

breedR: statistical methods for forest genetic resources analysis

Facundo Munoz, Leopoldo Sanchez Rodriguez

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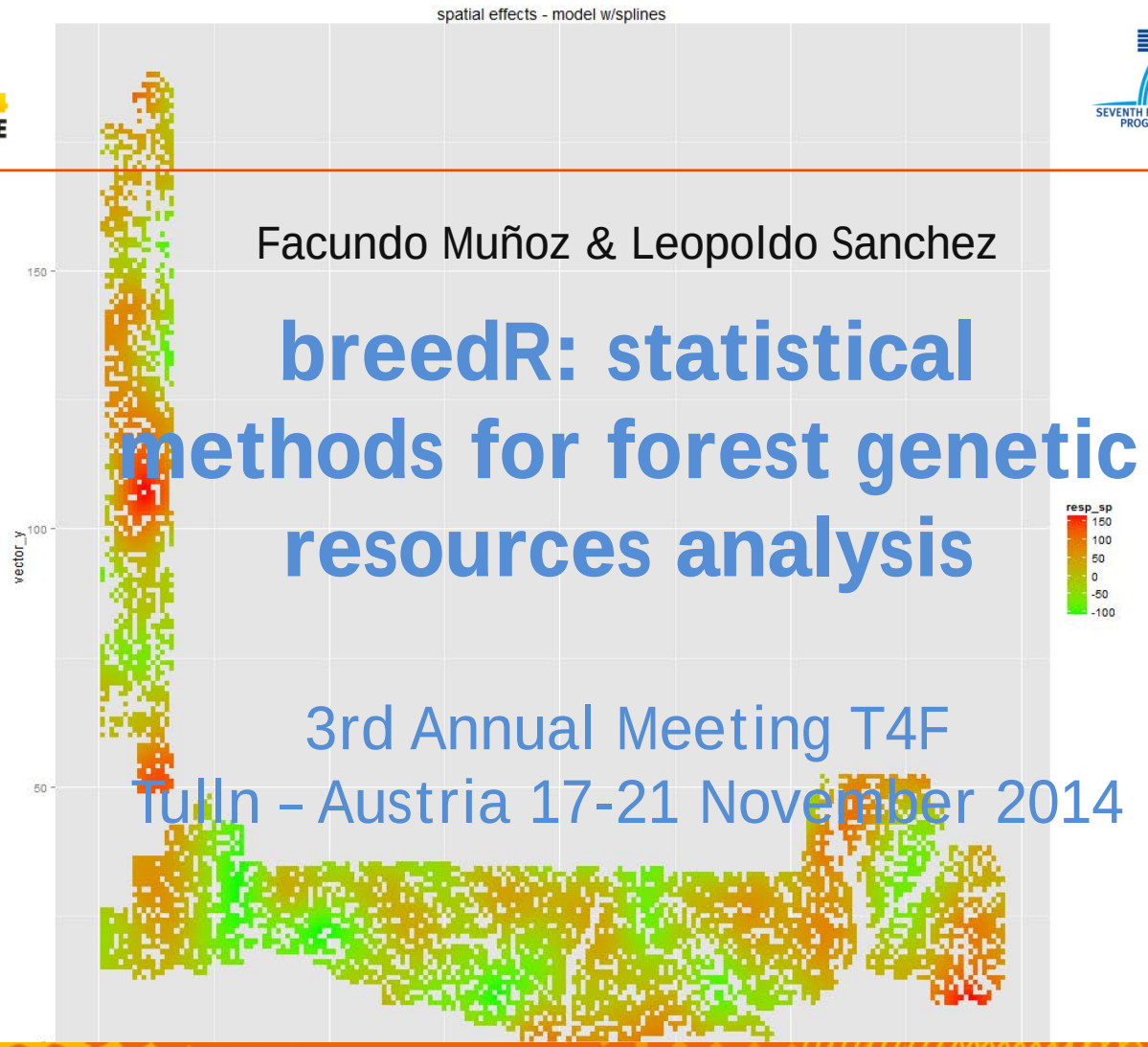
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Facundo Muñoz & Leopoldo Sanchez

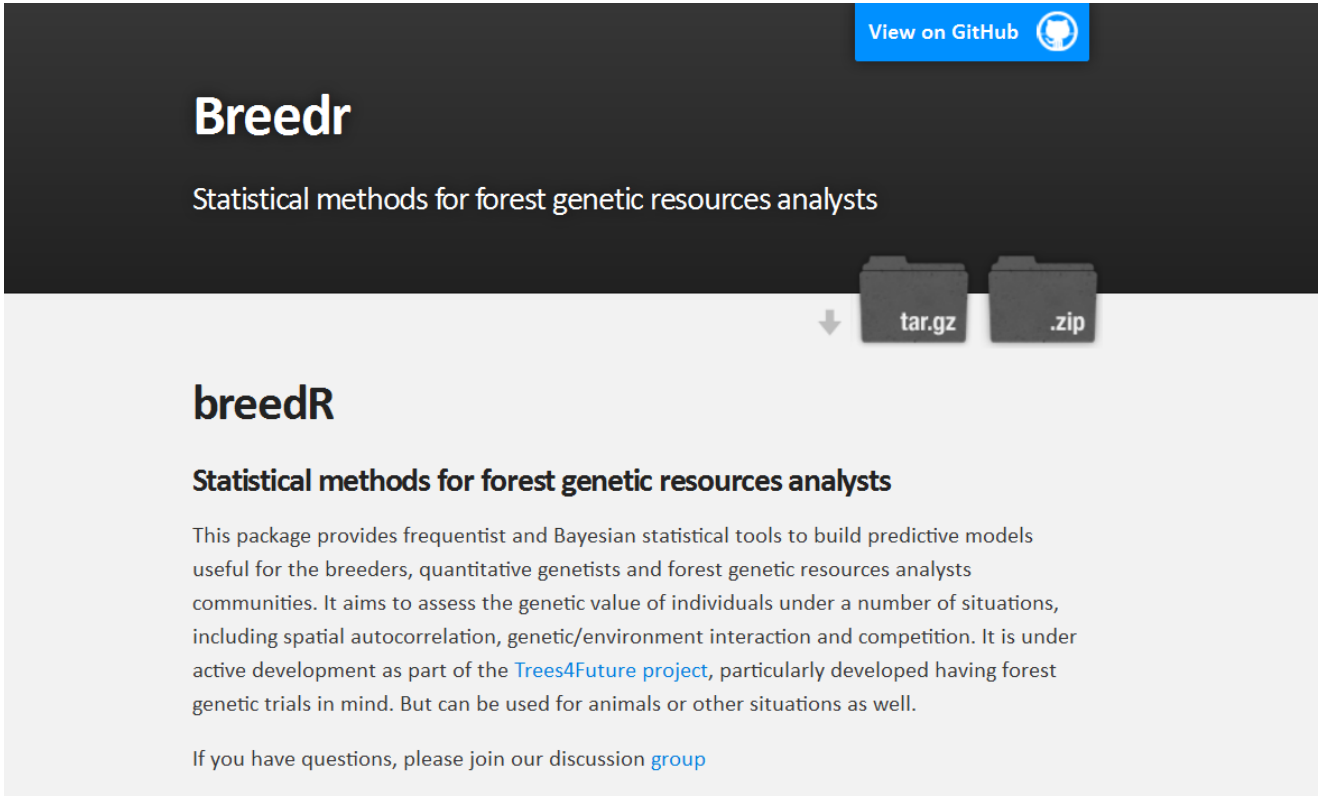
breedR: statistical methods for forest genetic resources analysis

3rd Annual Meeting T4F

Tulln – Austria 17-21 November 2014

Where to get BreedR?

- BreedR general web page: http://famuvie.github.io/breedR/
- BreedR Forge: https://github.com/famuvie/breedR



BreedR demo

- R-package implementing **statistical models** specifically suited for forest genetic resources evaluation.
- Ultimately Mixed Models, flexible, easy to implement and use
- **BreedR** acts as an **interface** which provides the means to:

1. **Combine** any number of explanatory factors into these models
2. Compute automatically **incidence** and **covariance matrices** (from explanations to data) from a few input parameters
3. **Fit** the model
4. Plot data and results, and perform **model diagnostics**

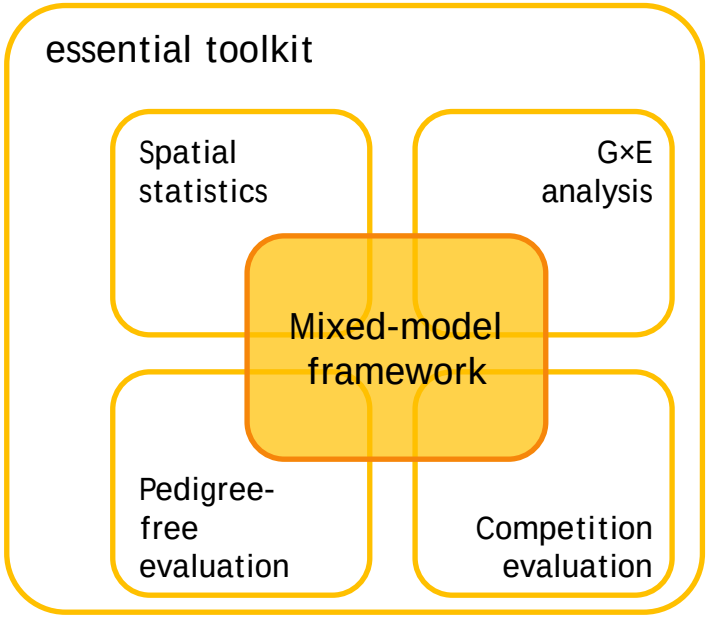
BreedR demo

- Mixed model:

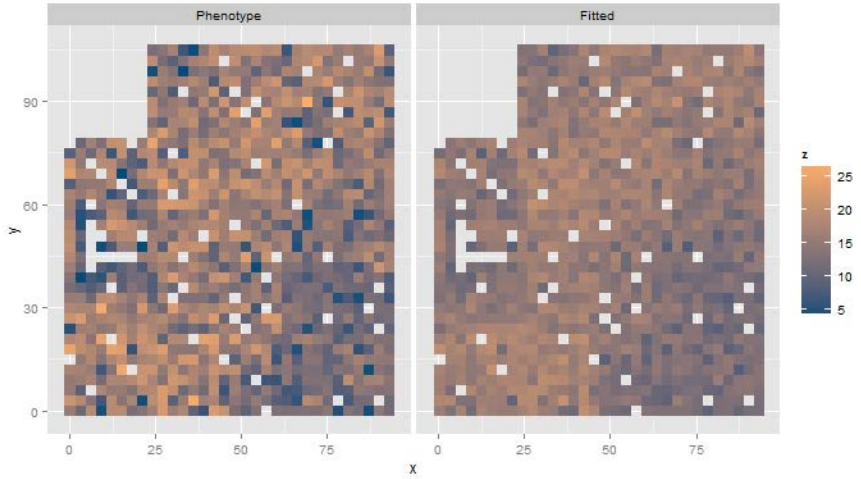
$$y = \mu + \beta x + Zu + \varepsilon$$

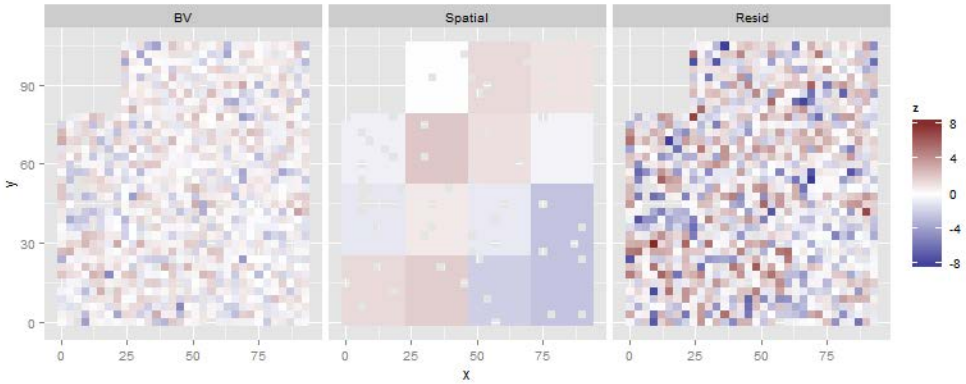
- Progeny testing:

  ✓ estimation of variance components
  ✓ prediction of breeding values



BreedR demo

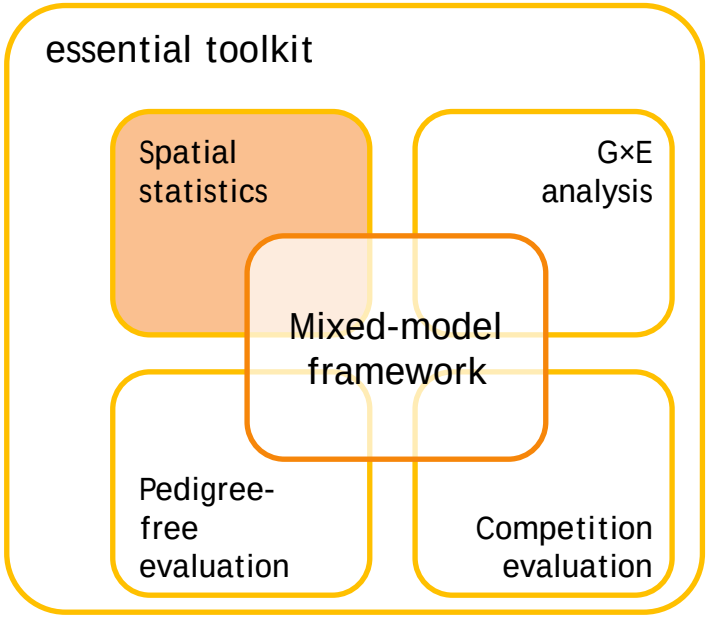




output example with globulus data set

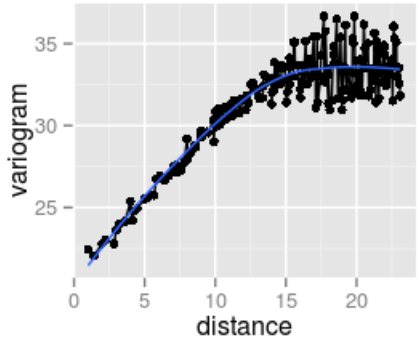
BreedR demo

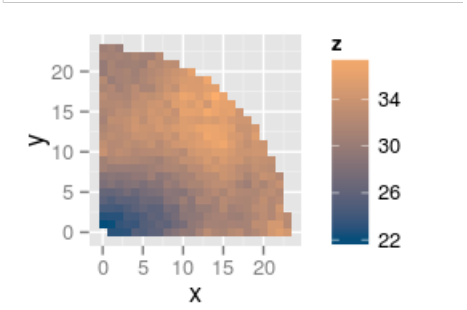
- **Spatial models**
- trials often occupy heterogeneous environments, partially accounted for by devising a priori block designs
- alternatives (BreedR) propose accounting for heterogeneity a posteriori together with the fitting of the evaluation model
- gain in flexibility whenever there is faulty design either by conception or by ageing of trial
- take the form of individual-tree mixed models

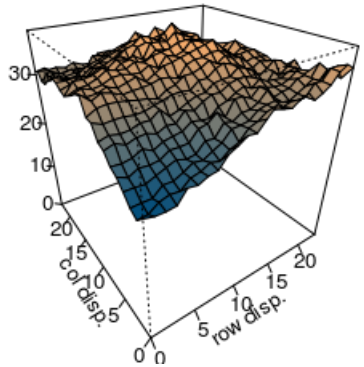


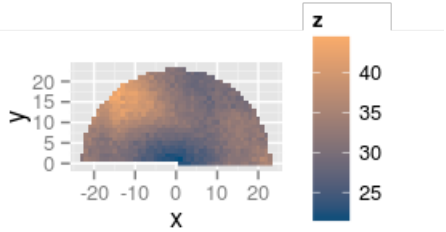
BreedR demo

without spatial adjustments

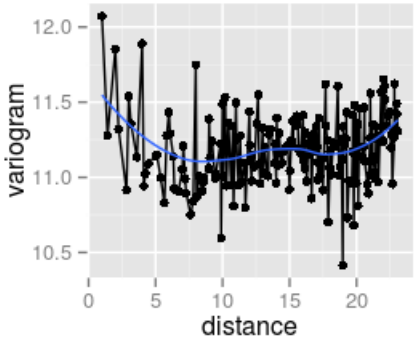


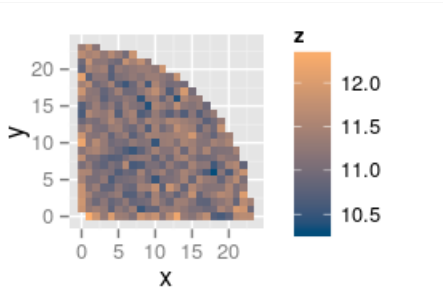


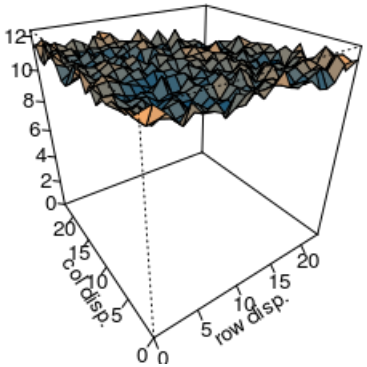


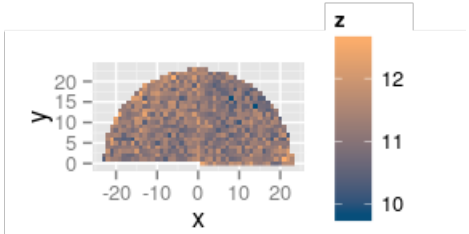


with spatial adjustments







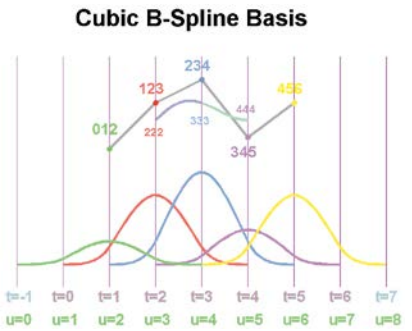


Variograms: diagnosis of spatially distributed patterns of residual variation

BreedR demo

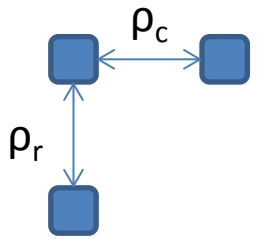
B-Splines model

• A continuous and smooth spatial surface built from a linear combination of basis functions, whose coefficients are modelled as a random effects

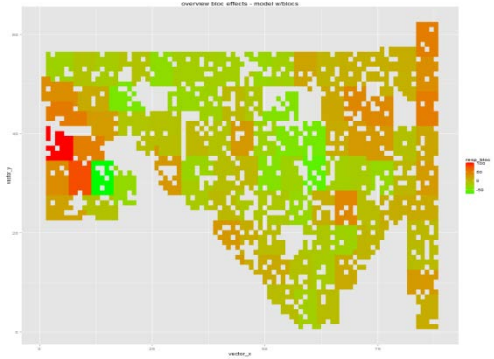


Autoregressive model

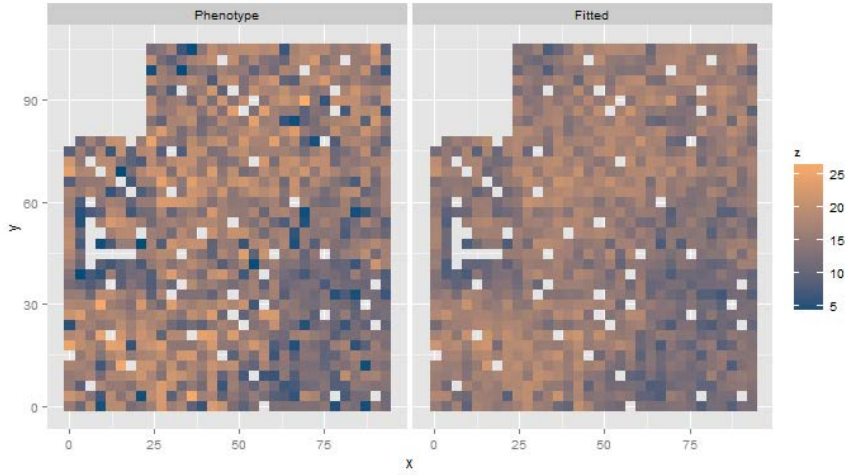
• A separable kronecker product of First order Autoregressive processes on the rows and the colums

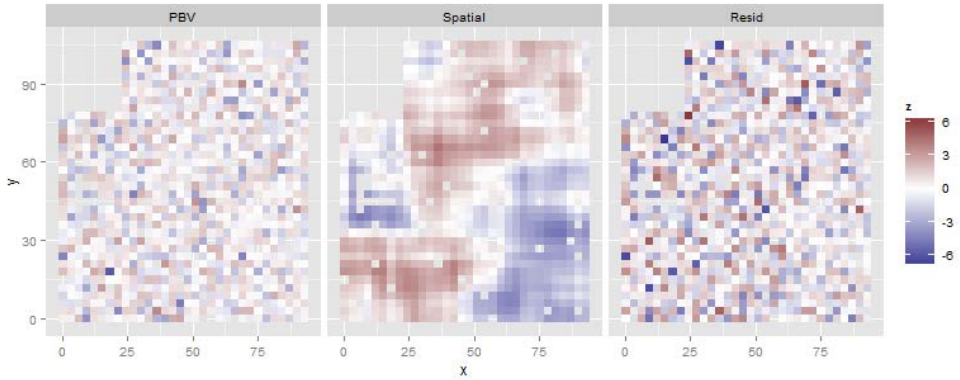


and old good Blocks models!



BreedR demo

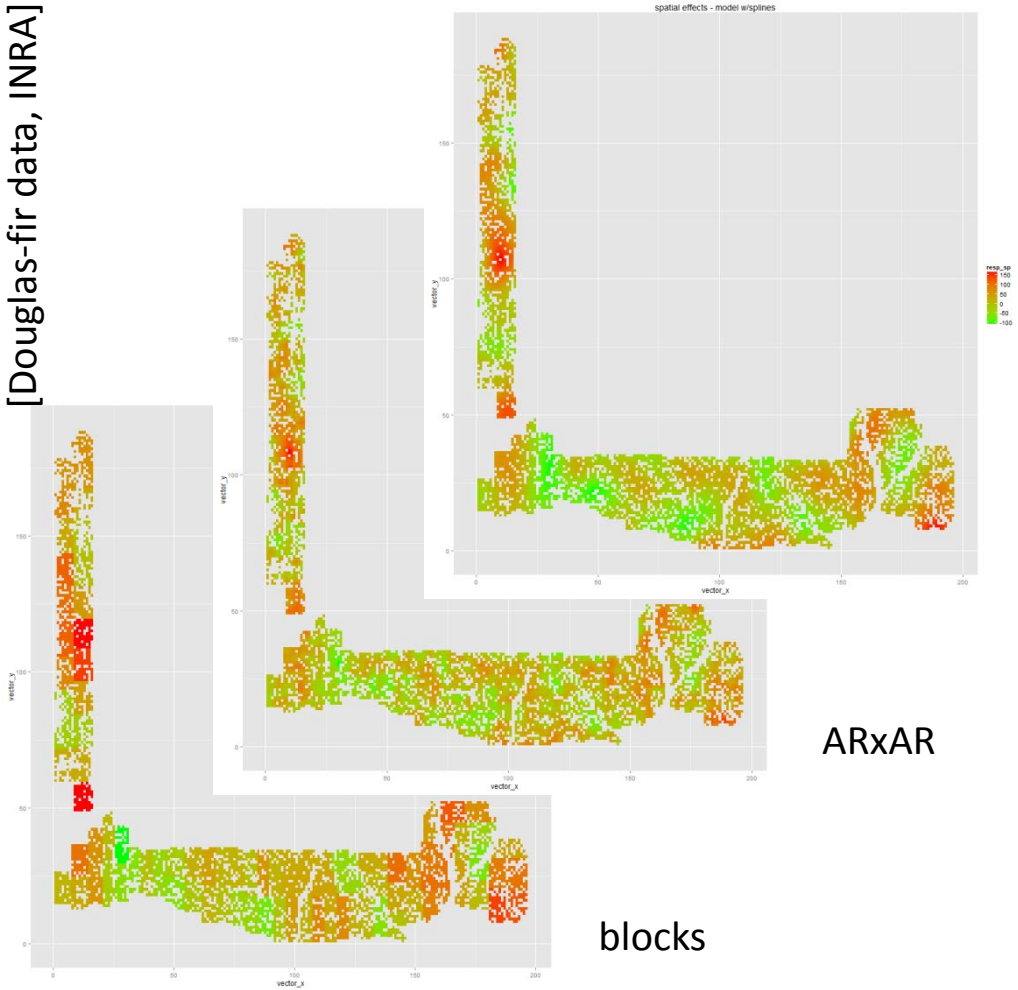




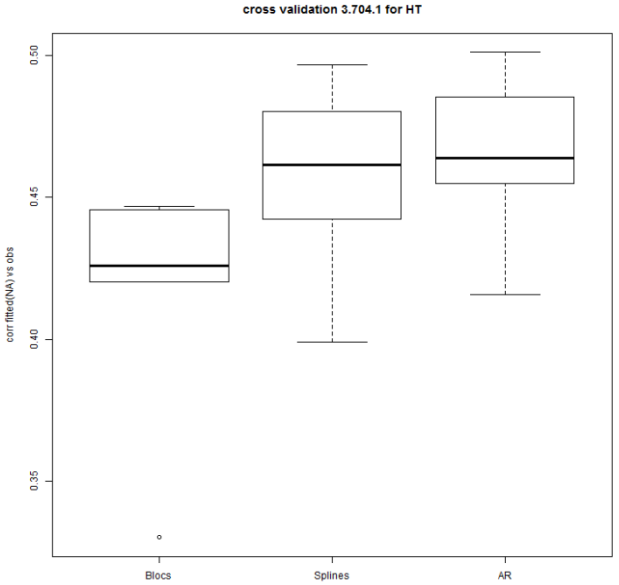
output example with *globulus* data set and spatial models

BreedR demo

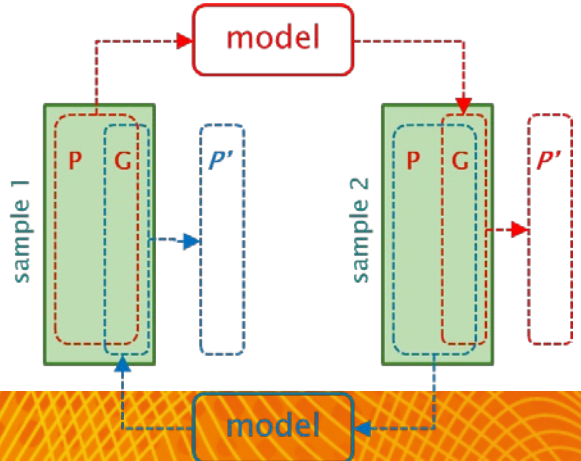
[Douglas-fir data, INRA]



Splines



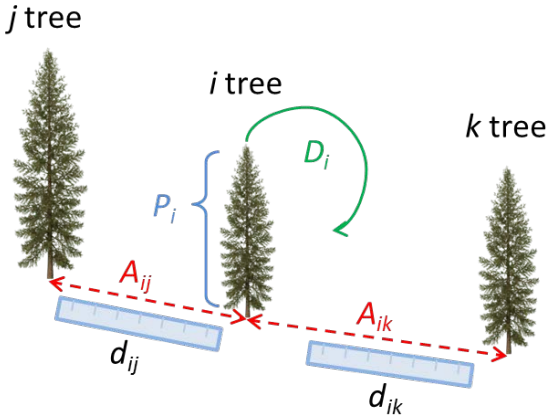
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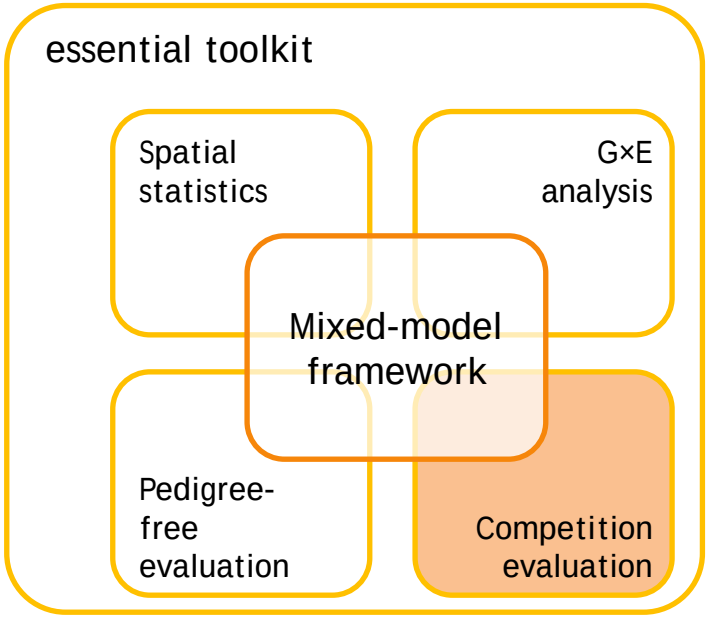
blocks

BreedR demo

- Competition models
- Competition reflects the impairing interplay of closely growing trees, often when local resources are limiting

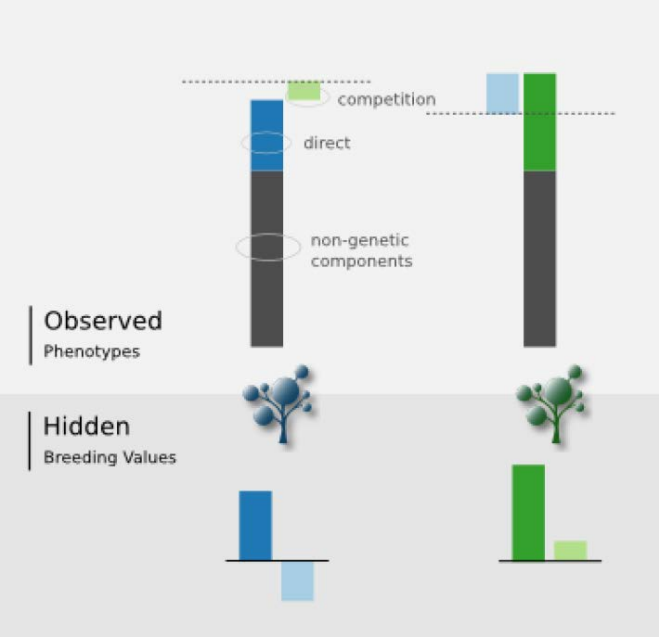


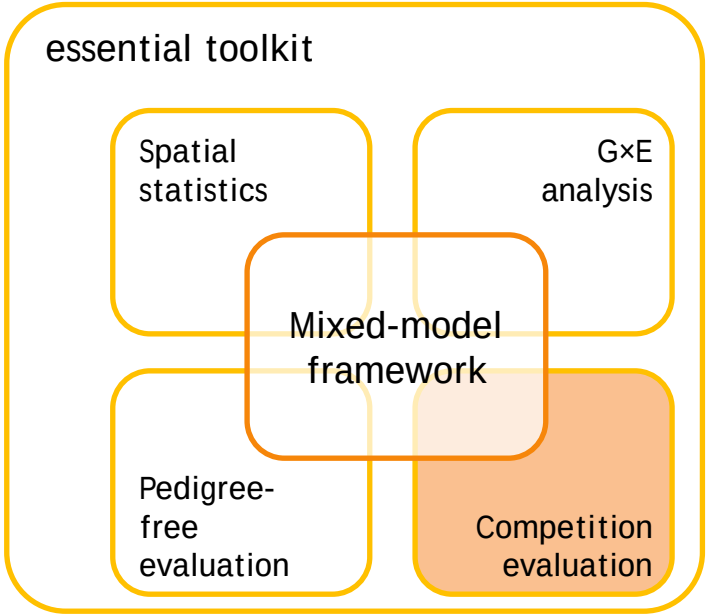
- Competition: an antagonism between direct and associative effects, that results ultimately into impaired phenotypes



BreedR demo

- Competition models





BreedR demo

- Other models developments to come in 2015

- multiple traits, multiple sites
- G by E
- longitudinal data
- Selection tools (index selection)
- Bayesian inference

