

Spatial and competition effects in tree breeding





- ▶ **Spatial** auto-correlation and **Competition** effects (*a.k.a.* Indirect Genetic Effects):
 - ▶ Motivation
 - ▶ Diagnostic tools
 - ▶ Statistical models available in **breedR** (Muñoz and Sanchez 2016, Poster **#S6.6**)
 - ▶ Examples using real Douglas-*fir* trial



Spatial autocorrelation

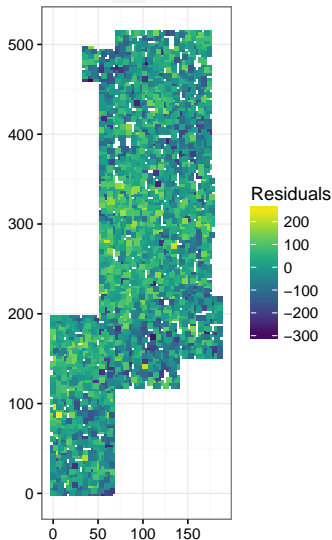


Motivation

- ▶ **Environmental** sources of variation
- ▶ **Bias** genetic estimates
- ▶ Recommended to **routinely** include spatial effects (Gilmour, Cullis, and Verbyla 1997; Dutkowski et al. 2002)

Diagnosis of spatial autocorrelation I

Residuals plot from *genetic-only* model



► Does this look like **random** noise?

► hint: no

Diagnosis of spatial autocorrelation II

Autocorrelation indices (e.g. Moran's I , Geary's C , etc.)

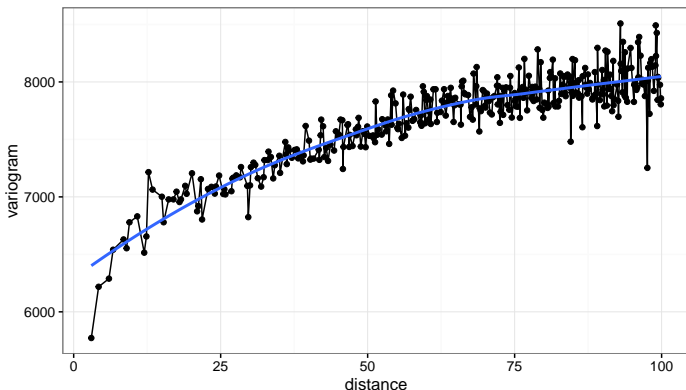
- ▶ $I \in [-1, 1]$
- ▶ Under H_0 : no spatial-autocorrelation, $E[I] = 0$

```
##  
## Moran I test under randomisation  
##  
## data: resid.df$Residuals  
## weights: doug_s1.wnb  
##  
## Moran I statistic standard deviate = 18.103, p-value < 2.2e-16  
## alternative hypothesis: greater  
## sample estimates:  
## Moran I statistic      Expectation      Variance  
##      0.2668934056      -0.0002570033      0.0002177654
```

Diagnosis of spatial autocorrelation III

Empirical (isotropic) semivariogram

$$\gamma(h) = \frac{1}{2}V[Z(\mathbf{u}) - Z(\mathbf{v})], \quad \text{dist}(\mathbf{u}, \mathbf{v}) = h$$

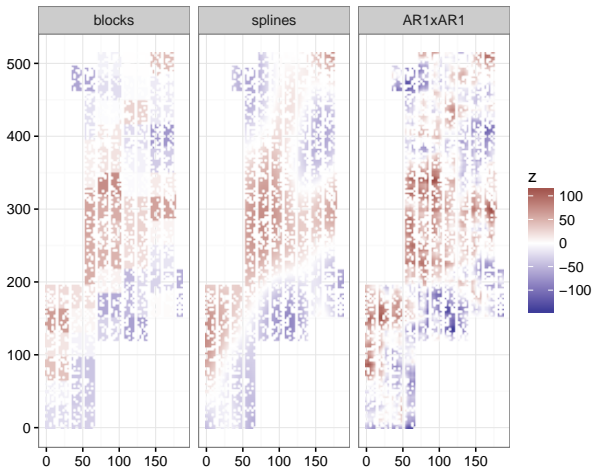




- ▶ 2-steps:
 1. **Remove spatial trend** with whatever spatial interpolation technique
 2. Model the spatially *adjusted* phenotype
- ▶ single-step: (generally preferable)
 - ▶ Use an **spatial effect** to account for autocorrelation
 - ▶ Including a **blocks** effect is sometimes good enough

Example of fitted spatial effects

Alternative spatial effects implemented into breedR





Competition

Competition effects

a.k.a. Indirect Genetic Effects

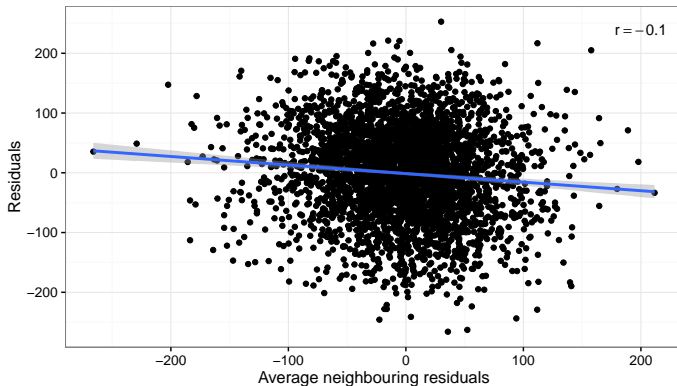
Motivation

- ▶ Some of the most fast-growing individuals can be extremely competitive, hampering **overall performance**
- ▶ *“IGEs can have profound effects on both the magnitude and the direction of response to selection”* (P. Bijma 2013)
- ▶ *“IGEs may enhance or diminish the response to natural or artificial selection”* (Costa e Silva et al. 2013)

Diagnosis of Competition I

Plot of residuals vs average neighbouring residuals

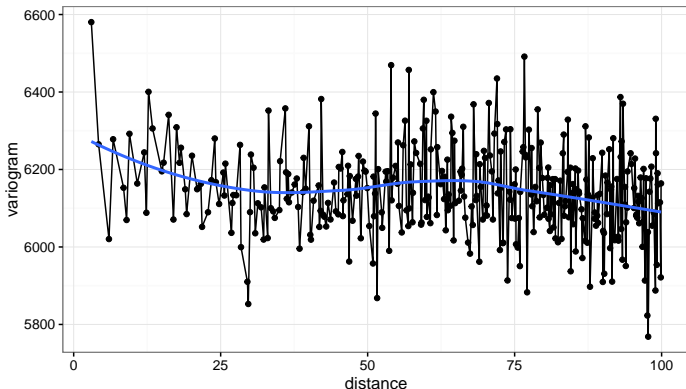
Negative correlation, after accounting for Direct Genetic Effects and Spatial Autocorrelation



Diagnosis of Competition II

Variogram assessment

Peak at the first lag in the variogram of residuals, after accounting for direct genetic effects and spatial autocorrelation



Diagnosis of Competition III

Model comparison

Compare (e.g. AIC) Competition model vs. DGE + Spatial effect

	Competition	Genetic.spatial
AIC	47965	47974
Direct	6235	6515
Competition	193	NA
Spatial	1356	1188
Residual	9457	9551

Competition model assumptions

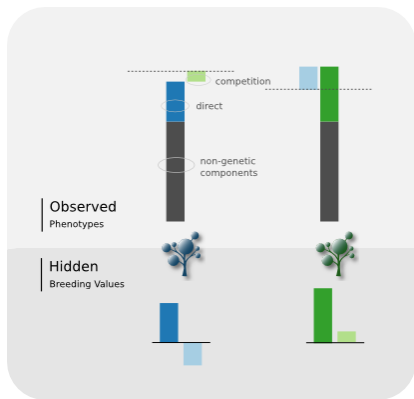
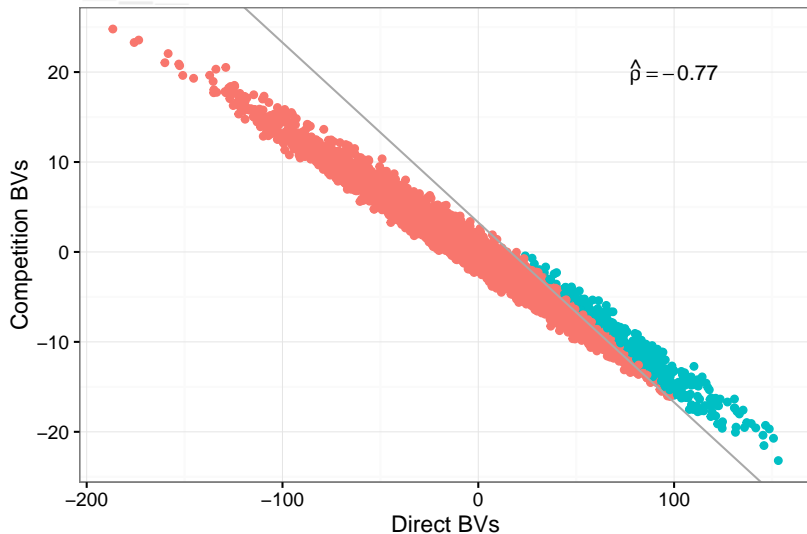


Figure 1: Competition model

- ▶ Each individual have **two** (unknown) Breeding Values (BV):
 - ▶ direct BV affects its **own** phenotype,
 - ▶ competition BV affects its **neighbours'**
- ▶ The total effect of the neighbouring competition BVs is given by their **distance-weighted sum**


Breeding under competition



Questions?



  famuvie

 <http://famuvie.github.io/breedR/>

 Poster #S6.6

 Code for reproduction 



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References

- Bijma, P. 2013. "The Quantitative Genetics of Indirect Genetic Effects: A Selective Review of Modelling Issues." *Heredity* 112 (1). Nature Publishing Group: 61–69. doi:10.1038/hdy.2013.15.
- Costa e Silva, João, Brad M. Potts, Piter Bijma, Richard J. Kerr, and David J. Pilbeam. 2013. "Genetic Control of Interactions Among Individuals: Contrasting Outcomes of Indirect Genetic Effects Arising from Neighbour Disease Infection and Competition in a Forest Tree." *New Phytologist* 197 (2): 631–41. doi:10.1111/nph.12035.
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- Gilmour, Arthur R., Brian R. Cullis, and Arūnas P. Verbyla. 1997. "Accounting for Natural and Extraneous Variation in the Analysis of Field Experiments." *Journal of Agricultural, Biological, and Environmental Statistics* 2 (3): 269+. doi:10.2307/1400446.
- Muñoz, Facundo, and Leopoldo Sanchez. 2016. "BreedR: Statistical Methods for Forest Genetic Resources Analysts." <http://famuvie.github.io/breedR/>.