breedR: statistical methods for forest genetic resources analysis
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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
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

essential toolkit

- Spatial statistics
- G\times E analysis
- Mixed-model framework
- Pedigree-free evaluation
- Competition evaluation
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
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 columns

and old good Blocks models!
BreedR demo

output example with *globulus* data set and spatial models
BreedR demo

Douglas-fir data, INRA

Splines

ARxAR

blocks

Designing Trees for the Future
• 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

**essential toolkit**

Spatial statistics

G×E analysis

Mixed-model framework

Pedigree-free evaluation

Competition evaluation
BreedR demo

- Other models developments to come in 2015
- multiple traits, multiple sites
- G by E
- longitudinal data
- Selection tools (index selection)
- Bayesian inference