1. Analyzing Ranking and Rating Data from Participatory On-Farm Trials[1]

Richard Coe[2]

Abstract
Responses in participatory on-farm trials are often measured as ratings (scores on an ordered but arbitrary scale) or rankings (respondents are simply asked to order treatments). Usual analyses of variance and linear model-based analyses are not appropriate for these data. Alternatives, based on generalized linear models, are described. These methods can be successfully used when the designs are irregular, as typically occurs in participatory trials, and when covariates are measured on each plot or farm in order to identify GxE interaction.

Key words: *ranking, on-farm trials, generalized linear models*

Résumé
Des réponses dans les essais participatifs en milieu réel sont souvent présentées sous forme d'indice (scores sur une échelle ordonnée mais arbitraire) ou classement (les répondants sont simplement invités à ordonner les traitements). L'analyse de la variance habituelle et les analyses des modèle-linéaires de base ne sont pas appropriées pour ces données. Des solutions de rechange, basées sur les modèles linéaires généraux sont décrites. Ces méthodes peuvent être employés avec succès quand les conceptions sont irrégulières, comme cela se passe dans les essais participatifs, et quand des covariantes sont mesurés sur chaque parcelle de terrain ou ferme afin d'identifier l'interaction de GxE.

Mots clés : *classement, essais participatifs en milieu réel, modèles linéaire général*

1. INTRODUCTION

Participatory methods have been widely by adopted by researchers working on applied agricultural problems, including crop breeding. This change in paradigm has implications for the methods used, both for design and analysis. Some of these are summarized in a companion paper (Coe 2007). An assumption of this paper is that formal analysis of systematically collected quantitative data collected from trials is still an important part of the process. Without this, it is difficult to see how the research activity can generate information of relevance to anyone other than the small numbers

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2 ICRAF, Nairobi, Kenya. Email: r.coe@cgiar.org

of farmers directly involved. Breeders adopting participatory methods have generally recognized this, but faced three difficulties:

- The experimental designs used are often irregular in layout due to the input by the participating farmers (e.g. choosing which varieties to test on their farm), or the constraints arising from the trials being conducted in farmers' fields.
- The focus of analysis often shifts from overall selection of varieties to understanding the variation in responses across farms. This is GxE interaction, but the 'E' may include social or economic variables in addition to biophysical environments.
- Much of the quantitative data collected may be ratings and rankings, for which the more usual methods of analysis may not be appropriate.

This paper seeks to demonstrate that analysis methods are available to deal simultaneously with each of these difficulties.

In Section 2 of the paper the nature of ranking and rating data are summarized and approaches to analysis are reviewed. Section 3 introduces the examples used to illustrate methods. Sections 4 and 5 present a detailed discussion of an approach to analysis of rating and ranking data respectively. The discussion in Section 6 highlights some outstanding problems and implications of the methods presented.

2. TYPES OF DATA AND ANALYSIS

This paper is concerned with the analysis of responses measured in experiments in the form of rankings and ratings, therefore I start with a summary of data types. The nature of the response variable is one determinant of the type of analysis that can be undertaken, whether conducting formal or informal analysis. It is therefore important to understand exactly how the data are collected and what the numbers represent.

2.1 Continuous

Quantities such as crop yield can be measured on a continuous scale, for example in kgm^{-2}. The numbers have the property that "2 really is the average of 1 and 3," making many common statistical procedures appropriate. Such quantities may be on a "ratio" or "interval" scale, the difference being whether the scale has a real zero. A yield of 1 tha^{-1} is 50 percent that of a

yield of 2tha^{-1}, but a temperature of 10°C is not 50 percent of a temperature of 20°C as the zero for temperature is arbitrary.

2.2 Scores or ratings

Here I refer to data that are recorded on a scale from "poor" to "excellent," or "less than enough" to "more than enough." The categories used are often given numeric labels, such as 1, 2, 3, 4, 5. These are called "scores" or "ratings" and such a scale is also described as "ordered categorical". The numerical labels are arbitrary. An observation of 3 is higher than that of 2, but we cannot say it is better by the same amount as an observation of 5 is better than that of 4. An analysis of the data would ideally use the ordering without using the actual numerical label, so the results would be the same whatever numerical labels were used as long as they described the same order. The word labels ("poor", "excellent" etc.) are not arbitrary, and will determine how respondents use the scale and award scores. The quality of data can be enhanced by giving careful thought to these word labels, and by providing explanations and examples to respondents regarding their meaning.

2.3 Binary

Data that are recorded with just two categories are common, for example "yes – no", "dead – alive", "acceptable – not acceptable." Analysis is based on the frequency with which the categories occur. Methods for these data are widely described and they are not elaborated further here.

2.4 Rankings

In many investigations of preference, data are collected by asking respondents to rank alternatives. The options available are placed in order without any attempt to describe by how much one differs from another, or whether any of the alternatives are "good" or "acceptable". We might have variety A ranked above B which is ranked above C, yet none of these varieties might be considered as good. The data would look the same in the case of a respondent who placed them in the same order, but where 1, 2 or all three were considered "acceptable."

Other scales may be hybrids between these.

2.5 Analysis

The steps in the analysis of any data set can be summarized as follows:

1. *Define the analysis objectives*. These drive the rest of the analysis. It is impossible to do a good analysis of data without clear objectives. Often the key graphs and tables can be defined at this stage, even though the results to fill them in may not yet be available.

2. *Prepare the data*. Data sets will have to be entered and checked, suitable transformations made (e.g. to dry weight per unit area), relevant information from different sources (e.g. farm household data and plot level yields) extracted to the same file, and so on.

3. *Exploratory and descriptive analysis*. The aim is to summarize the main patterns and notice further patterns that may be relevant. This step is only covered briefly in this paper as the methods used will depend on the context in which the analysis is carried out, and on the audience for the results.

4. *Formal statistical analysis*. The aim is to add measures of precision and provide estimates from complex situations.

5. *Interpretation and presentation*.

Iteration between the steps will be necessary. Training materials by Coe *et al.* (2001) provide much more information on analysis of experiments. Some comments on the roles of these steps in analysis of participatory experiments are given in Coe (2007).

A common objective in analysis of many participatory breeding trials is to understand the nature of variation in the responses given by different farmers. Many researchers report that participatory on-farm trials produce highly variable results, making interpretation difficult. Certainly, if a standard analysis aimed at identifying differences in varietal means is carried out, the result may well be a very high "residual" variation and a correspondingly large standard error of varietal difference, implying only vague knowledge about the relative performance of the entries. However, the variation can often be understood as GxE interaction.

The environment in which a participatory trial takes place is heterogeneous. There will be many sources of variation that are not apparent in trials in which a researcher has full control and performs the assessment, and these will include social or economic factors as well as the more usual biophysical definitions of environment. For example, male and female farmers may assess varieties differently; or ratings may depend on the level of a farmer's market

integration. The analyses carried out must therefore be able to identify and describe these GxE interactions. When this is done, the results are often the most useful output of the trial, as they allow recommendations to be tuned to particular local conditions.

A spreadsheet package such as Excel is useful for much of the descriptive analysis. Flexible facilities for data selection and transformation, tabulation, and graphics are useful. However, dedicated statistical software is needed for the analyses described here – they cannot be done in Excel. There are several packages with roughly equivalent facilities. All the examples cited here use Genstat (2000), as I find it often the easiest to understand, particularly as methods for different problems can be addressed with a similar sets of commands. The key commands used to produce each analysis are included in the text with the output they produce. SPSS is widely used by social scientists but is not particularly useful for the analyses described here. Further comments on software are made in the last section.

3. EXAMPLES

3.1 Agroforestry/ soil fertility in Malawi

Although this is not a breeding trial, it is included here as the design is typical of many participatory on-farm trials. Three soil fertility strategies are compared over a number of years:

g – mixed intercropping of maize and gliricidia
s – relay planting of maize and sesbania
c – the control of continuous maize.

Forty-one (41) farmers each compared the control with one or both of the other treatments. Crop yield is the response of interest. A number of covariates were measured at the plot or farm level to help identify the reasons for variation across farms. In the analyses below, the data structure "name" identifies the farmers, "trt" represents the treatments to compare, and "score98" the response of interest.

3.2 Maize varieties in Zimbabwe

This was a "baby" trial comparing 12 maize varieties. 146 farmers in 25 different sites took part, each one testing 4 of the 12 varieties. The varieties for each farmer to test were chosen by the researcher. Some household

and field covariates were recorded. The actual crop yields obtained were not available for analysis, so the examples here use simulated yield data but the original field design. In the analyses below, the data structure FARM identifies farmers, ENTRY the varieties to compare.

3.3 Maize varieties in Kenya

This was a "baby" trial comparing 18 varieties of maize, two of them being local controls. 29 farmers were involved, each planting two replicates of all 18 entries. Crop performance was rated on a scale of 1, 2, 3, 4, 5. Sex of the respondent and farm size were also recorded. In the analyses, IDNO identifies farmers and REP identifies blocks within farms.

4. ANALYZING RATINGS OR SCORES

Example 1

The crop yields in Example 1 were actually measured in tonnes per hectare. However, to illustrate the method of analyzing scores, I have here converted them. The conversion is "exact" (i.e. the scores farmers would give if asked to assess yield and could do it without error) so that, for illustration purposes, the results are comparable with those that can be obtained from actual yields. Scores were allocated as:

Yield	Score	Label
y < 1	1	poor
1 <= y < 2	2	ok
2 <= y < 3	3	good
3 <= y	4	excellent

Descriptive analyses of these data have been explained elsewhere. For example, we could tabulate frequencies as:

TABULATE [PRINT=nobs; CLASSIFICATION=trt,score98; MARGINS=no] score98

Nobservd				
score98	**poor**	**ok**	**good**	**excellent**
trt				
c	9	13	6	3
g	5	15	10	9
s	3	7	9	5

This is informative. For example, for treatment g the mode of the distribution is "ok." This shifts to "good" for treatment s. For treatment c the mode is also "ok" but the frequencies of other scores suggest that g is better than c.

This type of analysis has obvious drawbacks:

- It is difficult to know how to handle more complex patterns.
- It seems to ignore some of the structure in the data. For example, we have not used the fact that each farmer rates 2 or 3 treatments.
- It is not obvious how it could be extended to deal with more complex problems such as identifying and describing the effects of covariates to describe GxE.
- It is not obvious how to formalize it so we can give measures of uncertainty (standard errors, confidence intervals, or statistical hypothesis tests).

A common approach is to treat the scores as quantities measured on a continuous scale. Then means can be calculated (see below) and all the methods of analysis of variance, regression, and related modeling could be tried.

	Mean	**Variance**
trt		
c	2.097	0.8903
g	2.590	0.9852
s	2.667	0.9275

There are two reasons to be uncomfortable about this approach:

1. Many of the assumptions of analysis of variance or linear regression modeling may be inappropriate, given the limited range of the observations. A critical assumption is that the variance between observations of the same treatment is constant across treatments. This is commonly not the case, with the extreme entries showing less variation in score than those with a mean of 2 or 3.
2. The method makes some assumptions about the meaning of the scores that may not be appropriate. For example, is the average of "poor" and "good" really "ok"? The seriousness of this objection is plain when it is realized that the scores 1, 2, 3, 4 are just labels but the results depend critically on the labels given. If we used, for example, 0, 1, 5, 100 then the results using this method would look very different, yet logically these are equally acceptable labels.

There are situations in which both these objections are unimportant and a useful analysis can progress along these lines. However, we would like to have something that is theoretically more sound and robust, and which is applicable in a wider range of cases.

A second approach is to dichotomize the response – change it from a 4-level to a 2-level scale. For example, we could group "poor" and "ok" together, and "good" and "excellent" together to give a measure with just two possible values. There are well-established methods for analyzing such data, including models (e.g. logistic regression) that allow the effects of complex arrangements of covariates to be disentangled, and even methods (generalized linear mixed models) that allow random effects to be incorporated, as in the REML analysis of continuous data (Coe 2007). However, this approach is also unsatisfactory. If the variable is originally measured on a 4-point scale and we reduce it to a 2-point scale, then we must be losing information.

There have been methods developed that are valid, that use the all information without making unreasonable assumptions, and that can model the effect of covariates. In order to understand the model, we look first at the data for just two treatments, g and c, and forget about the fact that the observations are paired by farmer. The data are thus the frequencies:

treatment	poor	ok	good	excellent
c	9	13	6	3
g	5	15	10	9

If we combine the top three categories, the data reduce to the 2x2 table:

treatment	**poor**	**ok+good+excellent**
c	9	22
g	5	34

It looks as if g is better than c. A higher proportion of the plots are in the 'ok+good+excellent' category. A common measure of this association is the odds ratio, O, or log odds ratio log(O)=L.

$$O = \frac{\text{odds on g high}}{\text{odds on c high}} = \frac{34/5}{22/9} = 2.78$$

L = log(2.78) = 1.02

Now we could "cut" the categories at a different place, combining "poor" and "ok" to give the data:

treatment	**poor+ok**	**good+excellent**
c	22	9
g	20	19

This table has O=2.32, L=0.84.

A third "cut" is possible, combining "poor," "ok" and "good' to give:

treatment	**poor+ok+good**	**excellent**
c	28	3
g	30	9

O=2.80, L=1.02

In this case the values of O are similar for each cut. If we make the assumption of such "proportional odds," with a constant value of O, then its value and standard error can be estimated without choosing any particular cut. In Genstat the calculations are done using the regression modeling commands. Note that the data have to be arranged so that there is a response variable for each possible response category. The variable for each score contains the number of plots which had that score.

print treat,s1,s2,s3,s4

treat	s1	s2	s3	s4
c	9.000	13.00	6.000	3.000
g	5.000	15.00	10.000	9.000

model [dist=multinomial;yrel=cumulative;link=logit] s1,s2,s3,s4
fit [p=e,a] treat

***** Regression Analysis *****

*** Estimates of parameters ***

	estimate	s.e.	t(*)	antilog of estimate
Cut-point 0/1	-0.927	0.367	-2.53	0.3956
Cut-point 1/2	0.948	0.367	2.58	2.581
Cut-point 2/3	2.161	0.438	4.93	8.680
treat g	0.932	0.452	2.06	2.539

* MESSAGE: s.e.s are based on dispersion parameter with value 1

Parameters for factors are differences compared with the reference level:
Factor Reference level
treat c

*** Accumulated analysis of deviance ***

Change	d.f.	deviance	mean deviance	deviance ratio
+ treat	1	4.37545	4.37545	4.38
Residual	2	0.16035	0.08018	
Total	3	4.53580	1.51193	

* MESSAGE: ratios are based on dispersion parameter with value 1

The analysis of deviance is interpreted similarly to an analysis of variance, comparing the deviance with a chi squared distribution to judge the importance of the effect. In this case there seems to be a "significant" treatment difference.

The parameter estimate treat g measures the difference between treatments g and c. The estimate 0.932 is the log odds ratio = log (odds of g being high v low / odds of c being high v low). Here "high" and "low" refer to being above and below some cut point in the ordered set of scores. It doesn't matter which cut point, as the model constrains this odds ratio to be the same for any choice of cut point.

The value of 0.932 for the log odds ratio means the odds ratio is exp(0.932) = 2.539. This is similar to the average of the three odds ratios found directly from the data. The standard error can be used to test the hypothesis of no difference between g and c (log odds ratio of 0) or to give a confidence interval for the log odds ratio or odds ratio. The cut-point parameters listed by Genstat do not have a useful interpretation in this case.

Now we analyze the whole dataset using the same ideas, and including a term for farm to account for the fact that each farmer is evaluating 2 or 3 plots. There is a row of data for each plot and a column for each possible score (poor, ok, good, excellent or 1, 2, 3, 4), here given the names s98[1], s98[2], s98[3] and s98[4]. The data value is again the number of plots that were given that score, but now these are all just 0 or 1, with a single 1 in each row. A small part of the data is shown:

print name,trt,s98[1...4],score98;10;decimals=0

name	**trt**	**s98[1]**	**s98[2]**	**s98[3]**	**s98[4]**	**score98**
Chakame	g	0	0	0	1	excellent
Chakame	s	0	0	1	0	good
Chakame	c	1	0	0	0	poor
Thobola	g	0	1	0	0	ok
Thobola	s	1	0	0	0	poor
Thobola	c	0	1	0	0	ok
Adisani	g	0	1	0	0	ok
Adisani	c	1	0	0	0	poor
Majoni	g	0	0	0	1	excellent
Majoni	s	0	0	0	1	excellent

model [dist=multinomial;yrel=cumulative;link=logit] s98[1...4]

fit [p=*] name
add [p=a] trt

* MESSAGE: Term name cannot be fully included in the model because 2 parameters are aliased with terms already in the model

(name Komwa(died 97)) = 0
(name Lipenga(died 98)) = 0

***** Regression Analysis *****

*** Estimates of parameters ***

	estimate	**s.e.**	**t(*)**	**antilog of estimate**
Cut-point 0/1	1.90	2.00	0.95	6.716
Cut-point 1/2	7.23	2.27	3.18	1382.
Cut-point 2/3	10.72	2.43	4.41	45305.
name Belo	4.04	2.56	1.58	56.75
name Bisiwiki	0.00	2.76	0.00	1.000
name Chakame	5.63	2.51	2.24	278.9
name Chimimba	0.97	3.57	0.27	2.638
.				
.				
.				
name White	5.56	2.51	2.21	259.7
trt g	3.5898	0.770	4.67	36.51
trt s	2.722	0.786	3.47	15.21

* MESSAGE: s.e.s are based on dispersion parameter with value 1

Parameters for factors are differences compared with the reference level:
Factor Reference level
name Adisani
trt c

*** Accumulated analysis of deviance ***

Change	d.f.	deviance	mean deviance	deviance ratio
+ name	38	115.468	3.039	3.04
+ trt	2	30.218	15.109	15.11
Residual	51	105.977	2.078	
Total	91	251.663	2.766	

* MESSAGE: ratios are based on dispersion parameter with value 1

The analysis of deviance is interpreted in the usual way, using a chi squared distribution to assess the size of contributions. A deviance of 30.2 with 2 d.f. confirms that treatment is having a clear effect on the ratings.

The parameter estimates for each farmer are uninteresting – they reflect the fact that farmers can differ in the mean rating given. The estimates for the treatments are important and give the quantitative summary of the ratings. In this example the control treatment c is the baseline from which the others are measured. Hence the important results are in the table below. For comparison, analysis of the actual yields using a similar method (linear model fitting farmer+treatment effects) is also shown (details in Coe 2007). Remember the scales are different. We cannot hope to recover information on actual yield per hectare from data which have been recorded only as "poor," "ok," etc. What is important to note are the differences and similarities between treatments which are revealed by this analysis.

treatment	rating log odds ratio	s.e.*	yields adjusted mean	s.e.	scaled yields** adjusted mean	s.e.
g	3.60	0.77	2.62	0.15	3.60	0.53
s	2.72	0.79	2.37	0.17	2.68	0.61
c	0	-	1.64	-	0	-

* the s.e. is the standard error of the difference from c
** yield means scaled to match the log odds ratio scale

When the scales are aligned, then the results of the analyses are remarkably similar. The s.e. values for the rating data are higher as ratings contain less information than actual yields.

The value of the analysis becomes clear when we start looking at differences between groups of farmers, or trying to understand the effect of covariates. For example, slope2 is a factor classifying farms into flat or sloping. The variate cec is related to soil fertility. There were hypotheses that g would perform relatively better on flat land and that both g and s would be superior to c when cec is low. These are investigated in the following table:

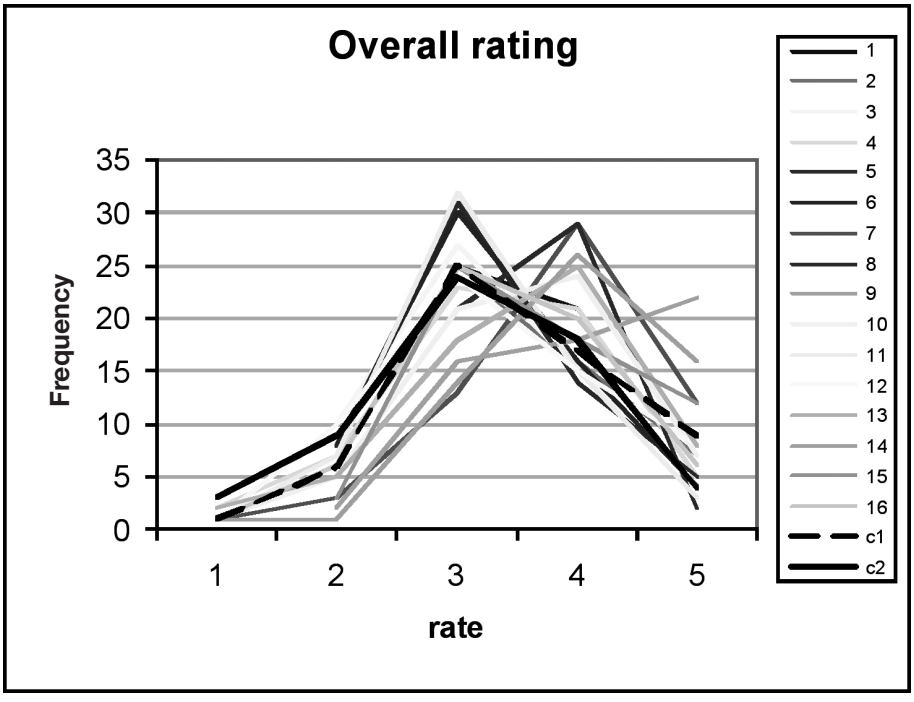
*** Accumulated analysis of deviance ***

Change	**d.f.**	**deviance**	**mean deviance**	**deviance ratio**
+ cec	1	1.945	1.945	1.94
+ slope2	1	8.959	8.959	8.96
+ trt	2	6.259	3.129	3.13
+ name	37	133.823	3.617	3.62
+ cec.trt	2	2.087	1.043	1.04
+ slope2.trt	2	2.543	1.271	1.27
Residual	44	90.606	2.059	

There is no clear evidence for either slope or cec showing an interaction with treatment.

Example 3

In this example, the performances of 18 varieties were rated on a scale from 1 (poor) to 5 (excellent). Criteria were yield, cob size, cob filling, and an overall assessment. The design was straightforward as each of 29 farmers evaluated all 18 varieties, with two plots of each. Simple descriptive statistics can therefore give a useful summary of some characteristics. For example, the graph below shows the frequency of responses for overall rating of each of the 18 varieties. Varieties 17 and 18 are local checks, so have been highlighted.



The varieties seem to fall into two main groups (those with a mode at 3 and those at 4), with entry 9 being rated more highly than all the others.

There are a number of reasons why the modeling analysis is still worthwhile:

- It provides simple, concise summaries with measures of precision.
- It makes inclusion of covariates straightforward. In this case both farm size and sex of the respondent have been recorded.
- It simplifies comparison of the ratings under different criteria.

The analysis follows a similar pattern to the previous example. Note that the layout with two replicates per farm can be explicitly included in the analysis if sensible. Here I have assumed the two replicates correspond to two blocks on each farm. Farms are distinguished by the factor IDNO and blocks within farmers by REP.

```
model [dist=multinomial;yrel=cumulative;link=logit] overall[]
fit [p=*]
add [p=*] IDNO
add [p=*] IDNO.REP
add [p=a,e] ENTRY
```

*** Accumulated analysis of deviance ***

Change	**d.f.**	**deviance**	**mean deviance**	**deviance ratio**
+ IDNO	28	342.309	12.225	12.23
+ IDNO.REP	29	82.354	2.840	2.84
+ ENTRY	17	123.623	7.272	7.27
Residual	966	2189.420	2.266	
Total	040	2737.706	2.632	

*** Estimates of parameters ***

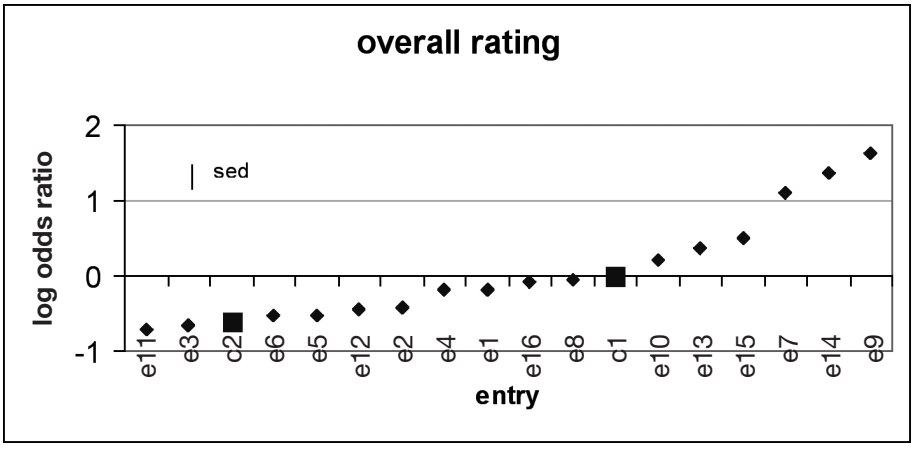
	estimate	**s.e.**	**t(*)**	**antilog of estimate**
Cut-point 0/1	-7.333	0.609	-12.05	0.0006534
Cut-point 1/2	-4.558	0.541	-8.43	0.01048
Cut-point 2/3	-1.560	0.522	-2.99	0.2102
Cut-point 3/4	0.848	0.520	1.63	2.335
IDNO 2	0.170	0.645	0.26	1.185
.				
..				
IDNO 29	-1.993	0.649	-3.07	0.1363
IDNO 1 .REP 2	-1.365	0.641	-2.13	0.2554
.				
..				
IDNO 29 .REP 2	-0.319	0.652	-0.49	0.7271
ENTRY c2	-0.610	0.361	-1.69	0.5433
ENTRY e1	-0.182	0.359	-0.51	0.8338
ENTRY e2	-0.419	0.360	-1.16	0.6575
ENTRY e3	-0.653	0.361	-1.81	0.5206
ENTRY e4	-0.196	0.359	-0.55	0.8219
ENTRY e5	-0.530	0.361	-1.47	0.5883

	estimate	s.e.	t(*)	antilog of estimate
ENTRY e6	-0.539	0.361	-1.49	0.5834
ENTRY e7	1.109	0.360	3.08	3.030
ENTRY e8	-0.049	0.359	-0.14	0.9523
ENTRY e9	1.625	0.365	4.45	5.078
ENTRY e10	0.223	0.358	0.62	1.250
ENTRY e11	-0.701	0.361	-1.94	0.4963
ENTRY e12	-0.438	0.360	-1.22	0.6453
ENTRY e13	0.377	0.358	1.05	1.458
ENTRY e14	1.380	0.362	3.81	3.974
ENTRY e15	0.510	0.358	1.43	1.666
ENTRY e16	-0.078	0.359	-0.22	0.9248

* MESSAGE: s.e.s are based on dispersion parameter with value 1

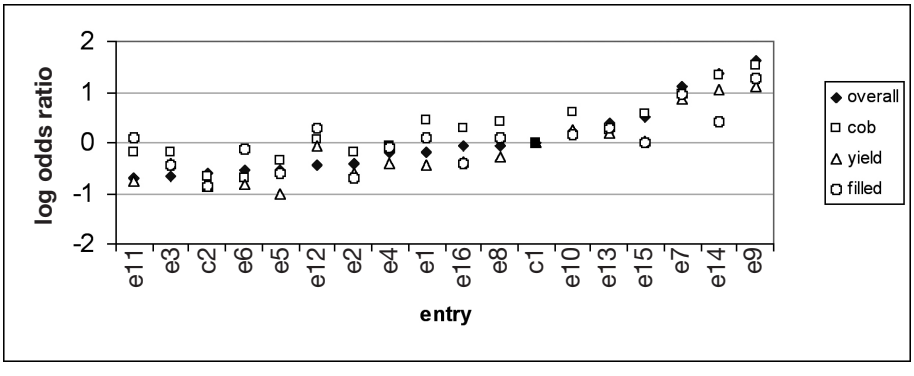
Parameters for factors are differences compared with the reference level:
Factor Reference level
IDNO 1
ENTRY c1

The analysis of deviance suggests that there are large differences between the entries. The parameter estimates summarize these. Remember the estimates are log odds ratios that describe the chance of being in a high response category rather than a low one, for each entry compared with the baseline. The data files have been set up so that the baseline is the first local check, c1. A simple graph reveals the patterns:



Apart from entries 9, 14 and 7, there is a continuous spread of ratings of these varieties, rather than any clear groupings, with one of the local checks towards the lower end of the spread and the other towards the upper end.

The ratings on each criteria can now be compared by repeating the analysis and putting the log odds ratio for each on the same graph. The pattern is much the same for each criterion. Of the three best performing entries, entry 14 does less well on cob filling.



There are two covariates of interest recorded: the sex of the respondent and the farm size. The question of interest is whether males and females tend to rate the entries differently, and whether the relative ratings depend on farm size.

```
model [dist=multinomial;yrel=cumulative;link=logit] overall[]
fit [p=*]
add [p=*] IDNO
add [p=*] IDNO.REP
add [p=*] ENTRY
add [p=*] SEX.ENTRY
add [p=a] SIZE.ENTRY
```

*** Accumulated analysis of deviance ***

Change	**d.f.**	**deviance**	**mean deviance**	**deviance ratio**
+ IDNO	28	342.309	12.225	12.23
+ IDNO.REP	29	82.354	2.840	2.84
+ ENTRY	17	123.623	7.272	7.27
+ ENTRY.SEX	17	21.404	1.259	1.26
+ SIZE.ENTRY	18	21.701	1.206	1.21
Residual	931	2146.315	2.305	
Total	1040	2737.706	2.632	

MESSAGE: ratios are based on dispersion parameter with value 1

Neither of the covariates shows any interaction with entry. Thus we can conclude that the overall rating of varieties is much the same for males and females, and does not have any linear relationship with farm size. The effect of farm size could perhaps be investigated further, for example by putting farms into a few (3 or 4) size categories. This approach removes the assumption of a linear relationship between farm size and the log odds ratios.

5. ANALYZING RANKINGS

At first glance, data from rankings look much the same as rating data. Like ratings, the observations are integers from a limited range, and we want to find out the same sort of information – are there consistencies in the rankings given to different treatments, that can allow us to reach conclusions about which treatments consistently ranked high? However, there are some important differences from rating data that will emerge.

Example 1

Again, to illustrate a method, I have converted yield data from Example 1 to ranks. Each farmer compared two or three treatments. Ranks have been allocated exactly, so that the treatment with the lowest yield on each farm is given rank 1, the next lowest rank 2, and the third (if there is one) rank 3. There were no ties. A small part of the data is shown.

name	**yield98**	**rank**	**trt**
Adisani	1.449	2.000	g
Adisani	0.801	1.000	c
Belo	*	*	c
Belo	2.071	2.000	s
Belo	1.246	1.000	g
Bisiwiki	0.643	1.000	c
Bisiwiki	1.514	2.000	g
Chakame	0.761	1.000	c
Chakame	3.380	3.000	g
Chakame	2.142	2.000	s
Chimimba	1.943	1.000	g
Chimimba	*	*	s
Chimimba	*	*	c
Chinzeka	2.356	3.000	g
Chinzeka	1.477	1.000	s
Chinzeka	1.713	2.000	c

Simple displays of the data can be designed. For example, we can tabulate the number of farmers who rank each treatment as 1, 2, or 3:

TABULATE [PRINT=counts; CLASSIFICATION=trt,rank; MARGINS=no] yield98

Count			
rank **trt**	**1.000**	**2.000**	**3.000**
c	24	6	1
g	9	16	14
s	6	12	6

Unknown Count 14

Treatment g is ranked 3 more often than s, an indication that it is superior. But a difficulty is clear straightaway: it is also ranked 2 and 1 more often than s. The problem arises from the fact that each farmer is only ranking the treatments s/he tests, and these are not the same for each. In the table above, when g=2, we cannot tell whether g was best out of 2 treatments or second out of 3. Changing the ranking method to 1=best does not help. Some authors suggest converting ranks to scores, but of course the problem cannot be fixed by a conversion that simply changes the ranks 1, 2, 3 to another set of numbers.

A more realistic summary comes from studying each treatment pair. If we take, for example, g and c, we can look at all those farmers that compared these two and calculate the proportion that ranked g higher than c.

Pair	**Number of comparisons**	**Number with first of pair ranked higher than second**	**Proportion with first of pair ranked higher than second**
g - c	31	28	0.903
s - c	21	16	0.762
g - s	24	16	0.667

This summary now correctly only relies on the rankings within each farm and is explicit about what is compared with what. Its shortcomings, and the reasons for wanting a formal analysis, are much the same as for the rating data. We need to put measures of precision on results and would like to extend the analysis to look at the effect of covariates or groupings of respondents. The analysis also seems unsatisfactory when we think of Example 2 with its 12 treatments and hence 66 pairs of treatments. A table such as the one

above but with 66 rows to describe performance of 12 varieties would be nothing but opaque!

The modeling approach to this type of data is based on the above table. The idea is to find a score s_i for each treatment such that the probability that treatment i is ranked higher than treatment j when the two are compared depends on the difference between the scores, $s_i - s_j$. If the relationship between scores and probability is a logistic function, then the model can be fitted using standard logistic regression software. Hence we put

p_{ij} = Prob(i ranked above j) and

$\log(p_{ij}/1-p_{ij}) = s_i - s_j$.

Setting up the data to fit the model is slightly messy. There has to be a row for each pair of treatments compared. Thus a farmer with just g and c will contribute one row of data for the pair g-c. A farmer with three treatments g, s and c will contribute three rows of data, g-c, s-c and g-s. Indicator variables are needed for each treatment and the response variable contains 0s and 1s. The first few rows of data are shown:

namel	**firstl**	**secondl**	**c**	**g**	**s**	**compl**
Adisini	g	c	-1	1	0	1
Belo	s	c	-1	0	1	*
Belo	s	g	0	-1	1	1
Belo	g	c	-1	1	0	*
Bisiwiki	g	c	-1	1	0	1
Chakame	g	c	-1	1	0	1
Chakame	s	c	-1	0	1	1
Chakame	s	g	0	-1	1	0
Chiminbo	g	c	-1	1	0	*
Chiminbo	s	g	0	-1	1	*
Chiminbo	s	c	-1	0	1	*
Chinzeka	g	c	-1	1	0	1
Chinzeka	s	g	0	-1	1	0
Chinzeka	s	c	-1	0	1	0

The first row of data shows that Adisini compared g and c. g was ranked higher than c, so when g is the first and c the second, the response is "suc-

cess," indicated by a 1 in the last column. Belo had all three treatments but the observation for c was missing, therefore both the s-c and g-c comparisons are missing.

The modeling now proceeds in a similar way as for other situations.

```
model [dist=b] compl; nbin=1
fit [con=o]g+s+c
```

*** Summary of analysis ***

d.f.	deviance	mean deviance	deviance ratio
Regression	2	*	*
Residual	74	73.49	0.9931
Total	76	*	*

* MESSAGE: ratios are based on dispersion parameter with value 1

*** Estimates of parameters ***

treatment	estimate	s.e.	t(*)	antilog of estimate
g	2.072	0.435	4.76	7.939
s	1.290	0.425	3.04	3.632

* MESSAGE: s.e.s are based on dispersion parameter with value 1

The output looks a little odd because Genstat does not know what to use as a null model when the constant is omitted, so cannot calculate a Total deviance, hence also cannot calculate a Regression deviance. In this case the sensible null model is one of "no preference" between treatments, corresponding to $p_{ij} = 0.5$ for all pairs, or $\log(p_{ij}/1\text{-}p_{ij})=0$. The deviance for this model is given by

```
model [dist=b] compl; nbin=1
fit [con=o]
```

Now the analysis of deviance can be reconstructed:

	d.f.	deviance	mean deviance	deviance ratio
Regression	2	31.91	15.96	15.96
Residual	74	73.49	0.9931	
Total	76	105.4	1.386	

The model appears to explain much of the variation, suggesting real difference between the treatments. When interpreting the parameter estimates, remember that the p_{ij} depend only on the differences s_i - s_j. Hence we only need to estimate two of them and can arbitrarily set the third, in this case c, to zero. Hence the estimates above give an ordering and even magnitude of differences between the treatments. They can be compared with the results from analyzing both actual yields and the scores.

	ranking		rating		yields		scaled yields**	
treatment	s_i	s.e.*	log odds ratio	s.e.	adjusted mean	s.e.	adjusted mean	s.e.
g	2.07	0.44	3.60	0.77	2.62	0.15	2.07	0.32
s	1.29	0.43	2.72	0.79	2.37	0.17	1.54	0.36
c	0	-	0	-	1.64	-	0	-

* the s.e. is the standard error of the difference from c
** yield means scaled to match the s scale of the ranking data

The analysis of ranks has, to within the arbitrary scaling, produced an order and relative difference between treatments which is remarkably similar to that from the actual yield data, yet with larger s.e.d. values: the ranks contain less information than actual yields.

Note the table of pairwise probabilities p_{ij} can be reconstructed from the scores s_i using the relationship

$$p_{ij} = \exp(s_i - s_j)/(1+\exp(s_i - s_j))$$

These are shown in the table below and indicate a reasonable fit of the model.

Pair	Number of comparisons	Number with first of pair ranked higher than second	Proportion with first of pair ranked higher than second	Fitted probabilities p_{ij}
g - c	31	28	0.903	0.888
s - c	21	16	0.762	0.784
g - s	24	16	0.667	0.686

As in other situations, an advantage of using an explicit model to analyze the ranks, rather than relying on more ad hoc methods, is that the effects of covariates can be identified. As an illustration I have looked at slope, classified into 2 levels (0=flat, 1=sloping), as one of the hypotheses was that g would perform relatively less well on sloping land.

add [p=a,e] slopel.(g+s+c)

*** Accumulated analysis of deviance ***

Change	d.f.	deviance	mean deviance	deviance ratio
- Constant				
+ g				
+ s				
+ c	1	*		
+ g.slopel				
+ s.slopel				
+ c.slopel	2	0.778	0.389	0.39
Residual	72	72.715	1.010	
Total	75	*		

* MESSAGE: ratios are based on dispersion parameter with value 1

The analysis of deviance suggests that there is no consistent difference in the way g, s and c are ranked on flat and sloping land. This conclusion is also reflected in the parameter estimates:

*** Estimates of parameters ***

	estimate	**s.e.**	**t(*)**	**antilog of estimate**
g	2.117	0.583	3.63	8.305
s	1.598	0.607	2.63	4.944
g.slopel 0	-0.056	0.901	-0.06	0.9454
g.slopel 1	0	*	*	1.000
s.slopel 0	-0.632	0.858	-0.74	0.5313
s.slopel 1	0	*	*	1.000

* MESSAGE: s.e.s are based on dispersion parameter with value 1

These can be put together into a table of scores, together with standard errors of the difference between treatments within slope categories.

Treatment	**slope=0**	**slope=1**
g	2.117-0.056=2.061	2.117
s	1.598-0.632=0.966	1.598
c	0	0

If the standard errors of the interaction effects were smaller, we would say the results were consistent with the hypothesis – the difference between g and s is greater on flat than on sloping land.

Remember that it is impossible to look at the "main effect" of slope. We cannot determine whether the treatments are generally assessed as better on flat land than sloping. Each participant ranks among the alternatives tested on their farm, and each farm is classed as either sloping or flat. Similarly, we cannot compare the two columns in the table above, comparing g on flat and sloping land. There is no information in the data on this comparison as all rankings are done within farms. The situation would be different if there were farms that had both flat and sloping land.

Example 2

Yields for Example 2 were also converted to ranks for the purpose of illustrating the analysis. Remember, this study has 12 varieties with 146 farmers comparing 4 varieties each. It is difficult to think of a useful simple, descriptive

analysis of this rank data that shows the differences between varieties. The design is very unbalanced, so any simple totaling of ranks will give a biased picture. We could look at all the 66 = 12 x 11 / 2 pairwise comparisons, and find the proportion in which one treatment ranks above another. It is not easy though to view a matrix of 66 values and understand the relative performance of 12 varieties. It has been suggested (Russell 1997) that an overall score be given to each variety by counting the number of times each one ranks above another. However, this requires each to occur equally often. Some sort of average proportion could be devised. However the modeling approach is simple once the data file is set up.

The data file structure and modeling proceeds as in Example 1. Twelve indicator variables, e[1],...e[12] are needed for the 12 varieties. In the statements below, the first FIT gives the correct Total deviance from which the analysis of deviance table is constructed.

```
model [dist=b] compl; nbin=1
fit [con=o]
fit [con=o] e[1...12]
```

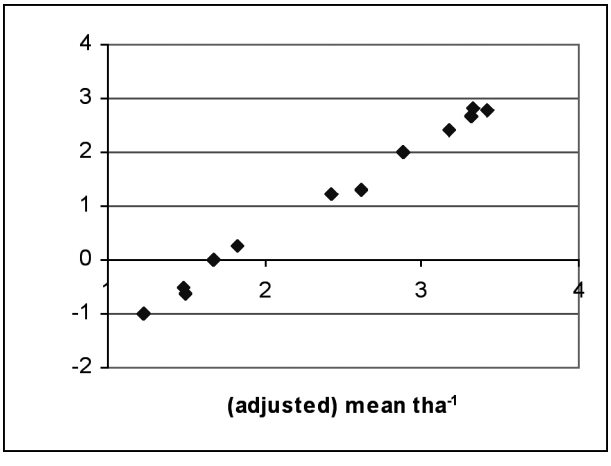
d.f.	**deviance**	**mean deviance**	**deviance ratio**
Regression	11	439.1	39.92
Residual	865	774.9	0.8959
Total	876	1214.	1.386

Genstat has put the score for the last treatment, s_{12}, to zero. The parameter estimates above then give the scores that show the relative performance for each variety. If these are compared with the results based on actual yields, it can be seen (graph below) that the method not only reproduces the ordering of the varieties very closely, but also the relative differences. Of course, in this case the ranks were calculated from the yields without error. Nonetheless, it still seems very surprising that this information about relative performance of the varieties can be recovered from just the four ranks on each farm.

*** Estimates of parameters ***

	estimate	s.e.	t(*)	antilog of estimate
e[1]	-0.996	0.293	-3.40	0.3692
e[2]	1.998	0.300	6.66	7.378
e[3]	1.282	0.284	4.52	3.606
e[4]	2.818	0.317	8.88	16.74
e[5]	-0.523	0.303	-1.73	0.5926
e[6]	2.655	0.312	8.51	14.22
e[7]	0.247	0.277	0.89	1.281
e[8]	1.205	0.281	4.29	3.336
e[9]	-0.637	0.299	-2.13	0.5289
e[10]	2.769	0.318	8.70	15.95
e[11]	2.423	0.303	8.00	11.28

* MESSAGE: s.e.s are based on dispersion parameter with value 1



As each score is relative to the score of zero for variety 12, the s.e.s listed with the estimates are for the comparison of that variety with variety 12. Other s.e. values are most easily found using predict. For example, the difference between scores for variety 1 and 2 is found by:

predict [back=n] e[1...11]; 1,-1,0,0,0,0,0,0,0,0,0

Prediction	s.e.
-2.995	0.335

More complex contrasts between treatments can be calculated in a similar way. For example, varieties 1, 5, 7, 9 and 12 are in one group, namely a. Varieties 4, 10 and 11 form group b. We can calculate the difference between the average scores for groups a and b by taking $(s_1+s_5+s_7+s_9+s_{12})/5 - (s_4+s_{10}+s_{11})/3$. Remembering $s_{12}=0$, predict can be used for this:

predict [back=n] e[1...11]; 0.2,0,0,-0.3333,0.2,0,0.2,0,0.2,-0.3333,-0.3333

Prediction	s.e.
-3.052	0.213

Group a is clearly worse than group b.

As in Example 1, it is simple to turn differences in scores into probabilities of one variety being ranked higher than another. For example, the chance that variety 1 is ranked higher than 2 is given by:

predict e[1...11]; 1,-1,0,0,0,0,0,0,0,0,0

Prediction	s.e.
0.0477	0.0152

Variety 2 is almost certain to be ranked higher than variety 1.

As before, the model can now be extended to look at the extent to which covariates interact with treatment differences. I use two continuous covariates, soil P and sand content. The data file has been set up with a column giving the sand and P for each pairwise comparison.

```
fit [p=*; con=o] e[1...11]
add [p=*; con=o] sandfl.e[1...11]
add [p=a; con=o] Pfl.e[1...11]
```

The analysis of deviance table can be constructed from this output. Note the total degrees of freedom has changed from earlier as there are missing values in the covariates.

	d.f.	**deviance**	**mean deviance**
e[1...11]	11	309.5	28.14
+sandfl.e[1..11]	11	15.64	1.42
+Pfl.e[1...11]	11	15.16	1.38
Residual	561	483.3	0.8614
Total	594	823.5	1.386

The results show that neither P nor sand has a strong interaction with variety. However, in order to show the types of results obtainable, the model with sand is refitted and parameter estimates produced.

fit [con=o;p=e] e[1...11]+sandfl.e[1...11]

*** Estimates of parameters ***

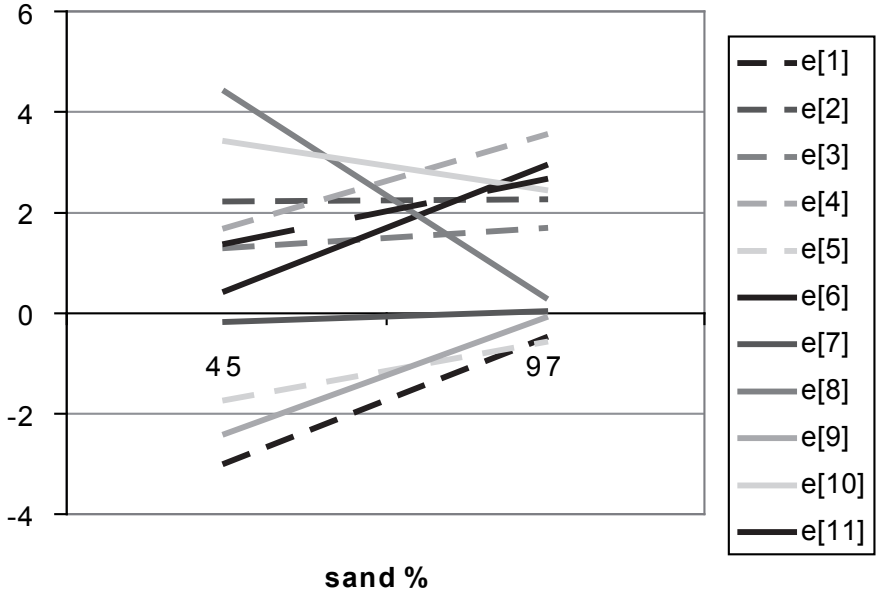
	estimate	**s.e.**	**t(*)**	**antilog of estimate**
e[1]	-5.11	2.83	-1.81	0.006012
e[2]	2.22	3.21	0.69	9.223
e[3]	0.97	2.49	0.39	2.631
e[4]	0.10	3.20	0.03	1.109
e[5]	-2.73	2.61	-1.04	0.06530
e[6]	-1.72	2.75	-0.62	0.1796
e[7]	-0.42	2.38	-0.18	0.6559
e[8]	7.90	3.70	2.14	2699.
e[9]	-4.38	2.64	-1.66	0.01248
e[10]	4.28	3.46	1.24	72.58
e[11]	0.28	4.01	0.07	1.317
e[1].sandfl	0.0475	0.0327	1.45	1.049

	estimate	**s.e.**	**t(*)**	**antilog of estimate**
e[2].sandfl	0.0004	0.0370	0.01	1.000
e[3].sandfl	0.0075	0.0290	0.26	1.008
e[4].sandfl	0.0357	0.0375	0.95	1.036
e[5].sandfl	0.0223	0.0301	0.74	1.023
e[6].sandfl	0.0478	0.0320	1.49	1.049
e[7].sandfl	0.0049	0.0280	0.17	1.005
e[8].sandfl	-0.0781	0.0417	-1.87	0.9249
e[9].sandfl	0.0444	0.0304	1.46	1.045
e[10].sandfl	-0.0187	0.0398	-0.47	0.9814
e[11].sandfl	0.0244	0.0460	0.53	1.025

The scores for each variety now depend on the sand content. For example, the score for variety 1 is

$s_1 = -5.11 + 0.0475$ sand

These are plotted below for the range of sand contents found in the trial, 45 to 97 percent.



Remembering that the scores show the relative performance of varieties, with variety 12 fixed at a score of zero, two main patterns emerge. Several varieties (1, 4, 5, 6, and 9) rank higher than 12 with increasing sand content. Variety 8 ranks distinctly worse with high sand content.

6. DISCUSSION

6.1 General

The methods described above for analysis of ranking and rating data are not new but they are not being routinely used in the analysis of agricultural trials. A discussion of the proportional odds model used for rating data can be found in Agresti (1996). The model for ranks is not so widely used, explaining why common statistical software does not make it immediately available. When the observations are paired comparisons (i.e., each participant is asked to state which of two treatments is superior), then the Bradley-Terry model (Bradley and Terry 1952) has been widely used, particularly in social science applications. Dittrich *et al.* (1998) use the method for paired comparisons when there are categorical covariates and mention that it is possible with continuous covariates. The approach used when more than two treatments are compared is described by Critchlow and Fligner (1991).

Both models involve making assumptions about the nature of the data, however this is true of all statistical analyses. It is a necessary part of attempting to reach conclusions about general patterns. Methods for checking the key assumptions are well developed for established linear model methods (for example, looking for various patterns in residuals) and similar tools need developing for these models. Alternative models may be more appropriate for either ranks or rates. The methods presented here appear to be the simplest that have proved useful in some common situations. Again this is common to all statistical modeling. For example, linear regression analysis is widely used but not because "nature has to be like that", but because the model has proved to be a useful approximation in many problems.

From the examples in this paper, it should be clear that statistical analysis of participatory breeding trials cannot be automatic. When researcher-designed trials were run using a very regular design, it was possible (though probably not wise) to run a standard analysis on each data set. Such an approach will not recover most of the useful information from participatory trials.

6.2 Further discussion on analysis of ranking

The method described above for analyzing data presented in the form of ranks seems to be appealing and powerful. It is able to produce an overall ordering of treatments, and even indicate the relative magnitudes of the differences between the treatments. It can handle awkward incomplete sets of data in which each farmer does not rank all treatments. Most importantly, it can show how treatments interact with covariates. In Example 1, the covariate was a categorical variable, dividing the sample of farmers into groups. In Example 2, continuous covariates were analyzed.

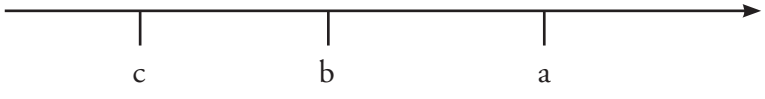
Unlike many other approaches to an analysis of ranks, the method uses estimation and not just testing. The distinction is often made when analyzing continuous variates such as crop yields. It is rarely useful simply to conclude that mean yields "differ significantly" between varieties, or even that variety A yields at a significantly higher level than variety B. We can draw useful conclusions when we can assess by how much A outyields B, and put a confidence interval around this. The same is true when analyzing ranks. It is rarely useful to simply report that treatments differ "significantly" in their ranks, yet this is all that most statistical procedures for an analysis of rankings do. The method presented here shows the relative magnitude of the differences and these can be interpreted. For example, we may show that A and B are ranked "significantly" differently. The scores for the varieties can be converted to a probability p_{AB} that A will be ranked higher than B.

If $p_{AB} = 0.95$ the interpretation is very different than if $p_{AB}=0.55$, yet both could be "significantly different" from the no-preference value of $p_{AB}=0.5$.

There are a number of questions about this analysis, some of which require some theoretical statistical investigation.

1. The model makes assumptions about the nature of the data and the effects of covariates. It is not clear how to check whether they are reasonable or how robust the results are to departures from the assumptions.

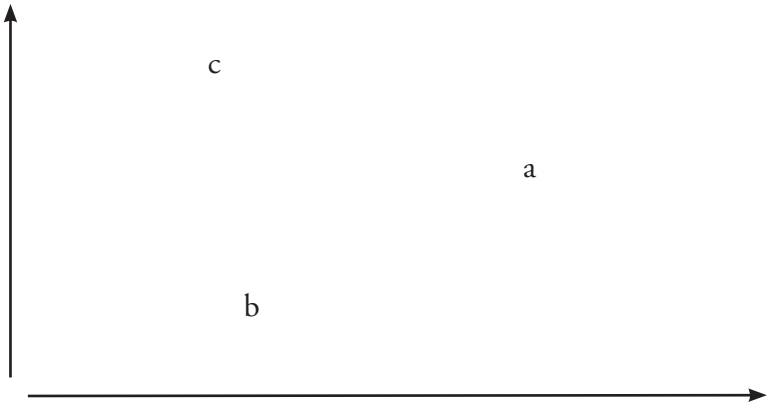
2. The analysis depends on the model, which assumes that the treatments can be allocated scores such that the probability of one ranking higher than another depends on the difference between the scores. This is the "linearity assumption" of Taplin (1997). It is helpful to represent it graphically. If farmers consistently rank a>b>c then we could derive scores that would put the treatments on a line:



It is easy to produce data for which this linearity assumption fails. For example, we can have a>b and a>c equally often, suggesting the ordering should look like the line below.

However, at the same time we can have b>c. This might occur if, for example, different farmers were making the comparisons and using different criteria for each one.

The problem occurs in other examples of "ordination," for example that used by ecologists to describe species occurrence. An answer is to introduce a second dimension. The distances between points a, b, and c can reflect the rankings if they are arranged as:



With just three treatments (as in Example 1), it is clear how an extra term can be introduced in the model to test whether a non-linear arrangement is superior (in Example 1 it is not). However, I do not know how to fit models that follow the usual, useful multivariate approach of gradually increasing the number of dimensions until a suitable fit is obtained.

3. In some ranking procedures, ties are allowed – for example, farmers are allowed to state that they have no preference between two or more of the treatments. Dittrich *et al.* (1998) show how the model can be modified to allow for ties. Extra parameters are included, so that for each pair we estimate the probability that they tie as well as the probability that one is ranked above the other.

4. Coe (2007) illustrates the value of being able to describe variation at different levels in the design with random effects. It is not clear if these ideas are useful or could be used here. In principle we can fit the model with random effects using the GLMM framework. However, this may not be necessary. All the information in the ranks is at the "within farm" level. Hence we can look at treatment differences and interactions of these with farm level (or higher level) covariates. However, we cannot look at any "between farm" effects. It is also not clear if plot-level covariates can be incorporated. For example, suppose farmers ranked treatments but also reported whether each plot was normally fertile or not, so that plots within one farm could have differing values of the fertility covariate. A model that uses these data would have to be built on the probability of a>b, depending on both the difference in treatment scores and the difference in fertility.

5. The analysis described here is suitable for one objective – that of determining treatment effects and their interaction with covariates when

the observations are ranks and the design is incomplete or irregular. If the design is more complete, for example with each respondent comparing all treatments, then other approaches are possible. Different objectives may be of interest, for example, comparison of the rankings under different criteria, or partitioning the sample of respondents into homogeneous groups, when again different methods will be appropriate. Remember also that if the data are rankings produced at, say, a group meeting, so that a consensus is arrived at, then no statistical analysis is necessary. Abeysekera (2001) and Riley and Fielding (2001) describe some of the simple alternatives. Taplin (1997) describes a number of the statistical tests available.

6.3 Ranks vs. rates

Having seen how data from these trials can be analyzed, it is worth looking again at the relative merits of using ranking or rating.

First it should be clear that a response measured on a continuous scale, using an accurate and unbiased instrument, contains more information that the equivalent observation using a rating scale with a few levels, or using ranks. Reasons for not using the continuous variate include:

1. *Time, money and logistics* (e.g. we may not be able to measure crop yield as we are uncertain when farmers will be ready to harvest).

2. *Lack of a suitable instrument*. If we want to assess taste or opinions, there is little alternative to rating or ranking.

3. *Participation*. Collection of ranking and rating data involves participants. Other measurement methods may be alienating.

Methods of collecting rating data have been described (e.g. Ashby 1990) and include tools that can give high-quality, repeatable, and reliable data. It appears that farmers are able to give scores to a large number of alternatives. There are statistical questions regarding the number of levels to use. There is no point in using too many levels, as small differences in rating will probably not reflect real differences in opinion. Note that we do not make a rating scale into a continuous variate simply by using many levels. The fundamental characteristic of a rating scale is that the numbers represent qualitative labels ("very good," "poor," etc.) and the quantitative analogue is missing. This may not be the case if the markers are used to represent the score.

There is a lot of theory and practice from the social science literature that is relevant here. Respondents are often reluctant to use the ends of a scale, particularly the lower end. Hence a 5-point scale may in practice be used as a 3-point scale. Note that some degree of consistency in the use of the scale by different participants, particularly in different locations, can be achieved by explaining what "poor," "excellent," etc. mean. For example, "poor" might correspond to "I would never consider growing this again," while "excellent" might mean, "I would like this to become a main variety for my farm each year."

Ranking is used when it is considered that participants find it easier to order alternatives than to give them a score. One reason for this is clear: participants might have a preference for two alternatives which might score the same (e.g. both "excellent"), and hence be able to give them different ranks. However, a shortcoming is immediately clear. The ranks may be the same if both are also considered "poor." This is an important problem. The information in ranks is all "within respondent," that is, we can identify whether, for example, participants consistently rank A above B, and we can determine whether this is true for both male and female respondents. However, we cannot determine what either group of participants actually thinks of A and B. An important part of any research is to make generalizations and extrapolations and ranked data are often not able to do this. Abeysekera (2001) makes the point that ranked information is considerably enhanced if some sort of baseline is also measured. For example, if a local control variety is included in each participant's set of alternatives, then we could get a rating for the local control, and rank the others relative to this. It is not clear exactly how such data could be analyzed.

A study by ICRAF (1996: 55) assessed the suitability of 12 tree species as firewood. The researcher thought that women could only realistically compare pairs of species. The participants ranked each pair tested, from which it was possible to produce an overall ordination. However, they were also asked the reasons for preferring one species to the other. An alternative design would have used a pilot study of this type to elicit important criteria, then asked for ratings on these for each species tested.

Remember that there is no ranked information on effects of quantities that vary across farms. In Example 1, we were unable to determine whether g was more effective on sloping or flat land.

Overall there seems little reason to collect ranked data unless they are specifically required by the objectives.

6. NOTE ON AVAILABLE SOFTWARE

Since the original version of this paper was published five years ago, there have been important changes in statistical software suitable for this type of analysis.

Genstat, used here to illustrate methods, has been updated to the 12th Edition. The basic commands needed to perform the analyses illustrated have not changed. Most are available to users through simple menus and dialogue boxes. Some details have changed. For example, when the MODEL command is used to fit ordered categorical regression models, the response variable no longer has to be arranged with a separate variate of counts for each category. A single response factor can be given. More importantly, VSNi, the company that produces Genstat, has made the Discovery Edition available free to researchers and educators in the developing world. Details are available from: http://www.vsn-intl.com/products/discovery/ or http://www.worldagroforestrycentre.org/rmg/GDE/index.html.

A second source of high-quality statistical software free to all is R. Development of this open-source software has been by a consortium with many contributors. Details are available and the software can be downloaded from http://cran.r-project.org/

It may take new users a while to learn the basics of R, but the effort is repaid by giving access to a very wide range of statistical tools, often including the very latest developments in statistics methods. As a starter, the following commands will give the analyses of Example 2 from this paper.

```
#Read the data, in this case from the clipboard after copying in Excel
soilfert<-read.table("clipboard", header=TRUE,na.strings="*")
attach(soilfert)

#Change the score column to an ordered factor, make sure name and trt are factors
score98<-ordered(score98, levels=c("poor", "ok","good","excellent"))
name<-as.factor(name)
trt<-as.factor(trt)

#Fit the ordered categorial (proportional odds) model
library(MASS)
ratemod<-polr(score98~name+trt)
summary(ratemod)
```

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