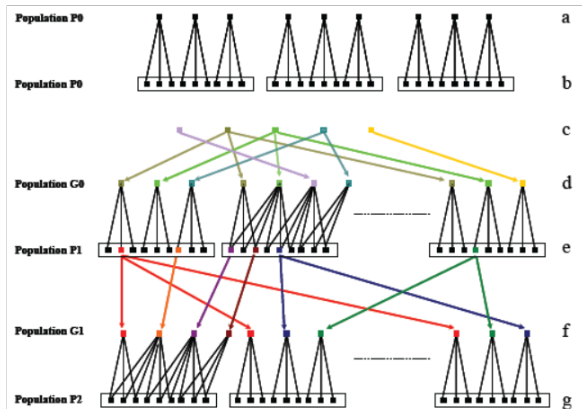


Plan

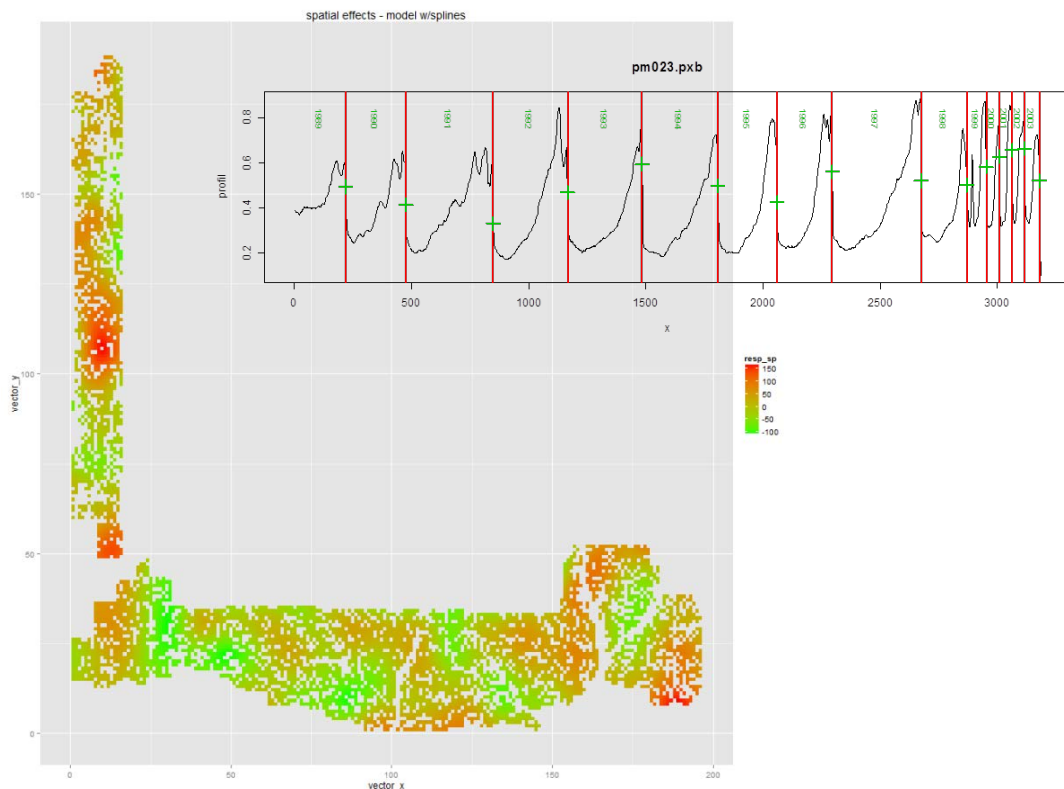
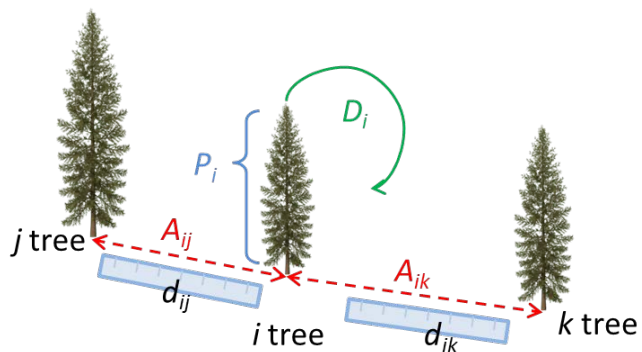
- **Why** do we need this?
- What are the **objectives**?
- What do we **need**?
- Where we are **now**?
- What are the **difficulties**?
- demo

- Statistical modelling: preliminary key step when assessing forest trials
- Experimental data is becoming increasingly complex and massive

[Bouffier thesis, 2007]



Maritime pine pedigree



[Douglas-fir data, INRA]

- Statistical modelling: preliminary key step when assessing forest trials
- Experimental data is becoming increasingly complex and massive
- Appropriate statistical tools are not an easy choice: daunting start for beginners / source of heterogeneity among advanced users
- Need of interchange & expertise & sharing in statistical issues

What are the objectives?

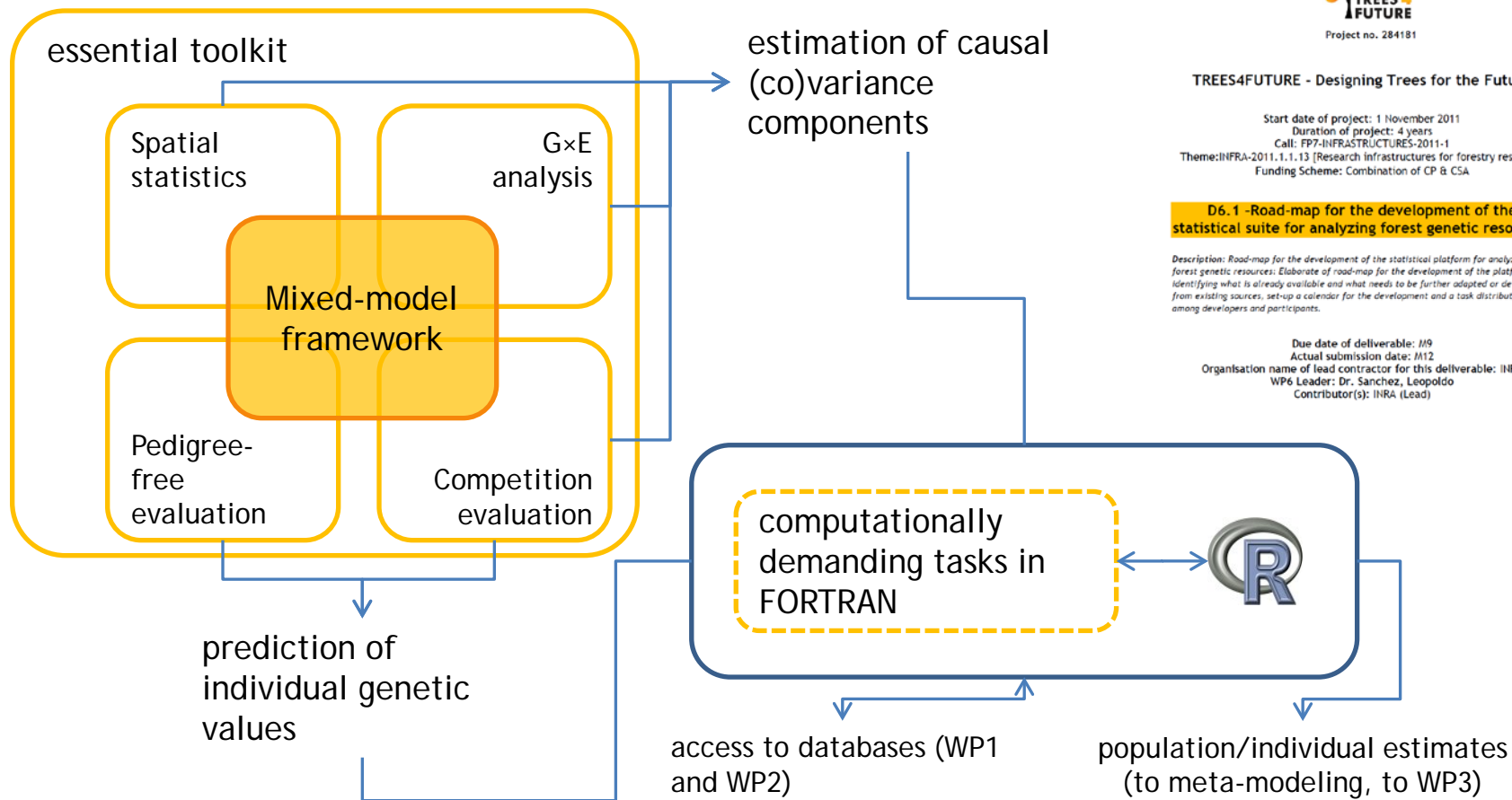
- Seek a consensual *starting seed* package comprising essential and novel statistical tools that are relevant to the community of forest genetics and breeding
- Develop a collaborative effort to make these tools reliable, readily available and conceptually accessible to the community
- Make all developments from publicly accessible open-source components and within a framework that allows for complete openness to new additions by the community of users
- Foster the interchange and expertise on statistical issues within the consortium and beyond

1. Elaborate a development plan, a road-map

D6.1 -Road-map for the development of the statistical suite for analyzing forest genetic resources

Description: Road-map for the development of the statistical platform for analyzing forest genetic resources: Elaborate of road-map for the development of the platform, identifying what is already available and what needs to be further adapted or developed from existing sources, set-up a calendar for the development and a task distribution among developers and participants.

Due date of deliverable: M9
Actual submission date: M12
Organisation name of lead contractor for this deliverable: INRA
WP6 Leader: Dr. Sanchez, Leopoldo
Contributor(s): INRA (Lead)

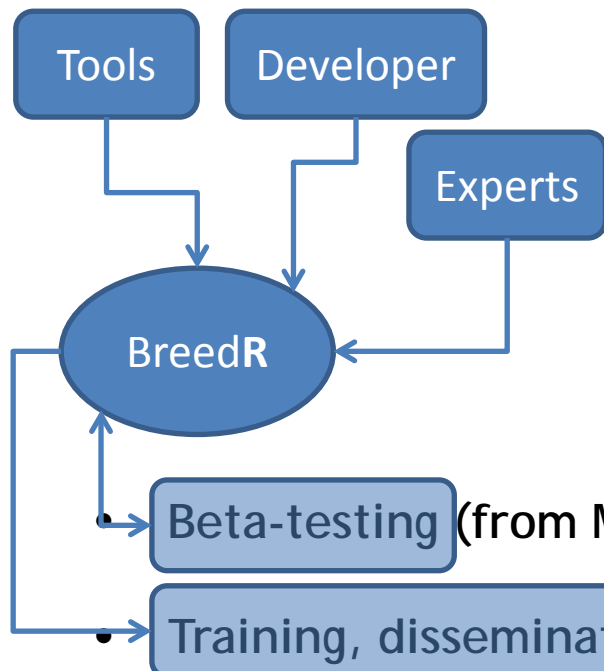


1. Elaborate a development plan, a road-map
2. Identify and test appropriate solutions

Module	Solution	Experts	Degree of accessibility and development
Mixed-model	BLUPF90 publicly available suite of 11 main programs, including several REML procedures and several Bayesian Gibbs samplers for solving general mixed-models. Briefly described in Misztal (2008) and downloadable from [1]	External: Ignacy Misztal, Jon Hallander and Luis Varona; internal: already in use for in-house simulation purposes at INRA	Readily available as FORTRAN90 codes and usable as standalone programs via the appropriate compilation. Some coding is expected and concerns mainly the input and output interfaces with users, among the different codes and with other modules
SS	Collection of independent programs for various phases of spatial analyses and developed by Eduardo Cappa and collaborators, and made available to T4F. Firstly described in Cappa and Cantet (2007)	External: Eduardo Cappa	Readily available as FORTRAN77 codes and usable as standalone programs via the appropriate compilation. Some substantial coding is needed in order for it to interface with the mixed-model module
G×E analyses	Module published for the R platform of statistical programming: <i>Agricolae</i> (downloadable from [2]) and random model alternatives as described by Smith et al (2001) and Piepho (1997)	Internal: Catherine Bastien (INRA)	Available as R module, readily usable and modifiable within R. Some substantial coding is needed in order for it to interface with the mixed-model module

1. Elaborate a development plan, a road-map
2. Identify and test appropriate solutions
3. **Organize a community for development/testing/training/dissemination**
 - **recruitment of a mathematician / developer**
September 2013 (up to end of T4F): development and integration of the different programs with help from local INRA team
 - **involving external experts into our development**
Up to 6 external experts with gradual involvements from late-2013 onwards
 - **setting-up a network of beta-testers**
Mostly belonging to T4F consortium: 13 people, 12 participants & up to 32MM + several volunteers without MM + several users outside T4F

- Programming and development



months		M20	M21	M22	M23	M24	M25	M26	M27	M28	M29	M30	M31	M32	M33	M34	M35	M36	M37	M38	M39	M40	M41	M42	M43
MM	developer	1	1	1	1		1	1	1	1	1														
	expert	0.25	0.25	0.25	0.25	0.25					0.25								0.5						
SS	developer					1										1									
	expert					0.25										0.5									
GxE	developer													1											
	expert								0.25	0.25	0.25	0.25	0.25	0.25	0.25										
	master								1	1	1	1	1	1	1										
PFEM	developer															1									
	expert								0.25	0.25	0.25	0.25	0.25	0.25	0.25	0.5									
	master								1	1	1	1	1	1	1										
CM	developer																1	1	1						
	expert															0.5	0.25								
Breed Tools	developer											1	1							1	1	1	1	1	1
	expert											0.25	0.25							0.25	0.25	0.25		0.25	0.25
Milestone & deliverable													MS27											D6.2	

1 developer
 0.25 internal expert
 0.25 external expert
 1 Master student

one international workshop and national follow-ups, repositories, wiki-documents, scientific publications using the tool

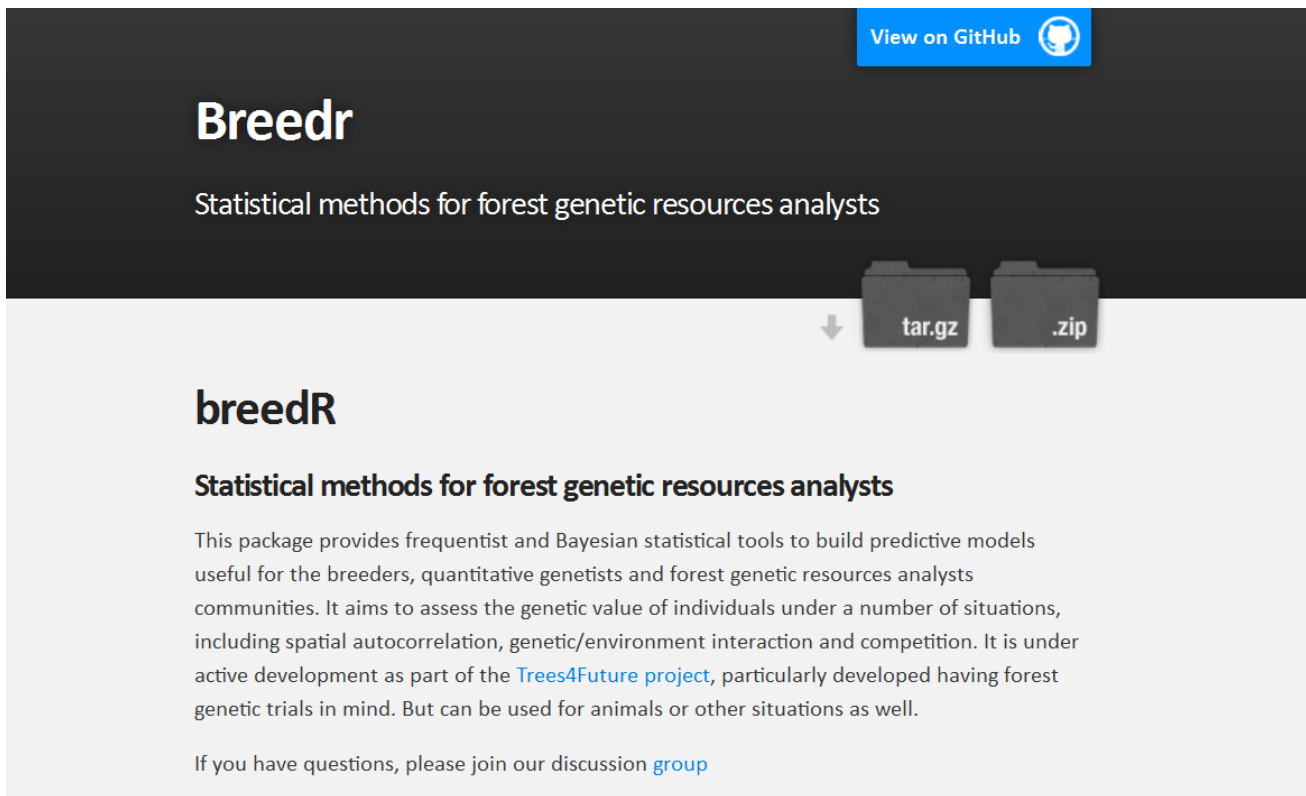
- Development is not a well paved way... but we are succeeding
- We rely very much on our own local circle of testers... but they tend to see things like us
- We desperately need feedback from (T4F) beta-testing

Beta-test NOW!



Where to get BreedR?

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



The screenshot shows the GitHub repository page for BreedR. At the top right, there is a blue button that says "View on GitHub" with the GitHub logo. The main heading is "Breedr" in a large, bold, white font. Below it, the subtitle "Statistical methods for forest genetic resources analysts" is displayed in a smaller white font. In the center, there are two dark gray folder icons labeled "tar.gz" and ".zip", with a downward arrow pointing to them. Below the repository name, the word "breedR" is written in a bold, black font. Underneath, the same subtitle "Statistical methods for forest genetic resources analysts" is repeated. A paragraph of text describes the package: "This package provides frequentist and Bayesian statistical tools to build predictive models useful for the breeders, quantitative genetists and forest genetic resources analysts communities. It aims to assess the genetic value of individuals under a number of situations, including spatial autocorrelation, genetic/environment interaction and competition. It is under active development as part of the [Trees4Future project](#), particularly developed having forest genetic trials in mind. But can be used for animals or other situations as well." At the bottom, there is a link: "If you have questions, please join our discussion [group](#)".

• Thanks!

