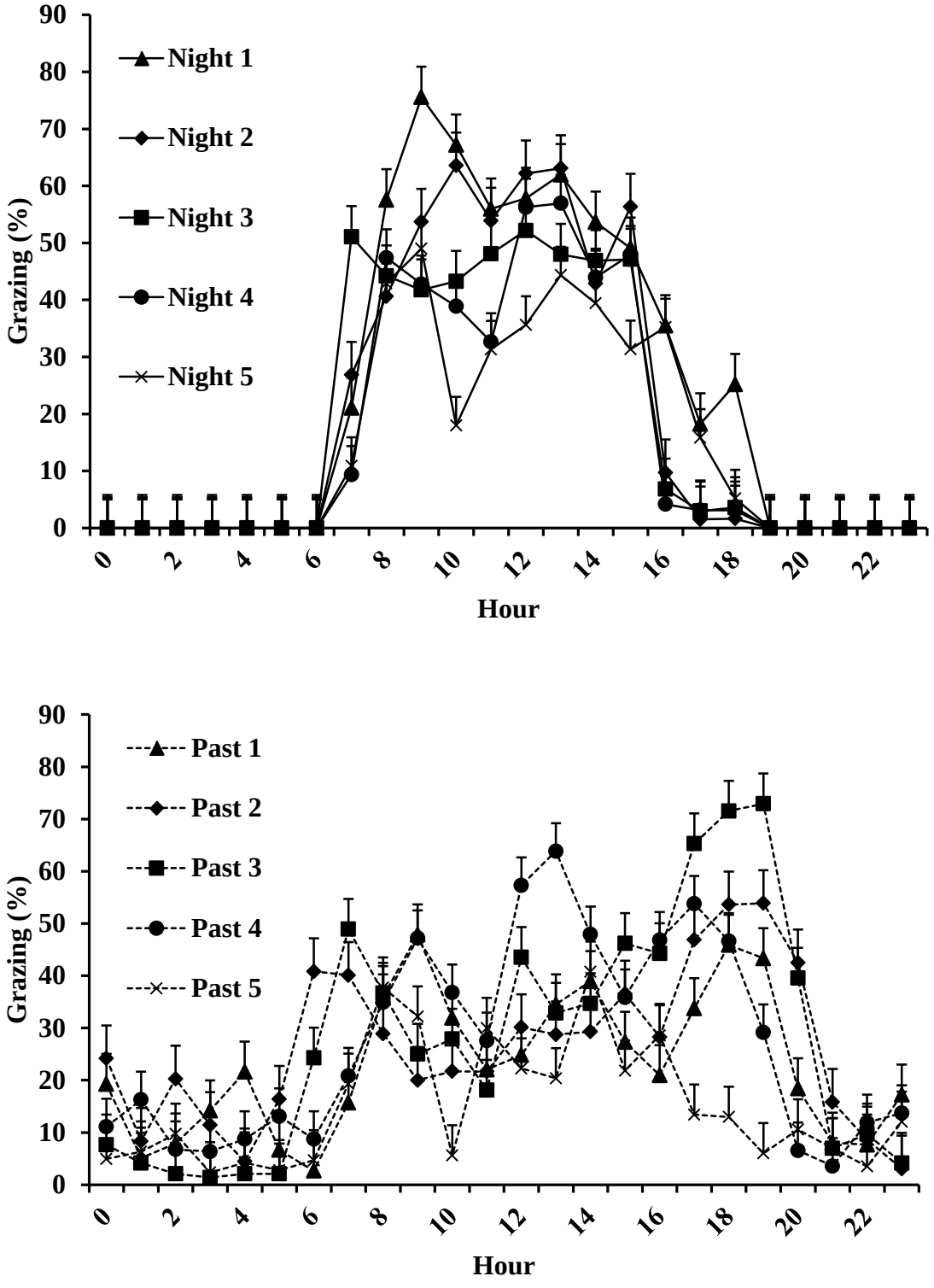


Figure 19. Effects of night-locking, stage of production, and hour of the day on time spent grazing by meat goat does grazing grass/legume pasture. Night = confined at night; Past = continuous pasture access. Period: 1 = late gestation, 2 = early lactation; 3 = late lactation; 4 = dry; 5 = early gestation.

Extension, Technology Transfer, Outreach

Introduction

One of the Technical Bulletins (number 37) of the ESGPIP is entitled "Methods in Sheep and Goat Technology Extension" (Tadesse, 2013). The quote below is an answer to the question "What is agricultural extension?".

- "Agricultural extension can be defined as the application of communication and learning activities to transfer "proven" technologies, practices, and skills to producers of agricultural commodities. Accordingly, the objective of sheep and goat extension is to sustainably improve production and productivity of sheep and goats through technological knowledge and skills combined with indigenous knowledge. Sheep and goat extension will result in better management of sheep and goats that produce more quality products and consequently generate higher income to the producer."

General Extension Delivery Systems

Cole (1981) and Tadesse (2013) outlined three delivery systems or teaching methods that are commonly used by extension educators: individual contact, group contact, and mass media. The most appropriate method varies with factors such as the nature of the information to be disseminated, resources available, and clientele characteristics such as literacy.

Although the individual contact method involves one-on-one interaction, it is important to obtain and consider views of all members of the group. Advantages and disadvantages listed below from Cole (1981) and Tadesse (2013) are of relatively greater pertinence to on-farm research conducted with the ISH than FGR approach.

Individual contact advantages:
- Easy to identify particular problems in real-time
- Immediate feedback on understanding of the message
- People listen to advice and suggestions of extension staff they know, like, and respect.

Individual contact disadvantages:
- Very expensive in terms of time and infrastructure support
- Very few producers reached within a given period of time
- Less opportunity to check on quality of technical advice provided
- A possibility that extension workers will select only a few beneficiaries
- Requires considerable effort of the extension agent
- Requires trust and respect of the extension agent

Methods of disseminating information via individual contact include written materials (e.g., fact sheets, technical bulletins, leaflets, pamphlets), verbal communications (e.g., general meetings, conferences), and audiovisuals (e.g., blackboards, flip charts, pictures, photographs, slide films, etc.). Home visits, telephone calls, office calls, music, songs, tales, and skits also can

be employed, and receipt of extension services through the internet is becoming common in some areas.

Most advantages and disadvantages of group contact extension are similar to those of individual contact. The considerations below, also from Cole (1981) and Tadesse (2013), have varying degrees of relevance to on-farm research conducted with both FRG and ISH at the village or community level.

Group contact advantages:

- Less expensive than individual contact in terms of staff time and cost of transportation per person
- More people reached within a given period of time
- Decisions are more effective since they are developed collectively.
- Beneficiaries can share resources.
- Members have common aims or ideas to bind them.
- Opportunities for strengthening friendships and team work, allowing members to share ideas, experiences, and problems
- Provides a forum for extension personnel to introduce ideas and skills that may be relevant to problems and needs of clientele
- Increased personal motivation
- Groups can seek funding and advice from NGO or donor organizations to support their development work.

Group contact disadvantages:

- Can take a long time to arrive at a decision
- Sometimes difficult to get people to agree on issues and work together
- Influential people may divert the group from desired courses of action.
- Groups may become dependent on donor organizations and NGO.
- Individual problems may not be adequately addressed.
- People who are not members will not be reached.
- Conflict may rise among members.
- Members must have similar interests and understanding about the group and what it will achieve.
- Benefits should be distributed fairly, according to amounts of effort contributed.

There are different tools or means of delivering services using the group contact method, which include method and result demonstrations. Method demonstrations create awareness of new technologies and their implementation, and are particularly effective because of the opportunity afforded for discussion in real-time. Although such demonstrations are for groups, the number of people should be limited to the most appropriate size for ample individual attention. In the context of on-farm livestock research, method demonstrations can be quite successful when major roles are assumed by the participating households implementing the technology while the activity is underway with both FRG and ISH approaches.

Result demonstrations are intended to arouse interest in a practice and provide evidence for benefits. The comparison of traditional and new practices is a main feature. Result demonstrations can occur during exchange visits, visits to institutions, field days, workshops, seminars, and study tours.

For on-farm research activities of the ESGPIP, field days and workshops encompassed aspects of both method and result demonstrations. The target audience was beyond particular households participating in research activities. In addition, many demonstrations were held in communities not involved in on-farm research.

The mass media method is designed to expose a large number of people to the same information. Radio, television, newspaper, newsletters, motion pictures, photographs, posters exhibitions, internet, etc. are the best tools to disseminate the necessary information. Drama can also be used to create public awareness of various issues. The delivery system depends on the nature of the information to be disseminated. One system or a combination can be used to deliver the same information. The mass media method is advantageous in that many people can be reached within a short period of time even in remote areas. One-way flow of information, limited access to media, and difficulty in evaluating impact without feedback are among drawbacks of the method. This method was not employed by the ESGPIP for on-farm research, but was important for other activities such as introduction of improver small ruminant breeds.

Technical Bulletins, Fact Sheets, Newsletters, Popular Press Articles

Many different types of publications can be used to disseminate useful findings from on-farm research to extension personnel who work directly with smallholder households. Most important considerations can be found by viewing Technical Bulletins (**TB**) of the ESGPIP, available at www.esgpip.org. These TB were one of the interventions to improve capacity of KDA to assist smallholder households in production of sheep and goats.

The TB of the ESGPIP were purposely limited in length, with text ranging from 7 to 16 pages excluding Foreword and Table of Contents sections. Most TB employed an appropriate font size and line spacing, although some contained too few or too many words per page. Each TB included a Table of Contents, although this may not have been necessary for shorter ones, particularly when the line spacing was large and words per page and in the entire TB were limited. Likewise, a Table of Contents would not be necessary for Fact Sheets with information on one or two pages. An attribute of the ESGPIP TB is their small size (i.e., 14.25 × 20.25 cm), which is convenient for carrying.

Only the most essential information should be included in publications such as TB, and the language and words used should be simple and common. In this regard, many ESGPIP TB include a Glossary section. If deemed useful for some individuals, more complex or detailed information could be included in an appendix, as is the case for a few TB of the ESGPIP.

Pictures, drawings, and diagrams can be very beneficial in publications primarily for use by extension personnel. Some TB of the ESGPIP provide examples of effective use of pictures, drawings, and diagrams. But, others contained an excessive number, resulting in size smaller

than can be comfortably viewed. The number of publications developed should be in accordance with useful technologies or practices identified or evaluated through on-farm research. Too many publications with overlapping or non-original information may minimize attention given by, and interest of, the target clientele. Some TB from the ESGPIP are very short and could have been combined with another TB on a similar topic.

A key feature of most ESGPIP TB is a section at or near the end with a title such as those below.

- "What can the KDA do to promote sustainable utilization" (number 23)
- "ROLES OF DEVELOPMENT AGENTS" (number 24)
- "The role of Kebele Development Agents in prevention and control of sheep and goat pox" (number 29)
- "WHAT CAN THE KEBELE DEVELOPMENT AGENT (KDA) DO?" (number 30)
- "Messages to Development Agents" (number 32)

This section consists of bullet statements, ranging in number from 3 to 11, which should be very useful for the KDA to implement the information in assistance of smallholder households.

Field Days, Workshops, Farm Tours, etc.

As noted above, field days, workshops, farm tours, etc. can be very effective instruments to disseminate useful findings of on-farm research as well as information derived from other sources. Nearly all on-farm research activities of the ESGPIP included a field day. For these events it is important to have considerable involvement of participating extension officers and households, rather than being primarily led by a researcher with whom the smallholders may not be comfortable and open with. It is desirable to have participating smallholder farmers share their experiences with others. This includes ones perhaps not officially part of the on-farm research activity but who adopted one or more of the interventions after observation and interaction with participants. The ESGPIP also capitalized on on-farm research field days to demonstrate other technologies that were not being addressed in a specific study. For example, at a field day for on-farm research dealing with ammoniation of a crop residue via urea treatment, construction of urea-molasses multi-nutrient blocks, ensiling of forage, and(or) production and use of improved forages were demonstrated as well.

Today there are many means of disseminating information that can be generated from on-farm research. One method used in the latter part of the ESGPIP was video clips for education of KDA, similar in purpose to TB. In fact, the AIGR of LU now has a series of educational videos on YouTube. However, internet conditions in some developing countries may limit present usefulness of this approach, and equipment and training for preparation may not be widely available.

Impact Assessment

Assessing impact of on-farm livestock research as well as other interventions is important but difficult. The challenge relates in part to change occurring over long periods of time relative to that of typical projects supported by entities such as USAID. To address baselines and track effects of on-farm research and other activities of the ESGPIP, the initial plan was to use questionnaires. One questionnaire was to be completed by KDA during annual 2-week periods of training in sheep and goat production. The second was to be completed later, again by KDA but through farm visits or other contacts such as field days and workshops. However, for a variety of reasons this questionnaire activity was not very successful in assessing impact. In addition to time, personnel, and fund constraints, the lack of adequate incentive for individuals to complete questionnaires was a significant issue. Nonetheless, the initial activity plans are overviewed below.

The first questionnaire was intended to provide an overall village characterization in regards to small ruminant productivity and, thus, included items such as general descriptions of production conditions and practices, etc. The second questionnaire was designed to more specifically address conditions on individual farms, with questions pertaining to current states of production, production cost, factors most constraining to production, prevailing practices, quantities and types of products marketed, prices received from marketed small ruminant products, how marketing decisions were made, profit, etc. The KDA were to select a certain proportion of smallholder households served. Moreover, households involved in on-farm research were included, with completion of the questionnaire annually during the life of the ESGPIP, which was to be a condition of participation. Likewise, KDA with farmers participating in ESGPIP activities such as on-farm research were to fill out the first questionnaire each year. These questionnaires and their repeated applications were to provide a geographically broad database to characterize small ruminant productivity in Ethiopia and track change due to interventions of the ESGPIP. Descriptions of the types of information in the questionnaires are shown below.

First Questionnaire

- General information on smallholder households served by KDA
  - ☐ Number of households or farms
  - ☐ Average family size
  - ☐ Average land holding
  - ☐ Average literacy
  - ☐ Percentage of households headed by women
  - ☐ Primary and secondary sources of income

- Characterization of small ruminant production conditions in recent years
  - ☐ Primary and secondary crops grown, yields, and uses
  - ☐ Average numbers of different types of livestock
  - ☐ Relative importance of different livestock species
  - ☐ Family member(s) caring for sheep and goats
  - ☐ Water supply for sheep and goats
  - ☐ Major feedstuffs for sheep and goats in different periods of the year
  - ☐ Average birthing rates for sheep and goats
  - ☐ Average birth weights for sheep and goats
  - ☐ Average weaning ages and weights for sheep and goats
  - ☐ Most prevalent sheep and goat breeds
  - ☐ Average mature weights of sheep and goat breeds raised
  - ☐ Average mortality rates of sheep and goats of different ages
  - ☐ Typical health management practices for sheep and goats
  - ☐ Primary and secondary factors limiting sheep and goat productivity

- Economic returns in recent years
  - ☐ Average ages of sheep and goats marketed
  - ☐ Average weights of sheep and goats marketed
  - ☐ Average body condition of sheep and goats typically marketed
  - ☐ Average market prices for sheep and goats, including possible seasonal fluctuations
  - ☐ Estimated value of sheep and goat products consumed on-farm
  - ☐ Reasons for marketing of sheep and goats
  - ☐ Primary and secondary factors limiting economic returns from sheep and goats

Second Questionnaire

- General farm information
  - ☐ Family size
  - ☐ Land holding
  - ☐ Literacy
  - ☐ Household head
  - ☐ Primary and secondary sources of income

- Characterization of small ruminant production conditions during the most recent year
  - ☐ Primary and secondary crops, uses, and yields
  - ☐ Numbers of different types of livestock
  - ☐ Relative importance of different livestock species
  - ☐ Family member(s) caring for sheep and goats
  - ☐ Water supply for sheep and goats
  - ☐ Major feedstuffs for sheep and goats in different periods of the year
  - ☐ Birthing rates for sheep and goats
  - ☐ Birth weights for sheep and goats
  - ☐ Weaning ages and weights for sheep and goats
  - ☐ Sheep and goat breeds
  - ☐ Mature weights of sheep and goat breeds raised
  - ☐ Mortality rates of sheep and goats of different ages
  - ☐ Health management practices for sheep and goats
  - ☐ Primary and secondary factors limiting sheep and goat productivity

- Economic returns
  - ☐ Ages sheep and goats marketed
  - ☐ Weights sheep and goats marketed
  - ☐ Number of different types of sheep and goats marketed
  - ☐ Markets used for sheep and goats
  - ☐ Other marketing options available and reasons for not using
  - ☐ Body condition of sheep and goats marketed
  - ☐ Market prices received for sheep and goats
  - ☐ Estimated value of sheep and goat products consumed on-farm
  - ☐ Reasons for marketing sheep and goats
  - ☐ Primary and secondary factors limiting economic returns from sheep and goats
  - ☐ Estimates of expenses in sheep and goat production
    - Feed
    - Health care
    - Animal purchase
    - Other

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Appendix 1. Statistical Analysis Statements

The 'lsmeans' statements below are for illustrative purposes. Most appropriate methods of means separation depend on specific objectives and treatments. The default covariance structure for SAS models is assumed, although that most appropriate would vary with the particular data set and variable. Appendix 2 lists results of these statements and analyses, and simulated data sets are in Appendix 3.

Described in Table 63 of Chapter 10 - Dissemination

SAS GLM

In order to compare treatments with and without a feeding period, animal was considered the experimental unit, although as noted earlier data for treatments with a feeding period were analyzed separately as a split-plot. For means separation, 12 non-orthogonal contrasts were employed. Treatments are described below.

Description of treatments in Table 63

Treatment number	Origin	Feeding	Length of feeding[1] or rest
1	Highland	No	1 day
2	Highland	No	2 days
3	Highland	No	3 days
4	Highland	Yes	2 weeks
5	Highland	Yes	2 weeks
6	Highland	Yes	4 weeks
7	Highland	Yes	4 weeks
8	Highland	Yes	6 weeks
9	Highland	Yes	6 weeks
10	Lowland	No	1 day
11	Lowland	No	2 days
12	Lowland	No	3 days
13	Lowland	Yes	2 weeks
14	Lowland	Yes	2 weeks
15	Lowland	Yes	4 weeks
16	Lowland	Yes	4 weeks
17	Lowland	Yes	6 weeks
18	Lowland	Yes	6 weeks

[1]There were two animal groups per feeding period treatment because supplements with and without added vitamin E were fed.

The SAS commands are given below.

```
proc glm;
classes treatment;
model variable = treatment;
contrast '1' treatment -2 -2 -2 1 1 1 1 1 1 -2 -2 -2 1 1 1 1 1 1;
contrast '2' treatment 2 2 2 -1 -1 -1 -1 -1 -1 -2 -2 -2 1 1 1 1 1 1;
```

```
contrast '3' treatment -1 -1 -1 0 0 0 0 0 0 1 1 1 0 0 0 0 0 0;
contrast '4' treatment -1 0 1 0 0 0 0 0 0 -1 0 1 0 0 0 0 0 0;
contrast '5' treatment -1 2 -1 0 0 0 0 0 0 -1 2 -1 0 0 0 0 0 0;
contrast '6' treatment 1 0 -1 0 0 0 0 0 0 -1 0 1 0 0 0 0 0 0;
contrast '7' treatment 1 -2 1 0 0 0 0 0 0 -1 2 -1 0 0 0 0 0 0;
contrast '8' treatment 0 0 0 -1 -1 -1 -1 -1 -1 0 0 0 1 1 1 1 1 1;
contrast '9' treatment 0 0 0 -1 -1 0 0 1 1 0 0 0 -1 -1 0 0 1 1;
contrast '10' treatment 0 0 0 -1 -1 2 2 -1 -1 0 0 0 -1 -1 2 2 -1 -1;
contrast '11' treatment 0 0 0 1 1 0 0 -1 -1 0 0 0 -1 -1 0 0 1 1;
contrast '12' treatment 0 0 0 1 1 -2 -2 1 1 0 0 0 -1 -1 2 2 -1 -1;
lsmeans treatment / stderr pdiff;
```

SAS MIXED

```
proc mixed method = reml covtest cl;
classes treatment animal;
model var = treatment;
random animal(treatment);
contrast '1' treatment -2 -2 -2 1 1 1 1 1 1 -2 -2 -2 1 1 1 1 1 1;
contrast '2' treatment 2 2 2 -1 -1 -1 -1 -1 -1 -2 -2 -2 1 1 1 1 1 1;
contrast '3' treatment -1 -1 -1 0 0 0 0 0 0 1 1 1 0 0 0 0 0 0;
contrast '4' treatment -1 0 1 0 0 0 0 0 0 -1 0 1 0 0 0 0 0 0;
contrast '5' treatment -1 2 -1 0 0 0 0 0 0 -1 2 -1 0 0 0 0 0 0;
contrast '6' treatment 1 0 -1 0 0 0 0 0 0 -1 0 1 0 0 0 0 0 0;
contrast '7' treatment 1 -2 1 0 0 0 0 0 0 -1 2 -1 0 0 0 0 0 0;
contrast '8' treatment 0 0 0 -1 -1 -1 -1 -1 -1 0 0 0 1 1 1 1 1 1;
contrast '9' treatment 0 0 0 -1 -1 0 0 1 1 0 0 0 -1 -1 0 0 1 1;
contrast '10' treatment 0 0 0 -1 -1 2 2 -1 -1 0 0 0 -1 -1 2 2 -1 -1;
contrast '11' treatment 0 0 0 1 1 0 0 -1 -1 0 0 0 -1 -1 0 0 1 1;
contrast '12' treatment 0 0 0 1 1 -2 -2 1 1 0 0 0 -1 -1 2 2 -1 -1;
lsmeans treatment / pdiff;
```

Described in Table 64 of Chapter 10 - Dissemination

SAS MIXED

```
proc mixed method = reml covtest cl;
class CPlevel feedstuffcomb period animal;
model variable = CPlevel feedstuffcomb CPlevel*feedstuffcomb;
repeated period / subject=animal;
contrast 'lin' feedstuffcomb -1 0 1;
contrast 'quad' feedstuffcomb 1 -2 1;
contrast 'lin int' CPlevel*feedstuffcomb -1 0 1 1 0 -1;
contrast 'qua int' CPlevel*feedstuffcomb 1 -2 1 -1 2 -1;
estimate 'lin' feedstuffcomb -1 0 1;
estimate 'quad' feedstuffcomb 1 -2 1;
estimate 'lin int' CPlevel*feedstuffcomb -1 0 1 1 0 -1;
estimate 'qua int' CPlevel*feedstuffcomb 1 -2 1 -1 2 -1;
lsmeans CPlevel feedstuffcomb CPlevel*feedstuffcomb / pdiff;
```

Simulated Data Set in Appendix 3 Table 163 and Described in Tables 1 and 2 of Chapter 5 – Experimental Design

SAS GLM (results in Appendix 2 Tables 69, 72, and 75)

```
proc glm;
classes origin ve pen length;
model variable = origin ve origin*ve pen(origin*ve) length length*origin length*ve
length*origin*ve;
test h = origin ve origin*ve e = pen(origin*ve);
lsmeans origin ve origin*ve / stderr pdiff e = pen(origin*ve);
lsmeans length length*origin length*ve length*origin*ve / stderr pdiff;
```

SAS MIXED (results in Appendix 2 Tables 70, 73, and 76)

```
proc mixed method = reml covtest cl;
classes origin ve pen length;
model variable = origin ve origin*ve length length*origin length*ve
length*origin*ve;
random pen(origin*ve) animal(length*origin*ve);
lsmeans origin ve origin*ve length length*origin length*ve
length*origin*ve / pdiff;
```

GenStat ANOVA-ARR (results in Appendix 2 Tables 71, 74, and 77)

Treatment structure statement:

- origin*ve*length

Blocking structure statement:

- origin.ve/pen

Described in Table 11 of Chapter 6 – Treatment Considerations

SAS GLM

```
proc glm;
classes breed supplement;
model variable = breed supplement breed*supplement;
lsmeans breed supplement breed*supplement / stderr pdiff;
```

SAS MIXED

```
proc mixed method = reml covtest cl;
classes breed supplement animal;
model variable = breed supplement breed*supplement;
random animal(breed*supplement);
lsmeans breed supplement breed*supplement / pdiff;
```

GenStat ANOVA-ARR

Treatment structure statement:

- breed*supplement

Described in Table 12 of Chapter 6 – Treatment Considerations

SAS MIXED

```
proc mixed method = reml covtest cl;
classes treatment animal time;
model variable = treatment time treatment*time;
random animal(treatment);
repeated time / subject = animal(treatment);
lsmeans treatment time treatment*time / pdiff;
```

GenStat - Repeated Measures option of Mixed Models (REML)

Subject:

- animal

Time point:

- time

Fixed effects:

- treatment*time

Described in Table 13 of Chapter 6 – Treatment Considerations

SAS GLM

```
proc glm;
classes treatment;
model variable = treatment;
lsmeans treatment / stderr pdiff;
```

SAS MIXED

```
proc mixed method = reml covtest cl;
classes treatment animal;
model variable = treatment;
random animal(treatment);
lsmeans treatment / pdiff;
```

GenStat ANOVA-ARR

Treatment structure statement is:

- treatment

Simulated Data Sets 1 and 2 in Appendix 3 Tables 166 and 169, respectively, and Described in Figure 10 and Table 30 of Chapter 9 – On-Farm Research Examples

SAS GLM (results in Appendix 2 Tables 78, 82, 85, and 88)

```
proc glm;
classes treatment frg household;
model variable = treatment frg treatment*frg household(frg);
test h = treatment frg e = treatment*frg;
test h = treatment*frg e = household(frg);
lsmeans treatment frg / stderr pdiff e = treatment*frg;
lsmeans treatment*frg / stderr pdiff e = household(frg);
lsmeans household(frg) / stderr pdiff;
```

SAS MIXED: A (results in Appendix 2 Tables 79, 83, 86, and 89)

```
proc mixed method = reml covtest cl;
classes treatment frg household;
model variable = treatment;
random frg treatment*frg household(frg);
lsmeans treatment / pdiff;
```

SAS MIXED: B (results in Appendix 2 Tables 79, 83, 86, and 89)

```
proc mixed method = reml covtest cl;
classes treatment frg household;
model variable = treatment frg;
random treatment*frg household(frg);
lsmeans treatment frg / pdiff;
```

GenStat ANOVA-ARR: A (results in Appendix 2 Tables 80, 84, 87, and 90)

Treatment structure statement:

- treatment

Blocking structure statement:

- frg + treatment.frg + frg/household

GenStat ANOVA-ARR: B (results in Appendix 2 Tables 81 and 91)

Treatment structure statement:

- treatment + frg

Blocking structure statement:

- treatment.frg + frg/household

Simulated Data Set in Appendix 3 Table 170 and Described in Figure 11 and Table 31 of Chapter 9 – On-Farm Research Examples

SAS GLM (results in Appendix 2 Table 92)

```
proc glm;
classes treatment woreda village household;
model variable = treatment woreda treatment*woreda village(woreda) treatment*village(woreda)
household(treatment*village*woreda);
test h = treatment woreda e = treatment*woreda;
test h = treatment*woreda e = village(woreda);
test h = village(woreda) treatment*village(woreda) e = household(treatment*village*woreda);
lsmeans treatment woreda / stderr pdiff e = treatment*woreda;
lsmeans treatment*woreda / stderr pdiff e = village(woreda);
lsmeans village(woreda) treatment*village(woreda) / stderr pdiff e =
household(treatment*village*woreda);
lsmeans household(treatment*village*woreda) / stderr pdiff;
```

SAS MIXED: A (results in Appendix 2 Table 93)

```
proc mixed method = reml covtest cl;
classes treatment woreda village household;
model variable = treatment;
random woreda treatment*woreda village(woreda) treatment*village(woreda)
household(treatment*village*woreda);
lsmeans treatment / pdiff;
```

SAS MIXED: B (results in Appendix 2 Table 93)

```
proc mixed method = reml covtest cl;
classes treatment woreda village household;
model variable = treatment woreda;
random treatment*woreda village(woreda) treatment*village(woreda)
household(treatment*village*woreda);
lsmeans treatment / pdiff;
```

GenStat ANOVA-ARR: A (results in Appendix 2 Table 94)

Treatment structure statement:

- treatment

Blocking structure statement:

- woreda + treatment.woreda + woreda/village + treatment.woreda/village + treatment.woreda/village/ household

GenStat ANOVA-ARR: B (results in Appendix 2 Table 95)

Treatment structure statement:

- treatment + woreda

Blocking structure statement:

- treatment.woreda + woreda/village + treatment.woreda/village + treatment.woreda/village/ household

However, statements for GenStat ANOVA-ARR: B result in 3 df for both woreda/village and treatment.woreda/village/household rather than 2 and 4, respectively, of the SAS GLM analysis shown above. But, if only treatment is considered fixed and entered in the Treatment structure statement shown for GenStat ANOVA-ARR: A, df for woreda/village and treatment.woreda/village/household are 2 and 4, respectively.

Simulated Data Sets 1 and 2 in Appendix 3 Tables 170 and 171, respectively, and Described in Figure 11 and Table 32 of Chapter 9 – On-Farm Research Examples

SAS GLM (results in Appendix 2 Tables 96, 100, and 104)

```
proc glm;
classes treatment village household;
model variable = treatment village treatment*village household(treatment*village);
test h = treatment village e = treatment*village;
test h = treatment*village e = household(treatment*village);
lsmeans treatment village / stderr pdiff e = treatment*village;
lsmeans treatment*village / stderr pdiff e = household(treatment*village);
lsmeans household(treatment*village) / stderr pdiff;
```

SAS MIXED: A (results in Appendix 2 Tables 97, 101, and 105)

```
proc mixed method = reml covtest cl;
classes treatment village household;
model variable = treatment;
random village treatment*village household(treatment*village);
lsmeans treatment / pdiff;
```

SAS MIXED: B (results in Appendix 2 Tables 97, 101, and 105)

```
proc mixed method = reml covtest cl;
classes treatment village household;
model variable = treatment village;
random treatment*village household(treatment*village);
lsmeans treatment / pdiff;
```

GenStat ANOVA-ARR: A (results in Appendix 2 Tables 98, 102, and 106)

Treatment structure statement:

- treatment

Blocking structure statement:

- village + treatment.village + treatment.village/household

GenStat ANOVA-ARR: B (results in Appendix 2 Tables 99, 103, and 107)

Treatment structure statement:

- treatment + village

Blocking structure statement:

- treatment.village + treatment.village/household

Simulated Data Set in Appendix 3 Table 173 and Described in Figure 12 and Table 33 of Chapter 9 – On-Farm Research Examples

SAS GLM (results in Appendix 2 Tables 108 and 112)

```
proc glm;
classes treatment village household;
model variable = treatment village treatment*village household(village);
test h = treatment village e = treatment × village;
test h = treatment*village e = household(village);
lsmeans treatment village / stderr pdiff e = treatment × village;
lsmeans treatment*village / stderr pdiff e = household(village);
```

SAS MIXED: A (results in Appendix 2 Tables 109 and 113)

```
proc mixed method = reml covtest cl;
classes treatment village household;
model variable = treatment;
random village treatment*village household(village);
lsmeans treatment / pdiff;
```

SAS MIXED: B (results in Appendix 2 Tables 109 and 113)

```
proc mixed method = reml covtest cl;
classes treatment village household;
model variable = treatment village;
random treatment*village household(village);
lsmeans treatment / pdiff;
```

GenStat ANOVA-ARR: A (results in Appendix 2 Tables 110 and 114)

Treatment structure statement:

- treatment

Blocking structure statement:

- village + treatment.village + village/household

GenStat ANOVA-ARR: B (results in Appendix 2 Tables 111 and 115)

Treatment structure statement:

- treatment + village

Blocking structure statement:

- treatment.village + village/household

Simulated Data Set in Appendix 3 Table 175 and Described in Figure 13 and Table 34 of Chapter 9 – On-Farm Research Examples

SAS GLM (results in Appendix 2 Table 116)

```
proc glm; classes treatment village household breed;
model lsone = treatment village treatment*village household(treatment*village) breed
treatment*breed
village*breed treatment*village*breed;
test h = treatment village e = treatment*village;
test h = treatment*village e = household(treatment*village);
```

SAS MIXED: A (results in Appendix 2 Table 117)

```
proc mixed method = reml covtest cl;
classes treatment village household breed;
model lsone = treatment breed treatment*breed;
random village treatment*village household(treatment*village);
lsmeans treatment breed treatment*breed / pdiff;
```

SAS MIXED: B (results in Appendix 2 Table 118)

```
proc mixed method = reml covtest cl;
classes treatment village household breed;
model lsone = treatment village breed treatment*breed village*breed;
random treatment*village household(treatment*village);
lsmeans treatment village breed treatment*breed village*breed / pdiff;
```

SAS MIXED: C (results in Appendix 2 Table 119)

```
proc mixed method = reml covtest cl;
classes treatment village household;
model lsone = treatment;
random village treatment*village household(treatment*village);
lsmeans treatment / pdiff;
```

SAS MIXED: D (results in Appendix 2 Table 120)

```
proc mixed method = reml covtest cl;
classes treatment village household;
model lsone = treatment village;
random treatment*village household(treatment*village);
lsmeans treatment village / pdiff;
```

SAS GLIMMIX: A (results in Appendix 2 Table 121)

```
proc glimmix;
classes treatment village household breed;
model lsone / total = treatment breed treatment*breed;
random village treatment*village household(treatment*village);
lsmeans treatment breed treatment*breed / odds or cl ilink diff;
```

SAS GLIMMIX: B (results in Appendix 2 Table 122)

```
proc glimmix;
classes treatment village household breed;
model lsone / total = treatment village breed treatment*breed village*breed;
random treatment*village household(treatment*village);
lsmeans treatment village breed treatment*breed village*breed / odds or cl ilink diff;
```

SAS GLIMMIX: C (results in Appendix 2 Table 123)

```
proc glimmix;
classes treatment village household;
model lsone / total = treatment;
random village treatment*village household(treatment*village);
lsmeans treatment / odds or cl ilink diff;
```

SAS GLIMMIX: D (results in Appendix 2 Table 124)

```
proc glimmix;
classes treatment village household;
model lsone / total = treatment village;
random treatment*village household(treatment*village);
lsmeans treatment village / odds or cl ilink diff;
```

Simulated Data Set in Appendix 3 Table 176 and Described in Figure 14 and Table 35 of Chapter 9 – On-Farm Research Examples

SAS GLM (results in Appendix 2 Table 125)

```
proc glm;
classes treatment season village household;
model variable = treatment season treatment*season village(season) village(treatment*season) household(treatment*village*season);
test h = treatment season treatment*season village(season) e = village(treatment*season);
test h = village(treatment*season) e = household(treatment*village*season);
lsmeans treatment season treatment*season village(season) / stderr pdiff e  =
village(treatment*season);
```

SAS MIXED (results in Appendix 2 Table 126)

```
proc mixed method = reml covtest cl;
classes treatment season village household;
model variable = treatment season treatment*season;
random village(treatment*season) household(village*treatment*season);
lsmeans treatment season treatment*season / pdiff;
```

GenStat ANOVA-ARR (results in Appendix 2 Table 127)

Treatment structure statement:

- treatment*season

Blocking structure statement is:

- treatment.season/village + treatment.season/village/household

Simulated Data Set in Appendix 3 Table 177 and Described in Figure 15 and Table 36 of Chapter 9 – On-Farm Research Examples

SAS MIXED: A (results in Appendix 2 Table 128)

```
proc mixed method = reml covtest cl;
classes treatment season village household;
model variable = treatment season treatment*season;
random village treatment*village village(treatment*season) household(treatment*village);
repeated season / subject = household(treatment*village);
lsmeans treatment season treatment*season / pdiff;
```

SAS MIXED: B (results in Appendix 2 Table 129)

```
proc mixed method = reml covtest cl;
classes treatment season village household;
model variable = treatment season treatment*season;
random village treatment*village village(treatment*season);
repeated season / subject = household(treatment*village);
lsmeans treatment season treatment*season / pdiff;
```

GenStat - Repeated Measurements option of Mixed Models (REML) (results in Appendix 2 Table 130)

Subject:

- household

Time point:

- season

Fixed model:

- treatment*season

GenStat - Linear Mixed Models option of Mixed Models (REML) (results in Appendix 2 Table 131)

Fixed model:

- treatment*season

Random model:

- village/household

Simulated Data Set in Appendix 3 Table 177 and Described in Figure 15 and Table 37 of Chapter 9 – On-Farm Research Examples

SAS MIXED: A (results in Appendix 2 Table 132)

```
proc mixed method = reml covtest cl;
classes treatment season village household;
model variable = treatment village treatment*village season treatment*season village*season treatment*village*season;
random household(treatment*village);
repeated season / subject = household(treatment*village);
lsmeans treatment village treatment*village season treatment*season village*season treatment*village*season / pdiff;
```

SAS MIXED: B (results in Appendix 2 Table 133)

```
proc mixed method = reml covtest cl;
classes treatment season village household;
model variable = treatment village treatment*village season treatment*season village*season treatment*village*season;
repeated season / subject = household(treatment*village);
lsmeans treatment village treatment*village season treatment*season village*season treatment*village*season / pdiff;
```

GenStat - Repeated Measurements option of Mixed Models (REML) (results in Appendix 2 Table 134)

Subject:

- household

Time point:

- season

Fixed model:

- treatment*village*season

GenStat - Linear Mixed Models option of Mixed Models (REML) (results in Appendix 2 Table 134)

Fixed model:

- treatment*village*season

Random model:

- village/household

Simulated Data Set in Appendix 3 Table 177 and Described in Table 38 of Chapter 9 – On-Farm Research Examples

SAS GLM (results in Appendix 2 Table 135

```
proc glm;
classes treatment village season household;
model variable = treatment village treatment*village household(treatment*village) season treatment*season village*season treatment*village season;
test h = treatment village e = treatment*village;
test h = treatment*village e = household(treatment*village);
lsmeans treatment village / stderr pdiff e = treatment*village;
lsmeans treatment*village / stderr pdiff e = household(treatment*village);
lsmeans season treatment*season village*season treatment*village*season / stderr pdiff;
```

GenStat ANOVA-ARR (results in Appendix 2 Table 136)

Treatment structure statement:

- treatment + village + season + treatment.season + village.season + treatment.village.season

Blocking structure statement:

- treatment.village + treatment.village/household

Simulated Data Set in Appendix 3 Table 178 and Described in Table 39 of Chapter 9 – On-Farm Research Examples

SAS MIXED (results in Appendix 2 Table 137)

```
proc mixed method = reml covtest cl;
classes month household;
model variable = month;
random household;
repeated month / subject = household;
lsmeans month / pdiff;
```

GenStat - Repeated Measurements option of Mixed Models (REML) (results in Appendix 2 Table 138)

Subject:

- household

Time point:

- month

Fixed model:

- month

GenStat - Linear Mixed Models option of Mixed Models (REML) (results in Appendix 2 Table 138)

Fixed model:

- month

Random model:

- household

Simulated Data Set in Appendix 3 Table 179 and Described in Table 40 of Chapter 9 – On-Farm Research Examples

SAS MIXED (results in Appendix 2 Table 139)

```
proc mixed method = reml covtest cl;
classes village month household;
model variable = village month village*month;
random household(village);
repeated month / subject = household(village);
lsmeans village month village*month / pdiff;
```

GenStat - Repeated Measurements option of Mixed Models (REML) (results in Appendix 2 Table 140)

Subject:

- household

Time point:

- month

Fixed model:

- village*month

GenStat - Linear Mixed Models option of Mixed Models (REML) (results in Appendix 2 Table 140)

Fixed model:

- village*month

Random model:

- village/household

Simulated Data Set in Appendix 3 Table 180 and Described in Table 41 of Chapter 9 – On-Farm Research Examples

SAS MIXED (results in Appendix 2 Table 141)

```
proc mixed method = reml covtest cl;
classes breed month household;
model variable = breed month breed*month;
random household(breed);
repeated month / subject = household(breed);
lsmeans breed month breed*month / pdiff;
```

GenStat - Repeated Measurements option of Mixed Models (REML) (results in Appendix 2 Table 142)

Subject:

- household

Time point:

- month

Fixed model:

- breed*month

GenStat - Linear Mixed Models option of Mixed Models (REML) (results in Appendix 2 Table 142)

Fixed model:

- breed*month

Random model:

- breed/household

Simulated Data Set in Appendix 3 Table 181 and Described in Table 42 of Chapter 9 – On-Farm Research Examples

SAS MIXED (results in Appendix 2 Table 143)

```
proc mixed method = reml covtest cl;
classes breed village month household;
model variable = breed village breed*village month breed*month village*month
breed*village*month;
random household(breed*village);
repeated month / subject = household(breed*village);
lsmeans breed village breed*village month breed*month village*month breed*village*month /
pdiff;
```

GenStat - Repeated Measurements option of Mixed Models (REML) (results in Appendix 2 Table 144)

Subject:

- household

Time point:

- month

Fixed model:

- breed*village*month

GenStat - Linear Mixed Models option of Mixed Models (REML) (results in Appendix 2 Table 144)

Fixed model:

- breed*village*month

Random model:

- breed.village/household

Simulated Data Set in Appendix 3 Table 182 and Described in Table 43 of Chapter 9 – On-Farm Research Examples

SAS GLIMMIX (results in Appendix 2 Table 145)

```
proc glimmix;
classes month household;
model lsone / total = month;
random household;
lsmeans month / odds or cl ilink diff;
```

Simulated Data Set in Appendix 3 Table 183 and Described in Table 44 of Chapter 9 – On-Farm Research Examples

SAS GLIMMIX (results in Appendix 2 Table 146)

```
proc glimmix;
classes village month household;
model lsone / total = village month village*month;
random household(village);
lsmeans village month village*month / odds or cl ilink diff;
```

Simulated Data Set in Appendix 3 Table 184 and Described in Table 45 of Chapter 9 – On-Farm Research Examples

SAS GLIMMIX (results in Appendix 2 Table 147)

```
proc glimmix;
classes breed month household;
model lsone / total = breed month breed*month;
random household(breed);
lsmeans breed month breed*month / odds or cl ilink diff;
```

Simulated Data Set in Appendix 3 Table 185 and Described in Table 46 of Chapter 9 – On-Farm Research Examples

SAS GLIMMIX (results in Appendix 2 Table 148)

```
proc glimmix;
classes village breed month household;
model lsone / total = village breed village*breed month village*month breed*month
village*breed*month;
random household(village*breed);
lsmeans village breed village*breed month village*month breed*month  village*breed*month
/ odds or cl ilink diff;
```

Simulated Data Set in Appendix 3 Table 186 and Described in Figure 16 and Table 47 of Chapter 9 – On-Farm Research Examples

SAS GLM (results in Appendix 2 Table 149)

```
proc glm; classes treatment village household;
model variable = treatment village(treatment) household(village*treatment);
test h = treatment e = village(treatment);
test h = village(treatment) e = household(village*treatment);
lsmeans treatment / stderr pdiff e = village(treatment);
lsmeans village(treatment) / stderr pdiff e = household(village*treatment);
```

SAS MIXED (results in Appendix 2 Table 150)

```
proc mixed method = reml covtest cl;
classes treatment village;
model variable = treatment;
random village(treatment);
lsmeans treatment / pdiff;
```

Simulated Data Set in Appendix 3 Table 187 and Described in Table 48 of Chapter 9 – On-Farm Research Examples

SAS MIXED (results in Appendix 2 Table 151)

```
proc mixed method = reml covtest cl;
classes order household period treatment;
model variable = order period treatment;
random household(order);
repeated period / subject = household(order);
lsmeans treatment period / pdiff;
```

GenStat - Repeated Measurements option of Mixed Models (REML) (results in Appendix 2 Table 152)

Subject:

- household

Time point:

- period

Fixed model:

- order+period+treatment

GenStat - Linear Mixed Models option of Mixed Models (REML) (results in Appendix 2 Table 153)

Fixed model:

- order+period+treatment

Random model:

- order/household

Simulated Data Set in Appendix 3 Table 188 and Described in Table 49 of Chapter 9 – On-Farm Research Examples

SAS MIXED (results in Appendix 2 Table 154)

```
proc mixed method = reml covtest cl;
classes village order household period treatment;
model variable = village order village*order period treatment treatment*village;
random household(village*order);
repeated period / subject = household(village*order);
lsmeans village period treatment / pdiff;
```

GenStat - Repeated Measurements option of Mixed Models (REML) (results in Appendix 2 Table 155)

Subject:

- village.household

Time point:

- period

Fixed model:

- village*order+period+treatment+treatment.village

GenStat - Linear Mixed Models option of Mixed Models (REML) (results in Appendix 2 Table 155)

Fixed model:

- village*order+period+treatment+treatment.village

Random model:

- village.order/household

Simulated Data Set in Appendix 3 Table 189 and Described in Table 50 of Chapter 9 – On-Farm Research Examples

SAS MIXED (results in Appendix 2 Table 156)

```
proc mixed method = reml covtest cl;
classes treatment period household;
model variable = treatment period;
repeated period / subject = household;
lsmeans treatment period / pdiff;
```

GenStat - Repeated Measurements option of Mixed Models (REML) (results in Appendix 2 Table 157)

Subject:

- household

Time point:

- period

Fixed model:

- treatment + period

GenStat - Linear Mixed Models option of Mixed Models (REML) (results in Appendix 2 Table 157)

Fixed model:

- treatment + period

Random model:

- household

Simulated Data Set in Appendix 3 Table 190 and Described in Table 51 of Chapter 9 – On-Farm Research Examples

SAS MIXED (results in Appendix 2 Table 158)

```
proc mixed method = reml covtest cl;
classes village treatment period household;
model variable = village treatment treatment*village period;
random household(village);
repeated period / subject = household(village);
```

GenStat - Repeated Measurements option of Mixed Models (REML) (results in Appendix 2 Table 159)

Subject:

- household

Time point:

- period

Fixed model:

- village*treatment+period

GenStat - Linear Mixed Models option of Mixed Models (REML) (results in Appendix 2 Table 159)

Fixed model:

- village*treatment+period

Random model:

- household

Appendix 2. Example Analyses Results

Simulated Data Set in Appendix 3 Table 163 and Described in Tables 1 and 2 of Chapter 5 – Experimental Design

No Missing Data

SAS GLM

Appendix 2 Table 69
Analysis of simulated data in Appendix 3 Table 163 and described in Tables 1 and 2 of Chapter 5 – Experimental Design by the SAS GLM procedure

Source of variation[1]	df	Type III SS	MS	P > *F*
Origin	1	3.34	3.34	0.284
VE	1	5.79	5.79	0.160
Origin*VE	1	1.57	1.57	0.463
Pen(origin*VE)	8	27.85	3.48	0.303
Length	2	1.46	0.73	0.776
Origin*length	2	1.69	0.84	0.747
VE*length	2	16.46	8.23	0.063
Origin*VE*length	2	13.57	6.79	0.101
Corrected total	107	324.99		
*Tests of hypotheses using the Type III MS for pen(origin*VE) as an error term*				
Origin	3	3.34	3.34	0.356
VE	3	5.79	5.79	0.233
Origin*VE	9	1.57	1.57	0.522

[1]VE = vitamin E.

SAS MIXED

Appendix 2 Table 70

Analysis of simulated data in Appendix 3 Table 163 and described in Tables 1 and 2 of Chapter 5 – Experimental Design by the SAS MIXED procedure

Source of variation[1]	df	P > *F*
Origin	1	0.356
VE	1	0.233
Origin*VE	1	0.522
Length	2	0.776
Origin*length	2	0.747
VE*length	2	0.063
Origin*VE*length	2	0.101

[1]VE = vitamin E.

GenStat ANOVA-ARR

Appendix 2 Table 71

Analysis of simulated data in Appendix 3 Table 163 and described in Tables 1 and 2 of Chapter 5 – Experimental Design by the GenStat ANOVA-ARR procedure

Source of variation[1]	df	SS	MS	P > *F*
Origin.VE.pen stratum				
Origin	1	3.34	3.34	0.356
VE	1	5.79	5.79	0.233
Origin.VE	1	1.57	1.57	0.521
Residual	8	27.85	3.48	
Origin.VE.pen.*Units* stratum				
Length	2	1.46	0.73	0.776
Origin.length	2	1.69	0.84	0.747
VE.length	2	16.46	0.82	0.063
Origin.VE.length	2	13.57	6.79	0.101
Residual	88	253.26	2.88	
Total	107			

[1]VE = vitamin E.

11 Observations Removed Without Regard to Treatment (i.e., Completely Random)

SAS GLM

Appendix 2 Table 72
Analysis of simulated data in Appendix 3 Table 164 and described in Tables 1 and 2 of Chapter 5 – Experimental Design by the SAS GLM procedure (11 observations removed without regard to treatment; i.e., completely random)

Source of variation[1]	df	Type III SS	MS	P > *F*
Origin	1	12.58	12.58	0.030
VE	1	7.12	7.12	0.099
Origin*VE	1	5.53	5.53	0.145
Pen(origin*VE)	8	28.21	3.53	0.219
Length	2	0.65	0.32	0.881
Origin*length	2	5.09	2.55	0.374
VE*length	2	13.22	6.61	0.092
Origin*VE*length	2	19.53	9.76	0.026
Corrected total	96	284.19		
*Tests of hypotheses using the Type III MS for pen(origin*VE) as an error term*				
Origin	3	12.58	12.58	0.096
VE	3	7.12	7.12	0.193
Origin*VE	9	5.53	5.53	0.246

[1]VE = vitamin E.

SAS MIXED

Appendix 2 Table 73
Analysis of simulated data in Appendix 3 Table 164 and described in Tables 1 and 2 of Chapter 5 – Experimental Design by the SAS MIXED procedure (11 observations removed without regard to treatment; i.e., completely random)

Source of variation[1]	df	P > *F*
Origin	1	0.103
VE	1	0.206
Origin*VE	1	0.236
Length	2	0.913
Origin*length	2	0.420
VE*length	2	0.077
Origin*VE*length	2	0.020

[1]VE = vitamin E.

GenStat ANOVA-ARR

Appendix 2 Table 74

Analysis of simulated data in Appendix 3 Table 164 and described in Tables 1 and 2 of Chapter 5 – Experimental Design by the GenStat ANOVA-ARR procedure (11 observations removed without regard to treatment; i.e., completely random)

Source of variation[1]	df	SS	MS	P > *F*
Origin.VE.pen stratum				
Origin	1	14.27	14.27	0.095
VE	1	8.08	8.08	0.192
Origin.VE	1	6.28	6.28	0.244
Residual	8	31.77	3.97	
Origin.VE.pen.*Units* stratum				
Length	2	0.69	0.35	0.874
Origin.length	2	5.60	2.88	0.339
VE.length	2	14.14	7.07	0.069
Origin.VE.length	2	22.37	11.18	0.016
Residual	77	196.72	2.56	
Total	96	284.19		

[1]VE = vitamin E.

10 Observations Removed Not in a Completely Random Manner

SAS GLM

Appendix 2 Table 75
Analysis of simulated data in Appendix 3 Table 165 and described in Tables 1 and 2 of Chapter 5 – Experimental Design by the SAS GLM procedure (10 observations removed not in a completely random manner)

Source of variation[1]	df	Type III SS	MS	P > *F*
Origin	1	2.06	2.06	0.403
VE	1	6.52	6.52	0.138
Origin*VE	1	2.07	2.07	0.402
Pen(origin*VE)	8	37.71	4.71	0.133
Length	2	3.22	1.61	0.577
Origin*length	2	1.12	0.56	0.825
VE*length	2	13.41	6.70	0.107
Origin*VE*length	2	12.52	6.26	0.123
Corrected total	97	306.34		
*Tests of hypotheses using the Type III MS for pen(origin*VE) as an error term*				
Origin	3	2.06	2.06	0.527
VE	3	6.52	6.52	0.273
Origin*VE	9	2.07	2.07	0.527

[1]VE = vitamin E.

SAS MIXED

Appendix 2 Table 76
Analysis of simulated data in Appendix 3 Table 165 and described in Tables 1 and 2 of Chapter 5 – Experimental Design by the SAS MIXED procedure (10 observations removed not in a completely random manner)

Source of variation[1]	df	P > *F*
Origin	1	0.508
VE	1	0.248
Origin*VE	1	0.553
Length	2	0.658
Origin*length	2	0.815
VE*length	2	0.119
Origin*VE*length	2	0.123

[1]VE = vitamin E.

GenStat ANOVA-ARR

Appendix 2 Table 77

Analysis of simulated data in Appendix 3 Table 165 and described in Tables 1 and 2 of Chapter 5 – Experimental Design by the GenStat ANOVA-ARR procedure (10 observations removed not in a completely random manner)

Source of variation[1]	df	SS	MS	P > *F*
Origin.VE.pen stratum				
Origin	1	2.36	2.36	0.524
VE	1	7.46	7.46	0.270
Origin.VE	1	2.34	2.34	0.526
Residual	8	42.57	5.32	
Origin.VE.pen.*Units* stratum				
Length	2	4.00	2.00	0.506
Origin.length	2	1.18	0.59	0.816
VE.length	2	14.45	7.23	0.090
Origin.VE.length	2	12.73	6.36	0.119
Residual	78	226.88	2.91	
Total	97	306.34		

[1]VE = vitamin E.

Simulated Data Set 1 in Appendix 3 Table 166 and Described in Figure 10 and Table 30 of Chapter 9 – On-Farm Research Examples

No Missing Data – Data Set 1

SAS GLM

Appendix 2 Table 78
Analysis of simulated data in Appendix 3 Table 166 and described in Figure 10 and Table 30 of Chapter 9 – On-Farm Research Examples by the SAS GLM procedure

Source of variation	df	Type III SS	MS	P > *F*
Treatment	3	6.23	2.08	0.953
FRG	3	23.23	7.74	0.740
Treatment*FRG	9	264.13	29.35	0.127
Household(FRG)	36	426.05	11.84	0.936
Error	108	1,994.15	18.46	
Corrected total	159	2,713.78		
*Tests of hypotheses using the Type III MS for treatment*FRG as an error term*				
Treatment	3	6.23	2.08	0.974
FRG	3	23.23	7.74	0.850
Tests of hypotheses using the Type III MS for household(FRG) as an error term				
Treatment*FRG	9	264.13	29.35	0.026

SAS MIXED

Appendix 2 Table 79
Analysis of simulated data in Appendix 3 Table 166 and described in Figure 10 and Table 30 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure

Analysis	Source of variation	df	P > *F*
FRG as random	Treatment	3	0.966
FRG as fixed	Treatment	3	0.974
	FRG	3	0.850

GenStat ANOVA-ARR: A

Appendix 2 Table 80
Analysis of simulated data in Appendix 3 Table 166 and described in Figure 10 and Table 30 of Chapter 9 – On-Farm Research Examples by the GenStat ANOVA-ARR procedure (treatment structure statement of 'treatment')

Source of variation	df	SS	MS	P > *F*
FRG stratum	3	23.22	7.74	
FRG.treatment stratum				
Treatment	3	6.23	2.08	0.974
Residual	9	264.12	29.35	
FRG.household stratum	36	426.05	11.83	
FRG.treatment.household stratum	108	1,994.15	18.46	
Total	159	2,713.78		

GenStat ANOVA-ARR: B

Appendix 2 Table 81
Analysis of simulated data in Appendix 3 Table 166 and described in Figure 10 and Table 30 of Chapter 9 – On-Farm Research Examples by the GenStat ANOVA-ARR procedure (treatment structure statement of 'treatment' and 'FRG')

Source of variation	df	SS	MS	P > *F*
Treatment.FRG stratum				
Treatment	3	6.23	2.08	0.974
FRG	3	23.22	7.74	0.850
Residual	9	264.12	29.35	
FRG.household stratum	39[1]	426.05	10.92	
Treatment.FRG.household stratum	105[1]	1,994.15	18.99	
Total	159	2,713.78		

[1]The df for FRG.household and treatment.FRG.household for GenStat ANOVA-ARR: A are 36 and 108, respectively (Appendix 2 Table 80), which is the same as for SAS GLM analysis in Appendix 2 Table 78. These differences between GenStat analyses may relate to only considering main effects of treatment and FRG to be fixed and their interaction random with GenStat ANOVA-ARR: B.

10 Observations Removed from Data Set 1 Without Regard to FRG or Treatment (i.e., Completely Random)

SAS GLM

Appendix 2 Table 82
Analysis of simulated data in Appendix 3 Table 167 and described in Figure 10 and Table 30 of Chapter 9 – On-Farm Research Examples by the SAS GLM procedure (10 observations removed without regard to FRG or treatment; i.e., completely random)

Source of variation	df	Type III SS	MS	P > *F*
Treatment	3	0.42	0.14	0.999
FRG	3	39.60	13.20	0.548
Treatment*FRG	9	245.00	27.78	0.161
Household(FRG)	36	450.35	12.51	0.910
Error	98	1,822.08	18.59	
Corrected total	149	2,569.49		
*Tests of hypotheses using the Type III MS for treatment*FRG as an error term*				
Treatment	3	0.42	0.14	0.999
FRG	3	39.60	13.20	0.707
Tests of hypotheses using the Type III MS for household(FRG) as an error term				
Treatment*FRG	9	250.00	27.78	0.044

SAS MIXED

Appendix 2 Table 83
Analysis of simulated data in Appendix 3 Table 167 and described in Figure 10 and Table 30 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure (10 observations removed without regard to FRG or treatment; i.e., completely random)

Analysis	Source of variation	df	P > *F*
FRG as random	Treatment	3	0.996
FRG as fixed	Treatment	3	0.997
	FRG	3	0.688

GenStat ANOVA-ARR: A

Appendix 2 Table 84

Analysis of simulated data in Appendix 3 Table 167 and described in Figure 10 and Table 30 of Chapter 9 – On-Farm Research Examples by the GenStat ANOVA-ARR procedure (10 observations removed without regard to FRG or treatment; i.e., completely random)

Source of variation	df	SS	MS	P > *F*
FRG stratum	3	61.04	20.35	
FRG.treatment stratum				
Treatment	3	5.25	1.75	0.980
Residual	9	266.08	29.56	
FRG.household stratum	36	374.10	10.39	
FRG.treatment.household stratum	98	1,721.64	17.57	
Total	149	2,405.04		

10 Observations Removed from Data Set 1 Not in a Completely Random Manner

SAS GLM

Appendix 2 Table 85
Analysis of simulated data in Appendix 3 Table 168 and described in Figure 10 and Table 30 of Chapter 9 – On-Farm Research Examples by the SAS GLM procedure (10 observations removed not in a completely random manner)

Source of variation	df	Type III SS	MS	P > *F*
Treatment	3	14.47	4.82	0.860
FRG	3	25.61	8.54	0.721
Treatment*FRG	9	254.24	28.25	0.168
Household(FRG)	36	431.04	11.97	0.944
Error	98	1,877.10	19.15	
Corrected total	149	2,605.17		
*Tests of hypotheses using the Type III MS for treatment*FRG as an error term*				
Treatment	3	14.47	4.82	0.914
FRG	3	25.61	8.54	0.823
Tests of hypotheses using the Type III MS for household(FRG) as an error term				
Treatment*FRG	9	254.24	28.25	0.033

SAS MIXED

Appendix 2 Table 86
Analysis of simulated data in Appendix 3 Table 168 and described in Figure 10 and Table 30 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure (10 observations removed not in a completely random manner)

Analysis	Source of variation	df	P > *F*
FRG as random	Treatment	3	0.941
FRG as fixed	Treatment	3	0.954
	FRG	3	0.755

GenStat ANOVA-ARR: A

Appendix 2 Table 87
Analysis of simulated data in Appendix 3 Table 168 and described in Figure 10 and Table 30 of Chapter 9 – On-Farm Research Examples by the GenStat ANOVA-ARR procedure (10 observations removed not in a completely random manner)

Source of variation	df	SS	MS	P > *F*
FRG stratum	3	23.29	9.46	
FRG.treatment stratum				
Treatment	3	16.04	5.35	0.920
Residual	9	299.43	33.27	
FRG.household stratum	36	488.30	13.56	
FRG.treatment.household stratum	98	1,877.10	13.56	
Total	149	2,605.17		

Simulated Data Set 2 in Appendix 3 Table 169 and Described in Figure 10 and Table 30 of Chapter 9 – On-Farm Research Examples

No Missing Data – Data Set 2

SAS GLM

Appendix 2 Table 88
Analysis of simulated data in Appendix 3 Table 169 and described in Figure 10 and Table 30 by the SAS GLM procedure

Source of variation	df	Type III SS	MS	P > *F*
Treatment	3	22.37	7.46	0.118
FRG	3	6.52	2.17	0.628
Treatment*FRG	9	22.66	2.52	0.730
Household(FRG)	36	45.18	1.25	1.000[1]
Error	108	402.73	3.73	
Corrected total	159	499.44		
*Tests of hypotheses using the Type III MS for treatment*FRG as an error term*				
Treatment	3	22.37	7.46	0.090
FRG	3	6.52	2.17	0.495
Tests of hypotheses using the Type III MS for household(FRG) as an error term				
Treatment*FRG	9	22.66	2.52	0.067

[1]0.9998.

SAS MIXED

Appendix 2 Table 89
Analysis of simulated data in Appendix 3 Table 169 and described in Figure 10 and Table 30 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure

Analysis	Source of variation	df	P > *F*
FRG as random	Treatment	3	0.132
FRG as fixed	Treatment	3	0.133
	FRG	3	0.572

GenStat ANOVA-ARR: A

Appendix 2 Table 90
Analysis of simulated data in Appendix 3 Table 169 and described in Figure 10 and Table 30 of Chapter 9 – On-Farm Research Examples by the GenStat ANOVA-ARR procedure (treatment structure statement of 'treatment')

Source of variation	df	SS	MS	P > *F*
FRG stratum	3	6.52	2.17	
FRG.treatment stratum				
Treatment	3	22.37	7.46	0.090
Residual	9	22.66	2.52	
FRG.household stratum	36	45.18	1.26	
FRG.treatment.household stratum	108	402.73	3.73	
Total	159	499.44		

GenStat ANOVA-ARR: B

Appendix 2 Table 91
Analysis of simulated data in Appendix 3 Table 169 and described in Figure 10 and Table 30 of Chapter 9 – On-Farm Research Examples by the GenStat ANOVA-ARR procedure (treatment structure statement of 'treatment' and 'FRG')

Source of variation	df	SS	MS	P > *F*
Treatment.FRG stratum				
Treatment	3	22.37	7.46	0.090
FRG	3	6.52	2.17	0.495
Residual	9	22.66	2.52	
FRG.household stratum	39[1]	45.18	1.16	
Treatment.FRG.household stratum	105[1]	402.73	3.84	
Total	159	499.44		

[1]The df for FRG.household and treatment.FRG.household for GenStat ANOVA-ARR: A are 36 and 108, respectively (Appendix 2 Table 90), which is the same as for SAS GLM analysis in Appendix 2 Table 88. These differences between GenStat analyses may relate to only considering main effects of treatment and FRG to be fixed and their interaction random with GenStat ANOVA-ARR: B.

Simulated Data Set in Appendix 3 Table 170 and Described in Figure 11 and Table 31 of Chapter 9 – On-Farm Research Examples

SAS GLM

Appendix 2 Table 92
Analysis of simulated data in Appendix 3 Table 170 and described in Figure 11 and Table 31 of Chapter 9 – On-Farm Research Examples by the SAS GLM procedure (considering woreda; animals of households subjected to the same treatment)

Source of variation	df	Type III SS	MS	P > *F*
Treatment	2	9.24	4.62	0.164
Woreda	1	2.37	2.37	0.333
Treatment*woreda	2	3.24	1.62	0.525
Village(woreda)	2	1.52	0.76	0.738
Treatment*village(woreda)	4	58.70	14.68	0.001
Household(treatment*woreda*village)	24	81.11	3.38	0.162
Corrected total	107	335.52		
*Tests of hypotheses using the Type III MS for treatment*woreda as an error term*				
Treatment	2	9.24	4.62	0.260
Woreda	1	2.37	2.37	0.350
Tests of hypotheses using the Type III MS for village(woreda) as an error term				
Treatment*woreda	2	3.24	1.62	0.319
*Tests of hypotheses using the Type III MS for household(treatment*woreda*village) as an error term*				
Village(woreda)	2	1.52	0.76	0.800
Treatment*village(woreda)	4	58.70	14.68	0.009

SAS MIXED

Appendix 2 Table 93
Analysis of simulated data in Appendix 3 Table 170 and described in Figure 11 and Table 31 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure (considering woreda; animals of households subjected to the same treatment)

Analysis	Source of variation	df	P > *F*
Woreda as random	Treatment	2	0.613
Woreda as fixed	Treatment	2	0.632
	Woreda	1	0.640

GenStat ANOVA-ARR: A

Appendix 2 Table 94
Analysis of simulated data in Appendix 3 Table 170 and described in Figure 11 and Table 31 of Chapter 9 – On-Farm Research Examples by the GenStat ANOVA-ARR procedure (considering woreda; animals of households subjected to the same treatment; treatment structure statement of 'treatment')

Source of variation	df	SS	MS	P > *F*
Woreda stratum	1	2.37		
Woreda.treatment stratum				
Treatment	2	9.24	4.62	0.260
Residual	2	3.24	1.62	
Woreda.village stratum	2	1.52	0.76	
Woreda.treatment.village stratum	4	58.70	14.68	
Woreda.treatment.village.household stratum	24	81.11	3.38	
Woreda.treatment.village.household.*Units* stratum	72	179.33	2.49	
Total	107	335.52		

GenStat ANOVA-ARR: B

Appendix 2 Table 95
Analysis of simulated data in Appendix 3 Table 170 and described in Figure 11 and Table 31 of Chapter 9 – On-Farm Research Examples by the GenStat ANOVA-ARR procedure (considering woreda; animals of households subjected to the same treatment; treatment structure statement of 'treatment' and 'woreda')

Source of variation	df	SS	MS	P > *F*
Treatment.woreda stratum				
Treatment	2	9.24	4.62	0.260
Woreda	1	2.37	2.37	0.350
Residual	2	3.24	1.62	
Woreda.village stratum	3[1]	1.52	0.51	
Treatment.woreda.village stratum	3[2]	58.70	19.57	
Treatment.woreda.village.household stratum	24	81.11	3.38	
Treatment.woreda.village.household.*Units* stratum	72	179.33	2.49	
Total	107	335.52		

[1]The SAS GLM analysis df is 2 (Appendix 2 Table 92). However, the df is 2 if treatment is the only fixed effect in the treatment structure statement, also yielding a treatment P > *F* of 0.260 but without an assessment of the effect of woreda.
[2]The SAS GLM analysis df is 4 (Appendix 2 Table 92). However, the df is 4 if treatment is the only fixed effect in the treatment structure statement, also yielding a treatment P > *F* of 0.260 but without an assessment of the effect of woreda.

Simulated Data Set in Appendix 3 Table 170 and Described in Figure 11 and Table 32 of Chapter 9 – On-Farm Research Examples

No Missing Data – Data Set 1

SAS GLM

Appendix 2 Table 96
Analysis of simulated data in Appendix 3 Table 170 and described in Figure 11 and Table 32 of Chapter 9 – On-Farm Research Examples by the SAS GLM procedure (not considering woreda; animals of households subjected to the same treatment)

Source of variation	df	Type III SS	MS	P > *F*
Treatment	2	9.24	4.62	0.164
Village	3	3.89	1.30	0.670
Treatment*village	6	61.94	10.32	0.001
Household(treatment*village)	24	81.11	3.38	0.162
Corrected total	107	335.52		
*Tests of hypotheses using the Type III MS for treatment*village as an error term*				
Treatment	2	9.24	4.62	0.659
Village	3	3.89	1.30	0.942
*Tests of hypotheses using the Type III MS for household(treatment*village) as an error term*				
Treatment*village	6	61.94	10.32	0.023

SAS MIXED

Appendix 2 Table 97
Analysis of simulated data in Appendix 3 Table 170 and described in Figure 11 and Table 32 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure (not considering woreda; animals of households subjected to the same treatment)

Analysis	Source of variation	df	P > *F*
Village as random	Treatment	2	0.564
Village as fixed	Treatment	2	0.659
	Village	3	0.942

GenStat ANOVA-ARR: A

Appendix 2 Table 98
Analysis of simulated data in Appendix 3 Table 170 and described in Figure 11 and Table 32 of Chapter 9 – On-Farm Research Examples by the GenStat ANOVA-ARR procedure (not considering woreda; animals of households subjected to the same treatment; treatment structure statement of 'treatment')

Source of variation	df	SS	MS	P > *F*
Village stratum	3	3.89	1.30	
Village.treatment stratum				
Treatment	2	9.24	4.62	0.659
Residual	6	61.94	10.32	
Village.treatment.household stratum	24	81.11	3.38	
Village.treatment.household.*Units* stratum	72	179.33	2.49	
Total	107	335.52		

GenStat ANOVA-ARR: B

Appendix 2 Table 99
Analysis of simulated data in Appendix 3 Table 170 and described in Figure 11 and Table 32 of Chapter 9 – On-Farm Research Examples by the GenStat ANOVA-ARR procedure (not considering woreda; animals of households subjected to the same treatment; treatment structure statement of 'treatment' and 'village')

Source of variation	df	SS	MS	P > *F*
Treatment.village stratum				
Treatment	2	9.24	4.62	0.659
Village	3	3.89	1.30	0.942
Residual	6	61.94	10.32	
Treatment.village.household stratum	24	81.11	3.38	
Treatment.village.household.*units* stratum	72	179.33	2.49	
Total	107	335.52		

Observations Removed from Data Set 1 Without Regard to Treatment, Village, or Household (i.e., Completely Random)

SAS GLM

Appendix Table 100
Analysis of simulated data in Appendix 3 Table 172 and described in Figure 11 and Table 32 of Chapter 9 – On-Farm Research Examples by the SAS GLM procedure (not considering woreda; animals of households subjected to the same treatment; 7 observations removed without regard to treatment, village, or household, i.e., completely random)

Source of variation	df	Type III SS	MS	P > *F*
Treatment	2	9.24	4.62	0.164
Village	3	3.89	1.30	0.670
Treatment*village	6	61.94	10.32	0.001
Household(treatment*village)	24	90.89	3.79	0.070
Corrected total	100	313.47		
*Tests of hypotheses using the Type III MS for treatment*village as an error term*				
Treatment	2	4.83	2.42	0.771
Village	3	2.41	0.80	0.963
*Tests of hypotheses using the Type III MS for household(treatment*village) as an error term*				
Treatment*village	6	53.49	8.92	0.063

SAS MIXED

Appendix 2 Table 101
Analysis of simulated data in Appendix 3 Table 172 and described in Figure 11 and Table 32 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure (not considering woreda; animals of households subjected to the same treatment; 7 observations removed without regard to treatment, village, or household, i.e., completely random)

Analysis	Source of variation	df	P > *F*
Village as random	Treatment	2	0.670
Village as fixed	Treatment	2	0.757
	Village	1	0.963

GenStat ANOVA-ARR: A

Appendix 2 Table 102
Analysis of simulated data in Appendix 3 Table 172 and described in Figure 11 and Table 32 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure (not considering woreda; animals of households subjected to the same treatment; 7 observations removed without regard to treatment, village, or household, i.e., completely random; treatment structure statement of 'treatment')

Source of variation	df	SS	MS	P > *F*
Village stratum	3	2.67	0.89	
Village.treatment stratum				
Treatment	2	5.24	2.62	0.777
Residual	6	59.78	9.96	
Village.treatment.household stratum	24	96.72	4.03	
Village.treatment.household.*Units* stratum	65	154.17	2.37	
Total	100	313.47		

GenStat ANOVA-ARR: B

Appendix 2 Table 103
Analysis of simulated data in Appendix 3 Table 172 and described in Figure 11 and Table 32 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure (not considering woreda; animals of households subjected to the same treatment; 7 observations removed without regard to treatment, village, or household, i.e., completely random; treatment structure statement of 'treatment' and 'village')

Source of variation	df	SS	MS	P > *F*
Treatment.village stratum				
Treatment	2	5.24	2.62	0.777
Village	3	2.67	0.89	0.963
Residual	6	59.78	9.96	
Treatment.village.household stratum	24	96.72	4.03	
Treatment.village.household.*units* stratum	65	154.17	2.37	
Total	100	313.47		

No Missing Data – Data Set 2

SAS GLM

Appendix 2 Table 104
Analysis of simulated data in Appendix 3 Table 171 and described in Figure 11 and Table 32 of Chapter 9 – On-Farm Research Examples by the SAS GLM procedure (not considering woreda; animals of households subjected to the same treatment)

Source of variation	df	Type III SS	MS	P > *F*
Treatment	2	268.46	134.23	0.017
Village	3	125.37	41.79	0.266
Treatment*village	6	228.13	38.02	0.304
Household(treatment*village)	24	476.67	19.86	0.890
Corrected total	107	3,334.63		
*Tests of hypotheses using the Type III MS for treatment*village as an error term*				
Treatment	2	268.46	134.23	0.097
Village	3	125.37	41.79	0.419
*Tests of hypotheses using the Type III MS for household(treatment*village) as an error term*				
Treatment*village	6	228.13	38.02	0.120

SAS MIXED

Appendix 2 Table 105
Analysis of simulated data in Appendix 3 Table 171 and described in Figure 11 and Table 32 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure (not considering woreda; animals of households subjected to the same treatment)

Analysis	Source of variation	df	P > *F*
Village as random	Treatment	2	0.097
Village as fixed	Treatment	2	0.097
	Village	3	0.419

GenStat ANOVA-ARR: A

Appendix 2 Table 106
Analysis of simulated data in Appendix 3 Table 171 and described in Figure 11 and Table 32 of Chapter 9 – On-Farm Research Examples by the GenStat ANOVA-ARR procedure (not considering woreda; animals of households subjected to the same treatment; treatment structure statement of 'treatment')

Source of variation	df	SS	MS	P > *F*
Village stratum	3	125.37	41.79	
Village.treatment stratum				
Treatment	2	268.46	134.23	0.097
Residual	6	228.13	38.02	
Village.treatment.household stratum	24	476.67	19.86	
Village.treatment.household.*Units* stratum	72	2,236.00	31.06	
Total	107	3,334.63		

GenStat ANOVA-ARR: B

Appendix 2 Table 107
Analysis of simulated data in Appendix 3 Table 171 and described in Figure 11 and Table 32 of Chapter 9 – On-Farm Research Examples by the GenStat ANOVA-ARR procedure (not considering woreda; animals of households subjected to the same treatment; treatment structure statement of 'treatment' and 'village')

Source of variation	df	SS	MS	P > *F*
Treatment.village stratum				
Treatment	2	268.46	134.23	0.097
Village	3	125.37	41.79	0.419
Residual	6	228.13	38.02	
Treatment.village.household stratum	24	476.67	19.86	
Treatment.village.household.*units* stratum	72	2,236.00	31.06	
Total	107	3,334.63		

Simulated Data Set in Appendix 3 Table 173 and Described in Figure 12 and Table 33 of Chapter 9 – On-Farm Research Examples

No Missing Data

SAS GLM

Appendix 2 Table 108
Analysis of simulated data in Appendix 3 Table 173 and described in Figure 12 and Table 33 of Chapter 9 – On-Farm Research Examples by the SAS GLM procedure (animals of households subjected to each of the treatments)

Source of variation	df	Type III SS	MS	P > *F*
Treatment	2	3.57	1.79	0.516
Village	3	3.89	1.30	0.694
Treatment*village	6	4.72	0.79	0.937
Household(village)	32	152.30	4.76	0.025
Corrected total	107	335.52		
*Tests of hypotheses using the Type III MS for treatment*village as an error term*				
Treatment	2	3.57	1.79	0.184
Village	3	3.89	1.30	0.276
Tests of hypotheses using the Type III MS for household(village) as an error term				
Treatment*village	6	4.72	0.79	0.984

SAS MIXED

Appendix 2 Table 109
Analysis of simulated data in Appendix 3 Table 173 and described in Figure 12 and Table 33 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure (animals of households subjected to each of the treatments)

Analysis	Source of variation	df	P > *F*
Village as random	Treatment	2	0.528
Village as fixed	Treatment	2	0.528
	Village	3	0.843

GenStat ANOVA-ARR: A

Appendix 2 Table 110
Analysis of simulated data in Appendix 3 Table 173 and described in Figure 12 and Table 33 of Chapter 9 – On-Farm Research Examples by the SAS GLM procedure (animals of households subjected to each of the treatments; treatment structure statement of 'treatment')

Source of variation	df	SS	MS	P > *F*
Village stratum	3	3.89	1.30	
Village.treatment stratum				
Treatment	2	3.57	1.79	0.184
Residual	6	4.72	0.79	
Village.household stratum	32	152.30	4.76	
Village.treatment.household stratum	64	171.04	2.67	
Total	107	335.52		

GenStat ANOVA-ARR: B

Appendix 2 Table 111
Analysis of simulated data in Appendix 3 Table 173 and described in Figure 12 and Table 33 of Chapter 9 – On-Farm Research Examples by the SAS GLM procedure (animals of households subjected to each of the treatments; treatment structure statement of 'treatment' and 'village')

Source of variation	df	SS	MS	P > *F*
Treatment.village stratum				
Treatment	2	3.57	1.79	0.184
Village	3	3.89	1.30	0.276
Residual	6	4.72	0.79	
Village.household stratum	35[1]	152.30	4.35	
Treatment.village.household stratum	61[2]	171.04	2.80	
Total	107	335.52		

[1]The SAS GLM analysis df in Appendix 2 Table 108 is 32.
[2]The SAS GLM analysis df in Appendix 2 Table 108 is 64

7 Observations Removed Without Regard to Treatment, Village, or Household (i.e., Completely Random)

GLM - SAS

Appendix 2 Table 112
Analysis of simulated data in Appendix 3 Table 174 and described in Figure 12 and Table 33 of Chapter 9 – On-Farm Research Examples by the SAS GLM procedure (animals of households subjected to each of the treatments; 7 observations removed without regard to treatment, village, or household, i.e., completely random)

Source of variation	df	Type III SS	MS	P > *F*
Treatment	2	3.57	1.79	0.516
Village	3	3.89	1.30	0.694
Treatment*village	6	4.72	0.79	0.937
Household(village)	32	147.60	4.60	0.029
Corrected total	100	309.80		
*Tests of hypotheses using the Type III MS for treatment*village as an error term*				
Treatment	2	7.07	3.54	0.062
Village	3	1.94	0.65	0.520
Tests of hypotheses using the Type III MS for household(village) an error term				
Treatment*village	6	4.72	0.79	0.984

SAS MIXED

Appendix 2 Table 113
Analysis of simulated data in Appendix 3 Table 174 and described in Figure 12 and Table 33 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure (animals of households subjected to each of the treatments; 7 observations removed without regard to treatment, village, or household, i.e., completely random)

Analysis	Source of variation	df	P > *F*
Village as random	Treatment	2	0.337
Village as fixed	Treatment	2	0.337
	Village	1	0.923

GenStat ANOVA-ARR: A

Appendix 2 Table 114
Analysis of simulated data in Appendix 3 Table 174 and described in Figure 12 and Table 33 of Chapter 9 – On-Farm Research Examples by the GenStat ANOVA-ARR procedure (animals of households subjected to each of the treatments; 7 observations removed without regard to treatment, village, or household, i.e., completely random; treatment structure statement of 'treatment')

Source of variation	df	SS	MS	P > *F*
Village stratum	3	2.09	0.70	
Village.treatment stratum	2	7.66	3.83	0.072
Residual	6	5.46	0.91	
Village.household stratum	32	160.23	5.01	
Village.treatment.household stratum	57	147.60	2.59	
Total	100	309.80		

GenStat ANOVA-ARR: B

Appendix 2 Table 115
Analysis of simulated data in Appendix 3 Table 174 and described in Figure 12 and Table 33 of Chapter 9 – On-Farm Research Examples by GenStat ANOVA-ARR analysis (animals of households subjected to each of the treatments; 7 observations removed without regard to treatment, village, or household, i.e., completely random; treatment structure statement of 'treatment' and 'village')

Source of variation	df	SS	MS	P > *F*
Treatment.village stratum				
Treatment	2	7.66	3.83	0.072
Village	3	2.09	0.70	0.554
Residual	6	5.46	0.91	
Village.household stratum	35	160.24	4.58	
Village.treatment.household stratum	54	147.60	2.73	
Total	100	309.80		

Simulated Data Set in Appendix 3 Table 175 and Described in Figure 13 and Table 34 of Chapter 9 – On-Farm Research Examples

Appendix 2 Table 116

Analysis of simulated continuous data in Appendix 3 Table 175 and described in Figure 13 and Table 34 of Chapter 9 – On-Farm Research Examples by the SAS GLM procedure

Source of variation	df	Type III SS	MS	P > *F*
Treatment	2	1.40	0.70	0.814
Village	3	1.21	0.40	0.948
Treatment*village	6	4.35	0.73	0.969
Household(treatment*village)	36	61.00	1.69	0.978
Breed	1	20.17	20.17	0.019
Treatment*breed	2	5.15	2.57	0.473
Village*breed	3	37.75	12.58	0.019
Treatment*village*breed	6	19.94	3.32	0.448
Corrected total	95	271.96		
*Tests of hypotheses using the Type III MS for treatment*village as an error term*				
Treatment	2	1.40	0.70	0.434
Village	3	1.21	0.40	0.664
*Tests of hypotheses using the Type III MS for household(treatment*village) an error term*				
Treatment*village	6	4.35	0.73	0.855

Appendix 2 Table 117

Analysis of simulated continuous data in Appendix 3 Table 175 and described in Figure 13 and Table 34 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure, with village as a random effect and considering the subplot of breed

Source of variation	df	P > *F*
Treatment[1]	2	0.782
Breed[2]	1	0.009
Treatment*breed[2]	2	0.397

[1]Denominator df = 6.
[2]Denominator df = 45.

Appendix 2 Table 118

Analysis of simulated continuous data in Appendix 3 Table 175 and described in Figure 13 and Table 34 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure, with village as a fixed effect and considering the subplot of breed

Source of variation	df	P > *F*
Treatment[1]	2	0.762
Village[1]	3	0.917
Breed[2]	1	0.007
Treatment*breed[2]	2	0.360
Village*breed[2]	3	0.004

[1]Denominator df = 6.
[2]Denominator df = 42.

Appendix 2 Table 119
Analysis of simulated continuous data in Appendix 3 Table 175 and described in Figure 13 and Table 34 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure, with village as a random effect and without considering the subplot of breed

Source of variation	df	P > *F*
Treatment[1]	2	0.794

[1]Denominator df = 6.

Appendix 2 Table 120
Analysis of simulated continuous data in Appendix 3 Table 175 and described in Figure 13 and Table 34 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure, with village as a fixed effect and without considering the subplot of breed

Source of variation	df	P > *F*
Treatment[1]	2	0.790
Village[1]	3	0.936

[1]Denominator df = 6.

Appendix 2 Table 121
Analysis of simulated continuous data in Appendix 3 Table 175 and described in Figure 13 and Table 34 of Chapter 9 – On-Farm Research Examples by the SAS GLIMMIX procedure, with village as a random effect and considering the subplot of breed

Source of variation	df	P > *F*
Treatment[1]	2	0.900
Breed[2]	1	0.002
Treatment*breed[2]	2	0.304

[1]Denominator df = 6.
[2]Denominator df = 45.

Appendix 2 Table 122
Analysis of simulated categorical data in Appendix 3 Table 175 and described in Figure 13 and Table 34 of Chapter 9 – On-Farm Research Examples by the SAS GLIMMIX procedure, with village as a fixed effect and considering the subplot of breed

Source of variation	df	P > *F*
Treatment[1]	2	0.856
Village[1]	3	0.792
Breed[2]	1	0.001
Treatment*breed[2]	2	0.439
Village*breed[2]	3	0.001

[1]Denominator df = 6.
[2]Denominator df = 42.

Appendix 2 Table 123
Analysis of simulated categorical data in Appendix 3 Table 175 and described in Figure 13 and Table 34 of Chapter 9 – On-Farm Research Examples by the SAS GLIMMIX procedure, with village as a random effect and without considering the subplot of breed

Source of variation	df	P > *F*
Treatment[1]	2	0.863

[1]Denominator df = 6.

Appendix 2 Table 124
Analysis of simulated continuous data in Appendix 3 Table 175 and described in Figure 13 and Table 34 of Chapter 9 – On-Farm Research Examples by the SAS GLIMMIX procedure, with village as a fixed effect and without considering the subplot of breed

Source of variation	df	P > *F*
Treatment[1]	2	0.861
Village[1]	3	0.811

[1]Denominator df = 6.

Simulated Data Set in Appendix 3 Table 176 and Described in Figure 14 and Table 35

SAS GLM

Appendix 2 Table 125
Analysis of simulated data in Appendix 3 Table 176 and described in Figure 14 and Table 35 of Chapter 9 – On-Farm Research Examples by the SAS GLM procedure

Source of variation	df	Type III SS	MS	P > *F*
Treatment	2	7.44	3.72	0.209
Season	1	0.22	0.22	0.757
Treatment*season	2	4.78	2.39	0.361
Village(treatment*season)	6	14.33	2.39	0.411
Household(treatment*season*village)	24	109.67	4.57	0.029
Corrected total	71	218.44		
*Tests of hypotheses using the Type III MS for village(treatment*season) as an error term*				
Treatment	2	7.44	3.72	0.285
Season	1	0.22	0.22	0.771
Treatment*season	2	4.78	2.39	0.422
*Tests of hypotheses using the Type III MS for household(treatment*season*village) as an error term*				
Village(treatment*season)	6	14.33	2.39	0.785

SAS MIXED

Appendix 2 Table 126
Analysis of simulated data in Appendix 3 Table 176 and described in Figure 14 and Table 35 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure

Source of variation	df	P > *F*
Treatment	2	0.455
Season	1	0.824
Treatment*season	2	0.590

GenStat ANOVA-AAR

Appendix 2 Table 127
Analysis of simulated data in Appendix 3 Table 176 and described in Figure 14 and Table 35 of Chapter 9 – On-Farm Research Examples by the GenStat ANOVA-ARR procedure

Source of variation	df	SS	MS	P > *F*
Treatment.season.village stratum				
Treatment	2	7.44	3.72	0.285
Season	1	0.22	0.22	0.771
Treatment.season	2	4.78	2.39	0.422
Residual	6	14.33	2.39	
Treatment.season.village.household stratum	24	109.67	4.57	
Treatment.season.villlage.household.*Units* stratum	36	82.00	2.28	
Total	71	218.44		

Simulated Data Set in Appendix 3 Table 177 and Described in Figure 15 and Table 36 of Chapter 9 – On-Farm Research Examples

SAS MIXED

Appendix 2 Table 128
Analysis of simulated data in Appendix 3 Table 177 and described in Figure 15 and Table 36 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure (assuming fixed effects of treatment, season, and treatment × season and random effects of village and household)

Source of variation	df	P > *F*
Treatment[1]	2	0.656
Season[2]	1	0.594
Treatment*season[2]	2	0.254

[1]Denominator df = 2.
[2]Denominator df = 3.

Appendix 2 Table 129
Analysis of simulated data in Appendix 3 Table 177 and described in Figure 15 and Table 36 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure (assuming fixed effects of treatment, season, treatment × season, and household and a random effect of village)

Source of variation	df	P > *F*
Treatment[1]	2	0.532
Season[2]	1	0.743
Treatment*season[2]	2	0.519

[1]Denominator df = 2.
[2]Denominator df = 3.

GenStat Repeated Measures option of Mixed Models (REML)

Appendix 2 Table 130
Analysis of simulated data in Appendix 3 Table 177 and described in Figure 15 and Table 36 of Chapter 9 – On-Farm Research Examples by the the GenStat Repeated Measures option of Mixed Models (REML) (assuming fixed effects of treatment, season, and treatment × season and a random effect of household)

Source of variation	df	P > *F*
Treatment	2	0.607
Season	1	0.561
Treatment.season	2	0.140

GenStat Linear Mixed Models option of Mixed Models (REML)

Appendix 2 Table 131
Analysis of simulated data in Appendix 3 Table 177 and described in Figure 15 and Table 36 of Chapter 9 – On-Farm Research Examples by the GenStat Linear Mixed Models option of Mixed Models (REML) (assuming fixed effects of treatment, season, and treatment × season and a random model of village/household)

Source of variation	df	P > *F*[1]
Treatment	2	0.603[2]
Season	1	0.561[3]
Treatment.season	2	0.140[3]

[1]Different from SAS MIXED analysis (Appendix 2 Table 128) because of omission of nesting of household within village. Likewise, P values are the same if village is not considered in SAS MIXED analysis.
[2]Slightly different from the P value of GenStat Repeated Measures option of Mixed Models (REML) in Appendix 2 Table 130.
[3]The same P values as derived from GenStat Repeated Measures option of Mixed Models (REML) in Appendix 2 Table 130.

Simulated Data Set in Appendix 3 Table 177 and Described in Figure 15 and Table 37 of Chapter 9 – On-Farm Research Examples

SAS MIXED

Appendix 2 Table 132
Analysis of simulated data in Appendix 3 Table 177 and described in Figure 15 and Table 37 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure (assuming effects and interactions of treatment, season, and village to be fixed and household to be random)

Source of variation[1]	df	P > *F*
Treatment	2	0.641
Village	1	0.317
Treatment*village	2	0.855
Season	1	0.562
Treatment*season	2	0.147
Village*season	1	0.441
Treatment*village*season	2	0.327

[1]Denominator df = 12.

Appendix 2 Table 133
Analysis of simulated data in Appendix 3 Table 177 and described in Figure 15 and Table 37 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure (assuming effects and interactions of treatment, season, village, and household to be fixed)

Source of variation[1]	df	P > *F*
Treatment	2	0.641
Village	1	0.317
Treatment*village	2	0.855
Season	1	0.562
Treatment*season	2	0.147
Village*season	1	0.441
Treatment*village*season	2	0.327

[1]Denominator df = 12.

GenStat Repeated Measurements and Linear Mixed Models options of Mixed Models (REML)

Appendix 2 Table 134
Analysis of simulated data in Appendix 3 Table 177 and described in Figure 15 and Table 37 of Chapter 9 – On-Farm Research Examples by the GenStat Repeated Measures and Linear Mixed Models options of Mixed Models (REML) (assuming effects and interactions of treatment, season, and village to be fixed)

Source of variation	df	P > *F*
Treatment	2	0.641
Village	1	0.317
Treatment.village	2	0.855
Season	1	0.562
Treatment.season	2	0.147
Village.season	1	0.441
Treatment.village.season	2	0.327

Simulated Data Set in Appendix 3 Table 177 and Described in Figure 15 and Table 38 of Chapter 9 – On-Farm Research Examples

GLM - SAS

Appendix 2 Table 135
Analyses of simulated data in Appendix 3 Table 177 and described in Figure 15 and Table 38 of Chapter 9 – On-Farm Research Examples by the SAS GLM procedure

Source of variation	df	Type III SS	MS	P > *F*
Treatment	2	3.39	1.69	0.131
Village	1	4.00	4.00	0.034
Treatment*village	2	1.17	0.58	0.459
Household(treatment*village)	12	44.08	3.67	0.004
Season	1	0.25	0.25	0.562
Treatment*season	2	3.17	1.58	0.147
Village*season	1	0.44	0.44	0.441
Treatment*village*season	2	1.72	0.86	0.327
Corrected total	35	66.64		
*Tests of hypotheses using the Type III MS for treatment*village as an error term*				
Treatment	2	3.39	1.69	0.256
Village	1	4.00	4.00	0.120
*Tests of hypotheses using the Type III MS for household(treatment*village) as an error term*				
Treatment*village	2	1.17	0.58	0.855

GenStat ANOVA-ARR

Appendix 2 Table 136
Analyses of simulated data in Appendix 3 Table 177 and described in Figure 15 and Table 38 of Chapter 9 – On-Farm Research Examples by the GenStat ANOVA-ARR procedure

Source of variation	df	SS	MS	P > *F*
Treatment.village stratum				
Treatment	2	3.39	1.69	0.256
Village	1	4.00	4.00	0.120
Residual	2	1.17	0.58	
Treatment.village.household stratum	12	44.08	3.67	
Treatment.village.household.*Units* stratum				
Season	1	0.25	0.25	0.562
Treatment.season	2	3.17	1.58	0.147
Village.season	1	0.44	0.44	0.441
Treatment.village.season	2	1.72	0.86	0.327
Residual	12	8.42	0.70	
Total	35	66.64		

Simulated Data Set in Appendix 3 Table 178 and Described in Table 39 of Chapter 9 – On-Farm Research Examples

SAS MIXED

Appendix 2 Table 137
Analysis of simulated data in Appendix 3 Table 178 and described in Table 39 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure (continuous variable; fixed effect and repeated measure of month)

Source of variation[1]	df	P > *F*
Month	11	0.095

[1]Denominator df = 99.

GenStat Repeated Measurements and Linear Mixed Models options of Mixed Models (REML)

Appendix 2 Table 138
Analysis of simulated data in Appendix 3 Table 178 and described in Table 39 of Chapter 9 – On-Farm Research Examples by the GenStat Repeated Measures and Linear Mixed Models options of Mixed Models (REML) (continuous variable; fixed effect and repeated measure of month)

Source of variation[1]	df	P > *F*
Month	11	0.125

[1]Denominator df = 99.

Simulated Data Set in Appendix 3 Table 179 and Described in Table 40 of Chapter 9 – On-Farm Research Examples

SAS MIXED

Appendix 2 Table 139
Analysis of simulated data in Appendix 3 Table 179 and described in Table 40 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure (continuous variable; fixed effect of village and fixed effect and repeated measure of month)

Source of variation	df	P > *F*
Village[1]	1	0.936
Month[2]	11	0.376
Village*month[2]	11	0.383

[1]Denominator df = 18.
[2]Denominator df = 198.

GenStat Repeated Measurements and Linear Mixed Models options of Mixed Models (REML)

Appendix 2 Table 140
Analysis of simulated data in Appendix 3 Table 179 and described in Table 40 of Chapter 9 – On-Farm Research Examples by the GenStat repeated Measures and Linear Mixed Models options of Mixed Models (REML) (continuous variable; fixed effect of village and fixed effect and repeated measure of month)

Source of variation	df	P > *F*
Village[1]	1	0.911
Month[2]	11	0.414
Village.month[2]	11	0.421

[1]Denominator df = 18.
[2]Denominator df = 198.

Simulated Data Set in Appendix 3 Table 180 and Described in Table 41 of Chapter 9 – On-Farm Research Examples

SAS MIXED

Appendix 2 Table 141
Analysis of simulated data in Appendix 3 Table 180 and described in Table 41 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure (continuous variable; fixed effect of breed and fixed effect and repeated measure of month)

Source of variation	df	P > *F*
Breed[1]	1	0.912
Month[2]	11	0.116
Breed*month[2]	11	0.733

[1]Denominator df = 8.
[2]Denominator df = 88.

GenStat Repeated Measurements and Linear Mixed Models options of Mixed Models (REML)

Appendix 2 Table 142
Analysis of simulated data in Appendix 3 Table 180 and described in Table 41 of Chapter 9 – On-Farm Research Examples by the GenStat Repeated Measures and Linear Mixed Models options of Mixed Models (REML) (continuous variable; fixed effect of breed and fixed effect and repeated measure of month)

Source of variation	df	P > *F*
Breed[1]	1	0.838
Month[2]	11	0.148
Breed.month[2]	11	0.772

[1]Denominator df = 8.
[2]Denominator df = 88.

Simulated Data Set in Appendix 3 Table 181 and Described in Table 42 of Chaper 9 – On-Farm Research Examples

SAS MIXED

Appendix 2 Table 143
Analysis of simulated data in Appendix 3 Table 181 and described in Table 42 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure (continuous variable; fixed effects of village and breed and fixed effect and repeated measure of month)

Source of variation	df	P > *F*[1]
Breed[1]	1	0.895
Village[1]	1	0.937
Breed*village[1]	1	0.979
Month[2]	11	0.386
Breed*month[2]	11	0.396
Village*month[2]	11	0.393
Breed*village*month[2]	11	0.532

[1]Denominator df = 16.
[2]Denominator df = 176.

GenStat Repeated Measurements and Linear Mixed Models options of Mixed Models (REML)

Appendix 2 Table 144
Analysis of simulated data in Appendix 3 Table 181 and described in Table 42 of Chapter 9 – On-Farm Research Examples by the GenStat Repeated Measures and Linear Mixed Models options of Mixed Models (REML) (continuous variable; fixed effects of village and breed and fixed effect and repeated measure of month)

Source of variation	df	P > *F*[1,2]
Breed[1]	1	0.860
Village[1]	1	0.916
Breed.village[1]	1	0.972
Month[2]	11	0.420
Breed.month[2]	11	0.431
Village.month[2]	11	0.427
Breed.village.month[2]	11	0.566

[1]Denominator df = 16.
[2]Denominator df = 176.

Simulated Data Set in Appendix 3 Table 182 and Described in Table 43 of Chapter 9 – On-Farm Research Examples

SAS GLIMMIX

Appendix 2 Table 145
Analysis of simulated data in Appendix 3 Table 182 and described in Table 43 of Chapter 9 – On-Farm Research Examples by the SAS GLIMMIX procedure (categorical variable; fixed effect of month)

Source of variance[1]	df	*P* > F
Month	11	0.009

[1]Denominator df = 99.

Simulated Data Set in Appendix 3 Table 183 and Described in Table 44 of Chapter 9 – On-Farm Research Examples

SAS GLIMMIX

Appendix 2 Table 146
Analysis of simulated data in Appendix 3 Table 183 and described in Table 44 of Chapter 9 – On-Farm Research Examples by the SAS GLIMMIX procedure (categorical variable; fixed effects of village and month)

Source of variance	df	*P* > F
Village[1]	1	0.034
Month[2]	11	0.006
Village*month[2]	11	0.002

[1]Denominator df = 18.
[2]Denominator df = 198.

Simulated Data Set in Appendix 3 Table 184 and Described in Table 45 of Chapter 9 – On-Farm Research Examples

SAS GLIMMIX

Appendix 2 Table 147
Analysis of simulated data in Appendix 3 Table 184 and described in Table 45 of Chapter 9 – On-Farm Research Examples by the SAS GLIMMIX procedure (categorical variable; fixed effects of breed and month)

Source of variance	df	*P* > F
Breed[1]	1	0.886
Month[2]	11	0.102
Breed*month[2]	11	0.005

[1]Denominator df = 8.
[2]Denominator df = 88.

Simulated Data Set in Appendix 3 Table 185 and Described in Table 46 of Chapter 9 – On-Farm Research Examples

SAS GLIMMIX

Appendix 2 Table 148
Analysis of simulated data in Appendix 3 Table 185 and described in Table 46 of Chapter 9 – On-Farm Research Examples by the SAS GLIMMIX procedure (categorical variable; fixed effects of village, breed, and month)

Source of variance	df	*P* > F
Village[1]	1	0.470
Breed[1]	1	0.456
Village*breed[1]	1	0.274
Month[2]	11	0.005
Village*month[2]	11	0.001
Breed*month[2]	11	0.233
Village*breed*month[2]	11	0.001

[1]Denominator df = 16.
[2]Denominator df = 176.

Simulated Data Set in Appendix 3 Table 186 and Described in Table 47 of Chapter 9 – On-Farm Research Examples

SAS GLM

Appendix 2 Table 149
Analysis of simulated data in Appendix 3 Table 186 and described in Figure 16 and Table 47 of Chapter 9 – On-Farm Research Examples by the SAS GLM procedure

Source of variation	df	Type III SS	MS	P > *F*
Treatment	1	0.33	3.72	0.897
Village(treatment)	4	29.07	7.27	0.829
Household(treatment*village)	30	389.67	12.99	0.894
Corrected total	72	1,830.41		
Tests of hypotheses using the Type III MS for village(treatment) as an error term				
Treatment	2	0.33	0.33	0.841
*Tests of hypotheses using the Type III MS for household(treatment*village) as an error term*				
Village(treatment)	6	29.07	7.27	0.694

SAS MIXED

Appendix 2 Table 150
Analysis of simulated data in Appendix 3 Table 186 and described in Figure 16 and Table 47 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure

Source of variation	df	P > *F*
Treatment	1	0.896

Simulated Data Set in Appendix 3 Table 187 and Described in Table 48 of Chapter 9 – On-Farm Research Examples

SAS MIXED

Appendix 2 Table 151
Analysis of simulated data in Appendix 3 Table 187 and described in Table 48 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure (switchback design; one village)

Source of variation	df	P > *F*
Order[1]	1	0.002
Period[2]	2	0.426
Treatment[2]	1	0.026

[1]Denominator df = 10.
[2]Denominator df = 21.

GenStat Repeated Measurements option of Mixed Models (REML)

Appendix 2 Table 152
Analysis of simulated data in Appendix 3 Table 187 and described in Table 48 of Chapter 9 – On-Farm Research Examples by the GenStat Repeated Measures option of Mixed Models (REML) (switchback design; one village)

Source of variation	df	P > *F*
Order[1]	1	0.003
Period[2]	2	0.427
Treatment[2]	1	0.026

[1]Denominator df = 12.6
[2]Denominator df = 21.

GenStat Linear Mixed Models options of Mixed Models (REML)

Appendix 2 Table 153
Analysis of simulated data in Appendix 3 Table 187 and described in Table 48 of Chapter 9 – On-Farm Research Examples by the GenStat Linear Mixed Models option of Mixed Models (REML) (switchback design; one village)

Source of variation[1]	df	P > *F*
Order	1	<0.001
Period	2	0.421
Treatment	1	0.022

[1]Denominator df = 31.

Simulated Data Set in Appendix 3 Table 188 and Described in Table 49 of Chapter 9 – On-Farm Research Examples

SAS MIXED

Appendix 2 Table 154
Analysis of simulated data in Appendix 3 Table 188 and described in Table 49 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure (switchback design; two villages)

Source of variation	df	P > *F*
Village[1]	1	0.250
Order[1]	1	0.007
Village*order[1]	1	0.439
Period[2]	2	0.325
Treatment[2]	1	0.026
Treatment*village	1	0.227

[1]Denominator df = 20.
[2]Denominator df = 44.

GenStat Repeated Measurements and Linear Mixed Models options of Mixed Models (REML)

Appendix 2 Table 155
Analysis of simulated data in Appendix 3 Table 188 and described in Table 49 of Chapter 9 – On-Farm Research Examples by the GenStat Repeated Measures and Linear Mixed Models options of Mixed Models (REML) (switchback design; two villages)

Source of variation	df	P > *F*
Village[1]	1	0.250
Order[2]	1	0.021
Village.order[1]	1	0.439
Period[3]	2	0.325
Treatment[3]	1	0.026
Treatment.village	1	0.227

[1]Denominator df = 20.
[2]Denominator df = 23.5.
[3]Denominator df = 44.

Simulated Data Set in Appendix 3 Table 189 and Described in Table 50 of Chapter 9 – On-Farm Research Examples

SAS MIXED

Appendix 2 Table 156
Analysis of simulated data in Appendix 3 Table 189 and described in Table 50 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure (4 × 4 Latin square; one village)

Source of variation[1]	df	P > *F*
Treatment	3	0.404
Period	3	0.669

[1]Denominator df = 6.

GenStat Repeated Measurements and Linear Mixed Models options of Mixed Models (REML)

Appendix 2 Table 157
Analysis of simulated data in Appendix 3 Table 187 and described in Table 50 of Chapter 9 – On-Farm Research Examples by the GenStat Repeated Measures and Linear Mixed Models options of Mixed Models (REML) (4 × 4 Latin square; one village)

Source of variation[1]	df	P > *F*
Treatment	3	0.427
Period	3	0.688

[1]Denominator df = 6.

Simulated Data Set in Appendix 3 Table 190 and Described in Table 51 of Chapter 9 – On-Farm Research Examples

SAS MIXED

Appendix 2 Table 158
Analysis of simulated data in Appendix 3 Table 190 and described in Table 51 of Chapter 9 – On-Farm Research Examples by the SAS MIXED procedure (simultaneous 4 × 4 Latin squares; four villages)

Source of variation	df	P > *F*
Village[1]	3	0.880
Treatment[2]	3	0.350
Treatment*village[2]	9	0.357
Period[2]	3	0.652

[1]Denominator df = 12.
[2]Denominator df = 33.

GenStat Repeated Measurements and Linear Mixed Models options of Mixed Models (REML)

Appendix 2 Table 159
Analysis of simulated data in Appendix 3 Table 190 and described in Table 51 of Chapter 9 – On-Farm Research Examples by the GenStat Repeated Measures and Linear Mixed Models options of Mixed Models (REML) (simultaneous 4 × 4 Latin squares; four villages)

Source of variation	df	P > *F*
Village[1]	3	0.767
Treatment[2]	3	0.701
Village.treatment[2]	9	0.413
Period[2]	3	0.462

[1]Denominator df = 12.
[2]Denominator df = 33.

Appendix 3. Simulated Data Sets

Data sets shown below are not from actual livestock experiments. Rather, values for variables were simply randomly entered without regard to distribution. Therefore, with analysis of real data, first normality should be evaluated. This test was not conducted with these data sets, which were used only for illustrative purposes.

Appendix 3 Table 160
Simulated data set (litter size and age) used for Chi-square and SAS GENMOD analyses, with P values given in Table 28 of Chapter 8 – Statistical Analyses (individual animal data, 2 treatments, 8 groups per treatment, 20 animals per groups, and without blocking)

Animal	Treatment	Group	Conception	Litter size	Age (years)
1	1	1	Yes	1	1.6
2	1	1	Yes	1	1.9
3	1	1	Yes	1	2.1
4	1	1	Yes	1	2.2
5	1	1	Yes	1	1.5
6	1	1	Yes	1	1.4
7	1	1	No	.	1.7
8	1	1	Yes	1	2.5
9	1	1	Yes	1	3.0
10	1	1	Yes	2	1.8
11	1	2	Yes	1	0.9
12	1	2	Yes	1	0.7
13	1	2	Yes	1	2.5
14	1	2	Yes	1	2.2
15	1	2	Yes	1	1.2
16	1	2	Yes	1	2.2
17	1	2	Yes	2	1.9
18	1	2	Yes	1	1.7
19	1	2	Yes	1	1.5
20	1	2	Yes	2	2.0
21	1	3	Yes	1	1.0
22	1	3	Yes	1	3.0
23	1	3	Yes	1	2.8
24	1	3	Yes	1	2.6
25	1	3	No	.	1.9
26	1	3	Yes	1	1.8
27	1	3	Yes	1	1.6
28	1	3	Yes	2	1.4
29	1	3	No	.	1.6
30	1	3	Yes	1	1.9

31	1	4	Yes	1	2.1
32	1	4	Yes	2	2.2
33	1	4	Yes	1	1.5
34	1	4	Yes	1	0.7
35	1	4	Yes	1	2.5
36	1	4	Yes	1	2.2
37	1	4	Yes	1	1.2
38	1	4	Yes	2	2.2
39	1	4	Yes	1	1.9
40	1	4	Yes	2	1.7
41	2	5	Yes	1	1.5
42	2	5	Yes	1	2.0
43	2	5	Yes	1	1.0
44	2	5	Yes	1	3.0
45	2	5	Yes	1	2.6
46	2	5	Yes	1	1.9
47	2	5	Yes	1	1.8
48	2	5	Yes	1	1.6
49	2	5	Yes	1	3.0
50	2	5	Yes	2	1.8
51	2	6	Yes	2	0.9
52	2	6	Yes	2	0.7
53	2	6	Yes	2	2.5
54	2	6	Yes	2	2.2
55	2	6	Yes	2	1.2
56	2	6	Yes	2	2.2
57	2	6	Yes	2	1.9
58	2	6	Yes	2	2.2
59	2	6	Yes	2	1.9
60	2	6	Yes	1	1.7
61	2	7	Yes	2	1.5
62	2	7	Yes	2	2.0
63	2	7	Yes	2	1.0
64	2	7	Yes	2	3.0
65	2	7	No	.	2.8
66	2	7	Yes	2	2.6
67	2	7	Yes	2	1.9
68	2	7	Yes	1	1.8
69	2	7	Yes	2	1.6
70	2	7	No	.	2.2
71	2	8	Yes	1	1.2
72	2	8	Yes	2	2.2
73	2	8	Yes	1	1.9
74	2	8	Yes	1	2.2

75	2	8	Yes	2	1.9
76	2	8	Yes	1	1.4
77	2	8	Yes	1	1.7
78	2	8	Yes	1	2.5
79	2	8	Yes	1	3.0
80	2	8	Yes	1	1.8
81	1	1	Yes	1	1.6
82	1	1	Yes	1	1.9
83	1	1	Yes	1	2.1
84	1	1	Yes	1	2.2
85	1	1	Yes	1	1.5
86	1	1	Yes	1	1.4
87	1	1	No	.	1.7
88	1	1	Yes	1	2.5
89	1	1	Yes	1	3.0
90	1	1	Yes	2	1.8
91	1	2	Yes	1	0.9
92	1	2	Yes	1	0.7
93	1	2	Yes	1	2.5
94	1	2	Yes	1	2.2
95	1	2	Yes	1	1.2
96	1	2	Yes	1	2.2
97	1	2	Yes	2	1.9
98	1	2	Yes	1	1.7
99	1	2	Yes	1	1.5
100	1	2	Yes	2	2.0
101	1	3	Yes	1	1.0
102	1	3	Yes	1	3.0
103	1	3	Yes	1	2.8
104	1	3	Yes	1	2.6
105	1	3	No	.	1.9
106	1	3	Yes	1	1.8
107	1	3	Yes	1	1.6
108	1	3	Yes	2	1.4
109	1	3	No	.	1.6
110	1	3	Yes	1	1.9
111	1	4	Yes	1	2.1
112	1	4	Yes	2	2.2
113	1	4	Yes	1	1.5
114	1	4	Yes	1	0.7
115	1	4	Yes	1	2.5
116	1	4	Yes	1	2.2
117	1	4	Yes	1	1.2
118	1	4	Yes	2	2.2
119	1	4	Yes	1	1.9

120	1	4	Yes	2	1.7
121	2	5	Yes	1	1.5
122	2	5	Yes	1	2.0
123	2	5	Yes	1	1.0
124	2	5	Yes	1	3.0
125	2	5	Yes	1	2.6
126	2	5	Yes	1	1.9
127	2	5	Yes	1	1.8
128	2	5	Yes	1	1.6
129	2	5	Yes	1	3.0
130	2	5	Yes	2	1.8
131	2	6	Yes	2	0.9
132	2	6	Yes	2	0.7
133	2	6	Yes	2	2.5
134	2	6	Yes	2	2.2
135	2	6	Yes	2	1.2
136	2	6	Yes	2	2.2
137	2	6	Yes	2	1.9
138	2	6	Yes	2	2.2
139	2	6	Yes	2	1.9
140	2	6	Yes	1	1.7
141	2	7	Yes	2	1.5
142	2	7	Yes	2	2.0
143	2	7	Yes	2	1.0
144	2	7	Yes	2	3.0
145	2	7	No	.	2.8
146	2	7	Yes	2	2.6
147	2	7	Yes	2	1.9
148	2	7	Yes	1	1.8
149	2	7	Yes	2	1.6
150	2	7	No	.	2.2
151	2	8	Yes	1	1.2
152	2	8	Yes	2	2.2
153	2	8	Yes	1	1.9
154	2	8	Yes	1	2.2
155	2	8	Yes	2	1.9
156	2	8	Yes	1	1.4
157	2	8	Yes	1	1.7
158	2	8	Yes	1	2.5
159	2	8	Yes	1	3.0
160	2	8	Yes	1	1.8

Appendix 3 Table 161
Simulated data set used for analysis by the SAS GLIMMIX procedure described in Chapter 8 – Statistical Analyses (animal group data; without blocking)

		Variable[1]			
Treatment	Group[2]	LSone	LStwo	Total	Age (years)
1	1	16	2	18	2.0000
1	2	16	4	20	1.6800
1	3	13	3	16	2.0125
1	4	15	5	20	1.8200
2	5	17	3	20	2.0200
2	6	10	10	20	1.7400
2	7	8	8	16	1.9250
2	8	16	4	20	1.9800

[1]LSone, LStwo, and Total = number of females per group with litter size of 1 and 2 and the number giving birth, respectively.
[2]20 animals per group.

Appendix 3 Table 162
Simulated data set used for analysis by the SAS GLIMMIX procedure described in Chapter 8 – Statistical Analyses (animal group data; blocking by village)

			Variable[1]			
Village	Household[2]	Treatment	LSone	LStwo	Total	Age (years)
1	1	1	5	0	5	2.0000
1	2	1	2	3	5	1.6800
1	3	1	4	0	4	2.0125
1	4	1	1	4	5	1.8200
1	5	2	0	5	5	1.6750
1	6	2	2	2	4	2.3000
1	7	2	2	3	5	2.5000
1	8	2	1	4	5	1.8000
1	9	3	0	4	4	1.7000
1	10	3	3	1	4	2.0000
1	11	3	4	1	5	2.0060
1	12	3	5	0	5	2.3000
2	13	1	0	4	4	2.0200
2	14	1	0	5	5	1.7400
2	15	1	2	3	5	1.9250
2	16	1	4	1	5	1.9800
2	17	2	2	2	4	1.9000
2	18	2	1	4	5	1.6000
2	19	2	2	3	5	2.2000
2	20	2	0	4	4	2.1000
2	21	3	2	3	5	2.1500
2	22	3	4	1	5	2.3400
2	23	3	2	3	5	1.8200
2	24	3	4	1	5	1.6750
3	25	1	2	3	5	2.0060
3	26	1	3	2	5	2.3000
3	27	1	5	0	5	2.0000
3	28	1	1	4	5	1.6800
3	29	2	0	5	5	2.0125
3	30	2	2	4	6	1.9800
3	31	2	0	4	4	1.9000
3	32	2	2	3	5	1.6000
3	33	3	5	0	5	2.2000
3	34	3	3	2	5	2.1500
3	35	3	3	2	5	2.3400
3	36	3	4	1	5	1.8200
4	37	1	1	4	5	2.1500
4	38	1	5	0	5	2.3400
4	39	1	0	3	3	1.8200

4	40	1	1	4	5	1.6750
4	41	2	0	5	5	2.0060
4	42	2	2	2	4	2.3000
4	43	2	1	3	4	2.0125
4	44	2	1	3	4	1.8200
4	45	3	3	2	5	1.6750
4	46	3	4	1	5	2.3000
4	47	3	5	0	5	2.5000
4	48	3	3	1	4	1.8000

[1]LSone, LStwo, and Total = number of females per group with litter size of 1 and 2 and the number giving birth, respectively.
[2]5 animals per household.

Appendix 3 Table 163
Simulated data set described in Tables 1 and 2 of Chapter 5 – Experimental Design for analysis by SAS and GenStat

Animal	Pen	Origin	VE[1]	Length	Variable	Feeding	Treatment
1	1	1	0	2	1	1	4
2	1	1	0	2	4	1	4
3	1	1	0	2	5	1	4
4	1	1	0	4	3	1	6
5	1	1	0	4	6	1	6
6	1	1	0	4	7	1	6
7	1	1	0	6	8	1	8
8	1	1	0	6	4	1	8
9	1	1	0	6	5	1	8
10	2	1	1	2	6	1	5
11	2	1	1	2	7	1	5
12	2	1	1	2	5	1	5
13	2	1	1	4	6	1	7
14	2	1	1	4	5	1	7
15	2	1	1	4	3	1	7
16	2	1	1	6	4	1	9
17	2	1	1	6	7	1	9
18	2	1	1	6	8	1	9
19	3	1	0	2	3	1	4
20	3	1	0	2	2	1	4
21	3	1	0	2	5	1	4
22	3	1	0	4	6	1	6
23	3	1	0	4	7	1	6
24	3	1	0	4	4	1	6
25	3	1	0	6	5	1	8
26	3	1	0	6	6	1	8
27	3	1	0	6	7	1	8
28	4	1	1	2	8	1	5
29	4	1	1	2	9	1	5
30	4	1	1	2	2	1	5
31	4	1	1	4	3	1	7
32	4	1	1	4	4	1	7
33	4	1	1	4	5	1	7
34	4	1	1	6	5	1	9
35	4	1	1	6	6	1	9
36	4	1	1	6	5	1	9
37	5	1	0	2	5	1	4
38	5	1	0	2	6	1	4
39	5	1	0	2	8	1	4
40	5	1	0	4	7	1	6

41	5	1	0	4	9	1	6
42	5	1	0	4	3	1	6
43	5	1	0	6	4	1	8
44	5	1	0	6	5	1	8
45	5	1	0	6	6	1	8
46	6	1	1	2	7	1	5
47	6	1	1	2	7	1	5
48	6	1	1	2	7	1	5
49	6	1	1	4	4	1	7
50	6	1	1	4	8	1	7
51	6	1	1	4	4	1	7
52	6	1	1	6	3	1	9
53	6	1	1	6	4	1	9
54	6	1	1	6	5	1	9
55	7	2	0	2	5	1	13
56	7	2	0	2	5	1	13
57	7	2	0	2	6	1	13
58	7	2	0	4	6	1	15
59	7	2	0	4	6	1	15
60	7	2	0	4	7	1	15
61	7	2	0	6	7	1	17
62	7	2	0	6	7	1	17
63	7	2	0	6	7	1	17
64	8	2	1	2	7	1	14
65	8	2	1	2	8	1	14
66	8	2	1	2	8	1	14
67	8	2	1	4	8	1	16
68	8	2	1	4	9	1	16
69	8	2	1	4	3	1	16
70	8	2	1	6	4	1	18
71	8	2	1	6	5	1	18
72	8	2	1	6	4	1	18
73	9	2	0	2	3	1	13
74	9	2	0	2	4	1	13
75	9	2	0	2	5	1	13
76	9	2	0	4	6	1	15
77	9	2	0	4	4	1	15
78	9	2	0	4	5	1	15
79	9	2	0	6	6	1	17
80	9	2	0	6	7	1	17
81	9	2	0	6	5	1	17
82	10	2	1	2	4	1	14
83	10	2	1	2	5	1	14
84	10	2	1	2	6	1	14
85	10	2	1	4	7	1	16

86	10	2	1	4	7	1	16
87	10	2	1	4	7	1	16
88	10	2	1	6	8	1	18
89	10	2	1	6	8	1	18
90	10	2	1	6	8	1	18
91	11	2	0	2	9	1	13
92	11	2	0	2	3	1	13
93	11	2	0	2	4	1	13
94	11	2	0	4	5	1	15
95	11	2	0	4	4	1	15
96	11	2	0	4	3	1	15
97	11	2	0	6	4	1	17
98	11	2	0	6	5	1	17
99	11	2	0	6	6	1	17
100	12	2	1	2	4	1	14
101	12	2	1	2	5	1	14
102	12	2	1	2	6	1	14
103	12	2	1	4	7	1	16
104	12	2	1	4	5	1	16
105	12	2	1	4	4	1	16
106	12	2	1	6	5	1	18
107	12	2	1	6	4	1	18
108	12	2	1	6	7	1	18

[1]Vitamin E.

Appendix 3 Table 164
Simulated data set described in Tables 1 and 2 of Chapter 5 – Experimental Design for analysis by SAS and GenStat (11 observations removed without regard to treatment; i.e., completely random)

Animal	Pen	Origin	VE[1]	Length	Variable	Feeding	Treatment
1	1	1	0	2	1	1	4
2	1	1	0	2	4	1	4
3	1	1	0	2	5	1	4
4	1	1	0	4	3	1	6
5	1	1	0	4	6	1	6
6	1	1	0	4	.	1	6
7	1	1	0	6	8	1	8
8	1	1	0	6	4	1	8
9	1	1	0	6	5	1	8
10	2	1	1	2	6	1	5
11	2	1	1	2	7	1	5
12	2	1	1	2	5	1	5
13	2	1	1	4	6	1	7
14	2	1	1	4	5	1	7
15	2	1	1	4	.	1	7
16	2	1	1	6	4	1	9
17	2	1	1	6	7	1	9
18	2	1	1	6	.	1	9
19	3	1	0	2	3	1	4
20	3	1	0	2	2	1	4
21	3	1	0	2	5	1	4
22	3	1	0	4	6	1	6
23	3	1	0	4	7	1	6
24	3	1	0	4	4	1	6
25	3	1	0	6	5	1	8
26	3	1	0	6	6	1	8
27	3	1	0	6	7	1	8
28	4	1	1	2	8	1	5
29	4	1	1	2	9	1	5
30	4	1	1	2	2	1	5
31	4	1	1	4	3	1	7
32	4	1	1	4	4	1	7
33	4	1	1	4	5	1	7
34	4	1	1	6	5	1	9
35	4	1	1	6	.	1	9
36	4	1	1	6	5	1	9
37	5	1	0	2	5	1	4
38	5	1	0	2	6	1	4
39	5	1	0	2	8	1	4
40	5	1	0	4	7	1	6

41	5	1	0	4	9	1	6
42	5	1	0	4	3	1	6
43	5	1	0	6	4	1	8
44	5	1	0	6	5	1	8
45	5	1	0	6	6	1	8
46	6	1	1	2	7	1	5
47	6	1	1	2	7	1	5
48	6	1	1	2	7	1	5
49	6	1	1	4	4	1	7
50	6	1	1	4	.	1	7
51	6	1	1	4	4	1	7
52	6	1	1	6	3	1	9
53	6	1	1	6	4	1	9
54	6	1	1	6	5	1	9
55	7	2	0	2	5	1	13
56	7	2	0	2	5	1	13
57	7	2	0	2	6	1	13
58	7	2	0	4	6	1	15
59	7	2	0	4	.	1	15
60	7	2	0	4	7	1	15
61	7	2	0	6	7	1	17
62	7	2	0	6	7	1	17
63	7	2	0	6	7	1	17
64	8	2	1	2	7	1	14
65	8	2	1	2	8	1	14
66	8	2	1	2	8	1	14
67	8	2	1	4	8	1	16
68	8	2	1	4	9	1	16
69	8	2	1	4	.	1	16
70	8	2	1	6	4	1	18
71	8	2	1	6	5	1	18
72	8	2	1	6	.	1	18
73	9	2	0	2	3	1	13
74	9	2	0	2	4	1	13
75	9	2	0	2	5	1	13
76	9	2	0	4	6	1	15
77	9	2	0	4	4	1	15
78	9	2	0	4	5	1	15
79	9	2	0	6	6	1	17
80	9	2	0	6	7	1	17
81	9	2	0	6	5	1	17
82	10	2	1	2	4	1	14
83	10	2	1	2	5	1	14
84	10	2	1	2	6	1	14
85	10	2	1	4	7	1	16

86	10	2	1	4	7	1	16
87	10	2	1	4	.	1	16
88	10	2	1	6	8	1	18
89	10	2	1	6	8	1	18
90	10	2	1	6	8	1	18
91	11	2	0	2	9	1	13
92	11	2	0	2	.	1	13
93	11	2	0	2	4	1	13
94	11	2	0	4	5	1	15
95	11	2	0	4	4	1	15
96	11	2	0	4	3	1	15
97	11	2	0	6	4	1	17
98	11	2	0	6	5	1	17
99	11	2	0	6	6	1	17
100	12	2	1	2	4	1	14
101	12	2	1	2	5	1	14
102	12	2	1	2	6	1	14
103	12	2	1	4	7	1	16
104	12	2	1	4	5	1	16
105	12	2	1	4	.	1	16
106	12	2	1	6	5	1	18
107	12	2	1	6	4	1	18
108	12	2	1	6	7	1	18

[1]Vitamin E.

Appendix 3 Table 165
Simulated data set described in Tables 1 and 2 of Chapter 5 – Experimental Design for analysis by SAS and GenStat (10 observations removed not in a completely random manner)

Animal	Pen	Origin	VE[1]	Length	Variable	Feeding	Treatment
1	1	1	0	2	1	1	4
2	1	1	0	2	4	1	4
3	1	1	0	2	5	1	4
4	1	1	0	4	3	1	6
5	1	1	0	4	6	1	6
6	1	1	0	4	7	1	6
7	1	1	0	6	.	1	8
8	1	1	0	6	4	1	8
9	1	1	0	6	5	1	8
10	2	1	1	2	6	1	5
11	2	1	1	2	7	1	5
12	2	1	1	2	5	1	5
13	2	1	1	4	6	1	7
14	2	1	1	4	5	1	7
15	2	1	1	4	3	1	7
16	2	1	1	6	.	1	9
17	2	1	1	6	7	1	9
18	2	1	1	6	8	1	9
19	3	1	0	2	3	1	4
20	3	1	0	2	2	1	4
21	3	1	0	2	5	1	4
22	3	1	0	4	6	1	6
23	3	1	0	4	7	1	6
24	3	1	0	4	4	1	6
25	3	1	0	6	.	1	8
26	3	1	0	6	6	1	8
27	3	1	0	6	7	1	8
28	4	1	1	2	8	1	5
29	4	1	1	2	9	1	5
30	4	1	1	2	2	1	5
31	4	1	1	4	3	1	7
32	4	1	1	4	4	1	7
33	4	1	1	4	5	1	7
34	4	1	1	6	.	1	9
35	4	1	1	6	6	1	9
36	4	1	1	6	5	1	9
37	5	1	0	2	5	1	4
38	5	1	0	2	6	1	4
39	5	1	0	2	8	1	4
40	5	1	0	4	7	1	6
41	5	1	0	4	9	1	6

42	5	1	0	4	3	1	6
43	5	1	0	6	.	1	8
44	5	1	0	6	.	1	8
45	5	1	0	6	6	1	8
46	6	1	1	2	7	1	5
47	6	1	1	2	7	1	5
48	6	1	1	2	7	1	5
49	6	1	1	4	4	1	7
50	6	1	1	4	8	1	7
51	6	1	1	4	.	1	7
52	6	1	1	6	3	1	9
53	6	1	1	6	4	1	9
54	6	1	1	6	5	1	9
55	7	2	0	2	5	1	13
56	7	2	0	2	5	1	13
57	7	2	0	2	6	1	13
58	7	2	0	4	6	1	15
59	7	2	0	4	6	1	15
60	7	2	0	4	7	1	15
61	7	2	0	6	.	1	17
62	7	2	0	6	7	1	17
63	7	2	0	6	7	1	17
64	8	2	1	2	7	1	14
65	8	2	1	2	8	1	14
66	8	2	1	2	8	1	14
67	8	2	1	4	8	1	16
68	8	2	1	4	9	1	16
69	8	2	1	4	3	1	16
70	8	2	1	6	.	1	18
71	8	2	1	6	5	1	18
72	8	2	1	6	4	1	18
73	9	2	0	2	3	1	13
74	9	2	0	2	4	1	13
75	9	2	0	2	5	1	13
76	9	2	0	4	6	1	15
77	9	2	0	4	4	1	15
78	9	2	0	4	5	1	15
79	9	2	0	6	.	1	17
80	9	2	0	6	7	1	17
81	9	2	0	6	5	1	17
82	10	2	1	2	4	1	14
83	10	2	1	2	5	1	14
84	10	2	1	2	6	1	14
85	10	2	1	4	7	1	16
86	10	2	1	4	7	1	16

87	10	2	1	4	7	1	16
88	10	2	1	6	8	1	18
89	10	2	1	6	8	1	18
90	10	2	1	6	8	1	18
91	11	2	0	2	9	1	13
92	11	2	0	2	3	1	13
93	11	2	0	2	4	1	13
94	11	2	0	4	5	1	15
95	11	2	0	4	4	1	15
96	11	2	0	4	3	1	15
97	11	2	0	6	4	1	17
98	11	2	0	6	5	1	17
99	11	2	0	6	6	1	17
100	12	2	1	2	4	1	14
101	12	2	1	2	5	1	14
102	12	2	1	2	6	1	14
103	12	2	1	4	7	1	16
104	12	2	1	4	5	1	16
105	12	2	1	4	4	1	16
106	12	2	1	6	5	1	18
107	12	2	1	6	4	1	18
108	12	2	1	6	7	1	18

[1]Vitamin E.

Appendix 3 Table 166
Simulated data set 1 for the FRG approach described in Figure 10 and Table 30 of Chapter 9 – On-Farm Research Examples used for analysis by SAS and GenStat

Animal	FRG	Household	Treatment	Variable
1	1	1	1	5
2	1	1	2	10
3	1	1	3	3
4	1	1	4	7
5	1	2	1	8
6	1	2	2	1
7	1	2	3	3
8	1	2	4	5
9	1	3	1	7
10	1	3	2	8
11	1	3	3	3
12	1	3	4	12
13	1	4	1	6
14	1	4	2	5
15	1	4	3	8
16	1	4	4	13
17	1	5	1	6
18	1	5	2	4
19	1	5	3	5
20	1	5	4	7
21	1	6	1	4
22	1	6	2	14
23	1	6	3	6
24	1	6	4	8
25	1	7	1	6
26	1	7	2	9
27	1	7	3	20
28	1	7	4	6
29	1	8	1	3
30	1	8	2	2
31	1	8	3	5
32	1	8	4	6
33	1	9	1	7
34	1	9	2	7
35	1	9	3	8
36	1	9	4	14
37	1	10	1	5
38	1	10	2	5
39	1	10	3	6
40	1	10	4	3
41	2	11	1	15

42	2	11	2	8
43	2	11	3	4
44	2	11	4	3
45	2	12	1	5
46	2	12	2	7
47	2	12	3	8
48	2	12	4	6
49	2	13	1	5
50	2	13	2	6
51	2	13	3	3
52	2	13	4	8
53	2	14	1	12
54	2	14	2	4
55	2	14	3	11
56	2	14	4	5
57	2	15	1	7
58	2	15	2	4
59	2	15	3	5
60	2	15	4	6
61	2	16	1	7
62	2	16	2	16
63	2	16	3	9
64	2	16	4	7
65	2	17	1	14
66	2	17	2	3
67	2	17	3	7
68	2	17	4	2
69	2	18	1	6
70	2	18	2	15
71	2	18	3	7
72	2	18	4	8
73	2	19	1	19
74	2	19	2	5
75	2	19	3	8
76	2	19	4	3
77	2	20	1	14
78	2	20	2	4
79	2	20	3	5
80	2	20	4	7
81	3	21	1	4
82	3	21	2	5
83	3	21	3	6
84	3	21	4	18
85	3	22	1	6
86	3	22	2	11

87	3	22	3	7
88	3	22	4	6
89	3	23	1	9
90	3	23	2	4
91	3	23	3	5
92	3	23	4	6
93	3	24	1	7
94	3	24	2	7
95	3	24	3	2
96	3	24	4	9
97	3	25	1	5
98	3	25	2	16
99	3	25	3	6
100	3	25	4	3
101	3	26	1	5
102	3	26	2	6
103	3	26	3	8
104	3	26	4	6
105	3	27	1	9
106	3	27	2	17
107	3	27	3	6
108	3	27	4	3
109	3	28	1	4
110	3	28	2	5
111	3	28	3	6
112	3	28	4	7
113	3	29	1	7
114	3	29	2	8
115	3	29	3	9
116	3	29	4	5
117	3	30	1	8
118	3	30	2	4
119	3	30	3	4
120	3	30	4	4
121	4	31	1	2
122	4	31	2	7
123	4	31	3	4
124	4	31	4	5
125	4	32	1	6
126	4	32	2	8
127	4	32	3	7
128	4	32	4	8
129	4	33	1	9
130	4	33	2	25
131	4	33	3	5

132	4	33	4	6
133	4	34	1	3
134	4	34	2	5
135	4	34	3	26
136	4	34	4	8
137	4	35	1	6
138	4	35	2	9
139	4	35	3	7
140	4	35	4	6
141	4	36	1	3
142	4	36	2	4
143	4	36	3	15
144	4	36	4	5
145	4	37	1	8
146	4	37	2	3
147	4	37	3	14
148	4	37	4	4
149	4	38	1	5
150	4	38	2	7
151	4	38	3	4
152	4	38	4	15
153	4	39	1	6
154	4	39	2	8
155	4	39	3	7
156	4	39	4	8
157	4	40	1	9
158	4	40	2	2
159	4	40	3	7
160	4	40	4	9

Appendix 3 Table 167
Simulated data set 1 for the FRG approach described in Figure 10 and Table 30 of Chapter 9 – On-Farm Research Examples used for analysis by SAS and GenStat (9 observations removed without regard to FRG or treatment; i.e., completely random)

Animal	FRG	Household	Treatment	Variable
1	1	1	1	5
2	1	1	2	10
3	1	1	3	3
4	1	1	4	7
5	1	2	1	8
6	1	2	2	1
7	1	2	3	3
8	1	2	4	5
9	1	3	1	7
10	1	3	2	8
11	1	3	3	3
12	1	3	4	12
13	1	4	1	6
14	1	4	2	5
15	1	4	3	8
16	1	4	4	13
17	1	5	1	6
18	1	5	2	4
19	1	5	3	5
20	1	5	4	7
21	1	6	1	.
22	1	6	2	14
23	1	6	3	6
24	1	6	4	8
25	1	7	1	6
26	1	7	2	9
27	1	7	3	20
28	1	7	4	.
29	1	8	1	3
30	1	8	2	2
31	1	8	3	5
32	1	8	4	6
33	1	9	1	7
34	1	9	2	7
35	1	9	3	.
36	1	9	4	14
37	1	10	1	5
38	1	10	2	5
39	1	10	3	6
40	1	10	4	3

41	2	11	1	15
42	2	11	2	8
43	2	11	3	4
44	2	11	4	3
45	2	12	1	5
46	2	12	2	7
47	2	12	3	8
48	2	12	4	6
49	2	13	1	5
50	2	13	2	6
51	2	13	3	3
52	2	13	4	8
53	2	14	1	12
54	2	14	2	4
55	2	14	3	11
56	2	14	4	5
57	2	15	1	7
58	2	15	2	4
59	2	15	3	5
60	2	15	4	6
61	2	16	1	7
62	2	16	2	16
63	2	16	3	9
64	2	16	4	.
65	2	17	1	14
66	2	17	2	.
67	2	17	3	7
68	2	17	4	2
69	2	18	1	6
70	2	18	2	15
71	2	18	3	7
72	2	18	4	8
73	2	19	1	19
74	2	19	2	5
75	2	19	3	8
76	2	19	4	3
77	2	20	1	14
78	2	20	2	4
79	2	20	3	5
80	2	20	4	7
81	3	21	1	4
82	3	21	2	5
83	3	21	3	6
84	3	21	4	18
85	3	22	1	6

86	3	22	2	11
87	3	22	3	7
88	3	22	4	6
89	3	23	1	9
90	3	23	2	4
91	3	23	3	5
92	3	23	4	6
93	3	24	1	7
94	3	24	2	7
95	3	24	3	2
96	3	24	4	9
97	3	25	1	5
98	3	25	2	16
99	3	25	3	6
100	3	25	4	3
101	3	26	1	5
102	3	26	2	6
103	3	26	3	8
104	3	26	4	6
105	3	27	1	9
106	3	27	2	.
107	3	27	3	6
108	3	27	4	3
109	3	28	1	4
110	3	28	2	5
111	3	28	3	6
112	3	28	4	7
113	3	29	1	7
114	3	29	2	8
115	3	29	3	.
116	3	29	4	5
117	3	30	1	8
118	3	30	2	4
119	3	30	3	4
120	3	30	4	4
121	4	31	1	2
122	4	31	2	7
123	4	31	3	4
124	4	31	4	5
125	4	32	1	6
126	4	32	2	8
127	4	32	3	7
128	4	32	4	8
129	4	33	1	9
130	4	33	2	25

131	4	33	3	5
132	4	33	4	6
133	4	34	1	3
134	4	34	2	5
135	4	34	3	26
136	4	34	4	8
137	4	35	1	6
138	4	35	2	9
139	4	35	3	7
140	4	35	4	6
141	4	36	1	3
142	4	36	2	4
143	4	36	3	15
144	4	36	4	5
145	4	37	1	8
146	4	37	2	3
147	4	37	3	14
148	4	37	4	.
149	4	38	1	.
150	4	38	2	7
151	4	38	3	4
152	4	38	4	15
153	4	39	1	6
154	4	39	2	8
155	4	39	3	.
156	4	39	4	8
157	4	40	1	9
158	4	40	2	2
159	4	40	3	7
160	4	40	4	9

Appendix 3 Table 168
Simulated data set 1 for the FRG approach described in Figure 10 and Table 30 of Chapter 9 – On-Farm Research Examples used for analysis by SAS and GenStat (10 observations removed not in a completely random manner)

Animal	FRG	Household	Treatment	Variable
1	1	1	1	5
2	1	1	2	10
3	1	1	3	3
4	1	1	4	7
5	1	2	1	.
6	1	2	2	1
7	1	2	3	3
8	1	2	4	5
9	1	3	1	7
10	1	3	2	8
11	1	3	3	3
12	1	3	4	12
13	1	4	1	6
14	1	4	2	5
15	1	4	3	8
16	1	4	4	13
17	1	5	1	6
18	1	5	2	4
19	1	5	3	5
20	1	5	4	7
21	1	6	1	4
22	1	6	2	14
23	1	6	3	6
24	1	6	4	8
25	1	7	1	6
26	1	7	2	.
27	1	7	3	20
28	1	7	4	6
29	1	8	1	3
30	1	8	2	2
31	1	8	3	5
32	1	8	4	6
33	1	9	1	.
34	1	9	2	7
35	1	9	3	8
36	1	9	4	14
37	1	10	1	5
38	1	10	2	5
39	1	10	3	6
40	1	10	4	3

41	2	11	1	15
42	2	11	2	8
43	2	11	3	4
44	2	11	4	3
45	2	12	1	.
46	2	12	2	7
47	2	12	3	8
48	2	12	4	6
49	2	13	1	5
50	2	13	2	6
51	2	13	3	3
52	2	13	4	8
53	2	14	1	12
54	2	14	2	4
55	2	14	3	11
56	2	14	4	5
57	2	15	1	7
58	2	15	2	4
59	2	15	3	5
60	2	15	4	6
61	2	16	1	7
62	2	16	2	16
63	2	16	3	9
64	2	16	4	7
65	2	17	1	14
66	2	17	2	3
67	2	17	3	7
68	2	17	4	2
69	2	18	1	6
70	2	18	2	15
71	2	18	3	7
72	2	18	4	8
73	2	19	1	19
74	2	19	2	5
75	2	19	3	8
76	2	19	4	3
77	2	20	1	.
78	2	20	2	4
79	2	20	3	5
80	2	20	4	7
81	3	21	1	4
82	3	21	2	5
83	3	21	3	6
84	3	21	4	18
85	3	22	1	6

86	3	22	2	11
87	3	22	3	7
88	3	22	4	6
89	3	23	1	9
90	3	23	2	.
91	3	23	3	5
92	3	23	4	6
93	3	24	1	7
94	3	24	2	7
95	3	24	3	2
96	3	24	4	9
97	3	25	1	.
98	3	25	2	16
99	3	25	3	6
100	3	25	4	3
101	3	26	1	5
102	3	26	2	6
103	3	26	3	8
104	3	26	4	6
105	3	27	1	9
106	3	27	2	17
107	3	27	3	6
108	3	27	4	3
109	3	28	1	4
110	3	28	2	5
111	3	28	3	6
112	3	28	4	7
113	3	29	1	7
114	3	29	2	8
115	3	29	3	9
116	3	29	4	5
117	3	30	1	8
118	3	30	2	4
119	3	30	3	4
120	3	30	4	4
121	4	31	1	.
122	4	31	2	7
123	4	31	3	4
124	4	31	4	5
125	4	32	1	6
126	4	32	2	8
127	4	32	3	7
128	4	32	4	8
129	4	33	1	9
130	4	33	2	25

131	4	33	3	5
132	4	33	4	6
133	4	34	1	3
134	4	34	2	5
135	4	34	3	26
136	4	34	4	8
137	4	35	1	6
138	4	35	2	9
139	4	35	3	7
140	4	35	4	6
141	4	36	1	3
142	4	36	2	.
143	4	36	3	15
144	4	36	4	5
145	4	37	1	8
146	4	37	2	3
147	4	37	3	14
148	4	37	4	4
149	4	38	1	5
150	4	38	2	7
151	4	38	3	4
152	4	38	4	15
153	4	39	1	.
154	4	39	2	8
155	4	39	3	7
156	4	39	4	8
157	4	40	1	9
158	4	40	2	2
159	4	40	3	7
160	4	40	4	9

Appendix 3 Table 169
Simulated data set 2 for the FRG approach described in Figure 10 and Table 30 of Chapter 9 – On-Farm Research Examples used for analysis by SAS and GenStat

Animal	FRG	Household	Treatment	Variable
1	1	1	1	5
2	1	1	2	4
3	1	1	3	7
4	1	1	4	3
5	1	2	1	8
6	1	2	2	5
7	1	2	3	4
8	1	2	4	6
9	1	3	1	3
10	1	3	2	7
11	1	3	3	9
12	1	3	4	2
13	1	4	1	5
14	1	4	2	3
15	1	4	3	6
16	1	4	4	8
17	1	5	1	3
18	1	5	2	5
19	1	5	3	8
20	1	5	4	3
21	1	6	1	5
22	1	6	2	2
23	1	6	3	8
24	1	6	4	9
25	1	7	1	3
26	1	7	2	3
27	1	7	3	4
28	1	7	4	7
29	1	8	1	4
30	1	8	2	9
31	1	8	3	6
32	1	8	4	7
33	1	9	1	5
34	1	9	2	4
35	1	9	3	5
36	1	9	4	7
37	1	10	1	6
38	1	10	2	5
39	1	10	3	6
40	1	10	4	8

41	2	11	1	2
42	2	11	2	8
43	2	11	3	6
44	2	11	4	5
45	2	12	1	4
46	2	12	2	6
47	2	12	3	7
48	2	12	4	8
49	2	13	1	9
50	2	13	2	3
51	2	13	3	1
52	2	13	4	6
53	2	14	1	4
54	2	14	2	7
55	2	14	3	8
56	2	14	4	5
57	2	15	1	6
58	2	15	2	4
59	2	15	3	5
60	2	15	4	6
61	2	16	1	5
62	2	16	2	4
63	2	16	3	6
64	2	16	4	7
65	2	17	1	4
66	2	17	2	8
67	2	17	3	2
68	2	17	4	8
69	2	18	1	9
70	2	18	2	5
71	2	18	3	4
72	2	18	4	7
73	2	19	1	8
74	2	19	2	5
75	2	19	3	6
76	2	19	4	4
77	2	20	1	7
78	2	20	2	4
79	2	20	3	7
80	2	20	4	8
81	3	21	1	3
82	3	21	2	6
83	3	21	3	4
84	3	21	4	8
85	3	22	1	4

86	3	22	2	7
87	3	22	3	5
88	3	22	4	4
89	3	23	1	7
90	3	23	2	4
91	3	23	3	5
92	3	23	4	6
93	3	24	1	8
94	3	24	2	3
95	3	24	3	8
96	3	24	4	5
97	3	25	1	4
98	3	25	2	7
99	3	25	3	6
100	3	25	4	7
101	3	26	1	8
102	3	26	2	5
103	3	26	3	6
104	3	26	4	4
105	3	27	1	5
106	3	27	2	7
107	3	27	3	4
108	3	27	4	7
109	3	28	1	4
110	3	28	2	7
111	3	28	3	5
112	3	28	4	4
113	3	29	1	8
114	3	29	2	3
115	3	29	3	5
116	3	29	4	9
117	3	30	1	4
118	3	30	2	4
119	3	30	3	6
120	3	30	4	7
121	4	31	1	4
122	4	31	2	5
123	4	31	3	7
124	4	31	4	6
125	4	32	1	7
126	4	32	2	6
127	4	32	3	7
128	4	32	4	6
129	4	33	1	7
130	4	33	2	5

131	4	33	3	8
132	4	33	4	6
133	4	34	1	8
134	4	34	2	5
135	4	34	3	7
136	4	34	4	4
137	4	35	1	7
138	4	35	2	5
139	4	35	3	8
140	4	35	4	6
141	4	36	1	5
142	4	36	2	7
143	4	36	3	6
144	4	36	4	8
145	4	37	1	3
146	4	37	2	6
147	4	37	3	4
148	4	37	4	8
149	4	38	1	6
150	4	38	2	4
151	4	38	3	7
152	4	38	4	5
153	4	39	1	8
154	4	39	2	4
155	4	39	3	6
156	4	39	4	5
157	4	40	1	5
158	4	40	2	5
159	4	40	3	7
160	4	40	4	6

Appendix 3 Table 170
Simulated data set 1 for the ISH approach described in Figure 11 and Tables 31 and 32 of Chapter 9 – On-Farm Research Examples used for analysis by SAS and GenStat (animals of households subjected to the same treatment)

Animal	Woreda	Village	Household	Treatment	Variable
1	1	1	1	1	5
2	1	1	1	1	6
3	1	1	1	1	3
4	1	1	2	2	7
5	1	1	2	2	8
6	1	1	2	2	4
7	1	1	3	3	3
8	1	1	3	3	5
9	1	1	3	3	7
10	1	1	4	1	8
11	1	1	4	1	3
12	1	1	4	1	5
13	1	1	5	2	6
14	1	1	5	2	7
15	1	1	5	2	8
16	1	1	6	3	3
17	1	1	6	3	4
18	1	1	6	3	4
19	1	1	7	1	5
20	1	1	7	1	7
21	1	1	7	1	4
22	1	1	8	2	5
23	1	1	8	2	6
24	1	1	8	2	8
25	1	1	9	3	6
26	1	1	9	3	9
27	1	1	9	3	7
28	1	2	10	1	6
29	1	2	10	1	3
30	1	2	10	1	4
31	1	2	11	2	5
32	1	2	11	2	6
33	1	2	11	2	7
34	1	2	12	3	7
35	1	2	12	3	8
36	1	2	12	3	9
37	1	2	13	1	5
38	1	2	13	1	5
39	1	2	13	1	6
40	1	2	14	2	3

41	1	2	14	2	7
42	1	2	14	2	8
43	1	2	15	3	4
44	1	2	15	3	3
45	1	2	15	3	5
46	1	2	16	1	7
47	1	2	16	1	8
48	1	2	16	1	3
49	1	2	17	2	5
50	1	2	17	2	6
51	1	2	17	2	7
52	1	2	18	3	8
53	1	2	18	3	3
54	1	2	18	3	4
55	2	3	19	1	4
56	2	3	19	1	5
57	2	3	19	1	7
58	2	3	20	2	4
59	2	3	20	2	5
60	2	3	20	2	6
61	2	3	21	3	8
62	2	3	21	3	6
63	2	3	21	3	9
64	2	3	22	1	7
65	2	3	22	1	6
66	2	3	22	1	3
67	2	3	23	2	4
68	2	3	23	2	5
69	2	3	23	2	6
70	2	3	24	3	7
71	2	3	24	3	7
72	2	3	24	3	8
73	2	3	25	1	9
74	2	3	25	1	5
75	2	3	25	1	8
76	2	3	26	2	3
77	2	3	26	2	4
78	2	3	26	2	4
79	2	3	27	3	5
80	2	3	27	3	7
81	2	3	27	3	4
82	2	4	28	1	5
83	2	4	28	1	6
84	2	4	28	1	8
85	2	4	29	2	6

86	2	4	29	2	9
87	2	4	29	2	7
88	2	4	30	3	6
89	2	4	30	3	3
90	2	4	30	3	4
91	2	4	31	1	5
92	2	4	31	1	6
93	2	4	31	1	7
94	2	4	32	2	7
95	2	4	32	2	8
96	2	4	32	2	9
97	2	4	33	3	5
98	2	4	33	3	5
99	2	4	33	3	6
100	2	4	34	1	3
101	2	4	34	1	5
102	2	4	34	1	6
103	2	4	35	2	8
104	2	4	35	2	6
105	2	4	35	2	9
106	2	4	36	3	7
107	2	4	36	3	6
108	2	4	36	3	3

Appendix 3 Table 171
Simulated data set 2 for the ISH approach described in Figure 11 and Tables 31 and 32 of Chapter 9 – On-Farm Research Examples used for analysis by SAS and GenStat (animals of households subjected to the same treatment)

Animal	Woreda	Village	Household	Treatment	Variable
1	1	1	1	1	1
2	1	1	1	1	6
3	1	1	1	1	9
4	1	1	2	2	7
5	1	1	2	2	5
6	1	1	2	2	4
7	1	1	3	3	3
8	1	1	3	3	5
9	1	1	3	3	7
10	1	1	4	1	3
11	1	1	4	1	8
12	1	1	4	1	5
13	1	1	5	2	6
14	1	1	5	2	7
15	1	1	5	2	8
16	1	1	6	3	3
17	1	1	6	3	4
18	1	1	6	3	4
19	1	1	7	1	5
20	1	1	7	1	12
21	1	1	7	1	4
22	1	1	8	2	5
23	1	1	8	2	6
24	1	1	8	2	1
25	1	1	9	3	6
26	1	1	9	3	9
27	1	1	9	3	7
28	1	2	10	1	6
29	1	2	10	1	13
30	1	2	10	1	4
31	1	2	11	2	5
32	1	2	11	2	6
33	1	2	11	2	7
34	1	2	12	3	7
35	1	2	12	3	8
36	1	2	12	3	19
37	1	2	13	1	5
38	1	2	13	1	5
39	1	2	13	1	16

40	1	2	14	2	3
41	1	2	14	2	3
42	1	2	14	2	8
43	1	2	15	3	4
44	1	2	15	3	8
45	1	2	15	3	5
46	1	2	16	1	17
47	1	2	16	1	8
48	1	2	16	1	23
49	1	2	17	2	5
50	1	2	17	2	6
51	1	2	17	2	7
52	1	2	18	3	18
53	1	2	18	3	3
54	1	2	18	3	4
55	2	3	19	1	14
56	2	3	19	1	5
57	2	3	19	1	7
58	2	3	20	2	4
59	2	3	20	2	5
60	2	3	20	2	6
61	2	3	21	3	1
62	2	3	21	3	26
63	2	3	21	3	9
64	2	3	22	1	17
65	2	3	22	1	6
66	2	3	22	1	3
67	2	3	23	2	4
68	2	3	23	2	5
69	2	3	23	2	6
70	2	3	24	3	27
71	2	3	24	3	7
72	2	3	24	3	8
73	2	3	25	1	9
74	2	3	25	1	5
75	2	3	25	1	18
76	2	3	26	2	3
77	2	3	26	2	4
78	2	3	26	2	4
79	2	3	27	3	5
80	2	3	27	3	7
81	2	3	27	3	4
82	2	4	28	1	5
83	2	4	28	1	6
84	2	4	28	1	18

85	2	4	29	2	6
86	2	4	29	2	1
87	2	4	29	2	7
88	2	4	30	3	6
89	2	4	30	3	3
90	2	4	30	3	4
91	2	4	31	1	5
92	2	4	31	1	36
93	2	4	31	1	7
94	2	4	32	2	7
95	2	4	32	2	8
96	2	4	32	2	9
97	2	4	33	3	5
98	2	4	33	3	5
99	2	4	33	3	6
100	2	4	34	1	13
101	2	4	34	1	5
102	2	4	34	1	6
103	2	4	35	2	8
104	2	4	35	2	6
105	2	4	35	2	4
106	2	4	36	3	7
107	2	4	36	3	6
108	2	4	36	3	3

Appendix 3 Table 172
Simulated data set for the ISH approach described in Figure 11 and Tables 31 and 32 of Chapter 9 – On-Farm Research Examples used for analysis by SAS and GenStat (animals of households subjected to the same treatment; 7 observations removed without regard to treatment, woreda, village, or household, i.e., completely random)

Animal	Woreda	Village	Household	Treatment	Variable
1	1	1	1	1	5
2	1	1	1	1	6
3	1	1	1	1	3
4	1	1	2	2	7
5	1	1	2	2	8
6	1	1	2	2	4
7	1	1	3	3	.
8	1	1	3	3	5
9	1	1	3	3	7
10	1	1	4	1	8
11	1	1	4	1	3
12	1	1	4	1	5
13	1	1	5	2	6
14	1	1	5	2	7
15	1	1	5	2	8
16	1	1	6	3	3
17	1	1	6	3	4
18	1	1	6	3	4
19	1	1	7	1	5
20	1	1	7	1	7
21	1	1	7	1	4
22	1	1	8	2	5
23	1	1	8	2	6
24	1	1	8	2	.
25	1	1	9	3	6
26	1	1	9	3	9
27	1	1	9	3	7
28	1	2	10	1	6
29	1	2	10	1	3
30	1	2	10	1	4
31	1	2	11	2	5
32	1	2	11	2	6
33	1	2	11	2	7
34	1	2	12	3	7
35	1	2	12	3	8
36	1	2	12	3	9
37	1	2	13	1	5
38	1	2	13	1	5
39	1	2	13	1	6

40	1	2	14	2	3
41	1	2	14	2	7
42	1	2	14	2	8
43	1	2	15	3	4
44	1	2	15	3	3
45	1	2	15	3	5
46	1	2	16	1	7
47	1	2	16	1	8
48	1	2	16	1	.
49	1	2	17	2	5
50	1	2	17	2	6
51	1	2	17	2	7
52	1	2	18	3	8
53	1	2	18	3	3
54	1	2	18	3	4
55	2	3	19	1	4
56	2	3	19	1	5
57	2	3	19	1	7
58	2	3	20	2	4
59	2	3	20	2	5
60	2	3	20	2	6
61	2	3	21	3	8
62	2	3	21	3	6
63	2	3	21	3	9
64	2	3	22	1	7
65	2	3	22	1	.
66	2	3	22	1	3
67	2	3	23	2	4
68	2	3	23	2	.
69	2	3	23	2	6
70	2	3	24	3	7
71	2	3	24	3	7
72	2	3	24	3	8
73	2	3	25	1	9
74	2	3	25	1	5
75	2	3	25	1	8
76	2	3	26	2	3
77	2	3	26	2	4
78	2	3	26	2	4
79	2	3	27	3	5
80	2	3	27	3	7
81	2	3	27	3	4
82	2	4	28	1	5
83	2	4	28	1	6
84	2	4	28	1	8

85	2	4	29	2	6
86	2	4	29	2	9
87	2	4	29	2	7
88	2	4	30	3	6
89	2	4	30	3	3
90	2	4	30	3	4
91	2	4	31	1	5
92	2	4	31	1	6
93	2	4	31	1	7
94	2	4	32	2	7
95	2	4	32	2	8
96	2	4	32	2	9
97	2	4	33	3	.
98	2	4	33	3	5
99	2	4	33	3	6
100	2	4	34	1	3
101	2	4	34	1	5
102	2	4	34	1	6
103	2	4	35	2	8
104	2	4	35	2	6
105	2	4	35	2	9
106	2	4	36	3	7
107	2	4	36	3	.
108	2	4	36	3	3

Appendix 3 Table 173
Simulated data set for the ISH approach described in Figure 12 and Table 33 of Chapter 9 – On-Farm Research Examples used for analysis by SAS and GenStat (animals of households subjected to each treatment)

Animal	Woreda	Village	Household	Treatment	Variable
1	1	1	1	1	5
2	1	1	1	2	6
3	1	1	1	3	3
4	1	1	2	1	7
5	1	1	2	2	8
6	1	1	2	3	4
7	1	1	3	1	3
8	1	1	3	2	5
9	1	1	3	3	7
10	1	1	4	1	8
11	1	1	4	2	3
12	1	1	4	3	5
13	1	1	5	1	6
14	1	1	5	2	7
15	1	1	5	3	8
16	1	1	6	1	3
17	1	1	6	2	4
18	1	1	6	3	4
19	1	1	7	1	5
20	1	1	7	2	7
21	1	1	7	3	4
22	1	1	8	1	5
23	1	1	8	2	6
24	1	1	8	3	8
25	1	1	9	1	6
26	1	1	9	2	9
27	1	1	9	3	7
28	1	2	10	1	6
29	1	2	10	2	3
30	1	2	10	3	4
31	1	2	11	1	5
32	1	2	11	2	6
33	1	2	11	3	7
34	1	2	12	1	7
35	1	2	12	2	8
36	1	2	12	3	9
37	1	2	13	1	5
38	1	2	13	2	5
39	1	2	13	3	6

40	1	2	14	1	3
41	1	2	14	2	7
42	1	2	14	3	8
43	1	2	15	1	4
44	1	2	15	2	3
45	1	2	15	3	5
46	1	2	16	1	7
47	1	2	16	2	8
48	1	2	16	3	3
49	1	2	17	1	5
50	1	2	17	2	6
51	1	2	17	3	7
52	1	2	18	1	8
53	1	2	18	2	3
54	1	2	18	3	4
55	2	3	19	1	4
56	2	3	19	2	5
57	2	3	19	3	7
58	2	3	20	1	4
59	2	3	20	2	5
60	2	3	20	3	6
61	2	3	21	1	8
62	2	3	21	2	6
63	2	3	21	3	9
64	2	3	22	1	7
65	2	3	22	2	6
66	2	3	22	3	3
67	2	3	23	1	4
68	2	3	23	2	5
69	2	3	23	3	6
70	2	3	24	1	7
71	2	3	24	2	7
72	2	3	24	3	8
73	2	3	25	1	9
74	2	3	25	2	5
75	2	3	25	3	8
76	2	3	26	1	3
77	2	3	26	2	4
78	2	3	26	3	4
79	2	3	27	1	5
80	2	3	27	2	7
81	2	3	27	3	4
82	2	4	28	1	5
83	2	4	28	2	6
84	2	4	28	3	8

85	2	4	29	1	6
86	2	4	29	2	9
87	2	4	29	3	7
88	2	4	30	1	6
89	2	4	30	2	3
90	2	4	30	3	4
91	2	4	31	1	5
92	2	4	31	2	6
93	2	4	31	3	7
94	2	4	32	1	7
95	2	4	32	2	8
96	2	4	32	3	9
97	2	4	33	1	5
98	2	4	33	2	5
99	2	4	33	3	6
100	2	4	34	1	3
101	2	4	34	2	5
102	2	4	34	3	6
103	2	4	35	1	8
104	2	4	35	2	6
105	2	4	35	3	9
106	2	4	36	1	7
107	2	4	36	2	6
108	2	4	36	3	3

Appendix 3 Table 174
Simulated data set for the ISH approach described in Figure 12 and Table 33 of Chapter 9 – On-Farm Research Examples used for analysis by SAS and GenStat (animals of households subjected to each treatment; 7 observations removed without regard to treatment, woreda, village, or household, i.e., completely random)

Animal	Woreda	Village	Household	Treatment	Variable
1	1	1	1	1	5
2	1	1	1	2	6
3	1	1	1	3	.
4	1	1	2	1	7
5	1	1	2	2	8
6	1	1	2	3	4
7	1	1	3	1	3
8	1	1	3	2	5
9	1	1	3	3	7
10	1	1	4	1	8
11	1	1	4	2	3
12	1	1	4	3	5
13	1	1	5	1	6
14	1	1	5	2	7
15	1	1	5	3	8
16	1	1	6	1	3
17	1	1	6	2	.
18	1	1	6	3	4
19	1	1	7	1	5
20	1	1	7	2	7
21	1	1	7	3	4
22	1	1	8	1	5
23	1	1	8	2	6
24	1	1	8	3	8
25	1	1	9	1	6
26	1	1	9	2	9
27	1	1	9	3	7
28	1	2	10	1	6
29	1	2	10	2	3
30	1	2	10	3	4
31	1	2	11	1	5
32	1	2	11	2	6
33	1	2	11	3	7
34	1	2	12	1	7
35	1	2	12	2	8
36	1	2	12	3	9
37	1	2	13	1	5
38	1	2	13	2	.
39	1	2	13	3	6

40	1	2	14	1	3
41	1	2	14	2	7
42	1	2	14	3	8
43	1	2	15	1	4
44	1	2	15	2	3
45	1	2	15	3	5
46	1	2	16	1	7
47	1	2	16	2	8
48	1	2	16	3	.
49	1	2	17	1	5
50	1	2	17	2	6
51	1	2	17	3	7
52	1	2	18	1	8
53	1	2	18	2	3
54	1	2	18	3	4
55	2	3	19	1	4
56	2	3	19	2	5
57	2	3	19	3	7
58	2	3	20	1	4
59	2	3	20	2	5
60	2	3	20	3	6
61	2	3	21	1	8
62	2	3	21	2	6
63	2	3	21	3	9
64	2	3	22	1	7
65	2	3	22	2	6
66	2	3	22	3	3
67	2	3	23	1	.
68	2	3	23	2	5
69	2	3	23	3	6
70	2	3	24	1	7
71	2	3	24	2	.
72	2	3	24	3	8
73	2	3	25	1	9
74	2	3	25	2	5
75	2	3	25	3	8
76	2	3	26	1	3
77	2	3	26	2	4
78	2	3	26	3	4
79	2	3	27	1	5
80	2	3	27	2	7
81	2	3	27	3	4
82	2	4	28	1	5
83	2	4	28	2	6
84	2	4	28	3	8

85	2	4	29	1	6
86	2	4	29	2	9
87	2	4	29	3	7
88	2	4	30	1	6
89	2	4	30	2	3
90	2	4	30	3	4
91	2	4	31	1	5
92	2	4	31	2	6
93	2	4	31	3	7
94	2	4	32	1	7
95	2	4	32	2	8
96	2	4	32	3	9
97	2	4	33	1	5
98	2	4	33	2	.
99	2	4	33	3	6
100	2	4	34	1	3
101	2	4	34	2	5
102	2	4	34	3	6
103	2	4	35	1	8
104	2	4	35	2	6
105	2	4	35	3	9
106	2	4	36	1	7
107	2	4	36	2	6
108	2	4	36	3	3

Appendix 3 Table 175
Simulated data set for the ISH approach with a split-plot treatment arrangement, entailing four villages, 12 households per village, two breeds of animals present at each household, and five animals per breed and household, described in Figure 13 and Table 34 of Chapter 9 – On-Farm Research Examples used for analysis by SAS

Village	Household	Breed	Treatment	LSone	LStwo	Total
1	1	1	1	4	1	5
1	1	2	1	3	1	4
1	2	1	1	2	3	5
1	2	2	1	1	3	4
1	3	1	1	5	0	5
1	3	2	1	3	2	5
1	4	1	1	4	0	4
1	4	2	1	4	1	5
1	5	1	2	5	0	5
1	5	2	2	1	2	3
1	6	1	2	0	4	4
1	6	2	2	3	1	4
1	7	1	2	2	3	5
1	7	2	2	1	4	5
1	8	1	2	5	0	5
1	8	2	2	4	0	4
1	9	1	3	3	0	3
1	9	2	3	3	1	4
1	10	1	3	4	0	4
1	10	2	3	4	1	5
1	11	1	3	5	0	5
1	11	2	3	1	3	4
1	12	1	3	5	0	5
1	12	2	3	1	1	2
2	13	1	1	1	2	3
2	13	2	1	5	0	5
2	14	1	1	1	2	3
2	14	2	1	5	0	5
2	15	1	1	4	1	5
2	15	2	1	4	1	5
2	16	1	1	5	0	5
2	16	2	1	1	2	3
2	17	1	2	2	3	5
2	17	2	2	4	0	4
2	18	1	2	3	0	3
2	18	2	2	3	1	4
2	19	1	2	4	0	4
2	19	2	2	4	1	5

2	20	1	2	3	1	4
2	20	2	2	2	3	5
2	21	1	3	1	3	4
2	21	2	3	5	0	5
2	22	1	3	1	3	4
2	22	2	3	5	0	5
2	23	1	3	1	1	2
2	23	2	3	5	0	5
2	24	1	3	1	2	3
2	24	2	3	5	0	5
3	25	1	1	5	0	5
3	25	2	1	1	3	4
3	26	1	1	5	0	5
3	26	2	1	5	0	5
3	27	1	1	1	2	3
3	27	2	1	4	0	4
3	28	1	1	4	1	5
3	28	2	1	5	0	5
3	29	1	2	1	3	4
3	29	2	2	5	0	5
3	30	1	2	1	2	3
3	30	2	2	5	0	5
3	31	1	2	4	1	5
3	31	2	2	3	0	3
3	32	1	2	3	1	4
3	32	2	2	4	0	4
3	33	1	3	4	1	5
3	33	2	3	2	3	5
3	34	1	3	1	3	4
3	34	2	3	5	0	5
3	35	1	3	1	3	4
3	35	2	3	5	0	5
3	36	1	3	1	1	2
3	36	2	3	5	0	5
4	37	1	1	1	2	3
4	37	2	1	1	3	4
4	38	1	1	5	0	5
4	38	2	1	5	0	5
4	39	1	1	1	3	4
4	39	2	1	5	0	5
4	40	1	1	1	2	3
4	40	2	1	5	0	5
4	41	1	2	4	1	5
4	41	2	2	5	0	5
4	42	1	2	1	3	4

4	42	2	2	5	0	5
4	43	1	2	1	1	2
4	43	2	2	5	0	5
4	44	1	2	5	0	5
4	44	2	2	1	2	3
4	45	1	3	1	3	4
4	45	2	3	5	0	5
4	46	1	3	1	2	3
4	46	2	3	5	0	5
4	47	1	3	4	1	5
4	47	2	3	4	1	5
4	48	1	3	2	3	5
4	48	2	3	1	3	4

Appendix 3 Table 176
Simulated data set for the ISH approach with different seasons described in Figure 14 and Table 35 of Chapter 9 – On-Farm Research Examples used for analysis by SAS and GenStat (different villages in each season; animals of each household subjected to the same treatment)

Animal	Season	Village	Household	Treatment	Variable
1	1	1	1	1	5
2	1	1	1	1	6
3	1	1	2	2	3
4	1	1	2	2	7
5	1	1	3	3	8
6	1	1	3	3	4
7	1	1	4	1	3
8	1	1	4	1	5
9	1	1	5	2	7
10	1	1	5	2	8
11	1	1	6	3	3
12	1	1	6	3	5
13	1	1	7	1	6
14	1	1	7	1	7
15	1	1	8	2	8
16	1	1	8	2	3
17	1	1	9	3	4
18	1	1	9	3	4
19	1	2	10	1	5
20	1	2	10	1	7
21	1	2	11	2	4
22	1	2	11	2	5
23	1	2	12	3	6
24	1	2	12	3	8
25	1	2	13	1	6
26	1	2	13	1	9
27	1	2	14	2	7
28	1	2	14	2	6
29	1	2	15	3	3
30	1	2	15	3	4
31	1	2	16	1	5
32	1	2	16	1	6
33	1	2	17	2	7
34	1	2	17	2	7
35	1	2	18	3	8
36	1	2	18	3	9
37	2	3	19	1	5
38	2	3	19	1	5
39	2	3	20	2	6
40	2	3	20	2	3

41	2	3	21	3	7
42	2	3	21	3	8
43	2	3	22	1	4
44	2	3	22	1	3
45	2	3	23	2	5
46	2	3	23	2	7
47	2	3	24	3	8
48	2	3	24	3	3
49	2	3	25	1	5
50	2	3	25	1	6
51	2	3	26	2	7
52	2	3	26	2	8
53	2	3	27	3	3
54	2	3	27	3	4
55	2	4	28	1	4
56	2	4	28	1	5
57	2	4	29	2	7
58	2	4	29	2	4
59	2	4	30	3	5
60	2	4	30	3	6
61	2	4	31	1	8
62	2	4	31	1	6
63	2	4	32	2	9
64	2	4	32	2	7
65	2	4	33	3	6
66	2	4	33	3	3
67	2	4	34	1	4
68	2	4	34	1	5
69	2	4	35	2	6
70	2	4	35	2	7
71	2	4	36	3	7
72	2	4	36	3	8

Appendix 3 Table 177
Simulated data set for the ISH approach with different seasons described in Figure 15 and Tables 36, 37, and 38 of Chapter 9 – On-Farm Research Examples used for analysis by SAS and GenStat (the same villages in each season; animals of each household subjected to the same treatment)

Observation	Village	Household	Season	Treatment	Variable
1	1	1	1	1	5.5
2	1	1	2	1	4.0
3	1	2	1	2	5.0
4	1	2	2	2	4.5
5	1	3	1	3	6.0
6	1	3	2	3	7.5
7	1	4	1	1	4.0
8	1	4	2	1	3.5
9	1	5	1	2	7.5
10	1	5	2	2	6.0
11	1	6	1	3	4.0
12	1	6	2	3	5.5
13	1	7	1	1	6.5
14	1	7	2	1	5.5
15	1	8	1	2	5.5
16	1	8	2	2	7.5
17	1	9	1	3	4.0
18	1	9	2	3	4.5
19	2	10	1	1	6.0
20	2	10	2	1	4.5
21	2	11	1	2	4.5
22	2	11	2	2	5.5
23	2	12	1	3	7.0
24	2	12	2	3	5.5
25	2	13	1	1	7.5
26	2	13	2	1	7.0
27	2	14	1	2	6.5
28	2	14	2	2	8.0
29	2	15	1	3	3.5
30	2	15	2	3	4.5
31	2	16	1	1	5.5
32	2	16	2	1	4.5
33	2	17	1	2	7.0
34	2	17	2	2	5.5
35	2	18	1	3	8.5
36	2	18	2	3	7.5

Appendix 3 Table 178
Simulated data set with a continuous variable used for the analysis described in Table 39 of Chapter 9 – On-Farm Research Examples with long-term and monthly monitoring of animal performance for ten households of one village with one breed (data averaged across animals of a household)

Household	Month	Variable
1	1	5
1	2	4
1	3	7
1	4	3
1	5	7
1	6	4
1	7	5
1	8	2
1	9	8
1	10	7
1	11	4
1	12	5
2	1	6
2	2	7
2	3	3
2	4	10
2	5	3
2	6	5
2	7	6
2	8	8
2	9	4
2	10	6
2	11	5
2	12	7
3	1	8
3	2	3
3	3	2
3	4	7
3	5	2
3	6	2
3	7	7
3	8	8
3	9	5
3	10	6
3	11	8
3	12	12
4	1	1
4	2	8

4	3	5
4	4	6
4	5	4
4	6	7
4	7	4
4	8	5
4	9	8
4	10	3
4	11	8
4	12	7
5	1	4
5	2	5
5	3	6
5	4	7
5	5	3
5	6	10
5	7	3
5	8	5
5	9	6
5	10	3
5	11	2
5	12	7
6	1	2
6	2	2
6	3	7
6	4	8
6	5	5
6	6	6
6	7	8
6	8	8
6	9	12
6	10	1
6	11	8
6	12	5
7	1	6
7	2	5
7	3	8
7	4	3
7	5	8
7	6	7
7	7	4
7	8	5
7	9	6
7	10	3
7	11	2

7	12	7
8	1	2
8	2	2
8	3	7
8	4	8
8	5	5
8	6	6
8	7	8
8	8	8
8	9	12
8	10	1
8	11	6
8	12	3
9	1	2
9	2	7
9	3	2
9	4	7
9	5	2
9	6	2
9	7	7
9	8	8
9	9	5
9	10	4
9	11	7
9	12	7
10	1	6
10	2	9
10	3	3
10	4	4
10	5	7
10	6	5
10	7	6
10	8	5
10	9	4
10	10	7
10	11	3
10	12	8

Appendix 3 Table 179
Simulated data set with a continuous variable used for the analysis described in Table 40 of Chapter 9 – On-Farm Research Examples with long-term and monthly monitoring of animal performance for two villages with ten households per village with one breed (data averaged across animals of a household)

Village	Household	Month	Variable
1	1	1	5
1	1	2	4
1	1	3	7
1	1	4	3
1	1	5	7
1	1	6	4
1	1	7	5
1	1	8	2
1	1	9	8
1	1	10	7
1	1	11	4
1	1	12	5
1	2	1	6
1	2	2	7
1	2	3	3
1	2	4	10
1	2	5	3
1	2	6	5
1	2	7	6
1	2	8	8
1	2	9	4
1	2	10	6
1	2	11	5
1	2	12	7
1	3	1	8
1	3	2	3
1	3	3	2
1	3	4	7
1	3	5	2
1	3	6	2
1	3	7	7
1	3	8	8
1	3	9	5
1	3	10	6
1	3	11	8
1	3	12	12
1	4	1	1
1	4	2	8

1	4	3	5
1	4	4	6
1	4	5	4
1	4	6	7
1	4	7	4
1	4	8	5
1	4	9	8
1	4	10	3
1	4	11	8
1	4	12	7
1	5	1	4
1	5	2	5
1	5	3	6
1	5	4	7
1	5	5	3
1	5	6	10
1	5	7	3
1	5	8	5
1	5	9	6
1	5	10	3
1	5	11	2
1	5	12	7
1	6	1	2
1	6	2	2
1	6	3	7
1	6	4	8
1	6	5	5
1	6	6	6
1	6	7	8
1	6	8	8
1	6	9	12
1	6	10	1
1	6	11	8
1	6	12	5
1	7	1	6
1	7	2	5
1	7	3	8
1	7	4	3
1	7	5	8
1	7	6	7
1	7	7	4
1	7	8	5
1	7	9	6
1	7	10	3
1	7	11	2

1	7	12	7
1	8	1	2
1	8	2	2
1	8	3	7
1	8	4	8
1	8	5	5
1	8	6	6
1	8	7	8
1	8	8	8
1	8	9	12
1	8	10	1
1	8	11	6
1	8	12	3
1	9	1	2
1	9	2	7
1	9	3	2
1	9	4	7
1	9	5	2
1	9	6	2
1	9	7	7
1	9	8	8
1	9	9	5
1	9	10	4
1	9	11	7
1	9	12	7
1	10	1	6
1	10	2	9
1	10	3	3
1	10	4	4
1	10	5	7
1	10	6	5
1	10	7	6
1	10	8	5
1	10	9	4
1	10	10	7
1	10	11	3
1	10	12	8
2	11	1	4
2	11	2	5
2	11	3	6
2	11	4	7
2	11	5	3
2	11	6	10
2	11	7	3
2	11	8	5

2	11	9	12
2	11	10	1
2	11	11	6
2	11	12	3
2	12	1	2
2	12	2	7
2	12	3	2
2	12	4	7
2	12	5	2
2	12	6	2
2	12	7	7
2	12	8	8
2	12	9	5
2	12	10	4
2	12	11	3
2	12	12	4
2	13	1	7
2	13	2	5
2	13	3	6
2	13	4	5
2	13	5	4
2	13	6	7
2	13	7	3
2	13	8	4
2	13	9	8
2	13	10	6
2	13	11	5
2	13	12	3
2	14	1	7
2	14	2	8
2	14	3	2
2	14	4	4
2	14	5	9
2	14	6	2
2	14	7	5
2	14	8	6
2	14	9	7
2	14	10	5
2	14	11	6
2	14	12	7
2	15	1	6
2	15	2	6
2	15	3	6
2	15	4	7
2	15	5	8

2	15	6	3
2	15	7	9
2	15	8	3
2	15	9	10
2	15	10	11
2	15	11	2
2	15	12	7
2	16	1	4
2	16	2	8
2	16	3	3
2	16	4	7
2	16	5	9
2	16	6	3
2	16	7	6
2	16	8	9
2	16	9	2
2	16	10	4
2	16	11	5
2	16	12	4
2	17	1	4
2	17	2	6
2	17	3	7
2	17	4	8
2	17	5	8
2	17	6	4
2	17	7	5
2	17	8	3
2	17	9	5
2	17	10	6
2	17	11	8
2	17	12	4
2	18	1	5
2	18	2	2
2	18	3	9
2	18	4	4
2	18	5	8
2	18	6	3
2	18	7	7
2	18	8	9
2	18	9	3
2	18	10	6
2	18	11	9
2	18	12	2
2	19	1	3
2	19	2	6

2	19	3	9
2	19	4	2
2	19	5	4
2	19	6	5
2	19	7	4
2	19	8	4
2	19	9	6
2	19	10	7
2	19	11	5
2	19	12	2
2	20	1	9
2	20	2	4
2	20	3	8
2	20	4	3
2	20	5	7
2	20	6	9
2	20	7	4
2	20	8	6
2	20	9	7
2	20	10	5
2	20	11	2
2	20	12	9

Appendix 3 Table 180
Simulated data set with a continuous variable used for the analysis described in Table 41 of Chapter 9 – On-Farm Research Examples with long-term and monthly monitoring of animal performance for ten households of one village with two breeds (data averaged across animals of a household)

Household	Breed	Month	Variable
1	1	1	5
1	1	2	4
1	1	3	7
1	1	4	3
1	1	5	7
1	1	6	4
1	1	7	5
1	1	8	2
1	1	9	8
1	1	10	7
1	1	11	4
1	1	12	5
2	1	1	6
2	1	2	7
2	1	3	3
2	1	4	10
2	1	5	3
2	1	6	5
2	1	7	6
2	1	8	8
2	1	9	4
2	1	10	6
2	1	11	5
2	1	12	7
3	1	1	8
3	1	2	3
3	1	3	2
3	1	4	7
3	1	5	2
3	1	6	2
3	1	7	7
3	1	8	8
3	1	9	5
3	1	10	6
3	1	11	8
3	1	12	12
4	1	1	1
4	1	2	8

4	1	3	5
4	1	4	6
4	1	5	4
4	1	6	7
4	1	7	4
4	1	8	5
4	1	9	8
4	1	10	3
4	1	11	8
4	1	12	7
5	1	1	4
5	1	2	5
5	1	3	6
5	1	4	7
5	1	5	3
5	1	6	10
5	1	7	3
5	1	8	5
5	1	9	6
5	1	10	3
5	1	11	2
5	1	12	7
6	2	1	2
6	2	2	2
6	2	3	7
6	2	4	8
6	2	5	5
6	2	6	6
6	2	7	8
6	2	8	8
6	2	9	12
6	2	10	1
6	2	11	8
6	2	12	5
7	2	1	6
7	2	2	5
7	2	3	8
7	2	4	3
7	2	5	8
7	2	6	7
7	2	7	4
7	2	8	5
7	2	9	6
7	2	10	3
7	2	11	2

7	2	12	7
8	2	1	2
8	2	2	2
8	2	3	7
8	2	4	8
8	2	5	5
8	2	6	6
8	2	7	8
8	2	8	8
8	2	9	12
8	2	10	1
8	2	11	6
8	2	12	3
9	2	1	2
9	2	2	7
9	2	3	2
9	2	4	7
9	2	5	2
9	2	6	2
9	2	7	7
9	2	8	8
9	2	9	5
9	2	10	4
9	2	11	7
9	2	12	7
10	2	1	6
10	2	2	9
10	2	3	3
10	2	4	4
10	2	5	7
10	2	6	5
10	2	7	6
10	2	8	5
10	2	9	4
10	2	10	7
10	2	11	3
10	2	12	8

Appendix 3 Table 181
Simulated data set with a continuous variable used for the analysis described in Table 42 of Chapter 9 – On-Farm Research Examples with long-term and monthly monitoring of animal performance for two villages with ten households per village and two breeds (data averaged across animals of a household)

Village	Household	Breed	Month	Variable
1	1	1	1	5
1	1	1	2	4
1	1	1	3	7
1	1	1	4	3
1	1	1	5	7
1	1	1	6	4
1	1	1	7	5
1	1	1	8	2
1	1	1	9	8
1	1	1	10	7
1	1	1	11	4
1	1	1	12	5
1	2	1	1	6
1	2	1	2	7
1	2	1	3	3
1	2	1	4	10
1	2	1	5	3
1	2	1	6	5
1	2	1	7	6
1	2	1	8	8
1	2	1	9	4
1	2	1	10	6
1	2	1	11	5
1	2	1	12	7
1	3	1	1	8
1	3	1	2	3
1	3	1	3	2
1	3	1	4	7
1	3	1	5	2
1	3	1	6	2
1	3	1	7	7
1	3	1	8	8
1	3	1	9	5
1	3	1	10	6
1	3	1	11	8
1	3	1	12	12
1	4	1	1	1
1	4	1	2	8

1	4	1	3	5
1	4	1	4	6
1	4	1	5	4
1	4	1	6	7
1	4	1	7	4
1	4	1	8	5
1	4	1	9	8
1	4	1	10	3
1	4	1	11	8
1	4	1	12	7
1	5	1	1	4
1	5	1	2	5
1	5	1	3	6
1	5	1	4	7
1	5	1	5	3
1	5	1	6	10
1	5	1	7	3
1	5	1	8	5
1	5	1	9	6
1	5	1	10	3
1	5	1	11	2
1	5	1	12	7
1	6	2	1	2
1	6	2	2	2
1	6	2	3	7
1	6	2	4	8
1	6	2	5	5
1	6	2	6	6
1	6	2	7	8
1	6	2	8	8
1	6	2	9	12
1	6	2	10	1
1	6	2	11	8
1	6	2	12	5
1	7	2	1	6
1	7	2	2	5
1	7	2	3	8
1	7	2	4	3
1	7	2	5	8
1	7	2	6	7
1	7	2	7	4
1	7	2	8	5
1	7	2	9	6
1	7	2	10	3
1	7	2	11	2

1	7	2	12	7
1	8	2	1	2
1	8	2	2	2
1	8	2	3	7
1	8	2	4	8
1	8	2	5	5
1	8	2	6	6
1	8	2	7	8
1	8	2	8	8
1	8	2	9	12
1	8	2	10	1
1	8	2	11	6
1	8	2	12	3
1	9	2	1	2
1	9	2	2	7
1	9	2	3	2
1	9	2	4	7
1	9	2	5	2
1	9	2	6	2
1	9	2	7	7
1	9	2	8	8
1	9	2	9	5
1	9	2	10	4
1	9	2	11	7
1	9	2	12	7
1	10	2	1	6
1	10	2	2	9
1	10	2	3	3
1	10	2	4	4
1	10	2	5	7
1	10	2	6	5
1	10	2	7	6
1	10	2	8	5
1	10	2	9	4
1	10	2	10	7
1	10	2	11	3
1	10	2	12	8
2	11	1	1	4
2	11	1	2	5
2	11	1	3	6
2	11	1	4	7
2	11	1	5	3
2	11	1	6	10
2	11	1	7	3
2	11	1	8	5

2	11	1	9	12
2	11	1	10	1
2	11	1	11	6
2	11	1	12	3
2	12	1	1	2
2	12	1	2	7
2	12	1	3	2
2	12	1	4	7
2	12	1	5	2
2	12	1	6	2
2	12	1	7	7
2	12	1	8	8
2	12	1	9	5
2	12	1	10	4
2	12	1	11	3
2	12	1	12	4
2	13	1	1	7
2	13	1	2	5
2	13	1	3	6
2	13	1	4	5
2	13	1	5	4
2	13	1	6	7
2	13	1	7	3
2	13	1	8	4
2	13	1	9	8
2	13	1	10	6
2	13	1	11	5
2	13	1	12	3
2	14	1	1	7
2	14	1	2	8
2	14	1	3	2
2	14	1	4	4
2	14	1	5	9
2	14	1	6	2
2	14	1	7	5
2	14	1	8	6
2	14	1	9	7
2	14	1	10	5
2	14	1	11	6
2	14	1	12	7
2	15	1	1	6
2	15	1	2	6
2	15	1	3	6
2	15	1	4	7
2	15	1	5	8

2	15	1	6	3
2	15	1	7	9
2	15	1	8	3
2	15	1	9	10
2	15	1	10	11
2	15	1	11	2
2	15	1	12	7
2	16	2	1	4
2	16	2	2	8
2	16	2	3	3
2	16	2	4	7
2	16	2	5	9
2	16	2	6	3
2	16	2	7	6
2	16	2	8	9
2	16	2	9	2
2	16	2	10	4
2	16	2	11	5
2	16	2	12	4
2	17	2	1	4
2	17	2	2	6
2	17	2	3	7
2	17	2	4	8
2	17	2	5	8
2	17	2	6	4
2	17	2	7	5
2	17	2	8	3
2	17	2	9	5
2	17	2	10	6
2	17	2	11	8
2	17	2	12	4
2	18	2	1	5
2	18	2	2	2
2	18	2	3	9
2	18	2	4	4
2	18	2	5	8
2	18	2	6	3
2	18	2	7	7
2	18	2	8	9
2	18	2	9	3
2	18	2	10	6
2	18	2	11	9
2	18	2	12	2
2	19	2	1	3
2	19	2	2	6

2	19	2	3	9
2	19	2	4	2
2	19	2	5	4
2	19	2	6	5
2	19	2	7	4
2	19	2	8	4
2	19	2	9	6
2	19	2	10	7
2	19	2	11	5
2	19	2	12	2
2	20	2	1	9
2	20	2	2	4
2	20	2	3	8
2	20	2	4	3
2	20	2	5	7
2	20	2	6	9
2	20	2	7	4
2	20	2	8	6
2	20	2	9	7
2	20	2	10	5
2	20	2	11	2
2	20	2	12	9

Appendix 3 Table 182
Simulated data set with a categorical variable used for the analysis described in Table 43 of Chapter 9 – On-Farm Research Examples with long-term and monthly monitoring of animal performance for ten households of one village with one breed

		Variable[1]		
Household[2]	Month	LSone	LStwo	Total
1	1	5	0	5
1	2	2	3	5
1	3	4	0	4
1	4	1	4	5
1	5	0	5	5
1	6	2	2	4
1	7	2	3	5
1	8	1	4	5
1	9	0	4	4
1	10	3	1	4
1	11	4	1	5
1	12	5	0	5
2	1	0	4	4
2	2	0	5	5
2	3	2	3	5
2	4	4	1	5
2	5	2	2	4
2	6	1	4	5
2	7	2	3	5
2	8	0	4	4
2	9	2	3	5
2	10	4	1	5
2	11	2	3	5
2	12	4	1	5
3	1	2	3	5
3	2	3	2	5
3	3	5	0	5
3	4	1	4	5
3	5	0	5	5
3	6	2	3	5
3	7	0	4	4
3	8	2	3	5
3	9	5	0	5
3	10	3	2	5
3	11	3	2	5
3	12	4	1	5
4	1	1	4	5
4	2	5	0	5

4	3	0	3	3
4	4	1	4	5
4	5	0	5	5
4	6	2	2	4
4	7	1	3	4
4	8	1	3	4
4	9	3	2	5
4	10	4	1	5
4	11	5	0	5
4	12	3	1	4
5	1	1	4	5
5	2	0	5	5
5	3	1	3	4
5	4	0	4	4
5	5	2	3	5
5	6	5	0	5
5	7	3	2	5
5	8	3	2	5
5	9	4	1	5
5	10	1	4	5
5	11	2	3	5
5	12	0	4	4
6	1	2	3	5
6	2	4	1	5
6	3	2	3	5
6	4	4	1	5
6	5	2	3	5
6	6	3	2	5
6	7	5	0	5
6	8	1	4	5
6	9	0	5	5
6	10	3	1	4
6	11	0	4	4
6	12	2	3	5
7	1	5	0	5
7	2	3	2	5
7	3	3	2	5
7	4	4	1	5
7	5	1	4	5
7	6	5	0	5
7	7	0	3	3
7	8	1	4	5
7	9	0	5	5
7	10	2	2	4
7	11	1	3	4

7	12	1	3	4
8	1	4	1	5
8	2	2	3	5
8	3	3	2	5
8	4	5	0	5
8	5	1	4	5
8	6	0	5	5
8	7	1	4	5
8	8	0	4	4
8	9	2	2	4
8	10	1	3	4
8	11	1	3	4
8	12	1	4	5
9	1	0	5	5
9	2	2	2	4
9	3	1	3	4
9	4	1	3	4
9	5	4	1	5
9	6	2	3	5
9	7	3	2	5
9	8	1	4	5
9	9	0	5	5
9	10	3	1	4
9	11	0	4	4
9	12	2	3	5
10	1	5	0	5
10	2	3	2	5
10	3	3	2	5
10	4	4	1	5
10	5	1	4	5
10	6	5	0	5
10	7	0	3	3
10	8	1	4	5
10	9	0	5	5
10	10	2	2	4
10	11	4	1	5
10	12	1	4	5

[1]LSone, LStwo, and Total = number of females per group with litter size of 1 and 2 and the number giving birth, respectively.
[2]5 animals per household.

Appendix 3 Table 183
Simulated data set with a categorical variable used for the analysis described in Table 44 of Chapter 9 – On-Farm Research Examples with long-term and monthly monitoring of animal performance for two villages with ten households per village with one breed

			Variable[1]		
Village	Household[2]	Month	LSone	LStwo	Total
1	1	1	5	0	5
1	1	2	2	3	5
1	1	3	4	0	4
1	1	4	1	4	5
1	1	5	0	5	5
1	1	6	2	2	4
1	1	7	2	3	5
1	1	8	1	4	5
1	1	9	0	4	4
1	1	10	3	1	4
1	1	11	4	1	5
1	1	12	5	0	5
1	2	1	0	4	4
1	2	2	0	5	5
1	2	3	2	3	5
1	2	4	4	1	5
1	2	5	2	2	4
1	2	6	1	4	5
1	2	7	2	3	5
1	2	8	0	4	4
1	2	9	2	3	5
1	2	10	4	1	5
1	2	11	2	3	5
1	2	12	4	1	5
1	3	1	2	3	5
1	3	2	3	2	5
1	3	3	5	0	5
1	3	4	1	4	5
1	3	5	0	5	5
1	3	6	2	3	5
1	3	7	0	4	4
1	3	8	2	3	5
1	3	9	5	0	5
1	3	10	3	2	5
1	3	11	3	2	5
1	3	12	4	1	5
1	4	1	1	4	5
1	4	2	5	0	5

1	4	3	0	3	3
1	4	4	1	4	5
1	4	5	0	5	5
1	4	6	2	2	4
1	4	7	1	3	4
1	4	8	1	3	4
1	4	9	3	2	5
1	4	10	4	1	5
1	4	11	5	0	5
1	4	12	3	1	4
1	5	1	1	4	5
1	5	2	0	5	5
1	5	3	1	3	4
1	5	4	0	4	4
1	5	5	2	3	5
1	5	6	5	0	5
1	5	7	3	2	5
1	5	8	3	2	5
1	5	9	4	1	5
1	5	10	1	4	5
1	5	11	2	3	5
1	5	12	0	4	4
1	6	1	2	3	5
1	6	2	4	1	5
1	6	3	2	3	5
1	6	4	4	1	5
1	6	5	2	3	5
1	6	6	3	2	5
1	6	7	5	0	5
1	6	8	1	4	5
1	6	9	0	5	5
1	6	10	3	1	4
1	6	11	0	4	4
1	6	12	2	3	5
1	7	1	5	0	5
1	7	2	3	2	5
1	7	3	3	2	5
1	7	4	4	1	5
1	7	5	1	4	5
1	7	6	5	0	5
1	7	7	0	3	3
1	7	8	1	4	5
1	7	9	0	5	5
1	7	10	2	2	4
1	7	11	1	3	4

1	7	12	1	3	4
1	8	1	4	1	5
1	8	2	2	3	5
1	8	3	3	2	5
1	8	4	5	0	5
1	8	5	1	4	5
1	8	6	0	5	5
1	8	7	1	4	5
1	8	8	0	4	4
1	8	9	2	2	4
1	8	10	1	3	4
1	8	11	1	3	4
1	8	12	1	4	5
1	9	1	0	5	5
1	9	2	2	2	4
1	9	3	1	3	4
1	9	4	1	3	4
1	9	5	4	1	5
1	9	6	2	3	5
1	9	7	3	2	5
1	9	8	1	4	5
1	9	9	0	5	5
1	9	10	3	1	4
1	9	11	0	4	4
1	9	12	2	3	5
1	10	1	5	0	5
1	10	2	3	2	5
1	10	3	3	2	5
1	10	4	4	1	5
1	10	5	1	4	5
1	10	6	5	0	5
1	10	7	0	3	3
1	10	8	1	4	5
1	10	9	0	5	5
1	10	10	2	2	4
1	10	11	4	1	5
1	10	12	1	4	5
2	11	1	0	5	5
2	11	2	2	2	4
2	11	3	1	3	4
2	11	4	1	3	4
2	11	5	4	1	5
2	11	6	2	3	5
2	11	7	3	2	5
2	11	8	1	4	5

2	11	9	0	5	5
2	11	10	3	1	4
2	11	11	0	5	5
2	11	12	3	1	4
2	12	1	0	4	4
2	12	2	2	3	5
2	12	3	5	0	5
2	12	4	3	2	5
2	12	5	3	2	5
2	12	6	4	1	5
2	12	7	1	4	5
2	12	8	5	0	5
2	12	9	0	3	3
2	12	10	1	4	5
2	12	11	0	5	5
2	12	12	2	2	4
2	13	1	2	2	4
2	13	2	1	3	4
2	13	3	1	3	4
2	13	4	1	4	5
2	13	5	0	5	5
2	13	6	2	2	4
2	13	7	1	3	4
2	13	8	1	3	4
2	13	9	4	1	5
2	13	10	2	3	5
2	13	11	3	2	5
2	13	12	1	4	5
2	14	1	0	5	5
2	14	2	3	1	4
2	14	3	0	4	4
2	14	4	3	2	5
2	14	5	3	2	5
2	14	6	4	1	5
2	14	7	1	4	5
2	14	8	5	0	5
2	14	9	0	3	3
2	14	10	1	4	5
2	14	11	0	5	5
2	14	12	2	2	4
2	15	1	2	2	4
2	15	2	1	3	4
2	15	3	1	3	4
2	15	4	1	4	5
2	15	5	0	5	5

2	15	6	2	2	4
2	15	7	1	3	4
2	15	8	1	3	4
2	15	9	3	1	4
2	15	10	0	4	4
2	15	11	3	2	5
2	15	12	3	2	5
2	16	1	4	1	5
2	16	2	1	4	5
2	16	3	5	0	5
2	16	4	0	3	3
2	16	5	1	4	5
2	16	6	0	5	5
2	16	7	2	2	4
2	16	8	0	5	5
2	16	9	2	2	4
2	16	10	2	2	4
2	16	11	1	3	4
2	16	12	1	3	4
2	17	1	1	4	5
2	17	2	0	5	5
2	17	3	2	2	4
2	17	4	1	3	4
2	17	5	1	3	4
2	17	6	3	1	4
2	17	7	0	4	4
2	17	8	3	2	5
2	17	9	3	2	5
2	17	10	4	1	5
2	17	11	1	4	5
2	17	12	5	0	5
2	18	1	0	3	3
2	18	2	2	2	4
2	18	3	2	2	4
2	18	4	1	3	4
2	18	5	1	3	4
2	18	6	1	4	5
2	18	7	0	5	5
2	18	8	2	2	4
2	18	9	1	3	4
2	18	10	0	5	5
2	18	11	2	2	4
2	18	12	1	3	4
2	19	1	1	3	4
2	19	2	3	1	4

2	19	3	0	4	4
2	19	4	3	2	5
2	19	5	3	2	5
2	19	6	4	1	5
2	19	7	1	4	5
2	19	8	5	0	5
2	19	9	0	3	3
2	19	10	1	4	5
2	19	11	0	5	5
2	19	12	2	2	4
2	20	1	1	3	4
2	20	2	0	5	5
2	20	3	2	2	4
2	20	4	1	3	4
2	20	5	1	3	4
2	20	6	3	1	4
2	20	7	0	4	4
2	20	8	3	2	5
2	20	9	3	2	5
2	20	10	4	1	5
2	20	11	0	4	4
2	20	12	3	2	5

[1]LSone, LStwo, and Total = number of females per group with litter size of 1 and 2 and the number giving birth, respectively.
[2]5 animals per household.

Appendix 3 Table 184
Simulated data set with a categorical variable used for the analysis described in Table 45 of Chapter 9 – On-Farm Research Examples with long-term and monthly monitoring of animal performance for ten households of one village with two breeds

			Variable[1]		
Household[2]	Breed	Month	LSone	LStwo	Total
1	1	1	5	0	5
1	1	2	2	3	5
1	1	3	4	0	4
1	1	4	1	4	5
1	1	5	0	5	5
1	1	6	2	2	4
1	1	7	2	3	5
1	1	8	1	4	5
1	1	9	0	4	4
1	1	10	3	1	4
1	1	11	4	1	5
1	1	12	5	0	5
2	1	1	0	4	4
2	1	2	0	5	5
2	1	3	2	3	5
2	1	4	4	1	5
2	1	5	2	2	4
2	1	6	1	4	5
2	1	7	2	3	5
2	1	8	0	5	5
2	1	9	2	2	4
2	1	10	2	3	5
2	1	11	1	4	5
2	1	12	0	4	4
3	1	1	3	1	4
3	1	2	4	1	5
3	1	3	5	0	5
3	1	4	0	4	4
3	1	5	0	5	5
3	1	6	2	3	5
3	1	7	0	4	4
3	1	8	2	3	5
3	1	9	5	0	5
3	1	10	3	2	5
3	1	11	3	2	5
3	1	12	0	5	5
4	1	1	2	3	5
4	1	2	4	1	5

4	1	3	2	2	4
4	1	4	0	4	4
4	1	5	0	5	5
4	1	6	2	3	5
4	1	7	0	4	4
4	1	8	2	3	5
4	1	9	5	0	5
4	1	10	0	4	4
4	1	11	5	0	5
4	1	12	3	1	4
5	1	1	1	4	5
5	1	2	0	5	5
5	1	3	1	3	4
5	1	4	0	4	4
5	1	5	2	3	5
5	1	6	5	0	5
5	1	7	3	2	5
5	1	8	2	2	4
5	1	9	1	4	5
5	1	10	2	3	5
5	1	11	0	5	5
5	1	12	2	2	4
6	2	1	2	3	5
6	2	2	1	4	5
6	2	3	0	4	4
6	2	4	3	1	4
6	2	5	4	1	5
6	2	6	5	0	5
6	2	7	0	4	4
6	2	8	0	5	5
6	2	9	2	3	5
6	2	10	0	4	4
6	2	11	2	3	5
6	2	12	5	0	5
7	2	1	3	2	5
7	2	2	3	2	5
7	2	3	0	5	5
7	2	4	2	3	5
7	2	5	4	1	5
7	2	6	2	2	4
7	2	7	0	4	4
7	2	8	1	4	5
7	2	9	0	5	5
7	2	10	2	2	4
7	2	11	1	3	4

7	2	12	1	3	4
8	2	1	4	1	5
8	2	2	2	3	5
8	2	3	3	2	5
8	2	4	5	0	5
8	2	5	1	4	5
8	2	6	2	3	5
8	2	7	0	5	5
8	2	8	2	2	4
8	2	9	2	3	5
8	2	10	1	4	5
8	2	11	0	4	4
8	2	12	3	1	4
9	2	1	4	1	5
9	2	2	5	0	5
9	2	3	0	4	4
9	2	4	0	5	5
9	2	5	2	3	5
9	2	6	0	4	4
9	2	7	2	3	5
9	2	8	1	4	5
9	2	9	0	5	5
9	2	10	3	1	4
9	2	11	0	4	4
9	2	12	2	3	5
10	2	1	5	0	5
10	2	2	3	2	5
10	2	3	3	2	5
10	2	4	4	1	5
10	2	5	1	4	5
10	2	6	0	4	4
10	2	7	2	3	5
10	2	8	5	0	5
10	2	9	3	2	5
10	2	10	3	2	5
10	2	11	4	1	5
10	2	12	1	4	5

[1]LSone, LStwo, and Total = number of females per group with litter size of 1 and 2 and the number giving birth, respectively.
[2]5 animals per household.

Appendix 3 Table 185
Simulated data set with a categorical variable used for the analysis described in Table 46 of Chapter 9 – On-Farm Research Examples with long-term and monthly monitoring of animal performance for two villages with ten households per village and two breeds

				Variable[1]		
Village	Household[2]	Breed	Month	LSone	LStwo	Total
1	1	1	1	5	0	5
1	1	1	2	2	3	5
1	1	1	3	4	0	4
1	1	1	4	1	4	5
1	1	1	5	0	5	5
1	1	1	6	2	2	4
1	1	1	7	2	3	5
1	1	1	8	1	4	5
1	1	1	9	0	4	4
1	1	1	10	3	1	4
1	1	1	11	4	1	5
1	1	1	12	5	0	5
1	2	1	1	0	4	4
1	2	1	2	0	5	5
1	2	1	3	2	3	5
1	2	1	4	4	1	5
1	2	1	5	2	2	4
1	2	1	6	1	4	5
1	2	1	7	2	3	5
1	2	1	8	0	4	4
1	2	1	9	2	3	5
1	2	1	10	4	1	5
1	2	1	11	2	3	5
1	2	1	12	4	1	5
1	3	1	1	2	3	5
1	3	1	2	4	1	5
1	3	1	3	5	0	5
1	3	1	4	0	4	4
1	3	1	5	0	5	5
1	3	1	6	2	3	5
1	3	1	7	4	1	5
1	3	1	8	2	2	4
1	3	1	9	1	4	5
1	3	1	10	2	3	5
1	3	1	11	0	4	4
1	3	1	12	2	3	5
1	4	1	1	1	4	5
1	4	1	2	5	0	5

1	4	1	3	0	3	3
1	4	1	4	1	4	5
1	4	1	5	0	5	5
1	4	1	6	2	2	4
1	4	1	7	1	3	4
1	4	1	8	2	3	5
1	4	1	9	4	1	5
1	4	1	10	2	3	5
1	4	1	11	4	1	5
1	4	1	12	2	3	5
1	5	1	1	4	1	5
1	5	1	2	5	0	5
1	5	1	3	0	4	4
1	5	1	4	0	5	5
1	5	1	5	2	3	5
1	5	1	6	4	1	5
1	5	1	7	2	2	4
1	5	1	8	1	4	5
1	5	1	9	2	3	5
1	5	1	10	0	4	4
1	5	1	11	2	3	5
1	5	1	12	1	4	5
1	6	2	1	5	0	5
1	6	2	2	0	3	3
1	6	2	3	1	4	5
1	6	2	4	4	1	5
1	6	2	5	2	3	5
1	6	2	6	3	2	5
1	6	2	7	5	0	5
1	6	2	8	1	4	5
1	6	2	9	0	5	5
1	6	2	10	3	1	4
1	6	2	11	0	4	4
1	6	2	12	2	3	5
1	7	2	1	5	0	5
1	7	2	2	3	2	5
1	7	2	3	3	2	5
1	7	2	4	4	1	5
1	7	2	5	1	4	5
1	7	2	6	5	0	5
1	7	2	7	0	3	3
1	7	2	8	1	4	5
1	7	2	9	0	5	5
1	7	2	10	2	2	4
1	7	2	11	1	3	4

1	7	2	12	1	4	5
1	8	2	1	0	5	5
1	8	2	2	3	1	4
1	8	2	3	0	4	4
1	8	2	4	2	3	5
1	8	2	5	5	0	5
1	8	2	6	3	2	5
1	8	2	7	3	2	5
1	8	2	8	4	1	5
1	8	2	9	1	4	5
1	8	2	10	5	0	5
1	8	2	11	0	3	3
1	8	2	12	1	4	5
1	9	2	1	0	5	5
1	9	2	2	2	2	4
1	9	2	3	1	3	4
1	9	2	4	1	3	4
1	9	2	5	4	1	5
1	9	2	6	2	3	5
1	9	2	7	3	2	5
1	9	2	8	1	4	5
1	9	2	9	0	5	5
1	9	2	10	3	1	4
1	9	2	11	0	4	4
1	9	2	12	2	3	5
1	10	2	1	5	0	5
1	10	2	2	3	2	5
1	10	2	3	3	2	5
1	10	2	4	4	1	5
1	10	2	5	1	4	5
1	10	2	6	5	0	5
1	10	2	7	0	3	3
1	10	2	8	1	4	5
1	10	2	9	0	5	5
1	10	2	10	2	2	4
1	10	2	11	4	1	5
1	10	2	12	4	1	5
2	11	1	1	2	3	5
2	11	1	2	3	2	5
2	11	1	3	1	4	5
2	11	1	4	0	5	5
2	11	1	5	3	1	4
2	11	1	6	0	4	4
2	11	1	7	2	3	5
2	11	1	8	5	0	5

2	11	1	9	3	2	5
2	11	1	10	3	2	5
2	11	1	11	4	1	5
2	11	1	12	1	4	5
2	12	1	1	5	0	5
2	12	1	2	0	3	3
2	12	1	3	5	0	5
2	12	1	4	3	2	5
2	12	1	5	3	2	5
2	12	1	6	4	1	5
2	12	1	7	1	4	5
2	12	1	8	5	0	5
2	12	1	9	0	3	3
2	12	1	10	1	4	5
2	12	1	11	0	5	5
2	12	1	12	2	2	4
2	13	1	1	2	2	4
2	13	1	2	1	3	4
2	13	1	3	1	4	5
2	13	1	4	5	0	5
2	13	1	5	0	3	3
2	13	1	6	1	4	5
2	13	1	7	0	5	5
2	13	1	8	2	2	4
2	13	1	9	4	1	5
2	13	1	10	4	1	5
2	13	1	11	2	3	5
2	13	1	12	3	2	5
2	14	1	1	1	4	5
2	14	1	2	0	5	5
2	14	1	3	3	1	4
2	14	1	4	3	2	5
2	14	1	5	3	2	5
2	14	1	6	4	1	5
2	14	1	7	1	4	5
2	14	1	8	5	0	5
2	14	1	9	0	3	3
2	14	1	10	1	4	5
2	14	1	11	0	5	5
2	14	1	12	2	2	4
2	15	1	1	2	2	4
2	15	1	2	1	3	4
2	15	1	3	1	3	4
2	15	1	4	1	4	5
2	15	1	5	0	5	5

2	15	1	6	2	3	5
2	15	1	7	3	2	5
2	15	1	8	1	4	5
2	15	1	9	0	5	5
2	15	1	10	3	1	4
2	15	1	11	3	2	5
2	15	1	12	3	2	5
2	16	2	1	4	1	5
2	16	2	2	1	4	5
2	16	2	3	5	0	5
2	16	2	4	0	3	3
2	16	2	5	1	4	5
2	16	2	6	0	5	5
2	16	2	7	2	2	4
2	16	2	8	2	2	4
2	16	2	9	2	2	4
2	16	2	10	2	2	4
2	16	2	11	1	3	4
2	16	2	12	1	3	4
2	17	2	1	1	4	5
2	17	2	2	0	5	5
2	17	2	3	2	2	4
2	17	2	4	1	3	4
2	17	2	5	1	3	4
2	17	2	6	3	1	4
2	17	2	7	0	4	4
2	17	2	8	3	2	5
2	17	2	9	3	2	5
2	17	2	10	4	1	5
2	17	2	11	1	4	5
2	17	2	12	5	0	5
2	18	2	1	0	3	3
2	18	2	2	2	2	4
2	18	2	3	2	2	4
2	18	2	4	1	3	4
2	18	2	5	1	3	4
2	18	2	6	1	3	4
2	18	2	7	1	4	5
2	18	2	8	0	5	5
2	18	2	9	2	2	4
2	18	2	10	1	3	4
2	18	2	11	1	3	4
2	18	2	12	3	1	4
2	19	2	1	0	4	4
2	19	2	2	3	2	5

2	19	2	3	3	2	5
2	19	2	4	4	1	5
2	19	2	5	1	4	5
2	19	2	6	5	0	5
2	19	2	7	0	3	3
2	19	2	8	2	2	4
2	19	2	9	2	2	4
2	19	2	10	1	3	4
2	19	2	11	1	3	4
2	19	2	12	1	4	5
2	20	2	1	0	5	5
2	20	2	2	2	2	4
2	20	2	3	1	3	4
2	20	2	4	0	5	5
2	20	2	5	2	2	4
2	20	2	6	1	3	4
2	20	2	7	1	3	4
2	20	2	8	3	2	5
2	20	2	9	3	2	5
2	20	2	10	4	1	5
2	20	2	11	0	4	4
2	20	2	12	3	2	5

[1]LSone, LStwo, and Total = number of females per group with litter size of 1 and 2 and the number giving birth, respectively.
[2]5 animals per household.

Appendix 3 Table 186
Simulated data set used for the analysis described in Table 47 of Chapter 9 – On-Farm Research Examples with six villages, two treatments, six households per village, three animals per household, and one treatment per village

Village	Household	Treatment	Animal	Variable
1	1	1	1	5
1	1	1	2	6
1	1	1	3	3
1	2	1	4	7
1	2	1	5	0
1	2	1	6	4
1	3	1	7	3
1	3	1	8	5
1	3	1	9	7
1	4	1	10	18
1	4	1	11	3
1	4	1	12	5
1	5	1	13	6
1	5	1	14	7
1	5	1	15	8
1	6	1	16	3
1	6	1	17	20
1	6	1	18	4
2	7	2	19	7
2	7	2	20	8
2	7	2	21	4
2	8	2	22	3
2	8	2	23	5
2	8	2	24	17
2	9	2	25	8
2	9	2	26	3
2	9	2	27	24
2	10	2	28	6
2	10	2	29	3
2	10	2	30	4
2	11	2	31	3
2	11	2	32	5
2	11	2	33	6
2	12	2	34	7
2	12	2	35	8
2	12	2	36	3
3	13	2	37	5
3	13	2	38	5
3	13	2	39	6

3	14	2	40	3
3	14	2	41	7
3	14	2	42	8
3	15	2	43	4
3	15	2	44	3
3	15	2	45	5
3	16	2	46	7
3	16	2	47	8
3	16	2	48	3
3	17	2	49	5
3	17	2	50	6
3	17	2	51	2
3	18	2	52	6
3	18	2	53	13
3	18	2	54	7
4	19	1	55	8
4	19	1	56	4
4	19	1	57	7
4	20	1	58	4
4	20	1	59	22
4	20	1	60	7
4	21	1	61	8
4	21	1	62	3
4	21	1	63	5
4	22	1	64	5
4	22	1	65	6
4	22	1	66	3
4	23	1	67	11
4	23	1	68	5
4	23	1	69	6
4	24	1	70	7
4	24	1	71	7
4	24	1	72	8
5	25	1	73	6
5	25	1	74	5
5	25	1	75	6
5	26	1	76	3
5	26	1	77	7
5	26	1	78	3
5	27	1	79	5
5	27	1	80	6
5	27	1	81	5
5	28	1	82	16
5	28	1	83	3
5	28	1	84	7

5	29	1	85	8
5	29	1	86	0
5	29	1	87	7
5	30	1	88	4
5	30	1	89	6
5	30	1	90	7
6	31	2	91	18
6	31	2	92	6
6	31	2	93	3
6	32	2	94	7
6	32	2	95	8
6	32	2	96	4
6	33	2	97	7
6	33	2	98	4
6	33	2	99	16
6	34	2	100	4
6	34	2	101	7
6	34	2	102	4
6	35	2	103	6
6	35	2	104	7
6	35	2	105	8
6	36	2	106	6
6	36	2	107	3
6	36	2	108	5

Appendix 3 Table 187
Simulated data set used for the analysis described in Table 48 of Chapter 9 – On-Farm Research Examples with a switchback design and observations of one village

Period	Household[1]	Treatment	Order	Variable
1	1	1	1	5
1	2	1	1	3
1	3	1	1	2
1	4	1	1	1
1	5	1	1	9
1	6	1	1	1
1	7	2	2	5
1	8	2	2	6
1	9	2	2	6
1	10	2	2	8
1	11	2	2	4
1	12	2	2	3
2	1	2	1	2
2	2	2	1	1
2	3	2	1	3
2	4	2	1	3
2	5	2	1	5
2	6	2	1	5
2	7	1	2	6
2	8	1	2	7
2	9	1	2	7
2	10	1	2	8
2	11	1	2	9
2	12	1	2	9
3	1	1	1	6
3	2	1	1	5
3	3	1	1	4
3	4	1	1	3
3	5	1	1	5
3	6	1	1	6
3	7	2	2	7
3	8	2	2	8
3	9	2	2	4
3	10	2	2	3
3	11	2	2	7
3	12	2	2	4

[1]Household is listed assuming observations are either averages of more than one animal per household, although in some cases this may be observations for individual animals.

Appendix 3 Table 188
Simulated data set used for the analysis described in Table 49 of Chapter 9 – On-Farm Research Examples with a switchback design and observations of two villages

Village	Period	Household[1]	Treatment	Order	Variable
1	1	1	1	1	5
1	1	2	1	1	3
1	1	3	1	1	2
1	1	4	1	1	1
1	1	5	1	1	9
1	1	6	1	1	1
1	1	7	2	2	5
1	1	8	2	2	6
1	1	9	2	2	6
1	1	10	2	2	8
1	1	11	2	2	4
1	1	12	2	2	3
1	2	1	2	1	2
1	2	2	2	1	1
1	2	3	2	1	3
1	2	4	2	1	3
1	2	5	2	1	5
1	2	6	2	1	5
1	2	7	1	2	6
1	2	8	1	2	7
1	2	9	1	2	7
1	2	10	1	2	8
1	2	11	1	2	9
1	2	12	1	2	7
1	3	1	1	1	6
1	3	2	1	1	5
1	3	3	1	1	7
1	3	4	1	1	3
1	3	5	1	1	5
1	3	6	1	1	6
1	3	7	2	2	3
1	3	8	2	2	8
1	3	9	2	2	4
1	3	10	2	2	3
1	3	11	2	2	7
1	3	12	2	2	4
2	1	1	1	1	5
2	1	2	1	1	3
2	1	3	1	1	2
2	1	4	1	1	1

2	1	5	1	1	6
2	1	6	1	1	7
2	1	7	2	2	7
2	1	8	2	2	8
2	1	9	2	2	9
2	1	10	2	2	8
2	1	11	2	2	4
2	1	12	2	2	1
2	2	1	2	1	3
2	2	2	2	1	3
2	2	3	2	1	5
2	2	4	2	1	5
2	2	5	2	1	6
2	2	6	2	1	7
2	2	7	1	2	9
2	2	8	1	2	7
2	2	9	1	2	6
2	2	10	1	2	5
2	2	11	1	2	4
2	2	12	1	2	8
2	3	1	1	1	3
2	3	2	1	1	6
2	3	3	1	1	7
2	3	4	1	1	6
2	3	5	1	1	8
2	3	6	1	1	9
2	3	7	2	2	7
2	3	8	2	2	8
2	3	9	2	2	4
2	3	10	2	2	3
2	3	11	2	2	7
2	3	12	2	2	4

[1]Household is listed assuming observations are either averages of more than one animal per household, although in some cases this may be observations for individual animals.

Appendix 3 Table 189
Simulated data set used for the analysis described in Table 50 of Chapter 9 – On-Farm Research Examples with a Latin square design and observations of one village

Period	Household[1]	Treatment	Variable
1	1	1	4
1	2	2	6
1	3	3	5
1	4	4	3
2	1	4	7
2	2	1	5
2	3	2	6
2	4	3	6
3	1	2	4
3	2	3	9
3	3	4	2
3	4	1	7
4	1	3	6
4	2	4	5
4	3	1	4
4	4	2	5

[1]Household is listed assuming observations are either averages of more than one animal per household, although in some cases this may be observations for individual animals.

Appendix 3 Table 190
Simulated data set used for the analysis described in Table 51 of Chapter 9 – On-Farm Research Examples with simultaneous Latin squares and observations of four villages

Village	Period	Household[1]	Treatment	Variable
1	1	1	1	4
1	1	2	2	6
1	1	3	3	5
1	1	4	4	3
1	2	1	4	7
1	2	2	1	5
1	2	3	2	6
1	2	4	3	6
1	3	1	2	4
1	3	2	3	9
1	3	3	4	2
1	3	4	1	7
1	4	1	3	6
1	4	2	4	5
1	4	3	1	4
1	4	4	2	5
2	1	5	1	3
2	1	6	2	7
2	1	7	3	5
2	1	8	4	6
2	2	5	4	6
2	2	6	1	5
2	2	7	2	4
2	2	8	3	5
2	3	5	2	3
2	3	6	3	2
2	3	7	4	2
2	3	8	1	7
2	4	5	3	6
2	4	6	4	9
2	4	7	1	6
2	4	8	2	4
3	1	9	1	9
3	1	10	2	2
3	1	11	3	7
3	1	12	4	6
3	2	9	4	5
3	2	10	1	4
3	2	11	2	6
3	2	12	3	3

3	3	9	2	4
3	3	10	3	9
3	3	11	4	2
3	3	12	1	5
3	4	9	3	6
3	4	10	4	7
3	4	11	1	5
3	4	12	2	4
4	1	13	1	5
4	1	14	2	6
4	1	15	3	5
4	1	16	4	3
4	2	13	4	2
4	2	14	1	7
4	2	15	2	6
4	2	16	3	5
4	3	13	2	6
4	3	14	3	4
4	3	15	4	2
4	3	16	1	6
4	4	13	3	6
4	4	14	4	5
4	4	15	1	4
4	4	16	2	5

[1]Household is listed assuming observations are either averages of more than one animal per household, although in some cases this may be observations for individual animals.

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