Two-dimensional P-spline smoothing for spatial analysis of field trials

Hans-Peter Piepho

Biostatistics Unit

Institute of Crop Science

University of Hohenheim

Germany



This is joint work with:

Martin Boer

Wageningen University & Research (WUR), Wageningen, NL

Emlyn Williams

Australian National University (ANU), Canberra, AUS

Spatial models



Spatial correlation among neighbouring plots

Figure: A single row of plots. Arrow indicates direction of spatial correlation.



 y_j = yield on *j*-th plot

Second differences:

$$y_j - \frac{y_{j-1} + y_{j+1}}{2}$$

An equivalent mixed model (spatial)

Linear Variance (LV) model (Williams 1986)

Covariance (\Rightarrow similarity of plots)



0 Distance of plots

 \Rightarrow Can implement NNA with mixed models

Random walk models (state-space models)

 t_1 , t_2 = trend values of two adjacent plots

First-order random walk \Rightarrow first differences:

$$t_1 - t_2 = a_2 \Leftrightarrow t_2 = t_1 + a_2$$
; $a_2 \sim N(0, \sigma_a^2) \implies \text{equivalent to LV}$

Second-order random walk \Rightarrow second differences:

$$(t_1 - t_2) - (t_2 - t_3) = t_1 - 2t_2 + t_3 = a_2 \Leftrightarrow t_2 = (t_1 + t_3)/2 + a_2 \quad ; \quad a_2 \sim N(0, \sigma_a^2)$$

First-order autoregressive model [AR(1)]:

$$t_2 = \rho t_1 + a_2$$
; $a_2 \sim N(0, \sigma_a^2)$ $0 < \rho < 1$ (Lee et al. 2021)

P-splines

(1) Use effects u_j to model trend values t_i for the plots

(2) Smear out the u_j over adjacent plots

(3) The u_j are regression coefficients for B-spline basis functions $B = \{b_{ij}\}$

Trend value for the *i*-th plot:

 $t_i = b_{i1}u_1 + b_{i2}u_2 + \dots + b_{im}u_m$; $b_{i1} + b_{i2} + \dots + b_{im} = 1$

 $P = penalized \implies penalty on regression coefficients u_j \\ \implies first differences or second differences!$

(Rodriguez-Alvarez et al. 2018; 'SpATS' package in R)



Figure 1. Example of a first-degree B-spline basis for a continuous coordinate *x*.

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Figure 2. Cubical B-spline basis for a continuous coordinate *x*.

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• Trend LV model

/ Trend 3rd degree P-spline

(Boer et al., 2020)

Figure 4. Comparison of plot effects u for the oats data. The red points are the estimates for the LV model and equivalent to first-order P-splines. The black curve is based on P-splines, using a third degree B-splines with 12 segments, so half the number of plots per replicates.

Cubical = third-degree, 7 knots at plots (including "outer" plots!):

$$B = \begin{pmatrix} 0.167 & 0.666 & 0.167 & 0 & 0 & 0 \\ 0 & 0.167 & 0.666 & 0.167 & 0 & 0 & 0 \\ 0 & 0 & 0.167 & 0.666 & 0.167 & 0 & 0 \\ 0 & 0 & 0 & 0.167 & 0.666 & 0.167 & 0 \\ 0 & 0 & 0 & 0 & 0.167 & 0.666 & 0.167 \end{pmatrix}$$

 \Rightarrow need $u_1, ..., u_7$

 $\Rightarrow t_1 = 0.167 \times u_1 + 0.666 \times u_2 + 0.167 \times u_3 + 0 \times u_4 + 0 \times u_5 + 0 \times u_6 + 0 \times u_7$ $\Rightarrow t_2 = 0 \times u_1 + 0.167 \times u_2 + 0.666 \times u_3 + 0.167 \times u_4 + 0 \times u_5 + 0 \times u_6 + 0 \times u_7$ etc.

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Cubical = third-degree, just 5 knots:

$$B = \begin{pmatrix} 0.167 & 0.666 & 0.167 & 0 & 0 \\ 0.021 & 0.479 & 0.479 & 0.021 & 0 \\ 0 & 0.167 & 0.666 & 0.167 & 0 \\ 0 & 0.021 & 0.479 & 0.479 & 0.021 \\ 0 & 0 & 0.167 & 0.666 & 0.167 \end{pmatrix}$$

 $\Rightarrow need u_1, ..., u_5$ $\Rightarrow t_1 = 0.167 \times u_1 + 0.666 \times u_2 + 0.167 \times u_3 + 0 \times u_4 + 0 \times u_5$ $\Rightarrow t_2 = 0.021 \times u_1 + 0.479 \times u_2 + 0.479 \times u_3 + 0.021 \times u_4 + 0 \times u_5$ etc.

First-degree, just 3 knots:

$$B = \begin{pmatrix} 1 & 0 & 0 \\ 0.5 & 0.5 & 0 \\ 0 & 1 & 0 \\ 0 & 0.5 & 0.5 \\ 0 & 0 & 1 \end{pmatrix}$$

$$\Rightarrow need u_1, ..., u_3$$

$$\Rightarrow t_1 = 1 \times u_1 + 0 \times u_2 + 0 \times u_3$$

$$\Rightarrow t_2 = 0.5 \times u_1 + 0.5 \times u_2 + 0 \times u_3$$

etc.

First-degree, **5** knots at plots:

$$B = \begin{pmatrix} 1 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 1 \end{pmatrix}$$

$$\Rightarrow \text{need } u_1, \dots, u_5$$

$$\Rightarrow t_1 = \mathbf{1} \times u_1 + \mathbf{0} \times u_2 + \mathbf{0} \times u_3 + \mathbf{0} \times u_4 + \mathbf{0} \times u_5 = u_1$$

$$\Rightarrow t_2 = \mathbf{0} \times u_1 + \mathbf{1} \times u_2 + \mathbf{0} \times u_3 + \mathbf{0} \times u_4 + \mathbf{0} \times u_5 = u_2$$

etc.

\Rightarrow This is LV when first differences are used to penalize $u_i!$



Intermediate summary on P-splines

- Modelling smooth trend
- Just another spatial covariance model
- All covariance structures linear in the variance components
- LV and random walk are special cases when using first differences
- Many knobs (degree of B-spline basis, number of knots, difference penalty)
- SpATS uses second differences, but often first differences sufficient

(Boer et al. 2020; Piepho et al. 2022)

Fitting P-splines as mixed models: one column of plots

t = Bu

- t = vector of trend values for k plots
- $B = \{b_{ij}\} = k \times m$ matrix of *m* B-spline bases of *q*-th degree
- u = m-vector of coefficients

Penalty for coefficients *u*:

 $\theta u^T D^T D u$

- θ = penalty parameter
- $D = (m p) \times m$ matrix of *p*-th differences

The penalty

 $\theta u^T P u$

 $P = D^T D$ = penalty matrix

 \Rightarrow equivalent to quadratic form for random effect in likelihood for random effects u

$$\sigma^{-2}u^T P u$$

where

 σ^2 = variance

P = precision matrix

Next question

What is the variance-covariance matrix for *u*?

 \Rightarrow needed for mixed model package

If *P* were positive-definite, we could just use $var(u) = P^{-1}\sigma^2$

But *P* is singular!

 \Rightarrow use spectral decomposition of *P*

Spectral decomposition of *P*

 $P = U diag(d) U^T$

- U = eigenvectors of $P = (U_+ \mid U_0)$
- d = eigenvalues of P

where

 $U_+ = (m - p)$ eigenvectors corresponding to d_+

 $U_0 = p$ eigenvectors corresponding to zero eigenvalues

 d_+ = sub-vector of (m - p) positive eigenvalues in d

Decomposing *Bu*

$$Bu = BUU^{T}u = BU_{0}U_{0}^{T}u + BU_{+}U_{+}^{T}u = X\beta + Zw$$

where

$$X = BU_0$$
 and $\beta = U_0^T u$ with precision zero! \Rightarrow fixed effect!
 $Z = BU_+$ and $w = U_+^T u$ with precision $\theta \ diag(d_+)$

The penalty

Using

$$P = U \operatorname{diag}(d) U^{T} = U_{+} \operatorname{diag}(d_{+}) U_{+}^{T}$$

and

$$w = U_+^T u$$

we find

$$\theta u^T P u = \theta u^T U_+ diag(d_+) U_+^T u = \theta w^T diag(d_+) w$$

$$\Rightarrow$$
 can assume var $(w) = \theta^{-1} diag(d_{+}^{-1}) = \sigma^{2} diag(d_{+}^{-1})$

The variance-covariance matrix for *u*

The penalty again:

$$\theta u^T P u = \theta u^T U_+ diag(d_+) U_+^T u = \theta w^T diag(d_+) w$$

Observing that

$$P^{+} = U_{+} diag (d_{+}^{-1}) U_{+}^{T}$$

is the Moore-Penrose inverse of P, we can also just fit the random effect Bu assuming that

 $\operatorname{var}(u) = \sigma^2 P^+$

But: Must also fit fixed effects $X\beta = BU_0^T u$

(Lee et al. 2021)

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What are the fixed effects? (What's in the null space?)

p = 1:

X = 1 (just an intercept)

p = 2:

 $X = \begin{pmatrix} 1 & h \end{pmatrix}$

- h = vector of plot numbers
 - \Rightarrow linear regression on plot numbers

Extending the model to two dimensions

Plots of a field trial on a regular grid with *k* rows and *s* columns

Model for spatial trend:

 $t = B_{rc} u_{rc}$

where

 $B_{rc} = B_r \otimes B_c$

 B_r = matrix of m_r B-spline bases for k rows

 B_c = matrix of m_c B-spline bases for *s* columns

A separable two-dimensional penalty

Consider differences $D_{rc}u_{rc}$ where

 $D_{rc} = D_r \otimes D_c$

 D_r = matrix of *p*-th differences for *k* rows

 D_c = matrix of *p*-th differences for *s* columns

$$\Rightarrow$$
 penalty $\theta_{rc} u_{rc}^T P_{rc} u_{rc}$

where

$$P_{rc} = P_r \otimes P_c = D_r^T D_r \otimes D_c^T D_c$$

What are the fixed effects?

 $(B_r \otimes B_c)(U_r \otimes U_c)(U_r^T \otimes U_c^T)u_{rc} = X_{00}\beta_{00} + X_{r0}\beta_{r0} + X_{0c}\beta_{0c} + Z_{rc}w_{rc},$

$$X_{00} = (B_r \otimes B_c) (U_{0r} \otimes U_{0c}) = X_r \otimes X_c,$$

$$X_{r0} = (B_r \otimes B_c) (U_{+r} \otimes U_{0c}) = Z_r \otimes X_c,$$

$$X_{0c} = (B_r \otimes B_c) (U_{0r} \otimes U_{+c}) = X_r \otimes Z_c,$$
 and

$$Z_{rc} = (B_r \otimes B_c) (U_{+r} \otimes U_{+c}) = Z_r \otimes Z_c$$

Fixed effects (null space) have dimension

$$m_r m_c - (m_r - p)(m_c - p)$$

 \Rightarrow need extra smoothing terms for row and column main effects

An important detail when p = 2

Have design matrices

$$X_r = \begin{pmatrix} 1 & h_r \end{pmatrix}$$
 and $X_c = \begin{pmatrix} 1 & h_c \end{pmatrix}$

When smoothing these using P-splines, have a random coefficient regression

- \Rightarrow need to allow for a covariance between intercept and slope
- \Rightarrow this is not nice but necessary to ensure invariance
- \Rightarrow to our knowledge this fact has been ignored in literature on P-splines
- \Rightarrow this complication is a good reason to favor p = 1

Special cases

Several older approaches turn out to be special cases when knots are at the plots and first differences are used (p = 1).

One particular one occurs when first-degree B-spline bases are used (q = 1). In this case the model is closely related to the

 $\mathsf{LV}\otimes\mathsf{LV}$

model (Piepho and Williams 2010; Boer et al. 2020).

This model, in turn, is a limiting case of the very popular

 $AR(1) \otimes AR(1)$

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model (Gilmour et al. 1997).
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Penalties derived from sum of Kronecker products

Lee and Durbán (2011) consider a penalty of the form

$$u_{rc}^{T} \left\{ \theta_{rc1} P_{r} \otimes I_{m_{c}} + \theta_{rc2} I_{m_{r}} \otimes P_{c} \right\} u_{rc}$$

Wood (2017, p. 232): This can provide smoother fits than interaction smooth

A major advantage: null space is $X_r \otimes X_c$ and only has dimension p^2

p = 1: null space is just the intercept (Dutta & Mondal 2015)

p = 2: null space also comprises regression on row and column numbers and their products (Rodríguez-Álvarez et al., 2018) \Rightarrow SpATS Interesting special case p = 1 & q = 1

Conditional expectation of $u_{i,j}$, the fertility value for the interior plot in the *i*-th row and *j*-th column (i.e., the *i*,*j*-th element of vector u_{rc}), given all other $u_{i',j'}$ -values:

$$E(u_{i,j}|...) = \frac{1}{2} \left[(1 - \alpha)(u_{i,j-1} + u_{i,j+1}) + \alpha(u_{i-1,j} + u_{i+1,j}) \right] \quad \text{with}$$

$$2\operatorname{var}(u_{i,j}|\cdots) = 1/(\theta_{rc1} + \theta_{rc2})$$
 , where

 $\alpha = \theta_{rc2} / (\theta_{rc1} + \theta_{rc2})$ (modified from Dutta and Mondal, 2015)

This is recognized as an NN model, where the central plot is regressed on the nearest row and column neighbours (Julian Besag, in discussion of Bartlett, 1978; Kempton and Howes, 1981).

Besag and Higdon (1999) refer to this as the intrinsic autoregressive (IAR) model.

More difficult to translate to a standard mixed model framework because inverse of the precision matrix is not linear in the parameters (Wood et al., 2013, p. 345).

Used here: profiling the residual log-likelihood for α , i.e., via a grid search over $\alpha \in [0,1]$ (Besag and Kooperberg, 1995).

Rodríguez-Álvarez et al. (2018) consider a simplified version of the IAR penalty:

$$\theta_{rc} w_{rc}^T \left\{ diag(d_{+r}) \otimes I_{m_c} + I_{m_r} \otimes diag(d_{+c}) \right\} w_{rc}$$

The models implemented in SpATS involve adding marginal smooths for rows and columns with diagonal variance-covariance structures

Two Examples

Barley data or Durban et al. (2003)

Wheat data of Stroup et al. (1994)

 \Rightarrow Fitted randomization-based baseline model and added spatial components

TABLE 5 Analysis of barley data of Durbán et al. (2003) and wheat data of Stroup et al. (1994) using other common models. All models have fixed effects for replicates, genotypes, row numbers h_r , column numbers h_c , and the product of row and column numbers

		Barley data		Wheat data		
Model	Description	Deviance	AIC	Deviance	AIC	
M53	Baseline ^a	410.19	412.19	1101.53	1103.53	
M54	Baseline + row & column ^b	352.40	358.40	1083.52	1089.52	
M55	AR1⊗AR1	299.60	305.60	1067.32	1073.32	
M56	AR1⊗AR1 + nugget	278.20	286.20	1050.34	1058.34	
M57	LV⊗LV	283.71	291.71	1051.33	1059.33	

^aModel with fixed effects for genotype, replicate, linear regression on row and column numbers as well as their product, and i.i.d. residual error. ^bBaseline, adding random effects for rows and columns nested within replicates.

The separable penalty (*p* = 1)

TABLE 3 Analysis of barley data of Durbán et al. (2003) and wheat data of Stroup et al. (1994) using P-spline approach with p = 1 (first differences) and the penalty in (3) for B_{rc} . All models have fixed effects for replicates, genotypes, row numbers h_r , column numbers h_c , and the product of row and column numbers. The marginal smooths use $var(u_r) = P_r^+ \otimes \sigma_r^2$, $X_c = 1_s$, $var(u_c) = \sigma_c^2 \otimes P_c^+$ and $X_r = 1_k$ for all models

					Barley data		Wheat data	
Model	q	i _r	i _c	$var(u_{rc})$	Deviance	AIC	Deviance	AIC
M21	3	k	S	-	293.37	299.37	1072.47	1078.47
M22	3	k	S	$\sigma_{rc}^2 P_r^+ \otimes P_c^+$	279.28	287.28	1046.40	1054.40
M23	2	k	S	-	293.56	299.56	1071.91	1077.91
M24	2	k	S	$\sigma_{rc}^2 P_r^+ \otimes P_c^+$	279.18	287.18	1046.06	1054.06
M25	1	k	S	-	295.78	301.78	1075.14	1081.14
M26	1	k	S	$\sigma_{rc}^2 P_r^+ \otimes P_c^+$	278.45	286.45	1047.12	1055.12
M27	3	10	20	-	292.92	298.92	1073.38	1079.38
M28	3	10	20	$\sigma_{rc}^2 P_r^+ \otimes P_c^+$	281.18	289.18	1056.41	1064.41
M29	2	10	20	-	291.61	297.61	1073.27	1079.27
M30	2	10	20	$\sigma_{rc}^2 P_r^+ \otimes P_c^+$	279.74	287.74	1057.09	1065.09
M31	1	10	20	-	296.75	302.75	1075.43	1081.43
M32	1	10	20	$\sigma_{rc}^2 P_r^+ \otimes P_c^+$	281.31	289.31	1052.41	1060.41

M26 is doing very well \Rightarrow mathematically close to LV \otimes LV

 \Rightarrow LVIS = Linear Variance with Interaction Splines

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The separable penalty (*p* = 2)

						Barley data			Wheat data				
						$\underline{q=1}$ $\underline{q=3}$		<u>q</u> = 3	<u>q</u> = 1		<u>q</u> = 3		
Model	$\operatorname{var}(u_r)^{\mathbf{a}}$	X_c^{b}	$var(u_c)^a$	$X_r^{\mathbf{b}}$	$var(u_{rc})$	Deviance	AIC	Deviance	AIC	Deviance	AIC	Deviance	AIC
M1	1	1_s	1	1_k	-	295.22	301.22	295.70	301.70	1076.03	1082.03	1075.93	1081.93
M2	1	1_s	1	1_k	$\sigma_{rc}^2 P_r^+ \otimes P_c^+$	292.20	300.20	293.09	301.09	1075.78	1083.78	1071.88	1079.88
M3	Σ	\ddot{X}_c	-	-	-	378.69	386.69	378.56	386.56	1075.45	1083.45	1075.51	1083.51
M4	Σ	$1_s \vdots h_s$	-	-	-	378.69	386.69	378.56	386.56	%	%	%	%
M5	Σ	$a_s \\\vdots \\ b_s$	-	-	-	378.69	386.69	378.56	386.56	%	%	%	%
M6	Ω	\widehat{X}_{c}	-	-	-	378.72	384.72	378.62	384.62	1078.49	1084.49	1075.15	1079.15
M7	Ω	$1_s \div h_s$	-	-	-	381.95	387.95	383.41	389.41	1082.32	1088.32	1081.92	1087.92
M8	Ω	$a_s \vdots b_s$	-	-	-	378.87	384.87	378.72	384.72	1081.76	1087.76	1081.08	1087.08
M9	I_2	\widehat{X}_{c}	I_2	\hat{X}_r	-	296.46	302.46	296.56	302.56	1058.02	1064.02	1060.05	1066.05
M10	I_2	$1_s \\ \vdots \\ h_s$	I_2	$1_k \vdots h_k$	-	317.58	323.58	316.77	322.77	1087.29	1093.29	1082.64	1088.64
M11	I_2	$a_s \vdots b_s$	I_2	$a_k \\ \vdots \\ b_k$	-	296.45	302.45	297.13	303.13	1058.02	1064.02	1059.84	1065.84
M12	Ω	\widehat{X}_{c}	Ω	\hat{X}_r	-	296.41	306.41	295.23	305.23	1049.91	1059.91	1057.51	1067.51
M13	Ω	$1_s \div h_s$	Ω	$1_k \stackrel{.}{\cdot} h_k$	-	291.15	301.15	291.52	301.52	1057.10	1067.10	1057.34	1067.34
M14	Ω	$a_s \vdots b_s$	Ω	$a_k \vdots b_k$	-	287.88	297.88	288.27	298.27	1057.45	1067.45	1059.24	1069.24
M15	Σ	\ddot{X}_c	Σ	\ddot{X}_r	-	283.65	297.65	284.12	298.12	1043.37	1057.37	1044.22	1058.22
M16	Σ	$1_s \\ \vdots \\ h_s$	Σ	$1_k \vdots h_k$	-	%	%	%	%	%	%	%	%
M17	Σ	$a_s \\ \vdots \\ b_s$	Σ	$a_k \\ \vdots \\ b_k$	-	%	%	%	%	%	%	%	%
M18	I_2	\widehat{X}_c	I_2	\hat{X}_r	$\sigma_{rc}^2 P_r^+ \otimes P_c^+$	293.23	301.23	293.60	301.60	1058.02	1066.02	1060.05	1068.05
M19	Ω	\widehat{X}_{c}	Ω	\hat{X}_r	$\sigma_{rc}^2 P_r^+ \otimes P_c^+$	293.16	305.16	292.28	304.28	1049.91	1061.91	1057.49	1067.49
M20	Σ	\ddot{X}_c	Σ	\ddot{X}_r	$\sigma_{rc}^2 P_r^+ \otimes P_c^+$	280.12	296.12	280.27	296.27	1042.80	1058.80	1044.22	1058.22

TABLE 2 Analysis of barley data of Durbán et al. (2003) and wheat data of Stroup et al. (1994) using P-spline approach with p = 2 (second differences), $i_r = k$, $i_c = s$, and the penalty in (3) for B_{rc} . All models have fixed effects for replicates, genotypes, row numbers h_r , column numbers h_c , and the product of row and column numbers

^a1: $P_r^+ \otimes \sigma_r^2$ or $\sigma_c^2 \otimes P_c^+$; I_2 : $P_r^+ \otimes \sigma_r^2 I_2$ or $\sigma_c^2 I_2 \otimes P_c^+$; Ω : $P_r^+ \otimes \Omega_r$ or $\Omega_c \otimes P_c^+$; Σ : $P_r^+ \otimes \Sigma_r$ or $\Sigma_c \otimes P_c^+$.

^bRepresentation of X_r or X_c in the marginal smooth; \hat{X} obtained using U_0 of spectral decomposition of P as obtained by software (IML procedure of SAS); \hat{X} obtained using near optimal orthogonal rotation (Figures 2 and 4).

% Did not converge due to poor scaling of X_r and/or X_c .

\Rightarrow Second differences not doing so well

				Barley data			Wheat data			
Model	q	р	Marginal smooth ^a	α	Deviance	AIC	α	Deviance	AIC	
M33	3	1	-	0.5	284.53	290.53	0.9	1052.33	1058.33	
M34	2	1	-	0.5	283.94	289.94	0.9	1053.18	1059.18	
M35	1	1	-	0.6	281.52	287.52	0.8	1055.06	1061.06	
M36	3	2	-	0.6	295.90	301.90	0.9	1063.35	1069.35	
M37	2	2	-	0.6	296.58	302.58	0.9	1064.66	1070.66	
M38	1	2	-	0.6	297.00	303.00	0.9	1064.94	1070.94	
M39	3	1	1	0.9	274.84	284.84	0.9	1050.84	1058.84	
M40	2	1	1	0.9	274.85	284.85	1.0	1050.61	1060.61	
M41	1	1	1	0.9	273.81	283.81	0.9	1053.08	1063.08	
M42	3	2	1	1.0	284.63	294.63	0.9	1059.55	1069.55	
M43	2	2	1	1.0	284.79	294.79	0.9	1060.54	1070.54	
M44	1	2	1	1.0	284.94	294.94	0.9	1061.39	1071.39	
M45 ^b	3	2	Ω	0.5	283.58	295.58	0.5	1063.57	1077.57	
M46 ^c	3	2	Ω	0.5	290.92	302.92	0.5	1052.70	1066.70	
M47	3	2	Ω	1.0	285.24	297.24	1.0	1049.40	1063.40	
M48	2	2	Ω	1.0	287.06	299.06	1.0	1044.35	1058.35	
M49	1	2	Ω	1.0	287.20	299.20	1.0	1046.99	1060.99	
M50	3	2	Σ	1.0	273.67	289.67	1.0	1044.28	1062.28	
M51	2	2	Σ	1.0	274.77	290.77	1.0	1041.51	1059.51	
M52	1	2	Σ	1.0	273.51	289.51	1.0	1038.81	1056.81	

TABLE 4 Analysis of barley data of Durbán et al. (2003) and wheat data of Stroup et al. (1994) using the IAR model with the penalty in (7) for u_{rc} with $i_r = k$ and $i_c = s$ with and without marginal smooths added. All models have fixed effects for replicates, genotypes, row numbers h_r , column numbers h_c , and the product of row and column numbers. Fits obtained by a grid search over $\alpha = 0, 1(0.1)$

^a1: for p = 1 just the intercepts for rows and columns. Ω : for p = 2 using $P_r^+ \otimes \Omega_r$ and $\Omega_c \otimes P_c^+$ with X_c and X_r , respectively. Σ : using $P_r^+ \otimes \Sigma_r$ and $\Sigma_c \otimes P_c^+$ with X_c and X_r , respectively; \hat{X} obtained using U_0 of spectral decomposition of P as obtained by software (IML procedure of SAS); \hat{X} : obtained using near optimal orthogonal rotation (Figures 2 and 4).

^bFit for fixed $\alpha = 0.5$; using \hat{X}_c and \hat{X}_r for X_c and X_r , respectively.

^cFit for fixed $\alpha = 0.5$; using $a_s \\\vdots \\ b_s$ and $a_k \\\vdots \\ b_k$ for X_c and X_r , respectively (Rodríguez-Álvarez et al., 2018).

IAR / SpATS

Brief summary

- P-splines are a very versatile option for spatial modelling in field trials
- Several choices to make (many knobs to turn)
- First differences simpler than second differences; work quite well
- Okay to place knots at plots and use first-degree B-spline bases
- Close ties with older approaches [NN-analysis, random walk, LV, AR(1)]
- Our philosophy: always start with a randomization-based model as baseline; any spatial modelling is just an add-on
- Important disclaimer: A sophisticated spatial analysis is no substitute for good experimental design

https://vsni.co.uk/blogs/top-5-must-have-features-for-effective-statistical-analysis/

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What does Genstat offer?

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Genstat provides extensive data analysis facilities, delivering reliable and insightful results no matter how complex your data may be. Our latest update provides even more functionality, including:

- The ability to analyse censored data using ANOVA and regression
- 2-dimensional spline models (i.e., LVIS and SpATS) for modelling spatial correlation
- Tools to design and analyse n-of-1 medical trials



(accessed on 8 August 2024)

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