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The analysis of the NSW wheat variety database. I. Modelling trial error variance

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Abstract The retrospective analysis of a large database on wheat variety testing in New South Wales (NSW) is considered. This analysis involved three key steps. Initially error variance heterogeneity is modelled, indicating significant differences in error variance due to trial location, year of trialling, sowing date and trial mean yield. The implication of this modelling for the estimation of variance components is discussed.

Key words Genotype-by-environment interaction · Variance heterogeneity

Introduction

The accurate assessment of the yield performance of new genotypes across a range of environments is crucial for plant improvement programmes. The cost of this evaluation is significant. New South Wales (NSW) Agriculture spends approximately $750,000 annually on wheat variety testing. Every year in southern and central NSW, there are over 100 wheat variety trials sown and harvested to assess the performance of new genotypes across a range of environments. Brennan (1988) has shown that the cost of sowing a single plot is $20. The optimum numbers of years, locations and replications per trial for testing new genotypes in NSW could either be determined from an economic or statistical viewpoint. That is, the numbers of years, locations and replications can be chosen so that the probability of releasing an inferior genotype (known as a type I error) can be chosen to be small. Alternatively, we can specify that the probability of releasing a superior genotype be large. That is, it may be preferable to set the number of years, locations and replicates per trial and the release criteria so that the probability is always high for any superior genotype to be accepted rather than protect against falsely releasing an inferior genotype. The economic cost to farmers of releasing an inferior genotype is much less than the economic cost of not releasing a superior genotype.

Whatever the strategy, it is necessary to determine the relative magnitude of the sources of variation in the NSW wheat trialling system. The components of variance which control the above decisions are due to genotype and the interaction of genotype with year, location and year and location. Once these components have been estimated, the efficiency (either statistical or economic) of various trialling systems can be determined.

There is a substantial amount of literature on genotype-by-environment interactions in Australia. Various approaches have been recommended for the analysis of such data dating back to the seminal work of Finlay and Wilkinson (1963) who proposed joint regression analysis. More recently, pattern analysis (Byth et al. 1976; Brennan and Byth 1979; Brennan and Shepherd 1985) and the additive main effects and multiplicative interaction (AMMI) model (Gollob 1968; Gauch 1988) have been recommended. The choice of the method of analysis depends on the aims of the study (Williams et al. 1992).

Most studies of variance component estimation in genotype-by-environment data have been restricted to either a smaller number of years (Gauch 1988; Thomson and Cunningham 1979; Nachit et al. 1992), locations (Mungomery et al. 1974) or genotypes (Seif et al. 1979; Zobel et al. 1988; Brandle and McVetty 1988). Many authors have dealt with reduced data sets for computational ease (Brennan and Byth 1979; Brennan et al. 1981), but the availability of software coinciding with the development of REML (Patterson and Thompson 1971) and the recent development of a new computer

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efficient algorithm for REML (Gilmour et al. 1996) has relieved these restrictions.

Patterson et al. (1977) presented the results of a similar study for several crops in the United Kingdom (UK), and Talbot (1984) updated these results and presented results for other crops not included in the original work of Patterson et al. These studies were conducted in the UK and cannot be reliably used to assess the effectiveness of trialling systems in NSW.

In this series of two papers (see also following article) we present the retrospective analysis of a large database of trials from 1982 to 1991 inclusive. The aim of this work is primarily to estimate the variance components due to genotype and the interaction of genotype with location, year and location by year. The structure of the papers broadly follows the sequence of analyses as they were undertaken. This paper reports on the modelling of within-trial error variance. The number of trials in the database and the length of the trialling period meant that a more statistically sound method of coping with error variance heterogeneity was possible. This modelling of error variance is crucial to the subsequent estimation of variance components, which is the subject of the second paper in this series. The second paper initially addresses the partitioning of genotype-by-environment interaction into explainable and unexplainable interactions. This partitioning is seen as sensible and necessary in order to obtain estimates of variance components that only reflect the unexplainable interactions of genotype with year and location. The second paper concludes with a comparison of the statistical efficiency of various trialling systems.

Description of the database

Wheat yield data from the trialling system for the years 1982–1991 inclusive were collated. This data represented experiments conducted in silo groups 3, 4, 5 and 6 in central and southern NSW. In all, there were 1071 experiments. For each experiment, the sowing date (measured in Julian days, 1 = 1 April), mean yield ($\bar{y}$), coefficient of variation of the yield (CV), average standard error of a difference between genotype means (sed), error degrees of freedom (v) and number of replicates (r) were recorded.

Table 1 Summary of experiment statistics for the NSW wheat database

Variable	Minimum	Maximum	Mean	Median
Sowing date	1 April	29 August	23 May	22 May
Yield(t ha^{-1})	0.12	8.02	3.03	2.98
Replicates	2	12	3.4	3
CV(%)	1.88	71.7	10.3	8.5
Error *df*	10	165	40	34
Entries/experiment	5	78	19	17

Table 1 presents a summary of this data. Sowing dates ranged from 1 April to late-August, and the experiment mean yield ranged from 0.12 t ha^{-1} to 8.02 t ha^{-1}. Most experiments had three replicates though data were included from some early generation experiments in which check plot replication can exceed ten. The CV varied substantially, being particularly high for the low-yielding experiments conducted in 1982, a year of severe drought.

Two measures of accuracy were available for each experiment, the sed and CV from which the error variance for the ith experiment, denoted by s_i^2, can be calculated using the usual formula for either a randomized block analysis or incomplete block or by an approximation for spatial analysis. These two estimates of s_i^2 were compared and remedial action taken if they differed by more than 1% (allowing for rounding errors). The range of s_i^2 was (0.000805, 0.903) with a mean of 0.08715 and median value of 0.0569.

The experiments were conducted across a wide range of sites from the high rainfall eastern boundary of the wheat belt (Bathurst, Molong, Orange) to sites on the marginal western edge of the wheat belt (Condobolin, Trangie, Bogan Gate). To identify key environments, we grouped these experiments into 60 locations, as shown in Fig. 1. Table 2 presents the number of experiments conducted at each location for each year. Often, two experiments were conducted at the same location in the same year (early and late sowing dates). Experiments were conducted either on cooperating farms or on NSW Agriculture research stations. In some cases experiment sites were chosen to represent a particular environmental condition, for example, soil acidity.

Experiment designs varied considerably from randomized complete blocks to incomplete block designs and more recently NN-balanced designs (Wilkinson et al. 1983). Methods of analysis varied from randomized block and incomplete block analysis for most experiments up to 1986, thence the spatial analysis procedures of Gleeson and Cullis (1987) from 1987 to 1989. The extended spatial analysis of Cullis and

Fig. 1 Map of NSW indicating the 60 locations

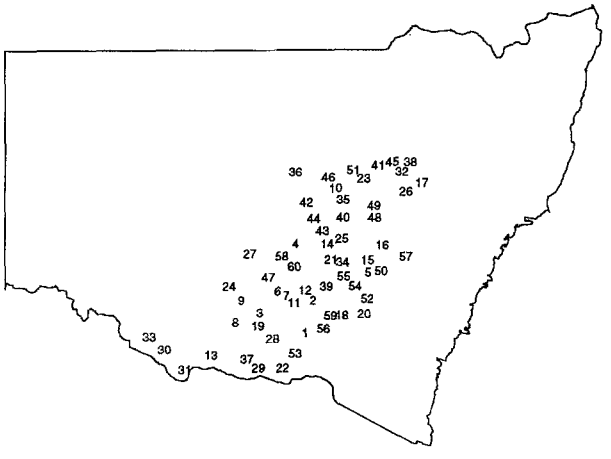

Table 2 Frequency of experiments classified by location and year

Number	Location Name	Year										Margin
		1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	
1	Wagga Wagga	9	5	5	6	5	6	1	2	2	1	42
2	Temora	6	4	3	3	3	3	2	1	2	1	28
3	Yanco	2	3	4	3	2	1	1	2	2	1	21
4	Condobolin	5	4	3	3	4	3	2	2	2	4	32
5	Cowra	1	2	0	2	2	2	2	2	3	2	18
6	Moombooldool	2	2	2	2	2	2	2	2	2	2	20
7	Beckom	2	2	2	2	2	2	2	2	2	2	20
8	Coleambally	2	2	1	1	1	0	0	0	0	1	8
9	Murrumbidgee	4	5	2	5	1	1	0	0	3	3	24
10	Trangie	3	4	2	2	2	2	2	1	1	1	20
11	Ariah Park	1	2	2	2	1	2	1	2	2	2	17
12	Barmedman	2	3	2	3	2	0	1	0	2	2	17
13	Blighty	2	2	1	2	2	0	0	1	2	2	14
14	Bogan Gate	1	1	2	3	0	2	1	1	1	1	13
15	Canowindra	2	2	2	4	1	2	3	1	1	1	19
16	Molong	1	3	1	2	0	0	2	2	3	2	16
17	Coolah	1	3	1	1	1	1	1	1	1	0	11
18	Cootamundra	2	2	2	1	1	2	2	2	2	2	18
19	Morundah	2	2	2	2	0	0	3	3	4	2	20
20	Galong	0	2	1	2	2	1	2	2	2	1	15
21	Garema	2	6	4	2	4	2	4	1	2	2	29
22	Gerogery	2	2	2	2	2	2	2	2	2	1	19
23	Gilgandra	2	1	1	2	2	2	3	2	5	2	22
24	Goolgowi	2	3	4	3	2	1	0	2	2	2	21
25	Goonumbla	0	3	3	3	4	2	1	2	2	2	22
26	Leadville	3	6	3	3	2	3	2	2	1	2	27
27	Lake Cargelligo	2	2	4	4	3	2	2	2	2	2	25
28	Lockhart	1	2	2	2	1	2	2	2	3	1	18
29	Lowesdale	0	2	2	2	0	2	1	2	2	1	14
30	Mallan	1	1	1	1	1	1	1	1	1	1	10
31	Mathoura	2	3	3	0	2	2	2	2	2	2	20
32	Mendooran	2	4	4	5	3	3	3	2	3	0	29
33	Moulamein	2	1	4	2	2	0	2	2	2	2	19
34	Mulyandry	1	2	2	2	2	2	2	2	1	2	18
35	Narromine	0	1	1	1	1	1	1	1	2	0	9
36	Nyngan	0	4	5	5	0	3	3	0	2	0	22
37	Oaklands	2	1	3	3	2	1	1	4	2	4	23
38	Purlewaugh	1	1	2	2	3	3	1	2	1	0	16
39	Quandialla	0	4	4	4	2	4	2	1	2	2	25
40	Tomingley	0	2	2	3	1	2	2	2	1	1	16
41	Tooraweenah	0	1	1	1	1	0	1	1	0	0	6
42	Tottenham	0	2	2	2	2	3	2	2	1	2	18
43	Trundle	1	3	1	1	1	1	1	1	2	1	13
44	Tullamore	0	1	1	2	2	2	1	0	1	1	11
45	Warkton	0	1	1	1	1	1	1	0	0	0	6
46	Warren	2	5	3	4	3	2	3	1	1	1	25
47	Weethalle	2	3	1	3	1	2	2	2	4	4	24
48	Wellington	1	5	4	2	0	0	0	1	1	3	17
49	Wongarbon	1	1	2	2	1	2	1	1	1	1	13
50	Woodstock	2	2	2	1	0	1	1	1	0	1	11
51	Collie	0	3	3	2	1	0	0	0	1	1	11
52	Young	2	0	3	5	0	0	0	1	2	3	16
53	Cookardinia	2	2	2	2	2	1	2	2	2	2	19
54	Greenethorpe	0	2	0	1	0	1	0	2	1	2	9
55	Grenfell	0	1	1	2	0	0	2	1	2	1	10
56	Eurongilly	2	3	1	2	1	3	1	0	0	0	13
57	Bathurst	0	1	1	1	1	1	1	1	0	0	7
58	Tullibigeal	1	2	1	1	0	0	3	3	2	2	15
59	Cootamundra 2	2	2	1	2	2	2	2	2	2	1	18
60	Lake Cowal	0	3	3	4	0	0	0	0	1	1	12
	Margin	93	149	130	143	92	94	91	87	103	89	1071

Gleeson (1991) was adopted for the analysis of experiments from 1990. Accompanying these changes in experiment analysis and design has been a significant change in field plot techniques and an improvement in awareness of the need for improved error control (Cullis and Gleeson 1989) among field workers in NSW Agriculture.

Modelling experiment error variance

Background

Variance heterogeneity is a common problem encountered in the analysis of a series of experiments (Cochran and Cox 1957). Nevertheless, the analysis of genotype-by-environment data is often conducted assuming constant variance (Patterson et al. 1977; Williams et al. 1992; Brennan et al. 1981). Other workers choose to transform to remove the mean-variance dependence. Commonly used transformations include logarithmic (Finlay and Wilkinson 1963) and square-root (Brennan and Shepherd 1985). The ability of a single transformation to achieve additivity, normality and constant variance has been questioned (Carroll and Ruppert 1989); however alternate approaches such as the use of quasi-likelihood or empirical weighted least-squares have not been exploited due to the computational burdens for the analysis of heterogeneous mixed models. Recently, Foulley et al. (1992) advocated modelling variance heterogeneity in mixed linear models and developed REML procedures for variance component estimation. It was not possible to adopt their procedures as only genotype experiment means, and the associated experiment standard errors were stored electronically.

Carroll and Ruppert (1989) present a very thorough account of methods for identifying variance heterogeneity in single strata designs. They also present several approaches for jointly modelling mean and variance parameters. In the context of genotype-by-environment data, variance heterogeneity presents serious difficulties. The existence of several strata or error terms (namely genotype-by-location, genotype-by-year, genotype-by-location-by-year and residual) precludes the simple application of the diagnostics discussed by Carroll and Ruppert (1989). There are various issues to be addressed concerning the homogeneity of the other variance components in the presence of error variance heterogeneity. If weights are taken as the reciprocal of the estimated variance for each experiment, this immediately implies that heritability (the ratio of genetic variance to error variance) will be proportional to error variance. It is perhaps more appropriate to assume all error terms have a common level of heterogeneity. This is equivalent, asymptotically, to the use of transformations or standardization techniques prior to analysis, i.e. assuming constant variance and additivity on a log scale implies strict conditions on the type of heterogeneity for each error term in the model.

The idea of modelling variance is not new. Aitken (1987) presents an approach to modelling variance using GLIM for normal data, and Box and Meyer (1986) consider the analysis of dispersion effects in replicated designs. Verbyla (1993) extends the ideas of Aitken (1987) and demonstrates how REML estimation is more appropriate for the joint estimation of mean and variance models. Carroll and Ruppert (1989) point out that the use of the sample variance as a weight when there is replication at each design point can be disastrous. In fact, Carroll and Cline (1988) note that weighted least squares is inconsistent for two replicates. Even for ten replicates, this approach leads to a variance inflation of 40% (Yates and Cochran 1938).

The problem is not as severe for most genotype-by-environment data in which replications are pooled within an experiment to increase the precision of variance estimation. For this data, the error degrees of freedom varied from 10 to 165 with a mean of 40.0 (Table 1). However, the use of only the sample experiment error variance as a weight is an equivalent procedure to estimating a regression function for the mean by linear interpolation (Carroll and Ruppert 1989).

Results

The variance model considered was the log-linear form

$$\log\sigma_i^2 = z_i'\lambda \quad \text{or} \quad \sigma_i^2 = e^{z_i'\lambda}, \tag{1}$$

where λ is a vector of unknown parameters. We assumed that the first component of each z_i satisfies $z_{i1} = 1$ so that if $\lambda_2 = \ldots = \lambda_q = 0$, we had constant variance, $\sigma_i^2 = e^{\lambda_1}$. As pointed out by Aitken (1987) and Smyth (1989), if the vector of experiment genotype means is known and we assume normality for the data then $s_i^2 \sim \sigma_i^2 \chi^2(v_i)$ where v_i is the error degrees of freedom for the ith experiment. Thus, maximum likelihood estimation of λ can proceed by application of a generalized linear model with Gamma errors and known scale parameter $2v_i^{-1}$ (McCullagh and Nelder 1989). The dependent variable was s_i^2 and link function was the log link.

Factors in these experiments which were likely to influence error variance include the year of sowing, (for reasons outlined earlier), the experiment mean yield, (given such wide variation in mean yield, Table 1) and sowing date. Experiments sown earlier in the season are often subject to more variability due to difficulties with crop establishment and intermittent frosting of spring-type genotypes. Additionally, some sites are inherently more variable than others.

Figure 2a,b presents the added variable plots (Atkinson 1985) of log (s_i^2) against log ($\bar{y}_i$) where $\bar{y}_i$ is the ith experiment mean and log (s_i^2) against t_i where t_i is the sowing date measured in Julian days from 1 April. The

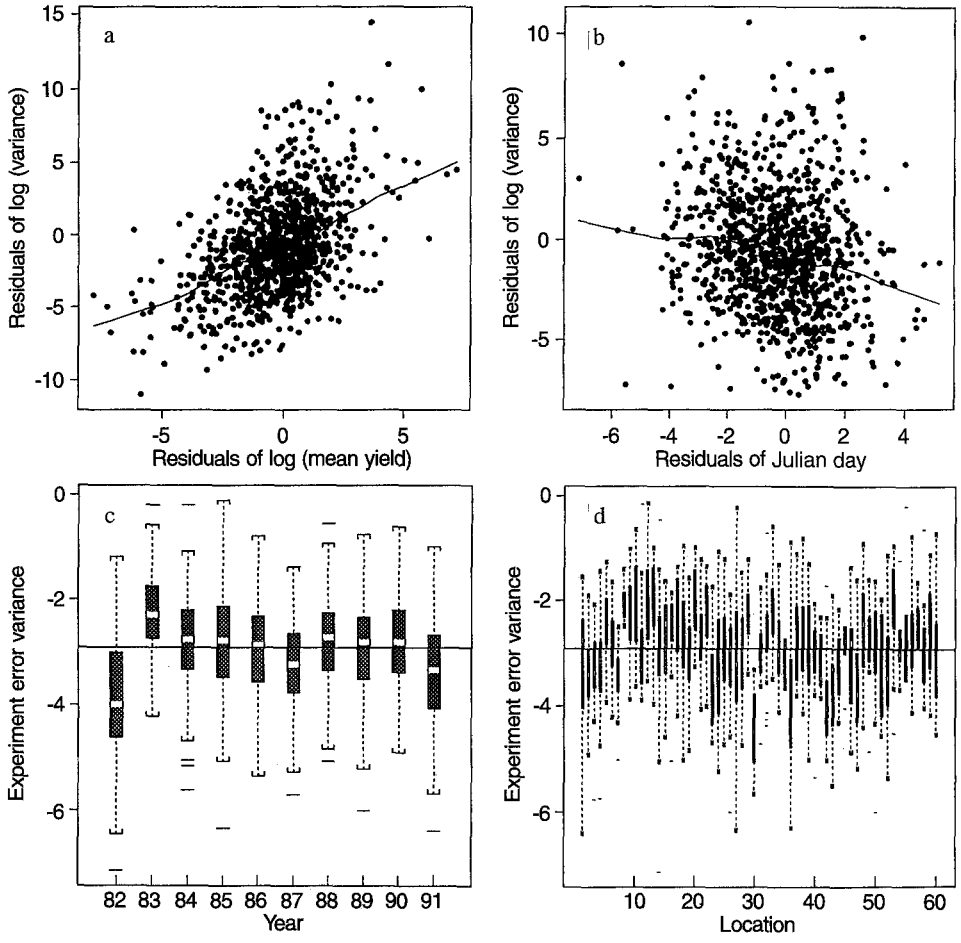

Fig. 2a–d Added variable plots of $\log(s_i^2)$

relationship between $\log(s_i^2)$ and $\log(\bar{y}_i)$ appeared to be linear, suggesting the 'power of the mean model' (as discussed by Carroll and Ruppert 1989).

Figure 2c, d also presents boxplots of error variance adjusted for t_i and $\log \bar{y}_i$ for each year and for each location, respectively. These indicate substantial variation both within and between years and locations.

Table 3 presents the analysis of deviance of error variance. In this table, terms appearing above the line have been adjusted only for other terms above the line, whereas terms below the line have been adjusted for all other terms in the model. The validity of the choice of the Gamma variance was examined by fitting the same model (including only the main effects) with log link and constant variance using the quasi-likelihood procedures of McCullagh and Nelder. Residual diagnostic plots supported the use of the Gamma variance function. There was evidence of year × $\log(\bar{y}_i)$ and year × t_i effects; however, closer inspection of the data revealed a limited range of yields and sowing dates in some years (1982 and 1987), and so we have excluded these interactions. Similarly, the year-by-location interaction has been excluded for reasons of parsimony.

Tables 4 and 5 present the relative variance of the years and locations, respectively. These were adjusted for experiment mean and sowing date and although

Table 3 Analysis of deviance of error variance log link, Gamma variance function, $n = 1071$

Source	df	Mean deviance	Residual mean deviance
$\log(\bar{y})$	1	2415	
(t)	1	211	
Year (Y)	9	122	
Location (L)	59	52.4	9.358
$\bar{y}$.Y	9	32.7	
t.Y	9	13.2	
Y.L	453	11.7	6.751

Table 4 Predicted experiment error variance for 10 years relative to 1987

Year	Experiment error variance
1987	1.00
1991	1.09
1986	1.40
1989	1.41
1988	1.42
1990	1.43
1982	1.45
1985	1.57
1984	1.96
1983	2.26

Table 5 Predicted experiment error variance for 60 locations in NSW relative to Mallan

Location name	Location number		Location name	Location number	
Mallan	30	1.00	Warkton	45	4.15
Beckom	7	1.91	Molong	16	4.23
• Temora	2	1.92	Moombooldool	6	4.24
Greenethorpe	54	2.05	Tullibigeal	58	4.25
Tottenham	42	2.09	Grenfell	55	4.36
• Yanco	3	2.17	Oaklands	37	4.50
Trundle	43	2.56	Wongarbon	49	4.51
Woodstock	50	2.64	Garema	21	4.52
Collie	51	2.70	Coolah	17	4.57
Weethalle	47	2.71	Nyngan	36	4.61
Tooraweenah	41	2.79	Cootamundra 2	59	4.66
Young	52	2.90	Murrumbidgee	9	4.66
Narromine	35	3.03	Bogan Gate	14	4.67
Lockhart	28	3.16	Bathurst	57	4.80
Mathoura	31	3.16	Lake Cargelligo	27	4.80
Gilgandra	23	3.17	Purlewaugh	38	4.83
• Wagga Wagga	1	3.24	Coleambally	8	4.83
Leadville	26	3.25	• Cowra	5	4.88
Morundah	19	3.25	Eurongilly	56	5.53
Goolgowi	24	3.26	Wellington	48	5.56
• Condobolin	4	3.36	Lowesdale	29	5.67
Tomingley	40	3.37	Gerogery	22	5.85
Mulyandry	34	3.61	Lake Cowal	60	5.85
Tullamore	44	3.72	Moulamein	33	6.21
Ariah Park	11	3.85	• Trangie	10	6.91
Canowindra	15	3.91	Blighty	13	7.02
Quandialla	39	4.00	Cootamundra	18	7.20
Goonumbla	25	4.09	Galong	20	7.46
Mendooran	32	4.11	Barmedman	12	9.38
Warren	46	4.13	Cookardinia	53	10.10

• = NSW Agriculture Research Station

mean sowing date and yield were affected by location and year, the range of yield and sowing date for each year and location was sufficient to cover the overall mean yield and sowing date. The most variable locations included locations chosen for soil acidity and the western low-yielding locations. Error variance has declined (though not consistently) over the 10-year period.

Discussion

This analysis not only provides insight into those factors affecting error variance, but potentially provides for an improved weight for the variance component estimation in the next stage of the analysis of the NSW wheat variety database described in the second paper in this series. With a 1000-fold range in error variance, it was clear that an unweighted analysis would be statistically inefficient. Much of the heterogeneity was attributable to the variation in mean yield (Fig. 2 and Table 3). However, there was significant heterogeneity between locations (10-fold) and years (3-fold) that warranted their inclusion in the model for error variance.

There are several options available for the choice of weight in the subsequent analyses. The most popular and simplest option is to use the number of replications in the experiment (r_i) as the weight. This was clearly inappropriate. Alternatively, we could have used the observed variance and weighted by r_i/s_i^2. This option had several disadvantages. Firstly, given the widely differing sources of the data, the chance of data errors and outliers being present was reasonably high. Several investigations of experiments with excessively low or high error variances uncovered errors of transcription and coding. Despite utmost care being taken in data collation it seemed unwise to condition subsequent analyses on the observed error variance.

Given the strong relationship between error variance and experiment mean yield, another option would have been to transform and use the experiment replication as the weight. The power transformation of $y^{0.592}$ removes the mean-variance dependence for this data. Although this transformation should have been performed on the original data, there would only be a small loss of efficiency by applying the transformation to the genotype experiment means as the genetic variance for each experiment usually was much larger than the error variance. This then assumed that models used in subsequent analyses were additive on this scale and that additional random effects such as genotype-by-year and genotype-by-location interactions were homogeneous on this scale.

A third alternative was to weight by $w_i = r_i\bar{s}^2/\hat{s}_i^2$ where $\bar{s}^2$ is the pooled experiment error variance and $\hat{s}_i^2$ is the predicted error variance for experiment i, using

our model. This option is appealing as it attempts to accommodate the major sources of heterogeneity, viz scale, year and location, without conditioning the subsequent analyses on the observed error variances nor does it assume additivity or homogeneity for the additional random effects on another scale.

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