

Rothamsted Repository Download

A - Papers appearing in refereed journals

De Resende, M. D. V., Thompson, R. and Welham, S. J. 2006.
Multivariate spatial statistical analysis of longitudinal data in perennial
crops. *Revista de Matemática e Estatística, São Paulo*,. 24 (1), pp. 147-
169.

The output can be accessed at: <https://repository.rothamsted.ac.uk/item/8q3zq>.

© Universidade Estadual Paulista "Julio de Mesquita Filho".

MULTIVARIATE SPATIAL STATISTICAL ANALYSIS OF LONGITUDINAL DATA IN PERENNIAL CROPS

Marcos Deon Vilela de RESENDE¹
Robin THOMPSON²
Sue WELHAM²

- **ABSTRACT:** *The advantages of using spatial analysis in annual crop experiments are well documented. There is much less evidence for perennial crops. For the sequence of measurements in perennial crops, apparently, there are no published articles in spatial analysis to date. This paper aimed at the comparison of several models, including auto-regressive, ante-dependence and character process models, in modelling sequences of measurements in perennial plants. The use of smoothed models, including splines, to give parsimonious response models, was also investigated. To assess model performance, residual maximum likelihood ratio tests (LRT) and Akaike Criterion Information (AIC), were used. We analysed a total of 22,320 observations from 2 trials of tea plant concerning 5 yield annual measures through different spatial and non-spatial models. The classes of methods used were: (1) univariate spatial models for individual annual measures on each trial; (2) longitudinal non-spatial models for the several measures on each trial; (3) longitudinal and spatial models simultaneously for repeated measures in each trial. The main results obtained were: for individual analysis, the best model out of 19 was the row-column analysis + a first-order spatial auto-regressive (AR1 x AR1) correlated error + independent term error, which provided efficiency (ratio between adjusted heritabilities associated with spatial and non spatial models) between 1.09 and 1.76 over block analysis, i.e., between 9% and 76% of improvement; the same model, however, with a second-order spatial auto-regressive (AR2 x AR2) correlated error, was not superior to (AR1 x AR1); the traits (sequence measurements in consecutive years) gave approximately the same behaviour in terms of results across models; the repeatability and the full unconstrained models were not adequate for the sequences of measures, which exhibited considerable variance heterogeneity between traits and high correlation between measures, revealing a need for new modelling. In general, the best approaches involved the modelling of treatment effects by ante-dependence (SAD) or auto-regressive models with heterogeneous variance (ARH). When the spatial effects are important, a combination of first order spatial auto-regressive approach for modelling errors and a multivariate (including simpler options such as SAD and ARH) approach for modelling treatments effects should be used.*
- **KEYWORDS:** *Repeated Measure; environmental trends; mixed models; REML; BLUP; auto-regressive models; ante-dependence models.*

¹ EMBRAPA FLORESTAS, Caixa Postal 319, CEP: 83411-000, Colombo, PR, Brasil. E-mail: marcos.deon@gmail.com

² Rothamsted Research Institute, AL5 2JQ, Harpenden, UK. E-mail: robin.thompson@bbsrc.ac.uk

1 Introduction

Traditional analysis of agricultural field trials considers measures taken from adjacent plants or plots as non-correlated and the spatial positions of the observations are ignored. Hence, the residual covariance matrix is modelled as a diagonal one, with errors assumed as independent. However, spatial dependence does exist and contributes to the increase of residual variance in such a way that it is relevant to consider it in the analysis of trials by approaching the correlated error structure through adequate models.

According to Fisher (1925) and Steel and Torrie (1980), randomisation of treatment plots across replications can provide neutralisation of the effects of spatial correlation, leading to a valid analysis of variance. However, the randomisation theory emphasises this kind of neutralisation, which is more efficient when spatial models are used. Besides, local control schemes relying on blocking can be inefficient in accounting all environmental gradients and trends and, additionally, incomplete blocks do not provide a complete evaluation of environmental effects. Once blocking is made before the establishment of the trials, the presence of patchy and environmental gradients within blocks is frequently observed (mainly in perennial crops) on the occasion of data collection. This reveals that blocks were not adequately designed a priori. In such situation, only spatial analysis techniques can circumvent estimation problems and provide efficient analysis.

The main procedures aimed at the control and account of spatial correlation among neighbouring observations are time series models (Gleeson and Cullis, 1987; Martin, 1990; Cullis and Gleeson, 1991; Gilmour et al., 1997; Gilmour et al., 1998; Cullis et al. 1998; Smith et al., 2001) using ARIMA models and REML estimates of variance components (Cooper and Thompson, 1977) and geostatistical models (Grondona and Cressie, 1991; Zimmerman and Harville, 1991; Cressie, 1993; Banerjee et al., 2003).

Time series models were first used by Gleeson and Cullis (1987) who considered the errors through an autoregressive integrated moving average process (ARIMA (p, q, d)) in one direction. This model was considered inefficient in some situations and Martin (1990) and Cullis and Gleeson (1991) extended such model to two directions: rows and columns. The extended model is of the form ARIMA (p₁, d₁, q₁) x ARIMA (p₂, d₂, q₂). This class of models is called error in variables and account for a tendency effect (ξ) plus an independent error η .

In annual crops experiments and the absence of knowledge concerning the correct correlation structure, Gilmour et al., (1997) suggested the modelling of ξ as a first order separable autoregressive process (AR1 x AR1). This auto-regressive process in two directions has shown efficiency in a range of situations (Grondona et al., 1996; Gilmour et al., 1997; Cullis et al., 1998; Apiolaza et al., 2000; Gilmour, 2000; Qiao et al., 2000; Smith et al., 2001; Stringer and Cullis, 2002). A process (AR1 x AR1) is flexible and permits to model local and global tendencies as well as extraneous variations, taking into account the three major sources of spatial variation, according to Gilmour et al. (1997). The ARIMA methods of Gleeson and Cullis (1987), Martin (1990) and Cullis and Gleeson (1991) encompass the nearest-neighbour (NN) methods of Papadakis (1937), the Papadakis' iterated NN method (Papadakis, 1970; Bartlett, 1978) and other previous

methods (Papadakis, 1984; Bartlett, 1938; Atkinson, 1969; Wilkinson et al., 1983; Green et al., 1985; Besag and Kempton, 1986; Williams, 1986) of neighbour analysis.

The geo-statistical procedures directly consider spatial heterogeneity through the inclusion of the tendency effects and error correlation in modelling the residual covariance matrix. According to Gleeson (1997), the geostatistical approach of Zimmerman and Harville (1991), called random field linear model, is equivalent to fitting separable ARIMA processes and according to Gilmour et al. (1995) it is equivalent to a first-order separable autoregressive process (AR1 x AR1) without the independent error. However, geostatistical models are often isotropic and Cullis and Gleeson (1991) and Gilmour et al. (1997) have shown that anisotropic models are often preferred for modelling the variance structure in field trials. Furthermore, the assumption of separability results in significant savings in computer time. Based on these facts, the ARIMA time series models are preferred as they encompass all the other main approaches.

The reports attesting the efficiency of spatial analysis refer to annual crops or forest trees with a single measure per plant. Spatial analysis concerning repeated measure data or multivariate data on each plant has not been accounted yet, despite the great number of crops that generate a large number of this sort of data. Perennial plants are of extreme importance in several tropical and subtropical parts of the world. The application of spatial analysis in these categories of plants involves modelling of the several random effects through different structures for each one, providing an adequate account of the repeated measures together with the spatial variation.

In modelling longitudinal or repeated measures data arising from perennial individuals, several approaches can be used such as repeatability, multivariate, random regression, spline, character process and ante-dependence models. The simplest (repeatability) and the more complete and parameterised (multivariate or full unconstrained) models are not likely to be useful in practice. Parsimonious approaches such as random regression or covariance functions (Kirkpatrick et al., 1994), smoothing cubic splines (White et al., 1999; Verbyla et al., 1999), character process and structured ante-dependence models (Nunez-Anton and Zimmermann, 2000) should be tried for the sake of practical efficiency. Character process and structured ante-dependence models have proven efficiency in a number of situations (Jaffrezic et al., 2002).

We analysed a total of 22,320 observations from 2 trials of tea plant concerning 5 yield annual measure, through different spatial and non-spatial models. The classes of methods applied were: (1) univariate spatial models for individual annual measures on each trial; (2) longitudinal non-spatial models for the several measures on each trial; (3) longitudinal and spatial models simultaneously for repeated measures in each trial. These situations are mandatory in any breeding program of a perennial crop and all data should be analysed simultaneously for the sake of maximum efficiency in the improvement program. Adequate modelling and computing are critical for obtaining reliable estimates and satisfactory practical results.

In section 2 of this paper we outline the statistical methodology emphasising general linear mixed modelling and REML estimation, the longitudinal and spatial models for repeated measured traits and model comparisons. In section 3, we present, discuss and compare the results of the several models applied to the data sets. In section 4, we present the final conclusions of the study.

2 Methodology

2.1 General linear mixed model and REML estimation

A general linear mixed model (GLMM) has the form (Henderson, 1984; Searle et al. 1992; Thompson et al., 2003):

$$y = X\beta + Z\tau + \varepsilon, \quad (1)$$

with the following distributions and structures of means and variances:

$$\begin{aligned} \tau &\sim N(0, G) & E(y) &= X\beta \\ \varepsilon &\sim N(0, R) & \text{Var}(y) &= V = ZGZ' + R \end{aligned}$$

where:

y : known vector of observations.

β : parametric vector of fixed effects, with incidence matrix X .

τ : parametric vector of random effects, with incidence matrix Z .

ε : unknown vector of errors.

G : variance-covariance matrix of random effects.

R : variance-covariance matrix of errors.

0 : null vector.

Assuming G and R as known, the simultaneous estimation of fixed effects and the prediction of random effects can be obtained through the mixed model equations given by:

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & Z'R^{-1}Z + G^{-1} \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \tilde{\tau} \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y \end{bmatrix}$$

When G and R are not known, the variance components associated can be estimated efficiently through the REML procedure (Patterson & Thompson, 1971). Except for a constant, the residual likelihood function (in terms of its log) to be maximised is given by:

$$\begin{aligned} L &= -\frac{1}{2} (\log|X'V^{-1}X| + \log|V| + v \log \sigma_\varepsilon^2 + y'Py / \sigma_\varepsilon^2) \\ &= -\frac{1}{2} (\log|C^*| + \log|R| + \log|G| + v \log \sigma_\varepsilon^2 + y'Py / \sigma_\varepsilon^2) \end{aligned}$$

where:

$$V = R + ZGZ; \quad P = V^{-1} - V^{-1}X (X'V^{-1}X)^{-1} X'V^{-1},$$

$v = N - r(x)$: degrees of freedom, where N is the total number of data and $r(x)$ is the rank of matrix X .

C^* : Coefficient matrix of the mixed model equations.

Being general, the model (1) encompasses several models inherent to different situations such as:

Univariate model

$$G = A\sigma_{\tau}^2; \quad R = I\sigma_{\varepsilon}^2$$

where:

σ_{τ}^2 : variance of random effects in τ .

A : known matrix of relationships between the τ elements.

σ_{ε}^2 : residual variance.

Repeated measures model including permanent effects (p)

$$y = X\beta + Z\tau + \varepsilon = X\beta + Z_1\tau^* + Z_2\rho + \varepsilon, \text{ where:}$$

$$\text{Var}(\tau^*) = A\sigma_{\tau^*}^2; \quad \text{Var}(\rho) = I\sigma_{\rho}^2; \quad R = I\sigma_{\varepsilon}^2$$

σ_{ρ}^2 : variance of permanent effects.

Multivariate models

In the bivariate case:

$$Z = \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix}; \quad \tau = \begin{bmatrix} \tau_1 \\ \tau_2 \end{bmatrix}; \quad G = A \otimes G_o; \quad R = I \otimes R_o;$$

$$G_o = \begin{bmatrix} \sigma_{\tau_1}^2 & \sigma_{\tau_{12}} \\ \sigma_{\tau_{21}} & \sigma_{\tau_2}^2 \end{bmatrix}; \quad R_o = \begin{bmatrix} \sigma_{\varepsilon_1}^2 & \sigma_{\varepsilon_{12}} \\ \sigma_{\varepsilon_{21}} & \sigma_{\varepsilon_2}^2 \end{bmatrix} \text{ or } R_o = \begin{bmatrix} \sigma_{\varepsilon_1}^2 & 0 \\ 0 & \sigma_{\varepsilon_2}^2 \end{bmatrix}, \text{ where:}$$

$\sigma_{\tau_{12}}$: random treatment effects of covariance between variables 1 and 2.

$\sigma_{\varepsilon_{12}}$: residual covariance between variables 1 and 2.

Spatial models (time series or geostatistical)

$R = \Sigma$: non-diagonal matrix that considers the correlation between residuals through ARIMA models or covariance based on adjusted semivariance.

2.2 Univariate spatial models for individual annual Measures on each trial

In the context of the agricultural experiments, the general spatial model developed by Martin (1990) and Cullis and Gleeson (1991) has the following form:

$$y = X\beta + Z\tau + \xi + \eta, \text{ where:}$$

Y : known vector of data ordered as columns and rows within columns;

τ : unknown vector of treatment effects;

β : unknown vector representing spatial variation at large scale or global tendency (block effects, polynomial tendency);

ξ : unknown vector representing spatial variation at small scale (within blocks) or local tendency, modelled as a random vector with zero mean and spatially dependent variance;

η : unknown vector of independent and identically distributed errors.

This model is dependent on normality. Through ARIMA models, error is modelled as a function of a tendency effect (ξ) plus a non correlated random residual (η). So, the vector of errors is partitioned into $\varepsilon = \xi + \eta$, where ξ and η refer to the spatially correlated and independent errors, respectively. The traditional models of analysis do not include the ξ component.

Considering an experiment with rectangular shape in a grid of c columns and r rows, the residuals can be arranged in a matrix in a way that they can be considered to be correlated within columns and rows. Writing these residuals in a vector following the field order (by putting each column beneath another), the variance of residuals is given by $Var(\varepsilon) = Var(\xi + \eta) = R = \Sigma = \sigma_{\xi}^2 [\sum_c(\Phi_c) \otimes \sum_r(\Phi_r)] + I\sigma_{\eta}^2$, where σ_{ξ}^2 is the variance due to local tendency and σ_{η}^2 is the variance of the independent residuals.

Matrices $\sum_c(\Phi_c)$ and $\sum_r(\Phi_r)$ refer to first-order autoregressive correlation matrices with auto-correlation parameters Φ_c and Φ_r and order equal to the number of columns and rows, respectively. In this case, ξ is modelled as a separable first order auto-regressive process (AR1 x AR1) with covariance matrix $Var(\xi) = \sigma_{\xi}^2 [\sum_c(\Phi_c) \otimes \sum_r(\Phi_r)]$ (Gilmour et al., 1997).

Using trials established in complete block designs the following models were fitted.

Model 1 : Model 1: Complete block design, block as fixed effects.

Model 2 : Model 2: Complete block design, block as fixed effects + (AR1 x AR1) without inclusion of the independent term error.

Model 3 : Model 3: Complete block design, block as random effects.

Model 4 : Model 4: Complete block design, block as random effects + (AR1 x AR1) without inclusion of the independent term error.

Model 5 : Model 5: Complete block design, block as fixed effects + (AR2 x AR2) without inclusion of the independent term error.

Model 6 : Model 6: Complete block design, block as fixed effects + (AR2 x AR2) without inclusion of the independent term error + inclusion of rows and columns as random effects.

- Model 7 :** Model 7: Complete block design, block as fixed effects + (AR1 x AR1) with inclusion of the independent term error.
- Model 8 :** Model 8: Complete block design, block as fixed effects + (AR2 x AR2) with inclusion of the independent term error.
- Model 9 :** Model 9: Complete block design, block as fixed effects + row and column as random effects (treatment and block are not orthogonal to row and column).
- Model 10 :** Model 10: Complete block design, block as fixed effects + row and column as random effects + (AR1 x AR1) with inclusion of the independent term error (treatment and block are not orthogonal to row and column).
- Model 11 :** Model 11: Row and column as random effects, not considering block and spatial structure.
- Model 12 :** Model 12: Row and column as random effects (not considering block) + (AR1 x AR1) with inclusion of the independent term error.
- Model 13 :** Model 13: Row as fixed and column as random effects, not considering block and spatial structure.
- Model 14 :** Model 14: Row as fixed and column as random effects (not considering block) + (AR1 x AR1) with inclusion of the independent term error.
- Model 15 :** Model 15: Row and column as fixed effects, not considering block and spatial structure.
- Model 16 :** Model 16: Linear trend across rows and columns, not considering block and spatial structure.
- Model 17 :** Model 17: Linear trend across rows and columns, considering block but not the spatial structure.
- Model 18 :** Model 18: Spatial structure (AR1 x AR1) with inclusion of the independent term error (equivalent to model 7 but without adjusting the block effect).
- Model 19 :** Model 19: Row and column as fixed effects, not considering block but considering the spatial structure (AR1 x AR1).

Other models including splines were also evaluated.

2.3 Longitudinal non-spatial models for several measures on each trial

Data analyses of repeated measures were approached by several models, including repeatability, multivariate, character process, ante-dependence, random regression and cubic spline models.

Character process models

Pletcher and Geyer (1999) suggested the use of character process models for the analysis of repeated measures. These models are based on the theory of stochastic process

and were extended by Jaffrezic and Pletcher (2000) aiming at relaxing its more restrictive assumption of stationarity of correlations. The simplest character process model uses the covariance function $C(t,s) = \sigma_t \sigma_s \rho^{(t-s)}$, where $C(t,s)$ is the covariance between repeated measures in times t , and s , σ_t is the standard deviation of the trait in time t , and $\rho^{(t-s)}$ is the correlation between measures in times t and s . For data collected at regularly spaced times, this character process is equivalent to an autoregressive model with heterogeneous variance (ARH).

Ante-dependence models

The basic idea of the ante-dependence models is that one observation in time t can be explained by previous observations. Nunez-Anton and Zimmerman (2000) proposed the structured ante-dependence model in which the number of parameters is smaller than that in the traditional ante-dependence models. These models can deal with highly non-stationary correlation patterns and correspond, in their simple specifications, to a non-stationary generalisation of autoregressive models. They also consider the heterogeneity of variance between measures. The covariance matrix is of the form

$$\Sigma = \begin{bmatrix} \sigma_1^2 & \sigma_1 \sigma_2 \rho_1 & \sigma_1 \sigma_3 \rho_1 \rho_2 & \sigma_1 \sigma_4 \rho_1 \rho_2 \rho_3 \\ & \sigma_2^2 & \sigma_2 \sigma_3 \rho_2 & \sigma_2 \sigma_4 \rho_2 \rho_3 \\ Sim. & & \sigma_3^2 & \sigma_3 \sigma_4 \rho_3 \\ & & & \sigma_4^2 \end{bmatrix}$$

Random regression models

By the random regression model (Meyer and Hill, 1997) the treatment effect is modelled by $\sum_{r=1}^l \beta_{ir} \Phi(a_{ik}^*)^r$, where term β_{ir} denotes the set of l random regressions coefficients for the i^{th} treatment, $\Phi(a_{ik}^*)^r$ is the r^{th} polynomial on standardised age (a_{ik}^*) of measurement k . The estimated G matrix for treatment effects is given by $G = \Phi B \Phi'$, where Φ is a matrix containing the random effects of the polynomials for the ages of measurements and B is the estimated variance-covariance matrix of the polynomial coefficients.

Cubic spline models

A cubic spline is a smooth curve over an interval formed by linked segments of cubic polynomials at certain knot points, such that the whole curve and its first and second differentials are continuous over the interval (Green and Silverman, 1994). Natural cubic splines can be incorporated into the standard mixed model framework (White et al., 1999; Verbyla et al., 1999). By the spline model, the treatment effect is modelled by $b_{i0} + b_{i1} t_{ik} + \sum_{l=2}^{q-1} b_{il} z_l(t_{ik})$, where b_{i0} denotes the intercept for treatment i , b_{i1} denotes the slope for treatment i and b_{il} denotes the random regression coefficient for the i^{th} treatment at knot l . t_{ik} denotes the age of measurement and $z_l(t_{ik})$ represents the spline coefficient for age t_{ik} . The estimated G matrix for treatment effects is given by $G = \Omega Z \Omega'$, where Ω is

a matrix containing the random effects of the spline for the ages of measurements and Z is the estimated variance-covariance matrix of the spline coefficients.

2.4 Longitudinal spatial models for repeated measures on each trial

In this case, the inverse of the correlated error covariance matrix is given by

$$R^{-1} = R_o^{-1} \otimes H^{-1} = \begin{bmatrix} H\sigma_{\xi_1}^2 & H\sigma_{\xi_{12}} \\ H\sigma_{\xi_{12}} & H\sigma_{\xi_2}^2 \end{bmatrix}^{-1}, \text{ where:}$$

$$R_o = \begin{bmatrix} \sigma_{\xi_1}^2 & \sigma_{\xi_{12}} \\ \sigma_{\xi_{12}} & \sigma_{\xi_2}^2 \end{bmatrix} \quad H = [\sum_c (\Phi_c) \otimes \sum_r (\Phi_r)];$$

2.5 Model comparisons

Residual maximum likelihood ratio tests (LRT) were used to compare fitted models provided they had a nested structure and the same fixed effects. Other criterion for model selection was the Akaike Information Criterion (AIC), which penalises likelihood by the number of independent parameters fitted. It can be pointed out that both depend on the basic quantity $-2 \log L$. All models were fitted using software ASREML (Gilmour and Thompson, 1998; Gilmour et al., 2002), which uses the REML procedure through the average information algorithm and sparse matrix techniques (Gilmour et al., 1995; Johnson and Thompson, 1995; Thompson et al., 2003). Software GENSTAT (Thompson and Welham, 2003) was also used. To date, there is no free software suitable for implementing these very complex models including spatial and temporal dependences simultaneously.

2.6 Application

The data set concerning tea plants came from two trials established in complete block designs with six plants per plot and in a spacing of 3 x 2 meters. The trait leaf weight was evaluated at individual level in several consecutive years. Trial 1 was established with 141 treatments (open pollinated progenies) and 10 replications, summing 8,460 plants and 16,920 observations (two consecutive years). Trial 2 provided 5,400 observations (60 treatments x 5 replications x 6 plants per plot x 3 annual measures). The basic model for all trials included block, treatments, plot and residual effects.

The trait leaf weight is a continuous variable with normal distribution. This was confirmed by means of statistical analyses that showed symmetry in the data distribution as well as normality through the Shapiro-Wilk test.

3 Results and discussion

3.1 Univariate spatial models for individual annual measures on each trial

Results concerning trial 1 are presented in Tables 1a and 1b.

Table 1a - Summary of results concerning models 1 to 19 for trait leaf weight in the first year of harvest in trial 1. The estimates are: genetic variance among treatments (progenies) ($\hat{\sigma}_\tau^2$), non-correlated residual variance ($\hat{\sigma}_\eta^2$), narrow sense heritability (\hat{h}^2), fitted narrow sense heritability ($\hat{h}_{adj}^2 = (4\hat{\sigma}_\tau^2) / (\hat{\sigma}_\tau^2 + \hat{\sigma}_\eta^2)$) proportional only to the unaccounted error (η), shrinkage factor ($\lambda_1 = (\hat{\sigma}_\eta^2 - 3\hat{\sigma}_\tau^2) / (4\hat{\sigma}_\tau^2)$) of genetic effects in the mixed model equations and efficiency (Effic.) of models over model1, in terms of \hat{h}_{adj}^2

Block as Fixed Effect							
Model (Spatial -S or Not-N)	Deviance	\hat{h}^2	\hat{h}_{adj}^2	λ_1	$\hat{\sigma}_\tau^2$	$\hat{\sigma}_\eta^2$	Effic.
1. N	-3105.78	0.1413	0.1905	4.250	0.0110	0.2214	1.00
2. S	-3862.28	0.1652			0.0126		
5. S	-4039.31	0.1667			0.0128		
6. S	-4045.31	0.1690			0.0128		
7. S	-4254.48	0.1737	0.3296	2.034	0.0134	0.1492	1.730
8. S	-4189.15	0.1788	0.3145	2.180	0.0132	0.1547	1.651
9. N	-3201.88	0.1416	0.1955	4.115	0.0111	0.2160	1.03
10. S	-4257.66	0.1728	0.3278	2.051	0.0133	0.1490	1.721
Row as Fixed Effect							
13. N	-3018.58	0.1439	0.1955	4.115	0.0111	0.2160	1.03
14. S	-4069.91	0.1737	0.3278	2.051	0.0133	0.1490	1.721
Linear trend across rows and columns							
16. N	-3085.37	0.1371	0.1864	4.366	0.0108	0.2210	0.98
17. N	-3083.82	0.1422	0.1913	4.227	0.0111	0.2210	1.004
Row and Column as Fixed Effect							
15. N	-2523.58	0.1600	0.2022	3.946	0.0115	0.2160	1.06
19. S	-3498.55	0.1792	0.3352	1.983	0.0136	0.1487	1.760
Constant as Fixed Effect							
3. N	-3137.40	0.1378	0.1905	4.250	0.0110	0.2214	1.00
4. S	-3894.34	0.1613			0.0126		
11. N	-3213.00	0.1391	0.1955	4.115	0.0111	0.2160	1.03
12. S	-4283.01	0.1725	0.3276	2.052	0.0134	0.1502	1.720
18. S	-4278.02	0.1717	0.3264	2.063	0.0134	0.1508	1.713

The deviance criterion is not adequate for comparing models with different fixed effects. So, efficiency in terms of the fitted heritability (proportional only to the unaccounted error) can be used for inference about the best models. The fitted narrow sense heritability estimates presented in the previous table refer to individual plant models rather than parent models.

The two traits (sequence measurements in consecutive years) presented approximately the same behaviour in terms of results across models. Among the non-spatial models, the row-column analyses (models 11, 13 and 15) performed better than the randomised block analyses (models 1 and 3). This can be explained by the local control in two directions provided by the row-column analysis and by the small block provided by rows since each original block was composed of six rows. Due to this last reason there was no need to fit blocks additionally to rows and columns (models 9, 10 and 17).

The spatial models (2, 4, 5, 6, 7, 8, 10, 12, 14, 18 and 19) were always much better than the non-spatial ones (1, 3, 9, 11, 13, 15, 16 and 17) as judged by deviances of the models as well as by selection efficiencies in terms of the fitted heritabilities or shrinkage factors for treatment effects in the mixed model equations (Tables 1a and 1b). The spatial

models with inclusion of η (models 7, 8, 10, 12, 14, 18 and 19) were always better than those without η (models 2, 4, 5 and 6) as judged by deviances of the models as well as selection efficiencies in terms of the fitted heritabilities or shrinkage factors for treatment effects in the mixed model equations (Tables 1a and 1b).

Table 1b - Summary of results concerning models 1 to 19 for trait leaf weight in the second year of harvest in trial 1. The estimates are: genetic variance among treatments (progenies) ($\hat{\sigma}_\tau^2$), non-correlated residual variance ($\hat{\sigma}_\eta^2$), narrow sense heritability (\hat{h}^2), fitted narrow sense heritability ($\hat{h}_{adj}^2 = (4\hat{\sigma}_\tau^2)/(\hat{\sigma}_\tau^2 + \hat{\sigma}_\eta^2)$) proportional only to unaccounted error (η), shrinkage factor ($\lambda_1 = (\hat{\sigma}_\tau^2 - 3\hat{\sigma}_\eta^2)/(4\hat{\sigma}_\tau^2)$) of genetic effects in the mixed model equations and efficiency (Effic.) of models over model1, in terms of \hat{h}_{adj}^2

Block as Fixed Effect							
Model	Deviance	\hat{h}^2	\hat{h}_{adj}^2	λ_1	$\hat{\sigma}_\tau^2$	$\hat{\sigma}_\eta^2$	Effic.
1. N	11853.72	0.1688	0.2346	3.262	0.083	1.339	1.00
2. S	11424.52	0.1900	-	-	0.094	-	-
5. S	11247.98	0.1887	-	-	0.093	-	-
6. S	11208.30	0.1905	-	-	0.092	-	-
7. S	11089.97	0.1927	0.3465	1.886	0.0965	1.0175	1.477
8. S	11084.85	0.1914	0.3630	1.755	0.0956	0.9669	1.547
9. N	1168990	0.1691	0.2438	3.101	0.084	1.294	1.04
10. S	11070.69	0.1933	0.3489	1.866	0.0965	1.0099	1.487
Row as Fixed Effect							
13. N	11767.86	0.1730	0.2438	3.101	0.084	1.294	1.04
14. S	11150.56	0.1961	0.3491	1.865	0.0965	1.0093	1.488
Linear trend across rows and columns							
16. N	11926.37	0.1620	0.2282	3.383	0.081	1.339	0.97
17. N	11872.48	0.1702	0.2361	3.235	0.084	1.339	1.006
Row and Column as Fixed Effect							
15. N	12027.38	0.1781	0.2493	3.012	0.086	1.294	1.06
19. S	11456.87	0.1974	0.3485	1.870	0.0964	1.0101	1.486
Constant as Fixed Effect							
3. N	11836.52	0.1654	0.2346	3.262	0.083	1.339	1.00
4. S	11407.16	0.1862	-	-	0.094	-	-
11. N	11683.96	0.1668	0.2438	3.101	0.084	1.294	1.04
12. S	11056.93	0.1920	0.3477	1.876	0.0966	1.0148	1.482
18. S	11080.62	0.1907	0.3438	1.909	0.0965	1.0263	1.465

Comparing models 7, 12 and 18, which led to almost the same efficiency, can see that keeping the design features in the analysis was not necessary. The rate of recovering of design features by spatial analysis is enhanced when the independent error is fitted. A model without plot and design features was fitted for the two traits and provided almost the same efficiency as model 12, showing that sometimes simple spatial models can be used.

For two dimension spatial models without η (models 2 and 5), model AR2 was better than AR1 (change in deviance of 176.54). However, that superiority was not kept (change in deviance of 5.12) when models (7 and 8) with η were fitted. So, there is no need for AR2 in models with inclusion of η .

Little difference (in terms of fitted heritability), if any, was noted in fitting local control as fixed or random effects in the non-spatial models (model 1 against 3; 11 against 13 or 15) and spatial models (12 against 14 and 19), with a slight superiority for fitting row and column as fixed effects.

Overall, the best methods for the two traits were 12 and 14, both corresponding to a row-column analysis + a spatial (AR1 x AR1) + independent term error. For these best models, efficiency over the traditional randomised complete block analysis ranged from 1.48 to 1.76, i.e., 48% to 76% of superiority. Improved designs can be used to have high efficiency when assuming a spatial model such as model 12 (establishing the experiment according to model 12). In other words, appropriate systematic designs are needed when spatial patterns are present in the field. Spatial analysis has been shown to improve the precision and accuracy of treatment estimates, even with designs not optimised spatially. It is expected that designs with good general spatial properties will further increase the efficiency of treatments estimates. This would permit the fitting of only one spatial model to all trials as advocated by Kempton et al. (1994).

The autocorrelation coefficients for models without independent errors were approximately 0.21 and 0.29 for AR Column and 0.13 and 0.14 for AR Row, for the two traits, respectively. For models with independent errors, the autocorrelation coefficients were approximately 0.79 and 0.75 for AR Column and 0.50 and 0.52 for AR Row, for the two traits, respectively. These high autocorrelation coefficients obtained show that the AR process is modelling fertility gradient rather than competition. This is coherent with the spacing used (3 by 2 meters) and with crop management in which all the leaves are harvested each year. These features tend to prevent above ground competition between plants.

Models with splines were also tried, some extending the previous model 12 and others using only splines to account for spatial variation. Results are presented in Table 2.

It can be seen that the extended model 12 did not improve the fit through the inclusion of splines. The deviances of the extended models were higher as the spline variance component is constrained to be positive, but the efficiencies in terms of the fitted heritability were practically the same (Table 2).

The approach using splines in place of AR(1) x AR(1) process for modelling spatial variation was suggested by Kempton (1999) and used by Durban et al. (2001). In our data set, such approach showed to be very inefficient, being comparable only with the random row and column analysis (model 11).

Results concerning individual analysis of trial 2 of tea plants are presented in Table 3.

It can be seen that the best models for all three traits were 7 (complete block design + (AR1 x AR1) + η) and 12 (row-column design + (AR1 x AR1) + η) in terms of efficiency over base model 1 (block analysis) and deviance values. The efficiencies (between 1.09 and 1.16) were in general much lower than the previous ones (of the order of 1.48 to 1.76) reported for trial 1. This is because there is much less environmental variability in this trial as revealed by the low significance of block effects for two of the three traits. Due to the same reason, the efficiencies of row-column over block designs were small or did not exist in this case. For the trait leaf weight 1, block and row effects should not be fitted as fixed because they were non-significant. So, the results concerning models 1, 11, 13 and 15 are not comparable for trait 1.

Table 2 - Results concerning some models for trait leaf weight in the first two years of harvest in trial 1. The estimates are: genetic variance among treatments (progenies) ($\hat{\sigma}_\tau^2$), non-correlated residual variance ($\hat{\sigma}_\eta^2$), fitted narrow sense heritability ($\hat{h}_{adj}^2 = (4\hat{\sigma}_g^2)/(\hat{\sigma}_g^2 + \hat{\sigma}_\eta^2)$) proportional only to the unaccounted error (η) and efficiency (Effic.) of models over model 1, in terms of \hat{h}_{adj}^2 . Spl(rc) means cubic splines applied on row and columns

Model	Deviance	\hat{h}_{adj}^2	$\hat{\sigma}_\tau^2$	$\hat{\sigma}_\eta^2$	Eff.
Leaf weight 1 – Trial 1					
1	-3105.78	0.1905	0.0110	0.2214	1.00
11	-2523.58	0.1955	0.0111	0.2160	1.03
Spl(rc)	-3202.72	0.1961	0.0112	0.2173	1.03
12	-4283.01	0.3276	0.0134	0.1502	1.72
12 + Spl(rc)	-4270.12	0.3302	0.0134	0.1489	1.73
Leaf weight 2 – Trial 1					
1	11853.72	0.2346	0.0830	1.3390	1.00
11	11683.96	0.2438	0.0840	1.2940	1.04
Spl(rc)	11731.32	0.2464	0.0852	1.2979	1.05
12	11056.93	0.3477	0.0966	1.0148	1.48
12 + Spl(rc)	11070.08	0.3492	0.0965	1.0088	1.49

Table 3 - Results concerning some models for trait leaf weight in the first three years of harvest in trial 2. The estimates are: genetic variance among treatments (progenies) ($\hat{\sigma}_\tau^2$), non-correlated residual variance ($\hat{\sigma}_\eta^2$) and fitted narrow sense heritability ($\hat{h}_{adj}^2 = (4\hat{\sigma}_g^2)/(\hat{\sigma}_g^2 + \hat{\sigma}_\eta^2)$) proportional only to unaccounted error (η) and efficiency (Effic.) of models over model 1, in terms of \hat{h}_{adj}^2

Model	Deviance	\hat{h}_{adj}^2	$\hat{\sigma}_\tau^2$	$\hat{\sigma}_\eta^2$	Eff	Local Control (signif.)
Leaf weight 1						
1	-1964.99	0.4778	0.0137±0.004	0.1010±0.004	1.00	Not sig.
7	-2038.17	0.5248	0.0140±0.004	0.0927±0.004	1.10	
11	-1995.02	0.4633	0.0131±0.004	0.1000±0.004	0.97	
12	-2059.70	0.5198	0.0138±0.004	0.0924±0.004	1.09	Not sig.
13	-1855.95	0.4602	0.0130±0.004	0.1000±0.004	0.96	Row (R)*
15	-1661.66	0.3899	0.0108±0.004	0.1000±0.004	0.82	C**;R*
Leaf weight 2						
1	830.15	0.7076	0.1038±0.03	0.483±0.02	1.00	* 6%
7	703.19	0.7931	0.1061±0.02	0.429±0.02	1.12	
11	795.78	0.7128	0.1017±0.03	0.469±0.02	1.01	
12	686.88	0.7934	0.1059±0.02	0.428±0.02	1.12	Not sig.
13	871.88	0.7134	0.1018±0.03	0.469±0.02	1.01	R**
15	984.87	0.6416	0.0896±0.03	0.469±0.02	0.91	C**;R*
Leaf weight 3						
1	3415.14	0.5887	0.345±0.10	1.999±0.07	1.00	**
7	3215.12	0.6852	0.351±0.08	1.698±0.07	1.16	
11	3379.20	0.6041	0.335±0.10	1.883±0.07	1.03	
12	3212.90	0.6849	0.350±0.08	1.694±0.07	1.16	Not sig.
13	3378.11	0.6069	0.337±0.10	1.884±0.07	1.03	R**
15	3401.23	0.5176	0.280±0.10	1.884±0.07	0.88	R**;C ns
18	3213.71	0.6858	0.352±0.08	1.701±0.07	1.16	

For this trial, column effects should not be fitted as fixed (model 15) as it is so small (size 30) and genetic information would be lost. With spatial analysis and inclusion of the independent error in the model, there was no need to include the design features in the model, even when the block effects were significant (trait 3). It can be seen from the deviance values that the model 7 and 18 were equivalent (Table 3). The auto-correlation coefficients were of the order of 0.80 and 0.90 between rows and columns, respectively, for the three traits (0.79 and 0.87; 0.79 and 0.87; 0.81 and 0.90, for traits 1, 2 and 3, respectively, according to the model 12).

3.2 Longitudinal non-spatial models for several measures on each trial

Results concerning repeatability and full unconstrained (bivariate in this case) models for the repeated measures in trial 1 are presented in Table 4. Block, measure and block x measure interaction effects were fitted as fixed.

Table 4 - Estimates of the variance parameters: genetic among treatments (progenies) ($\hat{\sigma}_\tau^2$), among plots ($\hat{\sigma}_\kappa^2$), permanent ($\hat{\sigma}_\rho^2$) and residual ($\hat{\sigma}_\eta^2$), using the repeatability and full unconstrained (bivariate) models

Original data in trial 1.				
Parameters estimates	Repeatability Model		Bivariate Model*	
	Both weights	Leaf weight 1	Leaf weight 2	Between weights
$\hat{\sigma}_\tau^2$	0.1913	0.0462	0.4397	0.1393
$\hat{\sigma}_\kappa^2$	0.0739	0.0365	0.13854	0.0711
$\hat{\sigma}_\rho^2$	0.3038	-	-	-
$\hat{\sigma}_\eta^2$	0.5413	0.2214	1.3390	0.3687
Deviance	14173.70		3357.02	
Standardised data in trial 1.				
Parameters estimates	Repeatability Model		Bivariate Model*	
	Both weights	Leaf weight 1	Leaf weight 2	Between weights
$\hat{\sigma}_\tau^2$	0.1799	0.1488	0.2184	0.1763
$\hat{\sigma}_\kappa^2$	0.0848	0.1176	0.0764	0.0982
$\hat{\sigma}_\rho^2$	0.4541	-	-	-
$\hat{\sigma}_\eta^2$	0.2465	0.7124	0.6649	0.4661
Deviance	7637.22		7316.52	

The associated repeatability coefficient was 0.51, which can be classified as intermediate. The genetic correlation coefficient between the two measures in the full unconstrained (bivariate) analysis was 0.98. These results show that the trait is probably not changing so much genetically from one another measure or age. However, it can be seen that there is heterogeneity of variance between the measures. The deviance values

show that the bivariate model is much better than the repeatability model. This justifies the preference for the bivariate model.

With standardised data (divided by the phenotypic standard deviation from individual analysis for each measure), the associated repeatability coefficient was 0.75, which is higher than the previous one. Standardisation led to an increased permanent variance estimate, while the others (except by the independent error) variance components were kept approximately constant (in comparison to the data in original scale) by the repeatability model. The genetic correlation coefficient between the two measures in the bivariate analysis was 0.98, which was the same as in the previous analysis. However, it can be seen that the heterogeneity of variance was reduced after standardisation. The deviance values show that the repeatability and bivariate models became closer after standardisation.

Nevertheless, the AIC values were 7334.52 and 7645.22 for the bivariate and repeatability models. This shows that the bivariate model, although less parsimonious, is still better than the repeatability model. So, in practice, the bivariate model should be used for selection. In case the repeatability model is chosen, the data should at least be standardised. The use of the bivariate model for selection implies giving weight to genetic values predicted for the two measures. These weights should be 0.5, if the two ages have equal importance. If the last measure provides a better representation of a mature trait, higher weight should be given to this measure. Nonetheless, the high genetic correlation may suggest that the weights should be 0.5 for each measure.

Estimates for the full (multivariate) model with original data in trial 2 are presented in Table 5. Block, measure and block x measure interaction effects were fitted as fixed.

Table 5 - Estimates of the variance and covariance parameters for the full (multivariate) model with original data in trial 2 concerning three repeated measures. Number of parameters equal to 18

Treatment (genetic)			Plot			Residual		
Covar.	Variance	Correl.	Covar.	Variance	Correl.	Covar.	Variance	Correl.
0.0134	0.9239	0.9984	0.0248	0.8638	0.7095	0.1011	0.6766	0.6128
0.0342	0.1020	0.9211	0.0422	0.0964	0.9123	0.1495	0.4827	0.7686
0.0673	0.1711	0.3380	0.0817	0.2072	0.5352	0.2755	0.7551	1.9990
Deviance = -787.172								

The deviance value (Table 5) reveals that the full multivariate model is far more suitable for the original data than the repeatability model (deviance 5070.64, results not shown). Such model gave high values for the genetic correlations between pairs of measures. The correlations were all within the parameter space but the model had to be constrained to achieve this. Without constraining the G matrix to be positive definite, correlations higher than 1 and negative variance components were obtained. In the constrained model, the G matrix is bent and this process involves shrinking the variances towards their mean. The unconstrained analysis is less biased because bias is introduced when constraining the solution to the parameter space. Convergence was more difficult as the number of measures increased. So, more suitable models needed to be searched.

Results concerning the character process model, called first-order autoregressive with heterogeneous variance (ARH) for the treatments effects, are presented in Table 6.

Table 6 - Estimates of the variance and covariance parameters for the character process model, called first order autoregressive with heterogeneous variance (ARH) applied to original data in trial 2, concerning three repeated measures. Number of parameters equal to 16

Treatment (genetic)			Plot			Residual		
Covar.	Variance	Correl.	Covar.	Variance	Correl.	Covar.	Variance	Correl.
0.0129	0.9761	0.9528	0.0254	0.8667	0.7532	0.1011	0.6766	0.6128
0.0357	0.1033	0.9761	0.0430	0.0968	0.9109	0.1495	0.4827	0.7686
0.0619	0.1792	0.3261	0.0891	0.2104	0.5510	0.2755	0.7551	1.9990
Deviance = -782.94								

The ARH and multivariate models presented almost the same deviance and the AIC values were -750.94 and -751.17, respectively, which are basically the same -751. So, the two models are equivalent by the parsimony criterion. However, ARH presented easy convergence without constraining the G matrix to be positive definite, fitted a small (two less than the full multivariate model) number of parameters and gave correlations within the parameter space. Besides, it gave a more realistic correlation between the most distant measures 1 and 3. The ARH model is then much preferred. Such model assumes stationarity and same correlation in all intervals of same lag.

An other model evaluated was the structured ante-dependence model (SAD), which also has parsimony and does not assume stationarity. Results are presented in Table 7.

Table 7 - Estimates of the variance and covariance parameters for the structured ante-dependence model (SAD) with original data in trial 2, concerning three repeated measures. Number of parameters equal to 17

Treatment (genetic)			Plot			Residual		
Covar.	Variance	Correl.	Covar.	Variance	Correl.	Covar.	Variance	Correl.
0.0128	0.9840	0.9580	0.0254	0.8667	0.7532	0.1011	0.6766	0.6128
0.0358	0.1032	0.9730	0.0430	0.0968	0.9109	0.1495	0.4827	0.7686
0.0618	0.1784	0.3250	0.0891	0.2104	0.5510	0.2755	0.7551	1.9990
Deviance = -783.04								

The SAD and ARH models presented basically the same deviance (-783) and are then equivalent by this criterion. Nonetheless, the SAD model fitted one parameter more than the ARH model and is not preferred, in terms of parsimony by the AIC rule. The results for plot and residual effects were exactly the same by the two models. The genetic components were slightly different but are both coherent in terms of the magnitude of the correlation coefficients, i.e., smaller for lag 1-3. This was not seen in the full multivariate model. Both models could be used efficiently in practice. The SAD model allows for different correlation for lags of same size.

These two classes of models were also used for modelling the other random terms of the model. Results concerning correlations for treatment and plot terms modelled by ARH and SAD are presented in Table 8.

Table 8 - Estimates of the correlation parameters for the structured ante-dependence model (SAD) and character process (ARH) for modelling both the treatment and plot effects. An original data set in trial 2 (three repeated measures) was used. Number of parameters equal to 16 and 14 for SAD and ARH, respectively.

Treatment (genetic)			Plot			Residual		
ARHSAD			ARHSAD			ARHSAD		
-	0.990	0.968	-	0.851	0.769	-	0.6766	0.6128
0.982	-	0.977	0.882	-	0.903	0.6766	-	0.7686
0.964	0.982	-	0.778	0.882	-	0.6128	0.7686	-
Deviance ARHSAD = -780.76/-782.20								

The results show that the plot effect can be perfectly modelled by the ARH or SAD process. The deviance values were close to the previous one where the plot effect was modelled in a full multivariate fashion. The AIC values here were -752.76 and -750.20 for ARH and SAD, respectively, which are close to values -751 and -749 for ARH and SAD, respectively, obtained with the two models but with multivariate plot effect. Comparing these four AIC values, the choice is for the ARH model for both treatments and plot effects (AIC -752.76).

The modelling of the residual term by the ARH was also evaluated. The resulting deviance for modelling the three effects simultaneously as an ARH process gave a deviance of only -677.46 . Also the residual correlations obtained were very different than the previous ones. Then, the residual should be modelled in a full multivariate way.

Other approaches were also evaluated. The banded correlation or Toeplitz model converged with a deviance of -794.28 . Nevertheless, it gave a genetic correlation higher than one, and only the correlation was supposed to be the small one. This model assumes equal correlation for lags of same size as does the ARH model, but the elements of the several diagonals are different and not a function of the correlation for lag 1.

Random regression models were also tried and results are presented in Table 9 for the full and reduced models.

Table 9 - Estimates of the variance and covariance parameters for the random regression model with original data in trial 2 concerning three repeated measures

Full model (quadratic fit) with number of parameters equal to 18.								
Treatment (genetic)			Plot			Residual		
Covar.	Variance	Correl.	Covar.	Variance	Correl.	Covar.	Variance	Correl.
0.0134	0.9239	0.9984	0.0248	0.8638	0.7095	0.1011	0.6766	0.6128
0.0342	0.1020	0.9211	0.0422	0.0964	0.9123	0.1495	0.4827	0.7686
0.0673	0.1711	0.3380	0.0817	0.2072	0.5352	0.2755	0.7551	1.9990
Deviance = -787.172								
Reduced model (linear fit) with number of parameters equal to 15.								
Treatment (genetic)			Plot			Residual		
Covar.	Variance	Correl.	Covar.	Variance	Correl.	Covar.	Variance	Correl.
0.0098	1.0552	1.0765	0.0248	0.8638	0.7095	0.1011	0.6766	0.6128
0.0331	0.1004	1.0040	0.0422	0.0964	0.9123	0.1495	0.4827	0.7686
0.0563	0.1677	0.2791	0.0817	0.2072	0.5352	0.2755	0.7551	1.9990
Deviance = -777.08								

Results were identical to those (which were not suitable) from the full multivariate analysis as expected for the full fitting of the random regression model, i.e., for fitting a quadratic polynomial. In a search for parsimony a reduced fit was tried. The deviance (-777) of the model is higher than that (-783) obtained from the ARH and SAD models for treatment effects (Tables 8 and 9). The AIC value is -747, which is higher than that obtained for the ARH (-751) and SAD (-749) models. So, the reduced random regression model is not a choice. Also, this model showed a poor reconstruction of the G matrix for treatment effects leading all correlations to be higher than 1 (Table 9). These results are in accordance with Apiolaza et al. (2000), who found that random regression models were often inappropriate.

The fit of smoothing cubic splines was also tried. The deviance obtained was only -748.33, which was the worst between the parsimonious models tried. This result was expected as function of the small number of ages available for fitting. In conclusion, the best approaches for trial 2 were the ARH and SAD models for treatment and plot effects. These models should be extended and used in conjunction with the spatial models for the residuals.

3.3 Longitudinal spatial models for repeated measures on each trial

Results concerning the multivariate spatial model for trial 1 are presented in Table 10.

Table 10 - Estimates of the variance parameters: genetic variance among treatments (progenies) ($\hat{\sigma}_\tau^2$), among plots ($\hat{\sigma}_\kappa^2$), residual ($\hat{\sigma}_\eta^2$) and respective covariance and correlation by the full multivariate spatial model for leaf weight in trial 1

Parameters estimates	Covariance		Variance		Correlation Between weights
	Between weights		Leaf weight 1	Leaf weight 2	
$\hat{\sigma}_\tau^2$ (Treatment)	0.1390		0.0465	0.4386	0.9736
$\hat{\sigma}_\kappa^2$ (Plot)	0.0251		0.0068	0.0975	0.9771
$\hat{\sigma}_\eta^2$ (Independent Error)	0.3378		0.1952	1.3030	0.6697

Deviance = 2764.12

It can be seen that the full multivariate spatial model is the best option for the analysis and selection concerning this experiment. The deviance of this model (2764.12) is much lower than that of the full multivariate (bivariate) non-spatial model (3357.02). The models fitted 11 and 9 random effects and the AIC values were 2786.12 and 3375.02 for the full multivariate spatial and non-spatial models, respectively. So, the choice is for the full multivariate spatial model. The genetic variance components stayed almost the same as in the multivariate non-spatial model. However, the plot variances were greatly reduced. The residual variances were also reduced by spatial analysis as expected. The genetic correlation showed about the same magnitude as in the non-spatial analysis. In conclusion, for trial 1, the selection should be practised according to the bivariate spatial analysis.

For trial 2, the superior approaches for analysing the repeated measures were extended by incorporating spatially correlated residuals. Three models were tried: ARH for treatments, ARH for treatments and plots and SAD for treatments and plots. The deviance values obtained were not lower than that obtained with the best non-spatial models and, the autocorrelation parameters approached 1, revealing that there is no need for spatial analysis for this multivariate data. This was expected as the efficiency of spatial analysis for the univariate case in this experiment was low as a function of the low environmental variability in the trial. In the multivariate case for the repeated measures, the amount of information about one individual increase and the model is automatically improved making it more difficult to add important information from the spatial analysis. Besides, the autocorrelation estimates approached 1, revealing that the estimated correlated error was of small magnitude.

4 Final conclusions

For longitudinal data or repeated measured traits (sequence measurements in consecutive years) in perennial crops, which exhibit considerable variance heterogeneity between traits and high correlation between measures, the repeatability and the full unconstrained models are not adequate, revealing a need for new modelling. In general, the best approaches involved the modelling of treatment effects by ante-dependence (SAD) or auto-regressive models with heterogeneous variance (ARH). When spatial effects are important, a combination of the first-order spatial auto-regressive approach for modelling errors and a multivariate (including simpler options such as SAD and ARH) approach for modelling treatments effects should be used.

RESENDE, M. D. V. de; THOMPSON, R.; WELHAM, S. Análise estatística espacial multivariada de dados longitudinais em culturas perenes. *Rev. Mat. Est.*, São Paulo, v. 24, n.1, p.147-169, 2006.

- RESUMO: As vantagens do uso da análise espacial em experimentos com culturas anuais estão bem documentadas. Para culturas perenes existem muito menos evidências. Aparentemente não existem artigos publicados tratando da análise espacial de medidas repetidas em culturas perenes. Este trabalho objetivou a comparação de vários modelos nesse contexto, incluindo as classes de modelos autoregressivos, de ante-dependência e de processo caráter, na modelagem de medidas repetidas em plantas perenes. O uso de modelos alisados parcimoniosos, incluindo splines, foram também investigados. Para a seleção de modelos foram utilizados o teste da razão de verossimilhança (LRT) e o critério de informação de Akaike (AIC). Foram analisadas, por meio de vários modelos espaciais e não espaciais, 22.320 observações associadas a cinco medições anuais repetidas em dois experimentos de erva-mate. As classes de modelos usados foram: (1) modelos espaciais univariados para medições anuais individuais em cada ensaio; (2) modelos não espaciais para dados longitudinais aplicados sobre todas as medidas repetidas em cada ensaio; (3) modelos espaciais para dados longitudinais aplicados sobre todas as medidas repetidas em cada ensaio, ou seja, simultânea análise da dependência espacial e temporal. Os principais resultados obtidos foram: para as análises individuais o melhor modelo, dentre 19 avaliados, contemplou os efeitos de linha e coluna da grade experimental mais um erro correlacionado espacial autoregressivo de primeira ordem (AR1 x AR1) (propiciando superioridade entre 9% e 76% sobre a tradicional análise em blocos, em termos da razão entre as herdabilidades ajustadas associadas aos modelos espaciais e não espaciais); modelos com erro espacial autoregressivo de segunda ordem (AR2 x AR2) não foram superiores aos modelos com

erro (AR1 x AR1); as diferentes medidas repetidas apresentaram aproximadamente o mesmo comportamento em termos de resultados através dos diferentes modelos; os modelos de repetibilidade e multivariado não foram totalmente adequados para a análise de medidas repetidas, as quais exibiram considerável heterogeneidade de variâncias, revelando a necessidade da adoção de novas modelagens. Em geral, as melhores abordagens envolveram a modelagem dos efeitos de tratamentos por modelos autoregressivos (ARH) e de ante-dependência (SAD) com variâncias heterogêneas. Quando os efeitos espaciais são importantes, a combinação de modelos autoregressivos para os resíduos e modelos SAD ou ARH para os efeitos de tratamentos, deve ser usada na análise de medidas repetidas em plantas perenes.

- PALAVRAS-CHAVE: Medidas repetidas; tendência ambiental; modelos mistos; reml; blup; modelos autoregressivos; modelos ante-dependência.

5 References

- APIOLAZA, L. A.; GILMOUR, A. R.; GARRICK, D. J. Variance modelling of longitudinal height data from a *Pinus radiata* progeny test. *Can. J. For. Res.*, Ottawa, v. 30, p. 645-654, 2000.
- ATKINSON, A.C. The use of residuals as a concomitant variable. *Biometrika*, London, v.56, p.33-41, 1969.
- BANERJEE, S.; CARLIN, B.; GELFAND, A. Hierarchical modelling and analysis for spatial data. London: Chapman & Hall, 2003. 488p.
- BARTLETT, M.S. The approximate recovery of information from replicated field experiments with large blocks. *J. Agric. Sci.*, Cambridge, v.28, p.418-427, 1938.
- BARTLETT, M.S. Nearest neighbour models in the analysis of field experiments. *J. R. Stat. Soc. Ser. B.*, London, v. 40, p.147-174, 1978.
- BESAG, J.; KEMPTON, R.A. Statistical analysis of field experiments using neighbouring plots. *Biometrics*, Washington, v. 42, p. 231 – 251, 1986.
- COOPER, D.M.; THOMPSON, R. A note on the estimation of the parameters of the autoregressive-moving average process. *Biometrika*, London, v. 64, p. 625-628, 1977.
- CRESSIE, N.A.C. *Statistics for spatial data analysis*. New York: John Wiley & Sons, 1993. 900p.
- CULLIS, B. R. et al. Spatial analysis of multi-environment early generation variety trials. *Biometrics*, Washington, v. 54, p.1-18, 1998.
- CULLIS, B.R.; GLEESON, A.C. Spatial analysis of field experiments-an extension at two dimensions. *Biometrics*, Washington, v.47, p.1449-1460, 1991.
- DURBAN, M.; CURRIE, I.; KEMPTON, R. Adjusting for fertility and competition in variety trials. *J. Agric. Sci.*, Cambridge, v.136, p.129-149, 2001.
- FISHER, R. A. *Statistical methods for research workers*. 1. ed. London: Oliver and Boyd, 1925. 314 p.
- GILMOUR, A.R.; CULLIS, B.R.; VERBYLA, A.P. Accounting for natural and extraneous variation in the analysis of field experiments. *J. Agric., Biol. Environ. Stat.*, Alexandria, v.2, p.269-293, 1997.

- GILMOUR, A.R. et al. (Co)variance structures for linear models in the analysis of plant improvement data. In: COMPSTAT98, 1998. *Proceedings ... Heidelberg: Physica - Verlag*, 1998. p.53-64.
- GILMOUR, A.R. Post blocking gone too far! Recovery of information and spatial analysis in field experiments. *Biometrics*, Washington, v. 56, p.944 – 946, 2000.
- GILMOUR, A. R.; THOMPSON, R. Modelling variance parameters in ASREML for repeated measures. In: WORLD CONGRESS ON GENETIC APPLIED TO LIVESTOCK PRODUCTION, 6., 1998, Armidale. *Proceedings...* Armidale: AGBU / University of New England, 1998. v. 27, p. 453-454.
- GILMOUR, A. R.; THOMPSON, R.; CULLIS, B. R. Average information REML: an efficient algorithm for parameter estimation in linear mixed models. *Biometrics*, Washington, v. 51, p.1440-1450, 1995.
- GILMOUR, A. R. et al. *ASReml reference manual*. Release 1.0, 2nd. ed. Harpenden: Biomathematics and Statistics Department - Rothamsted Research, 2002. 187 p.
- GLEESON, A.C. Spatial analysis. In: KEMPTON, R.A; FOX, P.N. Statistical methods for plant variety evaluation. London: Chapman & Hall, 1997. Chapter 5, p.68-85.
- GLEESON, A.C.; CULLIS, B.R. Residual maximum likelihood (REML) estimation of a neighbour model for field experiments. *Biometrics*, Washington, v.43, p.277-288, 1987.
- GREEN, P.J.; JENNISON, C.; SEHEULT, A. Analysis of field experiments by least square smoothing. *J.R. Statist. Soc. Ser. B.*, London, v. 47, n.2, p.299-315, 1985.
- GREEN, P. J.; SILVERMAN, B. W. *Nonparametric regression and generalized linear models*. London: Chapman & Hall. 1994. 182 p.
- GRONDONA, M.O.; CRESSIE, N. Using spatial considerations in the analysis of experiments. *Technometrics*, Washington, v. 33, p.381–392, 1991.
- GRONDONA, M. O. et al. Analysis of variety yield trials using two-dimensional separable ARIMA processes. *Biometrics*, Washington, v.52, p.763-770, 1996.
- HENDERSON, C.R. *Applications of linear models in animal breeding*. Guelph: University of Guelph, 1984. 462p.
- JAFFREZIC, F.; PLETCHER, S.D. Statistical models for estimating the genetic basis of repeated measures and other function valued traits. *Genetics*, Bethesda, v. 156, p. 913-922, 2000.
- JAFFREZIC, F. et al. Statistical models for the genetic analysis of longitudinal data. In: WORLD CONGRESS OF GENETICS APPLIED TO LIVESTOCK PRODUCTION, 7. Montpellier. *Communication n. 16-08*. Montpellier: INRA, 2002. 4p, 2002.
- JOHNSON, D. L.; THOMPSON, R. Restricted maximum likelihood estimation of variance components for univariate animal models using sparse matrix techniques and average information. *J. Dairy Sci.*, Savoy, v.78, p. 449-456, 1995.
- KEMPTON, R. A.; SERAPHIN, J.C.; SWORD, A.M. Statistical analysis of two dimensional variation in variety yield trials. *J. Agric. Sci.*, Cambridge, v.122, p.335 – 342. 1994.

- KEMPTON, R. A. Discussion on The analyses of designed experiments and longitudinal data using smoothing splines. (By VERBYLA, A.P; CULLIS, B.R.; KENWARD, M.G.; WELHAM, S.J.) *J. R. Stat. Soc., Ser. C.*, London, v.48, p.300-301, 1999.
- KIRKPATRICK, M.; HILL, W. G.; THOMPSON, R. Estimating the covariance structure of traits during growth and ageing, illustrated with lactations in dairy cattle. *Genet. Res.*, London, v. 64, p.57-69, 1994.
- MARTIN, R.J. The use of time-series models and methods in the analysis of agricultural field trials. *Commun. Stat. Theory Methods*, New York, v.19, n.1, p.55-81, 1990.
- MEYER, K.; HILL, W. G. Estimation of genetic and phenotypic covariance functions for longitudinal or repeated records by restricted maximum likelihood. *Livest. Prod. Sci.*, Amsterdam, v. 47, p.185-200, 1997.
- NUNEZ-ANTON V.; ZIMMERMANN, D.L. Modelling non-stationary longitudinal data. *Biometrics*, Washington, v.56, p.699-705, 2000.
- PAPADAKIS, J. Method statistique pour des experiences sur champ. *Bull.Inst. d'Amelioration Plantes Salonique*. Thessalonique, v.23, 1937.
- PAPADAKIS, J. *Agricultural research: principles, methodology, suggestions*. Buenos Aires: Edicion Argentina, 1970.
- PAPADAKIS, J. Advances in the analysis of field experiments. *Commun. Acad. Athenes*, Athenas, v.59, p.326-342, 1984.
- PATTERSON, H. D.; THOMPSON, R. Recovery of inter-block information when block sizes are unequal. *Biometrika*, London, v.58, p.545-554, 1971.
- PLETCHER, S.D.; GEYER, C.J. The genetic analysis of age-dependent traits: modelling a character process. *Genetics*, Bethesda, v.153, p.825-833, 1999.
- QIAO, C. G. et al. Evaluation of experimental designs and spatial analysis in wheat breeding trials. *Theor. Appl. Genet.*, Berlin, v. 100, p.9-16, 2000.
- SEARLE, S.R.; CASELLA, G.; Mc CULLOCH, C.E. *Variance Components*. New York: John Wiley, 1992. 528p.
- SMITH, A.; CULLIS, B.R.; THOMPSON, R. Analysing variety by environment data using multiplicative mixed models and adjustment for spatial field trend. *Biometrics*, Washington, v. 57, p. 1138-1147, 2001.
- STEEL, R.G.D.; TORRIE, J.H. *Principles and procedures of statistics*. 2th. ed. New York: Mac Graw-Hill, 1980. 633p.
- STRINGER, J.K.; CULLIS, B.R. Application of spatial analysis techniques to adjust for fertility trends and identify interplot competition in early stage sugarcane selection trials. *Aust. J. Agric. Res.*, Collingwood, v.53, n.8, p.911-918, 2002.
- THOMPSON, R.; WELHAM, S. J. REML analysis of mixed models. In: PAYNE et al. (Ed). *GenStat 6 release 6.1. The guide to GenStat, Statistics*. Harpenden: Rothamsted Research, 2003. p.469-560.
- THOMPSON, R. et al. A sparse implementation of the average information algorithm for factor analytic and reduced rank variance models. *Aust. N. Z. J. Stat.*, Thredbo, v.45, n.4, p.445-459, 2003.

VERBYLA, A.P.; CULLIS, B.R.; KENWARD, M.G.; WELHAM, S.J. The analyses of designed experiments and longitudinal data using smoothing splines. *J. R. Stat. Soc., Ser. C.*, London, v.48, p.269-311, 1999.

WHITE, I. M. S.; THOMPSON, R.; BROTHERSTONE, S. Genetic and environmental smoothing of lactation curves with cubic splines. *J. Dairy Sci.*, Savoy, v.82, p.632-638, 1999.

WILKINSON, G.N.; ECKERT, S.R.; HANCOCK, T.W.; MAYO, O. Nearest neighbor (NN) analysis of field experiments. *J. R. Stat. Soc. Ser. B.*, London, v.45, p.151-211, 1983.

WILLIAMS, E.R. A neighbor model for field experiments. *Biometrika*, London, v.73, p.279-287, 1986.

ZIMMERMAN, D.I.; HARVILLE, D.A. A random field approach to the analysis of field-plot experiments and other spatial experiments. *Biometrics*, Washington, v.47, p.223-239, 1991.

Recebido em 01.12.2005.

Aprovado após revisão em 27.03.2006.