Empirical comparison of times series models and tensor product penalised splines for modelling spatial dependence in plant breeding field trials ...

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Outline of talk ...

- background information ...
- introduce auto-regressive time-series models and spline models for field trial data ...
  - algebraic description ...
- give an overview of the empirical study we've conducted ...
  - data set we used / approach we took ...
- share the results of the study ...
- summary ...

Background ...

Background ...

- spatial dependence between neighbouring plots occurs naturally in plant breeding field trials laid out as a rectangular lattice ...

- this is due to local variation in soil conditions ... *fertility/ moisture content* ...
- has impacts in terms of producing accurate and reliable estimates of the treatments being tested (or contrasts between them) and their standard errors ...

Background ...

- as early as the 1920's Fisher was concerned that yield observations on neighbouring plots were more highly correlated than they were on plots that were further apart ...
- since then there is a rich literature on methods to deal with spatial dependence in field trial data .. for example ...
  - using the values on neighbouring plots as covariates .. **Papadakis (1937)** [12], **Bartlett (1978)** [12] ...
  - differencing the data to remove non-stationarity .. **Wilkinson *et al.* (1983)** [21], **Green *et al.* (1985)** [9], **Green (1985)** [10], **Besag and Kempton (1986)** [1] ...
  - modelling spatial correlation *directly* using low order time series models ...
    - in one dimension and within a linear mixed model (LMM) .. **Gleeson and Cullis (1987)** [8] ...
    - in two dimensions using separable lattice processes .. **Cullis and Gleeson *et al.* (1991)**, **Martin (1990)** [11] ...
  - adding an independent error term to the 2-d process ... **Besag (1977)** [2], **Gilmour *et al.* (1997)** [7] ...
  - LMMs that include extra terms to model non-stationary effects .. **Martin (1990)** [11], **Gilmour *et al.* (1997)** [7] ...

Background: time-series models ...

- empirical evidence over many years has shown that LMMs with ...
  - a separable first order autoregressive process for the lattice of residuals ...
    - called **AR1** $\times$ **AR1** or **A** $\times$ **A** for simplicity ...
  - plus extra terms to account for non-stationarity ...
- generally works well for the analysis of field trial data ...
- is still in widespread use in practice ...

Background: time-series models ...

- the **AR1** process ...
  - models a pattern of *exponential decay* as the lag between plots increases ...
  - is one of the simplest from the class of **ARIMA** time series models ...

    Auto-**R**egressive **I**ntegrated **M**oving **A**verage
- means that if the **A** $\times$ **A** model doesn't provide an adequate fit to the data there's a whole class of **ARIMA** models to choose from ...
- this provides a rich and very flexible framework for modelling spatial dependence ...

Background: tensor product penalised splines ...

- recently tensor-product penalised-splines (**TPS**) have been introduced to explicitly model smooth variation in field trial data **Rodriguez-Alvarez *et al.* 2017** [17] ...
- they are fitted as 2-dimensional surface within an LMM ...
- with multiple smooth components to account for small- and large-scale continuous trend effects across the trial area ...

Background: tensor product penalised splines ...

- concerns have been raised about the behaviour/performance of **AR1** models ...
  - iterations and convergence behaviour ... **Piepho *et al.* 2015** [14] , **Velazco et al. 2017** [18], **Rodriguez-Alvarez *et al.* 2018** [16] ...
  - a model selection process which some consider to be complex and unnecessary **Velazco et al. 2017** [18], **Rodriguez-Alvarez *et al.* 2018** [16] ...
- this has prompted us to conduct an empirical study in which we've compared ...
  - two **AR1** models and a **baseline** model ...
  - to the **TPS** model ...

Background: tensor product penalised splines ...

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  - a model selection process which some consider to be complex and unnecessary **Velazco et al. 2017** [18], **Rodriguez-Alvarez *et al.* 2018** [16] ...
- this has prompted us to conduct an empirical study in which we've compared ...
  - two **AR1** models and a **baseline** model ... **stochastic models** ... *model a correlation structure* ...
  - to the **TPS** model ... **non-stochastic model** ... *models a spatial surface* ...
- all four models can be considered within the same statistical framework ...

Background: tensor product penalised splines ...

- the four models we have considered are ...
  - the **A** $\times$ **A** model ...
  - the **A** $\times$ **A** model plus an independent error term .. called the **A** $\times$ **Ae** model ...
    - together the **A** $\times$ **A** and **A** $\times$ **Ae** are the **AR** models ... .
  - the **TPS** model ...
  - a **baseline** model for which there is no modelling of spatial dependence ...

Background: tensor product penalised splines ...

- the **TPS** model is available through the **SpATS** package [17] in **R** [15] ...
- **ARIMA** models available through **ASReml-R** .. **Butler et al. (2018)** [4] in **R** [15] ...

Background: tensor product penalised splines ...

- the **TPS** model is available through the **SpATS** package [17] in **R** [15] ...
- **ARIMA** models available through **ASReml-R** .. **Butler et al. (2018)** [4] in **R** [15] ...
- the **SpATS** package is limited to the assumption of *independent genetic effects* ...
- alternatively, the **TPSbits** package .. **Welham (2020)** [20] `www.mmade.org` ...
  - generates the design matrices required to fit the **TPS** model in **ASReml-R** ...
  - for LMM that include information on genetic relatedness through either pedigree information or molecular marker data ...
- has allowed us to conduct our study using more plausible models for the genetic effects ...

Algebraic form of the models ...

Linear mixed model: general algebraic form ...

- the LMM for a single trial has this general form ...

$$\boldsymbol{y} = \mathbf{1}_n\mu + \boldsymbol{X_p}\boldsymbol{\tau_p} + \boldsymbol{Z_g}\boldsymbol{u_g} + \boldsymbol{Z_p}\boldsymbol{u_p} + \boldsymbol{e}$$

  - $\boldsymbol{y}$ is the vector of data ...
  - μ is the overall mean and $\mathbf{1}_n$ is a vector of 1's ...
  - $\boldsymbol{\tau_p}$ is a vector of fixed effects with design matrix $\boldsymbol{X_p}$ ...
  - $\boldsymbol{u_g}$ is a vector of random genetic effects with design matrix $\boldsymbol{Z_g}$ ...
  - $\boldsymbol{u_p}$ is a vector of non-genetic (or peripheral) random effects with design matrix $\boldsymbol{Z_p}$ ...
    - includes blocking terms ...
    - random row and column terms to deal with non-stationarity, mostly to do with trial management practices ...
  - $\boldsymbol{e}$ is the vector of plot errors ...

Linear mixed model: random effects ...

- $\boldsymbol{u_g}$, $\boldsymbol{u_p}$ and $\boldsymbol{e}$ are assumed to be independent sets of effects with zero mean and block diagonal variance structure ...

$$\begin{bmatrix} \boldsymbol{u_g} \\ \boldsymbol{u_p} \\ \boldsymbol{e} \end{bmatrix} \sim \mathcal{N}\left(\begin{bmatrix} \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \end{bmatrix}, \begin{bmatrix} \boldsymbol{G_g}(\boldsymbol{\sigma_g}) & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \boldsymbol{G_p}(\boldsymbol{\sigma_p}) & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \boldsymbol{R}(\boldsymbol{\sigma_r}) \end{bmatrix} \right)$$

Linear mixed model: genetic effects ...

- when there is information on genetic relatedness the total effects in $\boldsymbol{u_g}$ are written as the sum of ...
  - a set of additive genetic effects, $\boldsymbol{u_a}$ ... *linked to the pedigree or the molecular marker data* ...
  - a set of non-additive (or residual) genetic effects, $\boldsymbol{u_e}$ ...

$$\boldsymbol{u_g} = \boldsymbol{u_a} + \boldsymbol{u_e}$$

- with this variance structure ...

$$\begin{aligned} \text{var}\left(\boldsymbol{u_g}\right) &= \text{var}\left(\boldsymbol{u_a}\right) + \text{var}\left(\boldsymbol{u_e}\right) \\ &= \sigma_a^2 \boldsymbol{A} + \sigma_e^2 \boldsymbol{I}_m \end{aligned}$$

  - $\boldsymbol{A}$ is a known relationship matrix ... *linked to the pedigree or marker information* ...

- this genetic model was assumed for all four models in our empirical study .. **A** $\times$ **A**, **A** $\times$ **Ae**, **TPS**, **baseline** ...

Linear mixed model: non-genetic fixed/random effects and residuals ...

model	fixed terms: $\boldsymbol{X_p}$	non-genetic random terms: $\boldsymbol{Z_p}$	residual variance structure: $\boldsymbol{R}(\boldsymbol{\sigma_r})$	total variance parameters
baseline	$\mathbf{1}_n$	$[\boldsymbol{Z_b}\ \boldsymbol{Z_{row}}\ \boldsymbol{Z_{col}}]$	$\sigma^2 \boldsymbol{I}_n$	$p+5$
A $\times$ **A**	$[\mathbf{1}_n\ \boldsymbol{r}\ \boldsymbol{c}]$	$[\boldsymbol{Z_b}\ \boldsymbol{Z_{row}}\ \boldsymbol{Z_{col}}]$	$\sigma^2\ \boldsymbol{\Sigma}_c(\rho_c) \otimes \boldsymbol{\Sigma}_r(\rho_r)$	$p+7$
A $\times$ **Ae**	$[\mathbf{1}_n\ \boldsymbol{r}\ \boldsymbol{c}]$	$[\boldsymbol{Z_b}\ \boldsymbol{Z_{row}}\ \boldsymbol{Z_{col}}]$	$\sigma^2\ (\boldsymbol{\Sigma}_c(\rho_c) \otimes \boldsymbol{\Sigma}_r(\rho_r) + \alpha \boldsymbol{I}_n)$	$p+8$
TPS	$[\mathbf{1}_n\ \boldsymbol{r}\ \boldsymbol{c}\ \boldsymbol{rc}\ \boldsymbol{X_b}]$	$[\boldsymbol{Z_{row}}\ \boldsymbol{Z_{col}}\ \boldsymbol{Z_s}]$	$\sigma^2 \boldsymbol{I}_n$	10

- **baseline** model includes ...
  - an overall mean ... *the only fixed model term* ...
  - IID random terms for blocks, and the row and column effects ...
  - a simple independent error model with no modelling of spatial dependence ...

Linear mixed model: non-genetic fixed/random effects and residuals ...

model	fixed terms: $\boldsymbol{X_p}$	non-genetic random terms: $\boldsymbol{Z_p}$	residual variance structure: $\boldsymbol{R}(\boldsymbol{\sigma_r})$	total variance parameters
baseline	$\mathbf{1}_n$	$[\boldsymbol{Z_b}\ \boldsymbol{Z_{row}}\ \boldsymbol{Z_{col}}]$	$\sigma^2 \boldsymbol{I}_n$	$p+5$
A $\times$ **A**	$[\mathbf{1}_n\ \boldsymbol{r}\ \boldsymbol{c}]$	$[\boldsymbol{Z_b}\ \boldsymbol{Z_{row}}\ \boldsymbol{Z_{col}}]$	$\sigma^2\ \boldsymbol{\Sigma}_c(\rho_c) \otimes \boldsymbol{\Sigma}_r(\rho_r)$	$p+7$
A $\times$ **Ae**	$[\mathbf{1}_n\ \boldsymbol{r}\ \boldsymbol{c}]$	$[\boldsymbol{Z_b}\ \boldsymbol{Z_{row}}\ \boldsymbol{Z_{col}}]$	$\sigma^2\ (\boldsymbol{\Sigma}_c(\rho_c) \otimes \boldsymbol{\Sigma}_r(\rho_r) + \alpha \boldsymbol{I}_n)$	$p+8$
TPS	$[\mathbf{1}_n\ \boldsymbol{r}\ \boldsymbol{c}\ \boldsymbol{rc}\ \boldsymbol{X_b}]$	$[\boldsymbol{Z_{row}}\ \boldsymbol{Z_{col}}\ \boldsymbol{Z_s}]$	$\sigma^2 \boldsymbol{I}_n$	10

- the **A** $\times$ **A** model includes ...
  - linear trends in the row and column directions to model this form of non-stationarity ...
  - an **AR1** $\times$ **AR1** process for the residuals ...

Linear mixed model: non-genetic fixed/random effects and residuals ...

model	fixed terms: $\boldsymbol{X_p}$	non-genetic random terms: $\boldsymbol{Z_p}$	residual variance structure: $\boldsymbol{R}(\boldsymbol{\sigma_r})$	total variance parameters
baseline	$\mathbf{1}_n$	$[\boldsymbol{Z_b}\ \boldsymbol{Z_{row}}\ \boldsymbol{Z_{col}}]$	$\sigma^2 \boldsymbol{I}_n$	$p+5$
A $\times$ **A**	$[\mathbf{1}_n\ \boldsymbol{r}\ \boldsymbol{c}]$	$[\boldsymbol{Z_b}\ \boldsymbol{Z_{row}}\ \boldsymbol{Z_{col}}]$	$\sigma^2\ \boldsymbol{\Sigma}_c(\rho_c) \otimes \boldsymbol{\Sigma}_r(\rho_r)$	$p+7$
A $\times$ **Ae**	$[\mathbf{1}_n\ \boldsymbol{r}\ \boldsymbol{c}]$	$[\boldsymbol{Z_b}\ \boldsymbol{Z_{row}}\ \boldsymbol{Z_{col}}]$	$\sigma^2\ (\boldsymbol{\Sigma}_c(\rho_c) \otimes \boldsymbol{\Sigma}_r(\rho_r) + \alpha \boldsymbol{I}_n)$	$p+8$
TPS	$[\mathbf{1}_n\ \boldsymbol{r}\ \boldsymbol{c}\ \boldsymbol{rc}\ \boldsymbol{X_b}]$	$[\boldsymbol{Z_{row}}\ \boldsymbol{Z_{col}}\ \boldsymbol{Z_s}]$	$\sigma^2 \boldsymbol{I}_n$	10

- the **A** $\times$ **Ae** model is the **A** $\times$ **A** model plus a set of independent errors ...

Linear mixed model: non-genetic fixed/random effects and residuals ...

model	fixed terms: $\boldsymbol{X_p}$	non-genetic random terms: $\boldsymbol{Z_p}$	residual variance structure: $\boldsymbol{R(\sigma_r)}$	total variance parameters
baseline	$\mathbf{1}_n$	$[\boldsymbol{Z_b}\ \boldsymbol{Z_{row}}\ \boldsymbol{Z_{col}}]$	$\sigma^2 \boldsymbol{I}_n$	$p+5$
A × A	$[\mathbf{1}_n\ \boldsymbol{r}\ \boldsymbol{c}]$	$[\boldsymbol{Z_b}\ \boldsymbol{Z_{row}}\ \boldsymbol{Z_{col}}]$	$\sigma^2\ \boldsymbol{\Sigma}_c(\rho_c) \otimes \boldsymbol{\Sigma}_r(\rho_r)$	$p+7$
A × Ae	$[\mathbf{1}_n\ \boldsymbol{r}\ \boldsymbol{c}]$	$[\boldsymbol{Z_b}\ \boldsymbol{Z_{row}}\ \boldsymbol{Z_{col}}]$	$\sigma^2\ (\boldsymbol{\Sigma}_c(\rho_c) \otimes \boldsymbol{\Sigma}_r(\rho_r) + \alpha \boldsymbol{I}_n)$	$p+8$
TPS	$[\mathbf{1}_n\ \boldsymbol{r}\ \boldsymbol{c}\ \boldsymbol{rc}\ \boldsymbol{X_b}]$	$[\boldsymbol{Z_{row}}\ \boldsymbol{Z_{col}}\ \boldsymbol{Z_s}]$	$\sigma^2 \boldsymbol{I}_n$	10

- for the **TPS** model ...
  - we use a cubic spline basis with second-order differencing ... **d = 2**, the **SpATS** default ...
  - the blocking terms are included in the fixed part of the model ($\boldsymbol{X_b}$)...
  - the *fixed part of the* **TPS** consists of bilinear trend across the lattice surface ...
    - linear trends in rows ($\boldsymbol{r}$) and columns ($\boldsymbol{c}$) and their interaction ($\boldsymbol{rc}$) ...
  - the *random part of the* **TPS** represents smooth 2-d variation across the lattice surface ...
    - written as partitioned matrix $\boldsymbol{Z_s} = [\boldsymbol{Z_r}\ \ \boldsymbol{Z_{rl}}\ \ \boldsymbol{Z_c}\ \ \boldsymbol{Z_{cl}}\ \ \boldsymbol{Z_{rc}}]$ where each partition (5) has its own variance component ...
  - a simple IID variance structure is assumed for the plot errors ...

Empirical study ...

Empirical study: overview ...

- we have compared the **A** $\times$ **A**, **A** $\times$ **Ae**, **TPS** and **baseline** models ...
- for a set of 110 early generation lentil and field pea trials ...
- considered to be representative of early stage plant breeding data in Australia ...

Empirical study: data set ...

- 110 Stage 0, 1 and 2 trials: 48 lentil trials and 62 field pea trials ...
- 73 environments in New South Wales, South Australia, Western Australia and Victoria ...
- each trial was laid out as a rectangular lattice ...
- trials at each stage were either p-rep trials, RCB trials or a mix of both ...
  - blocking in either 1 or 2 directions ...
- before 2019 the trials were generated as model based designs *without the use of* pedigree information ...
  - **DiGGer Coombes (2109)** [5] or **Butler (2013)** [3] ...
- since 2019 they have been generated as model based designs *utilizing* pedigree information **Cullis et al. (2020)** [6] ...
- for analysis, pedigree information was available for 5771 individuals for the lentil data set and 11482 individuals for the field pea data set ...

Empirical study: approach ...

- analysed each trial using the **A** $\times$ **A**, **A** $\times$ **Ae**, **TPS** and **baseline** models ...
- for the **TPS** model we specified equally spaced knots at a rate of about 1 knot per 2 rows or columns ...
- we have compared the models based on ...
  - iterations and convergence behaviour ...
  - goodness of fit using information criteria ...
  - measures of discrepancy based on the predicted genetic effects ...
    - *correlation and rates of mis-classification for selection* ...
- our main question ...

  ... is there any real difference in the fit of the different models?

Empirical study results: approach ...

- judged models using AIC of **Verbyla (2019)** [19] ...
- model with lowest AIC = judged **Best**
  - **14%, 67%, 15%, 4%** ...
  - our assumption is that the outputs for the **Best** model are closest to those of the underlying true model ...
- in comparing models for a trial, we were most interested in ...
  - the performance of each model relative to the best fitting model for that trial ...
  - *if a model wasn't the best fitting model, how close did it get to the best fitting model ...*
- so our measures are *mostly* based on **95** (**A × A**), **35** (**A × Ae**), **94** (**TPS**), **105** (**baseline**) trials ...
- going to ignore **baseline** model as it wasn't competitive ...

best model	trial number	Model: A × A	A × Ae	TPS	baseline	total trials	% of total
A × A	1	B	✓	✓	✓		
	2	B	✓	✓	✓		
	⋮	⋮	⋮	⋮	⋮		
	15	B	✓	✓	✓	**15**	**14%**
A × Ae	16	✓	B	✓	✓		
	17	✓	B	✓	✓		
	⋮	⋮	⋮	⋮	⋮		
	89	✓	B	✓	✓	**74**	**67%**
TPS	90	✓	✓	B	✓		
	91	✓	✓	B	✓		
	⋮	⋮	⋮	⋮	⋮		
	105	✓	✓	B	✓	**16**	**15%**
baseline	106	✓	✓	✓	B		
	107	✓	✓	✓	B		
	⋮	⋮	⋮	⋮	⋮		
	110	✓	✓	✓	B	**5**	**4%**
total trials		**95**	**35**	**94**	**105**	**110**	**100%**

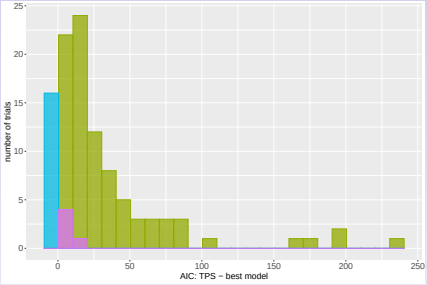
Empirical study results ...

Empirical study results: iterations and convergence behaviour ...

- for the full set of 440 analyses ... **4** *models* $\times$ **110** *trials* ...
  - just one analysis for the **A** $\times$ **Ae** model failed to converge ...
  - represents an almost 100% rate of convergence for our study ...
- differences in run time between the **AR** and **TPS** models were negligible ...

Empirical study results: goodness of fit ...

- histogram of the difference in AIC between the **TPS** model and the **best** model ...
  - **blue** = 14.5% of trials where **TPS** was best ...
  - **green** = 81% of trials where **AR** were best ...
  - **purple** = 4.6% of trials where **baseline** was best ...



- on average, the best model was an improvement over **TPS** by 34 AIC units ...
- the **TPS** model was best by at most 9.6 AIC units ...
- the **AR** models were best by as much as 240 AIC units ...

- ultimately what we found ...
  - in general, when the **TPS** model outperforms the **AR** models it does so by only a small amount while the **AR** models can win by a substantial margin ...

Empirical study results: predicted genetic effects ...

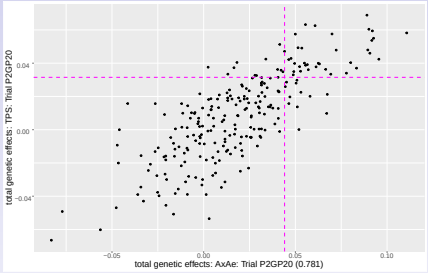
- in field trial analysis the predicted additive and total genetic effects are of key importance as they drive selection decisions ...
- for each trial we determined ...
  - the predicted genetic effects for the two sets for each of the four models ...
  - their correlation with those of the **best** fitting model ...

effect type	model	number of trials	median	mean
additive	**A** $\times$ **A**	95	0.994	0.988
	A $\times$ **Ae**	35	0.998	0.996
	TPS	94	0.986	0.968
	baseline	105	0.969	0.936
total	**A** $\times$ **A**	95	0.991	0.982
	A $\times$ **Ae**	35	0.997	0.994
	TPS	94	0.983	0.965
	baseline	105	0.963	0.932

- median and mean correlations were *highest* for the **A** $\times$ **Ae** model ...
- **TPS** model was *less correlated* with the best fitting model than both **AR** models ...

Empirical study results: mis-classification of entries ...

- plot of the predicted total effects for a FP trial for **TPS** vs **A** $\times$ **Ae** ...
  - difference in AIC = -200 units ...
  - correlation between predicted genetic effects = 0.78 ...
  - **A** $\times$ **Ae** model the **best** model ...
- pink horizontal line separates out top 20% of entries under the **TPS** model ... 49 entries above line ...
- pink vertical line separates out top 20% of entries under the **A** $\times$ **Ae** model ... 49 entries to right of line ...



- top right and bottom left quadrants contain the sets of 37 and 180 entries that would be selected or rejected under both models ...
- the top left and bottom right quadrants contain the 12 entries that would be selected by one model but rejected by the other model ...
- represents a 24.5% rate of mis-classification for the **TPS** model given the **A** $\times$ **Ae** model was the **best** fitting model ...

Empirical study results: mis-classification of entries for the full set of trials ...

- we have summarised the % mis-classification for the four models across the full set of trials ...
- this is the median % mis-classification for the **TPS**, **A** $\times$ **A** and **A** $\times$ **Ae** models ...

10.42%	additive,	**11.52%**	total	for **TPS** ...
6.52%	additive,	**8.33%**	total	for **A** $\times$ **A** ...
4.08%	additive,	**4.17%**	total	for **A** $\times$ **Ae** ...

- the **A** $\times$ **Ae** model had the *lowest median rate of mis-classification* ...
- the **TPS** model had a *higher median rate of mis-classification than both* **AR** *models* ...
- this is important information for breeding programs since **maximising genetic gain can only be achieved through accurate selection decisions** ...

Technicalities with the TPS model ...

Technicalities with the TPS model ...

- **Piepho et al. (2022) [13]** have pointed out that an extra correlation parameter is needed to make the **TPS** model with second order differencing (**d = 2**) invariant to any choice of basis for the *unpenalised* terms ...
- **Welham (2022)** has found that additional parameters are needed to achieve this same invariance for the *penalised* terms ... *for any order of differencing ...*
- **Piepho et al. (2022)** recommend a process of **model selection** that uses a **TPS** model with first-order differencing (**d = 1**) in response to the issue they have raised ...
- given ...
  - lack of invariance in the **TPS** model ...
  - that the process of model selection is not avoided in using the **TPS** model ...
  - the relative performance of the **AR** models compared to the **TPS** model ...
- we recommend the use of low order **ARIMA** models for field trial analysis ...

Summary ...

Summary ...

- the **AR** and **TPS** models offer different approaches for the analysis of field trial data ...
  - modelling spatial correlation .. *the* **AR** *models* ...
  - modelling spatial trend .. *the* **TPS** *model* ...
- in our study ...
  - the **AR** models generally outperformed the **TPS** based on AIC ... *particularly the* **A** $\times$ **Ae** *model* ...
  - we found that when the **TPS** model is best it is generally by only a small amount compared to the **AR** models which can the best model by a large amount ...
  - the **TPS** model had consistently higher rates of mis-classification for selection than the **AR** models ...
- to achieve high rates of genetic gain plant breeding programs need to be making accurate selection decisions ...
- again, based on our study results, we recommend **AR** models in preference to the **TPS** model for use in field trial analysis and evaluation systems ...

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