



Statistical Analysis of Field Trials with Changing Treatment Variance

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ABSTRACT

This is a discussion paper that presents no new material but challenges the way that field trials with changing treatment variances have been traditionally analyzed. We argue that one should always expect the variance of yield to change when the yields are obtained from plots with different plant densities. To illustrate, a turnip (*Brassica rapa* L.) sowing density by sowing date experiment is analyzed using analysis of variance and residual maximum likelihood methods. Deviance is used to compare the statistical models and demonstrate that residual maximum likelihood provides a better analysis when a linear mixed model is fitted to account for a changing variance due to sowing density. The analysis is further improved when sowing date, which also has a changing variance, is incorporated into the model. Plant density trials should always be assumed to have changing variance. Linear mixed models (with a residual maximum likelihood algorithm for estimating variance parameters) can be used to obtain superior analyses and make better research decisions.

WHEN USING ANOVA to analyze experiments with different harvest times, sowing times or plant densities, do you routinely challenge the assumption of equal variance? We argue in this paper that your starting assumption should always be that the variance changes with treatment.

Let Y_1, \dots, Y_n represent n individual plant yields in a plot and assume for the moment that σ^2 represents the common variance on a per plant basis, so that $\text{var}(Y_i) = \sigma^2$ for each i . Then statistical theory tells us that, for independently growing plants,

$$\text{var}(\text{total plot yield}) = \text{var}(Y_1 + \dots + Y_n) = n \sigma^2$$

Consequently, if you analyze total plot yield for plants growing independently in plots of a density trial, you should use a weighted ANOVA, with the weights inversely proportional to the number of plants in a plot. That is one extreme.

In field trials, it is unlikely that plants are growing independently within a plot unless widely spaced. Indeed, it is quite common now for field trials to be checked for the presence of spatial correlations (Payne, 2006). In the event of strong plant competition within a plot, the variance of total plot yield may well be constant across different plant spacings. Plants with more space tend to grow larger; plants with less space smaller, but there are more of them, so the variance of the total plot yield may even out. This is the other extreme. The reality is

probably somewhere between proportional variance and constant variance. How is this checked?

A harvest or sowing date treatment also raises the separate issue of whether the variance of the yield from plants grown for various lengths of time can be constant. For example, Fig. 1A shows dry weights of transplanted lettuce (*Lactuca sativa* L.) seedlings for the first 35 d of growth (J. Moodie, personal communication, 1994). It is clear that the variance of dry weight increases over time; once logged (Fig. 1B), the variance appears stable.

DATA

By way of illustration, Table 1 presents the data from page 206 of McConway et al. (1999). This is a randomized block experiment, with four 3- by 32-m blocks each with 16 3- by 2-m plots. Turnip (*Brassica rapa* L.) seed was sown after a main crop was removed, with the sole purpose to provide food for farm animals to graze on in winter. The 16 treatments were combinations of two varieties, 'Barkant' and 'Marco', two sowing dates, 21 and 28 Aug. 1990, and four sowing densities, 1, 2, 4, or 8 kg ha⁻¹. Treatments were allocated to plots within blocks at random.

ANALYSIS AND DISCUSSION

Classical Analysis of Variance Approach

Table 2 presents the standard, unweighted ANOVA for turnip data using GenStat (Payne et al., 2007). One way of detecting a change in variance is to check the (standardized) residuals plotted against fitted values. A fanning of the residuals suggests that a power or log-transformation is required. The standardized residual plot in Fig. 2A indicates marked fanning, which is somewhat alleviated by using a weighted ANOVA (Fig. 2B). Analyzing log(dry weight) appears to over-correct (Fig. 2C), with the fanning reduced with increasing fitted value. With the analysis of untransformed data, negative fitted values are produced. The outliers in the log-transformed analysis cor-

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Abbreviations: LMM, Linear Mixed Model; BLUP, Best Linear Unbiased Predictor; REML, Residual Maximum Likelihood.

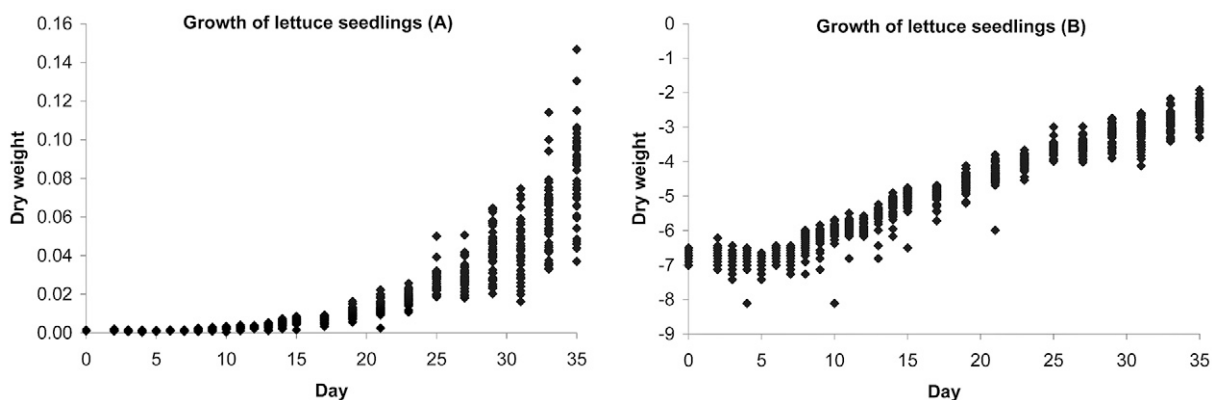


Fig. 1. Dry weights (A), and log-transformed dry weights (B), of lettuce seedlings over the first 35 d after transplanting.

respond to different plots than those from the two untransformed analyses. While logging the data may induce common variance over sowing dates, mathematically it does not work over sowing densities. So how do we proceed?

Linear Mixed Models (REML) Approach

A linear mixed model (LMM) is simply a model that contains a collection of fixed effects and random effects:

$$Y = \text{overall mean} + \text{fixed effects} + \text{random effects} + \text{Error}$$

The random effects are assumed to be independent of each other (and of the random Error), however the variance structures of all the random terms are flexible, allowing the levels of a factor to be correlated and/or have changing variance. Variance parameters of the random terms are estimated using Residual Maximum Likelihood (REML), which produces estimates that are unbiased (or at least less biased) than those obtained by Maximum Likelihood (Galwey, 2006).

Generally in agriculture blocks are considered random, so for the current experiment the random part of the model is Block + Error. Accordingly, we need to specify the variance structure for the random model in such a way as to allow an investigation

Table 1. Yield of turnips from McConway et al. (1999).

Variety	Sowing date (1990)	Sowing density kg ha ⁻¹	Block			
			1	2	3	4
Barkant	21 Aug.	1	2.7	1.4	1.2	3.8
		2	7.3	3.8	3.0	1.2
		4	6.5	4.6	4.7	0.8
		8	8.2	4.0	6.0	2.5
	28 Aug.	1	4.4	0.4	6.5	3.1
		2	2.6	7.1	7.0	3.2
		4	24.0	14.9	14.6	2.6
		8	12.2	18.9	15.6	9.9
Marco	21 Aug.	1	1.2	1.3	1.5	1.0
		2	2.2	2.0	2.1	2.5
		4	2.2	6.2	5.7	0.6
		8	4.0	2.8	10.8	3.1
	28 Aug.	1	2.5	1.6	1.3	0.3
		2	5.5	1.2	2.0	0.9
		4	4.7	13.2	9.0	2.9
		8	14.9	13.3	9.3	3.6

into changing variances across the levels of two of our factors, density and planting date.

To investigate whether the variance changes across the levels of a factor, we calculate the change in deviance between the constant-variance and changing-variance models. Deviance plays the role in LMM (REML) that the Residual Sum of Squares plays in ANOVA. The change in deviance is distributed approximately as χ^2 with degrees of freedom (df) equal to the change in individual df between the two models.

Some packages use a statistic known as the scaled Wald statistic and an associated *P* value from a χ^2 distribution. For a balanced design, the scaled Wald statistic is the same as the *F* statistic from the ANOVA. In that case one is free to replace the *P* value with one based on an *F* distribution. Other packages such as ASReml (Gilmour et al., 2006) use an *F* statistic with (sometimes approximate) denominator degrees of freedom, as explained later. This is the preferred approach, because the *P* value from the Wald statistic assumes known variances and hence is underestimated, especially for small-scale experiments.

We chose GenStat for this paper, because (i) it is easy to use and (ii) it is free to “not-for-profit research organizations, charities, and educational institutes based in the developing world” (www.vsnl.co.uk/products/discovery, verified 5 Mar. 2008). (For users of GenStat, the Wald statistic is the only test statistic produced before Version 10.) The Appendix also provides the code to perform the analyses in SAS (SAS Institute, Inc., 2004) and R (R Development Core Team, 2006).

Table 2. Standard GenStat unweighted ANOVA of turnip yield data.

Source of variation	df	Sum of squares	Mean square	Variance ratio	<i>P</i>
Block stratum	3	163.737	54.579	5.69	
Block × Units × Stratum					
Variety	1	83.951	83.951	8.75	0.005
Density	3	470.378	156.793	16.35	<0.001
Date	1	233.708	233.708	24.37	<0.001
Variety × Density	3	8.647	2.882	0.30	0.825
Variety × Date	1	36.451	36.451	3.80	0.057
Density × Date	3	154.793	51.598	5.38	0.003
Variety × Density × Date	3	17.999	6.000	0.63	0.602
Residual	45	431.611	9.591		
Total	63	1601.275			

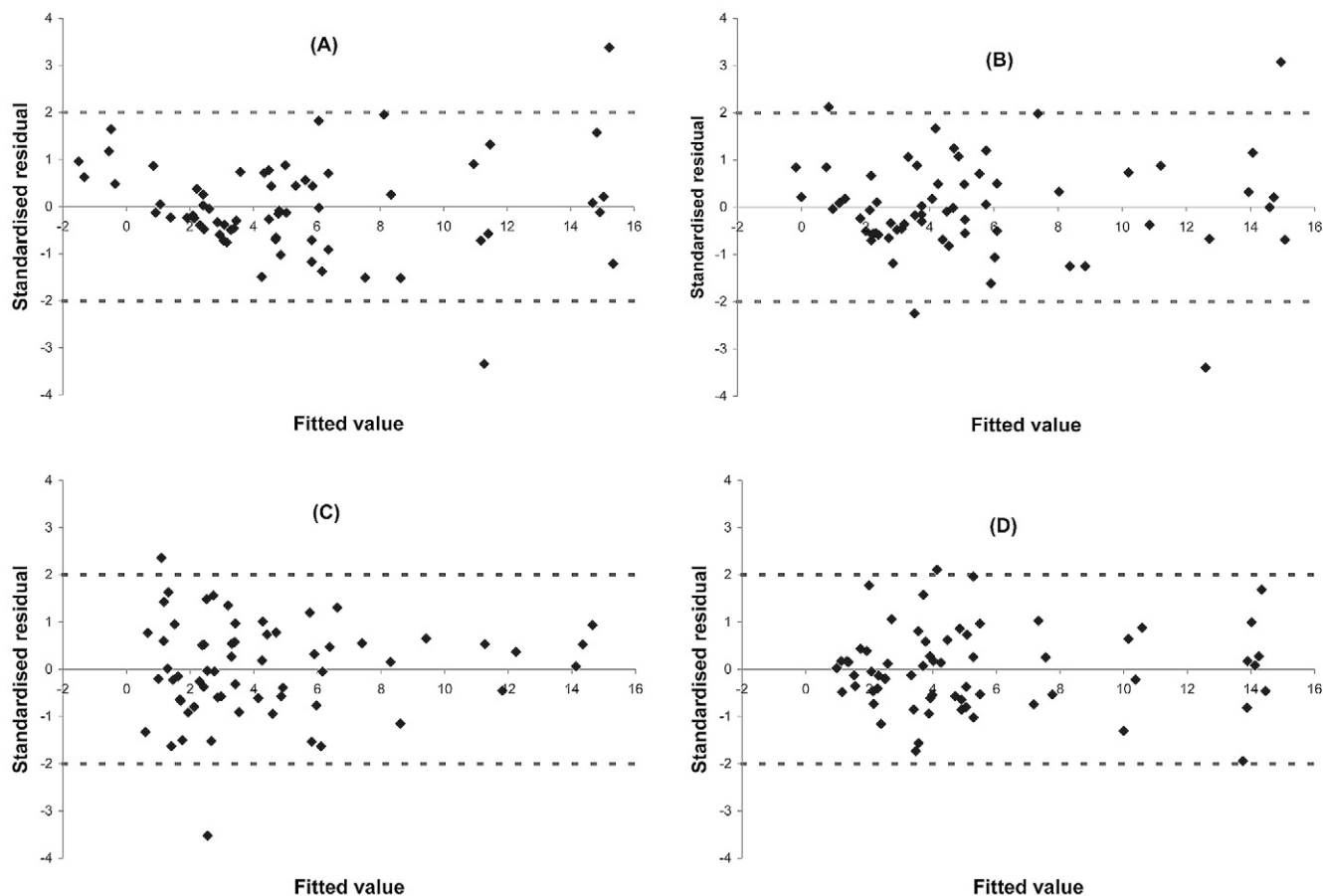


Fig. 2. Standardized residual plots from (A) standard ANOVA of the turnip yields, (B) weighted ANOVA of the turnip yields, with weights inversely proportional to the densities, (C) standard ANOVA of log-transformed turnip yields, and (D) a linear mixed model (LMM) (Residual Maximum Likelihood, REML) analysis with variances changing across sowing dates and sowing densities.

Variance Structures in the Error Term

In addition to a constant variance assumption, there are two possible assumptions for a changing variance across dates and densities for the turnip data. In both cases we assume a constant variance across blocks and varieties.

The first allows the variance to change across densities in a pattern that is the same across all dates. In this case the variance may also change across dates. This variance model is multiplicative across dates and densities, with five parameters to estimate (four variances and one multiplicative constant for the

second date). Note that this form of the model could be explored to allow a changing variance across dates but not densities.

The second allows the variance to change across all combinations of dates and densities in no particular pattern. This is an unstructured variance model, with eight variances to estimate. For the turnip data, this says that any change in variance across densities for turnips planted on 21 August is different than any change in variance for turnips planted on 28 August. Since these sowing dates are close, we might expect this not to be the case.

The first assumption for density/date variances is a special case of the second assumption, and hence can be tested using change in deviance. The deviances for various models are presented in Table 3.

First, the constant variance model is a significantly worse model compared to both the multiplicative ($183.92 - 162.05 = 21.87$ with $46 - 42 = 4$ df, $P < 0.001$) and unstructured ($183.92 - 159.99 = 23.93$ with $46 - 39 = 7$ df, $P = 0.001$) variance model. This has repercussions on the precision of treatment comparisons, as we will discuss later.

Next we compare the unstructured vs. multiplicative model for densities and dates. The change in deviance is 2.06 with $42 - 39 = 3$ df and is not significant ($P = 0.560$). This indicates that any change in the variance across densities is proportionately the same at each date.

We now explore whether the variance for the multiplicative model is constant across dates (but not densities). The change

Table 3. Deviances for different variance structures in the Error term of the random model *Block + Error* for turnip yield data.

Block	Variety	Density	Date	Deviance	df
<u>Multiplicative variance model across densities and dates</u>					
Identity	Identity	Identity	Identity	183.92	46
Identity	Identity	Identity	Diagonal	175.71	45
Identity	Identity	Diagonal	Identity	168.10	43
Identity	Identity	Diagonal	Diagonal	162.05	42
Dropping <i>Block</i> from <i>Block + Error</i>					
Identity	Identity	Diagonal	Diagonal	162.41	43
<u>Unstructured variance model across density/date combinations</u>					
Identity	Identity	Diagonal		159.99	39
Dropping <i>Block</i> from <i>Block + Error</i>					
Identity	Identity	Diagonal		160.02	40

in deviance, $168.10 - 162.05 = 6.05$ with $43 - 42 = 1$ df, is significant ($P = 0.014$). The variance therefore changes across dates, which we had expected from biological considerations. To test if it also changes across densities, we use $175.71 - 162.05 = 13.66$ with $45 - 42 = 3$ df, which is also significant ($P = 0.003$). We had expected this from mathematical considerations.

The LMM (REML) analysis from GenStat (Version 10) for the final model with a random block term and a random error term with a constant variance across blocks and varieties and a variance that changes multiplicatively across densities and dates is given in Table 4. Notice that GenStat produces sequential (i.e., Type I) tests, as well as conditional tests for the current model. We dropped the three-factor interaction to illustrate the conditional tests for the three two-factor interactions.

Estimated error variances are 1.03, 2.26, 10.79, and 7.91 for the four densities sown on 21 August, and 3.05 times these values, namely 3.14, 6.90, 32.94 and 24.15, for the four densities sown on 28 August. You can see how clearly different these variances are.

Finally, we note that the change in deviance is also used to assess whether a random factor can be dropped. Technically, a random factor has no role to play in a model if the variance of that random term is zero. For the multiplicative model of the turnip data, the variance component for the random block term is only 0.16. The change in deviance for the same model with the random block term removed is $162.41 - 162.05 = 0.36$ (based on $43 - 42 = 1$ df, $P = 0.546$) and hence it is clear that there is no block variation. This of itself is extremely interesting, since the ANOVA (which assumes constant variance) indicated a strongly significant block effect. The analysis has a strong block effect associated with low values in block 4. Block 4 has the lowest yield in 13 of the 16 treatments, the high values being with the lowest density. Thus, allowing a larger variance for the higher densities has moved block variation into the residual.

Estimated variety means are 6.552 (Barkant) and 4.231 (Marco). The estimated standard error of the mean (SE) is 0.547 from the ANOVA and 0.623 from the LMM (REML). The estimated standard error of the difference (SED) is 0.774 from the ANOVA and 0.834 from the LMM (REML). There are clear advantages to the LMM (REML) analysis when we compare density by date means. From the ANOVA (which assumes a common variance), the SE is 1.095 for all means and the SED is 1.548 for all com-

parisons. Using the LMM (REML) analysis, these depend on the comparison being made. Table 5 presents the individual means, SE and SED values for date and density. While the average SE is 1.071, the minimum is only 0.411 (for the lowest density planted on 21 August) and the maximum 2.039 (for a density of 4 kg ha^{-1} planted on 28 August). Similarly, while the average SED is 1.579, the minimum is 0.641 (for the lowest density planted on 21 August) and the maximum is 2.671 (for the highest density planted on 28 August). The variances across dates and densities vary, hence means are compared with appropriate SED values. At this point, a couple of questions remain.

Table 4. GenStat's Linear Mixed Model (REML) analysis of the turnip yield with a random block effect and a random error whose variance is constant over blocks and varieties but changes over dates and densities.

Estimated variance components						
Random term	component	SE				
Block	0.160	0.328				
Residual variance model						
Term	Factor	Model (order)	Parameter	Estimate	SE	
Block.Variety.Date.Density			Sigma2	1	fixed	
	Block	Identity	-	-	-	
	Variety	Identity	-	-	-	
	Date	Diagonal	d_1	1	fixed	
			d_2	3.053	1.328	
	Density	Diagonal	d_1	1.030	0.507	
			d_2	2.260	1.019	
			d_3	10.790	5.550	
			d_4	7.910	3.546	
Tests for fixed effects						
Sequentially adding terms to fixed model						
Fixed term	Wald statistic	ndf†	F statistic	ddf‡	P	
Variety	9.35	1	9.35	22.2	0.006	
Date	7.86	1	7.86	21.9	0.010	
Density	38.47	3	12.09	18.9	<0.001	
Variety × Date	2.03	1	2.03	21.9	0.168	
Variety × Density	0.40	3	0.13	18.9	0.944	
Date × Density	14.50	3	4.56	18.8	0.014	
Variety × Date × Density	1.44	3	0.45	18.8	0.719	
In a model with no three factor information						
Dropping individual terms from full fixed model						
Fixed term	Wald statistic	ndf	F statistic	ddf	P	
Variety × Date	2.11	1	2.11	23.3	0.160	
Variety × Density	0.41	3	0.13	20.1	0.941	
Date × Density	15.21	3	4.80	20.8	0.011	

† ndf = numerator degrees freedom.

‡ ddf = denominator degrees freedom.

Table 5. Table of predicted density by date means (\pm SE) and standard errors of differences from the linear mixed model (LMM) (Residual Maximum Likelihood, REML) analysis.

Sowing date (1990)	Sowing density	Mean \pm SE	Treatment	SED table							
				1	2	3	4	5	6	7	
		kg ha^{-1}									
21 Aug.	1	1.763 ± 0.411	1	-							
	2	3.012 ± 0.568	2	0.641	-						
	4	3.912 ± 1.179	3	1.216	1.277	-					
	8	5.175 ± 1.014	4	1.057	1.127	1.529	-				
28 Aug.	1	2.513 ± 0.658	5	0.722	0.822	1.320	1.175	-			
	2	3.688 ± 0.950	6	0.996	1.070	1.487	1.361	1.120	-		
	4	10.738 ± 2.039	7	2.061	2.098	2.338	2.260	2.124	2.232	-	
	8	12.213 ± 1.749	8	1.774	1.817	2.090	2.002	1.847	1.970	2.671	

What degrees of freedom should be used for the SED values?

Sometimes this is very easy to work out. Clearly in the absence of changing variance or correlated data, the df will be identical to the residual df from the ANOVA. Sometimes component mean squares are averages of other variance estimates, in which case use of the combined df is appropriate only when those components are estimating a common variance. However, even in the latter case, the df to use for particular mean differences are not always easy to calculate, because the SED could be based on error terms from more than one stratum. A typical example of this is a standard split-plot ANOVA when the comparison of two-way means involves different levels of the whole-plot treatment: a Satterthwaite approximation is used by most statistical packages in the calculation of the df to use in those cases.

For the turnip experiment with no random block effect and with the variance assumed constant, the df to use are the combined df from the individual variance estimates from all 16 treatments, thus, $16 \times (4 - 1) = 48$. For the unstructured variance model, the variance component for a particular date and density must be the average of two estimates, each from a different cultivar and each with $(4 - 1)$ df. This gives 6 df for each variance component, which will drop slightly if a block effect is included: $45/8 = 5.625$ would be a reasonable value to use.

For the variance components in the multiplicative variance model with a random block effect, 6 df is an underestimate: we have only five, not eight, different variance parameters to estimate, and these are obtained, in part, from all dates and densities. Again, $45/5 = 9$ would be a reasonable value to use.

The SED values that GenStat calculates are based on estimates of variances appropriate to the comparison under consideration. The analysis suggests that there are two tables of means of interest.

First, there is a significant varietal mean difference. We suggest using 17.6 df for this comparison, which are the denominator df of the Variety F statistic.

Next, we look at the table of date and density means. In this case, each mean is based on a different variance, and a Satterthwaite approximation is one option for calculating approximate df. The Satterthwaite formula for a comparison involving means based on n_1 and n_2 observations and respective variance estimates s_1^2 and s_2^2 is

$$\text{df} = \frac{\left(\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2} \right)^2}{\left(\frac{s_1^2/n_1}{\text{df of } s_1^2} + \frac{s_2^2/n_2}{\text{df of } s_2^2} \right)} = \frac{(s_1^2 + s_2^2)^2}{s_1^4 + s_2^4} \times (\text{df of } s^2)$$

for equal replication and df.

For the current multiplicative model, $s_2^2 = 3.053 \times s_1^2$, and hence the approximate df for a comparison across dates for a particular density simplifies to $(1 + 3.053)^2 / (1 + 3.053^2) = 1.6$ times the df of any one component (which we suggested were 9); this gives 14.4 df for all densities. For comparisons across densities for a given date, the multiplier changes from a mini-

um of 1.2 for the most different variance components (densities 1 and 3) to 2.0 for the most similar (densities 3 and 4).

Standardized residuals

Many packages do not produce standardized residuals for LMM. With such a change in variance across the units of this experiment, these are important. How are they obtained?

With blocks considered random effects with mean zero, there are two types of fitted values and residuals available. One has only the fixed effects removed, in which case the fitted values will be the same for all plots in a block. The other has the fixed effects and what are known as the best linear unbiased predictors (BLUPs) of the block effects removed. We suggest that these are the ones to look at here: in GenStat, for example, they are obtained by selecting "Form residuals from final term only" (as opposed to "from all random terms") in the Save menu.

The standard error of the theoretical error term is σ , however the standard error of the observed residuals is not simply $\hat{\sigma}$, the square root of the Residual MS from the ANOVA. For example, in an unblocked design the standard error of the raw residuals is $\hat{\sigma}\sqrt{(r-1)/r}$, where r is the number of replicates in a treatment; for a randomized block design with t treatments and r blocks, it is $\hat{\sigma}\sqrt{(r-1)(t-1)/(rt)}$. For a LMM model, the standard errors of the raw residuals are much more complex. However, using $\hat{\sigma}$ would be a close approximation, especially for larger designs. For the current analysis this becomes $\hat{\sigma}_i$, the square root of the variance component for the i th date/density combination. This is the approach used in R. The effect of using $\hat{\sigma}_i$ as a divisor is to bring into line large raw residuals from treatments with large variation, and reduce the effect of small raw residuals from treatments with small variation. The actual standardized residuals may be slightly under-dispersed, but should eliminate any fanning, as shown in the standardized residual plot in Fig. 2(D).

CONCLUSIONS

This paper does not present any new material, rather it draws attention to several possible shortcomings of standard analyses of experiments that involve changing plant densities, target plant populations, and/or sowing dates. Many such analyses have been used in monographs in the past with no investigation of the underlying assumptions.

We recommend that a fundamental starting point of such an analysis is that the variance of yield changes. If a constant variance model is warranted in a density trial, this simply means that plant competition is sufficiently strong for the varying numbers of plants in plots to produce yields that vary similarly.

A LMM analysis is a very flexible tool that allows for changing variances and spatial or temporal correlations for random effects. Many modern statistical packages implement a REML algorithm for estimating the variance matrices, and produce sufficient information in their output to make informed decisions about model assumptions and mean comparisons.

APPENDIX

GenStat

In GenStat, specifying a changing variance is achieved by supplying an error term that indexes over all blocks and treatments. In the submenu Correlated Error Terms, Identity for any factor represents constant variance (as well as uncorrelated), Diagonal represents different variances (as well as uncorrelated) across the levels of a factor. The REML menu becomes:

(a) For the multiplicative variance model over densities and dates

```
Fixed Model: Variety*Density*Date
Random Model: Block+Block.Variety.
Density.Date
Correlated Error Terms... Identity+Identity,
Identity, Diagonal, Diagonal
```

(b) For the unstructured variance model over densities and dates, define a new factor called (say) DensityDate which indexes over the eight density/date combinations

```
Fixed Model: Variety*Density*Date
Random Model: Block+Block.Variety.
DensityDate
Correlated Error Terms... Identity+Identity,
Identity, Diagonal
```

SAS

(a) For the multiplicative variance model over densities and dates

```
proc mixed data=Density covtest;
class Variety Date Density Block;
model Yield= Variety Density Date
Variety|Density|Date/
ddfm=kr;
random block;
repeated Date Density/
subject=Block*Variety type=un@un;
parms (1)
(1)
(0) (1)
(1)
(0) (1)
(0) (0) (1)
(0) (0) (0) (1)
/hold=3,5,6,8,9,11,12,13;
lsmeans date*density/diff;
ods output covparms=covest;
run;
```

(b) For the unstructured variance model over densities and dates

```
proc mixed data=Density;
class Variety Date Density Block;
model Yield= Variety Density Date
Variety|Density|Date/ddfm=kr;
random Block;
repeated/group=Density*Date;
run;
```

R

(a) For the multiplicative variance model over densities and dates

```
library(nlme)
McConway.lme
<-lme(Yield~Variety*Date*Density, random=
.~1|Block, data=McConway)
summary(McConway.lme)
anova(McConway.lme)
McConway.lme.mult
<-update(McConway.lme, weights=varComb(va
rIdent(form=~1|Density),
+ varIdent(form=~1|Date)))
summary(McConway.lme.mult)
anova(McConway.lme.mult)
```

(b) For the unstructured variance model over densities and dates

```
McConway.lme.unst <
update(McConway.lme, weights=varIdent(form
=~1|Density*Date))
summary(McConway.lme.unst)
anova(McConway.lme.unst)
```

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REFERENCES

- Galwey, N.W. 2006. Introduction to mixed modeling: Beyond regression and ANOVA. John Wiley & Sons Ltd., West Sussex, England.
- Gilmour, A.R., B.J. Gogel, B.R. Cullis, and R. Thompson. 2006. ASReml user guide Release 2.0 VSN International Ltd, Hemel Hempstead, UK.
- McConway, K.J., M.C. Jones, and P.C. Taylor. 1999. Statistical modeling using GenStat. Arnold Publ., London.
- Payne, R.W. 2006. New and traditional methods for analysis of unreplicated experiments. *Crop Sci.* 46:2476–2481.
- Payne, R.W., and D.A. Murray, S.A., Harding, D.B. Baird, and D.M. Soutar. 2007. GenStat for Windows (10th ed.) Introduction. VSN International, Hemel Hempstead, UK.
- R Development Core Team. 2006. R: A language and environment for statistical computing. R. Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0, URL <http://www.R-project.org> (verified 9 Jan. 2008).
- SAS Institute. 2004. SAS OnlineDoc 9.1.3. SAS Inst., Cary, NC.