

Hierarchical Modelling for Large Spatial Datasets

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1

The Big n issue

Univariate spatial regression

$$\mathbf{Y} = \mathbf{X}\beta + \mathbf{w} + \epsilon,$$

- Estimation involves $(\sigma^2 R(\phi) + \tau^2 I)^{-1}$, which is $n \times n$.
- Matrix computations occur in each MCMC iteration.
- Known as the “Big-N problem” in geostatistics.
- Approach: Use a model $\mathbf{Y} = \mathbf{X}\beta + \mathbf{Z}\mathbf{w}^* + \epsilon$. But what \mathbf{Z} ?

2

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- Consider “knots” $\mathcal{S}^* = \{\mathbf{s}_1^*, \dots, \mathbf{s}_{n^*}^*\}$ with $n^* \ll n$.
- Let $\mathbf{w}^* = \{w(\mathbf{s}_i^*)\}_{i=1}^{n^*}$
- $\mathbf{Z}(\theta) = \{\text{cov}(w(\mathbf{s}_i), w(\mathbf{s}_j^*))\}' \{\text{var}(\mathbf{w}^*)\}^{-1}$ is $n \times n^*$.

Predictive process regression model

$$\mathbf{Y} = \mathbf{X}\beta + \mathbf{Z}(\theta)\mathbf{w}^* + \epsilon,$$

- Fitting requires only $n^* \times n^*$ matrix computations ($n^* \ll n$).
- **Key attraction:** The above arises as a process model: $\tilde{w}(\mathbf{s}) \sim GP(0, \sigma_w^2 \tilde{\rho}(\cdot; \phi))$ instead of $w(\mathbf{s})$.
- $\tilde{\rho}(\mathbf{s}_1, \mathbf{s}_2; \phi) = \text{cov}(w(\mathbf{s}_1), \mathbf{w}^*) \text{var}(\mathbf{w}^*)^{-1} \text{cov}(\mathbf{w}^*, w(\mathbf{s}_2))$

3

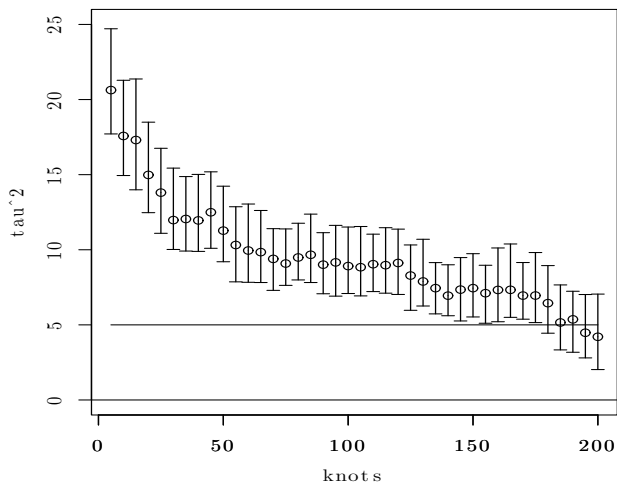
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Knots: A “Knotty” problem??

- Knot selection: Regular grid? More knots near locations we have sampled more?
- Formal spatial design paradigm: maximize information metrics (Zhu and Stein, 2006; Diggle & Lophaven, 2006)
- Geometric considerations: space-filling designs (Royle & Nychka, 1998); various clustering algorithms
- Compare performance of estimation of range and smoothness by varying knot size.
- Stein (2007, 2008): method may not work for fine-scale spatial data
- Still a popular choice – seamlessly adapts to multivariate and spatiotemporal settings.

4

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5

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A rectified predictive process is defined as

$$\tilde{w}_{\tilde{\epsilon}}(\mathbf{s}) = \tilde{w}(\mathbf{s}) + \tilde{\epsilon}(\mathbf{s}), \text{ where}$$

$$\tilde{\epsilon}(\mathbf{s}) \stackrel{\text{indep}}{\sim} N(0, \sigma_w^2 (1 - \mathbf{r}(\mathbf{s}, \phi)' R^{*-1}(\phi) \mathbf{r}(\mathbf{s}, \phi))).$$

Maximum likelihood estimates of τ^2 :

# of Knots	Predictive Process	Rectified Predictive Process
25	1.56941	1.00786
36	1.65688	1.15386
64	1.45169	1.08358
100	1.37916	1.09657
225	1.27391	1.08985
400	1.22429	1.09489
625	1.21127	1.09998
exact	1.14414	1.14414

6

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Illustration from:

Banerjee, S., A.O. Finley, P. Waldmann, and T. Ericsson. (2009). Hierarchical multivariate modeling of large spatially referenced genetic trial datasets. *Journal of the American Statistical Association*.

Finley, A.O., S. Banerjee, P. Waldmann, and T. Ericsson. (2008) Hierarchical spatial modeling of additive and dominance genetic variance for large spatial trial datasets. *Biometrics*. DOI:10.1111/j.1541-0420.2008.01115.x

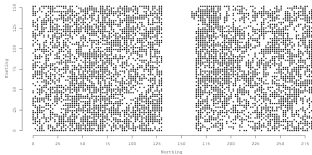
Univariate random effects models

Modeling genetic variation in Scots pine (*Pinus sylvestris* L.), long-term progeny study in northern Sweden.

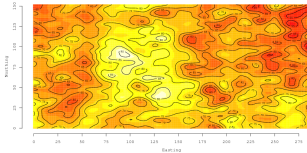
Quantitative genetics: studies the inheritance of polygenic traits, focusing upon estimation of additive genetic variance, σ_a^2 , and the heritability $h^2 = \sigma_a^2 / \sigma_{Tot}^2$, where the σ_{Tot}^2 represents the total genetic and unexplained variation.

A high heritability, h^2 , should result in a larger selection response (i.e., a higher probability for genetic gain in future generations).

Observed trees



Observed height



Data overview:

- established in 1971 (by Skogforsk)
- partial diallel design of 52 parent trees
- 8,160 planted randomly on 2.2m squares
- 1997 reinventory of 4,970 surviving trees, height, DBH, branch angle, etc.

Genetic effects model:

$$Y_i = \mathbf{x}_i^T \boldsymbol{\beta} + a_i + d_i + \epsilon_i,$$

- $\mathbf{a} = [a_i]_{i=1}^n \sim MVN(\mathbf{0}, \sigma_a^2 \mathbf{A})$
- $\mathbf{d} = [d_i]_{i=1}^n \sim MVN(\mathbf{0}, \sigma_d^2 \mathbf{D})$
- $\epsilon = [\epsilon_i]_{i=1}^n \sim N(\mathbf{0}, \tau^2 \mathbf{I}_n)$

\mathbf{A} and \mathbf{D} are fixed relationship matrices (See e.g., Henderson, 1985; Lynch and Walsh, 1998)

Note, genetic variance is further partitioned into additive and the non-additive *dominance* component σ_d^2

Genetic effects model:

$$Y_i = \mathbf{x}_i^T \boldsymbol{\beta} + a_i + d_i + \epsilon_i,$$

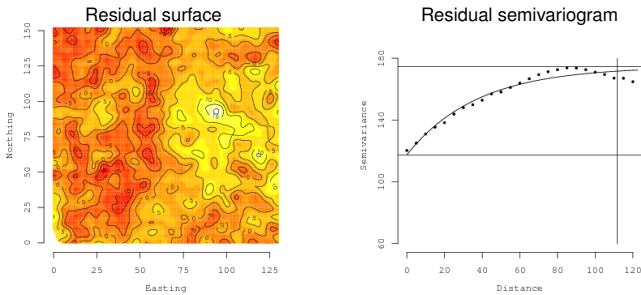
- Common feature is systematic heterogeneity among observational units (i.e., violation of $\epsilon \sim N(\mathbf{0}, \tau^2 \mathbf{I}_n)$)
- Spatial heterogeneity arises from:
 - soil characteristics
 - micro-climates
 - light availability
- Residual correlation among units as a function of distance and/or direction = erroneous parameter estimates (e.g., biased h^2)

Genetic model results

Parameter credible intervals, 50% (2.5%, 97.5%) for the non-spatial Scots pine trial.

Parameter	Non-spatial	
	Add.	Add. Dom.
β	72.53 (69.66, 75.08)	72.27 (70.04, 74.57)
σ_a^2	31.94 (18.30, 49.85)	25.23 (14.12, 43.96)
σ_d^2	–	22.37 (11.24, 40.11)
τ^2	133.60 (121.18, 144.70)	116.14 (100.51, 127.76)
h^2	0.19 (0.12, 0.28)	0.15 (0.09, 0.26)

Genetic model results, cont'd.



So, $\epsilon \sim N(\mathbf{0}, \tau^2 I_n)$. Consider a spatial model.

Previous approaches to accommodating residual spatial dependence:

- Manipulate the mean function
 - constructing covariates using residuals from neighboring units (see e.g., Wilkinson et al., 1983; Besag and Kempton, 1986; Williams, 1986)
- Geostatistical
 - spatial process formed $AR(1)_{col} \otimes AR(1)_{row}$ (Martin, 1990; Cullis et al., 1998)
 - classical geostatistical method (Zimmerman and Harville, 1991)

All are computationally feasible, but **ad hoc** and/or **restrictive** from a modeling perspective.

Spatial model for genetic trials:

$$Y(\mathbf{s}_i) = \mathbf{x}^T(\mathbf{s}_i)\beta + a_i + d_i + w(\mathbf{s}_i) + \epsilon_i,$$

- $\mathbf{a} = [a_i]_{i=1}^n \sim MVN(\mathbf{0}, \sigma_a^2 \mathbf{A})$
- $\mathbf{d} = [d_i]_{i=1}^n \sim MVN(\mathbf{0}, \sigma_d^2 \mathbf{D})$
- $\mathbf{w} = [w(\mathbf{s}_i)]_{i=1}^n \sim MVN(\mathbf{0}, \sigma_w^2 C(\theta))$
- $\epsilon = [\epsilon_i]_{i=1}^n \sim N(\mathbf{0}, \tau^2 I_n)$

Tools used to estimate parameters:

- Markov chain Monte Carlo (MCMC) - iterative
 - Gibbs sampler ($\beta, \mathbf{a}, \mathbf{d}, \mathbf{w}$)
 - Metropolis-Hastings and Slice samplers (θ)

Here MCMC is computationally infeasible because of Big-N!

Trick to sample genetic effects:

Gibbs draw for random effects, e.g., $\mathbf{a} | \cdot \sim MVN(\boldsymbol{\mu}_{a|\cdot}, \Sigma_{a|\cdot})$, where calculating $\Sigma_{a|\cdot} = \left[\frac{1}{\sigma_a^2} \mathbf{A}^{-1} + \frac{I_n}{\tau^2} \right]^{-1}$ is **computationally expensive!**

However \mathbf{A} and \mathbf{D} are known, so use initial spectral decomposition i.e., $\mathbf{A}^{-1} = P^T \Lambda^{-1} P$.

Thus, $\Sigma_{a|\cdot} = P^T \left(\frac{1}{\sigma_a^2} \Lambda^{-1} + \frac{1}{\tau^2} I \right)^{-1} P$ to achieve computational benefits.

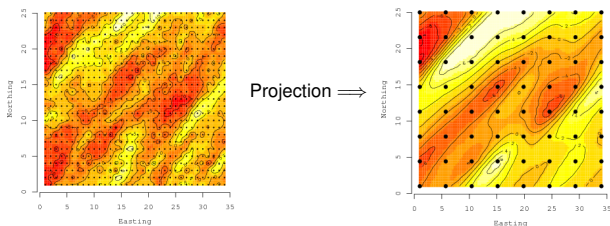
Unfortunately, this *trick* does not work for \mathbf{w} . Rather, we proposed the knot-based *predictive process*.

Corresponding *predictive process* model:

$$Y(\mathbf{s}_i) = \mathbf{x}^T(\mathbf{s}_i)\beta + a_i + d_i + \tilde{w}(\mathbf{s}_i) + \epsilon_i,$$

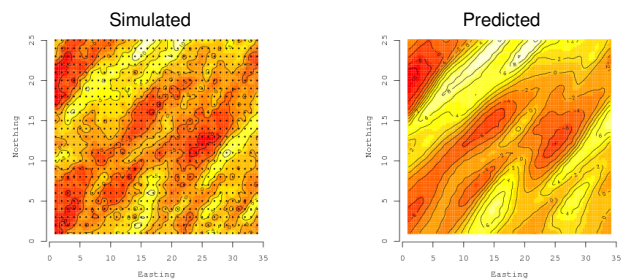
$$\bullet \tilde{w}(\mathbf{s}_i) = \mathbf{c}(\mathbf{s}_i; \theta)^T C(\theta)^{-1}(\theta) \mathbf{w}^*$$

where, $\mathbf{w}^* = [w(\mathbf{s}_i^*)]_{i=1}^m \sim MVN(\mathbf{0}, C^*(\theta))$ and $C^*(\theta) = [C(\mathbf{s}_i^*, \mathbf{s}_j^*; \theta)]_{i,j=1}^m$



\tilde{w} can accommodate complex spatial dependence structures, E.g., anisotropic Matérn correlation function:

$\rho(\mathbf{s}_i, \mathbf{s}_j; \theta) = (1/\Gamma(\nu)2^{\nu-1}) (2\sqrt{\nu d_{ij}})^\nu \kappa_\nu(2\sqrt{\nu d_{ij}})$, where $d_{ij} = (\mathbf{s}_i - \mathbf{s}_j)^T \Sigma^{-1} (\mathbf{s}_i - \mathbf{s}_j)$, $\Sigma = G(\psi)\Lambda^2 G^T(\psi)$. Thus, $\theta = (\nu, \psi, \Lambda)$.



Genetic + spatial effects models

- Candidate spatial models (i.e., specifications of $C^*(\theta)$):
 - 1 $AR(1)_{col} \otimes AR(1)_{row}$
 - 2 isotropic Matérn
 - 3 anisotropic Matérn
- Each model evaluated using 64, 144, and 256 knot grids.
- Model choice using Deviance Information Criterion (DIC) (Spiegelhalter et al., 2002)

Table: Model comparisons using the DIC criterion for the Scots pine dataset.

Model	p_D	DIC
<i>Non-spatial</i>		
Add.	306.40	15,618.09
Add. Dom.	555.92	15,547.85
<i>Spatial Isotropic</i>		
64 Knots	639.77	14,877.51
144 Knots	739.61	14,814.89
256 Knots	802.29	14,771.64
<i>Spatial Anisotropic</i>		
64 Knots	678.82	14,884.13
144 Knots	748.89	14,823.90
256 Knots	806.46	14,781.53

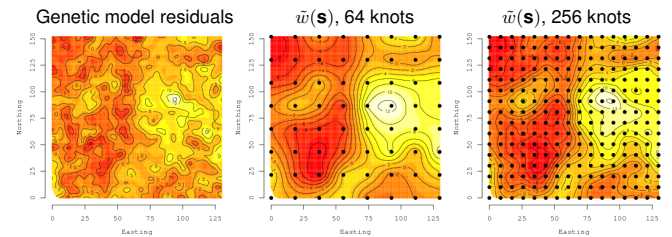
Genetic + spatial effects models results

Parameter credible intervals, 50% (2.5%, 97.5%) for the isotropic Matérn and 64 and 256 knots Scots pine trial.

Parameter	Spatial	
	64 Knots	256 Knots
β	72.53 (69.00, 76.05)	74.21 (69.66, 79.66)
σ_a^2	26.87 (17.14, 41.82)	33.03 (18.19, 53.69)
σ_d^2	11.69 (6.00, 34.27)	13.96 (7.65, 27.05)
σ_w^2	41.84 (23.71, 73.34)	50.36 (30.24, 88.10)
τ^2	89.55 (72.11, 99.65)	80.75 (67.90, 96.16)
ν	0.83 (0.31, 1.46)	0.47 (0.26, 1.28)
ϕ	0.05 (0.02, 0.09)	0.04 (0.02, 0.09)
Eff. Range	71.00 (44.66, 127.93)	74.59 (45.22, 129.83)
h^2	0.21 (0.13, 0.31)	0.25 (0.15, 0.39)

- Decrease in τ^2 due to removal of spatial variation, results in increase in h^2 (i.e., ~ 0.25 vs. ~ 0.15 with confounding).

Genetic + spatial effects models results, cont'd.



Predictive process – balance model richness with computational feasibility (e.g., $4,970 \times 4,970$ vs. 64×64).

Summary

Challenge - to meet modeling needs:

- ensure computationally feasible
 - reduce algorithmic complexity = cheap tricks (e.g., spectral decomp. of \mathbf{A} prior to MCMC)
 - reduce dimensionality = *predictive process*
- maintain richness and flexibility
 - focus on the model **not** how to estimate the parameters = embrace new tools (MCMC) for estimating highly flexible hierarchical models
- truly acknowledge sources of uncertainty
 - propagate uncertainty through hierarchical structures (e.g., recognize uncertainty in $C(\theta)$)