A robust and versatile, componentized statistical genetic pipeline for plant breeding

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H³

Within plant breeding new data generating techniques in the field of genotyping, phenotyping, omics and envirotyping present new opportunities for increasing the efficiency of breeding programmes. To take advantage of these developments we provide new statistical techniques and software that can be customized to your specific needs.

High throughput phenotyping

The pipeline embeds new spline based algorithms for spatial and temporal analysis of experiments in the field and on phenotyping platforms.
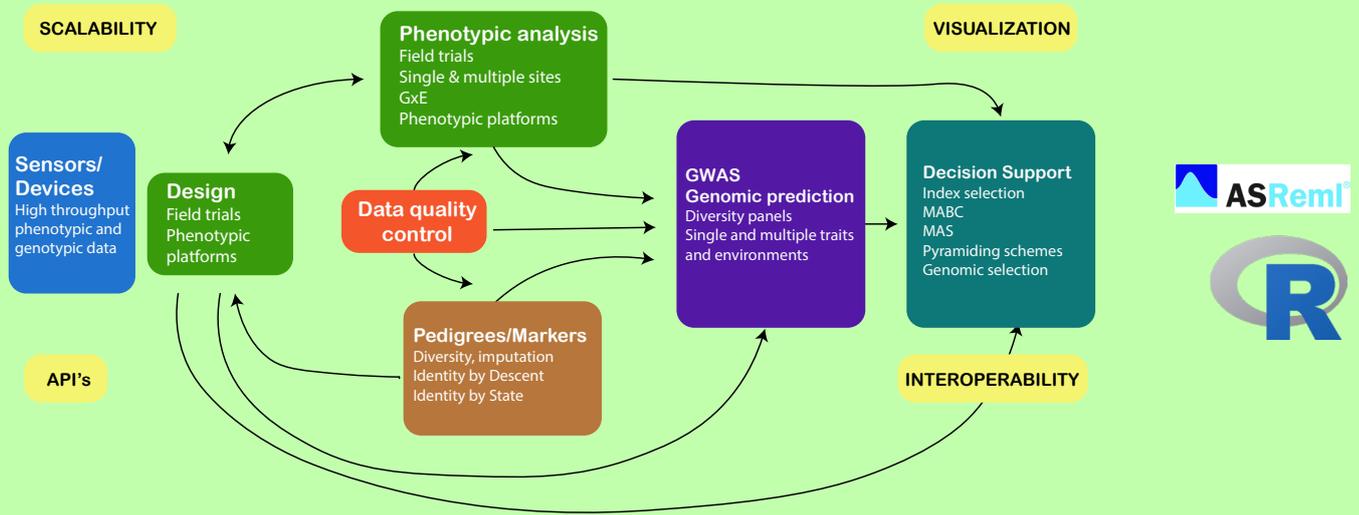
High throughput genotyping

Calculation of IBD probabilities by a special Hidden Markov Model feeds into a universal map construction algorithm for bi- and multi-parental populations of in- and out breeders, diploids and tetraploids. The same HMM facilitates imputation and general QTL mapping.

High throughput data analytics

Extensive suite of mixed model driven methods to investigate and visualize genetic architecture of bi- and multi-parental populations as well diversity panels. Includes single and multiple traits / environments, QTL mapping and genomic prediction.

SCALABILITY

VISUALIZATION

Phenotypic analysis
Field trials
Single & multiple sites
GxE
Phenotypic platforms

Sensors/ Devices
High throughput phenotypic and genotypic data

Design
Field trials
Phenotypic platforms

Data quality control

GWAS Genomic prediction
Diversity panels
Single and multiple traits and environments

Decision Support
Index selection
MABC
MAS
Pyramiding schemes
Genomic selection

ASReml®

R

API's

Pedigrees/Markers
Diversity, imputation
Identity by Descent
Identity by State

INTEROPERABILITY

Why Choose Us?

WAGENINGEN UNIVERSITY & RESEARCH Wageningen University and its associated research collaborations offer unparalleled resource and expertise in bioscience and statistical genetics.

VSNi VSNi is a world leader in the advancement of statistical and data analytical tools and solutions for the biotechnology sector. These tools are widely used in plant and animal breeding both in lab and field applications.

The James Hutton Institute The Information and Computational Sciences (ICS) Group brings together an exceptional combination of expertise from bioinformatics to the modelling of climate information on a geographical scale.

About Us

Drawing on our complementary world-class expertise, tools and experience in plant breeding, analytics and visualization collected in projects in collaboration with the Integrated Breeding Platform, CGIAR institutes, national and EU research programs (e.g. EPPN2020), and breeding companies (e.g. SESVanderHave), Biometris, VSNi and James Hutton have come together to form H3.

The Team

Fred van Eeuwijk, Martin Boer, Chaozhi Zheng, Bart-Jan van Rossum, Maikel Verouden, Willem Kruijer, Ron Wehrens, Emilie Millet, Joao Paulo, Daniela Bustos-Korts, Darren Murray, David Marshall, Iain Milne, Gordon Stephen, Jim Twynam
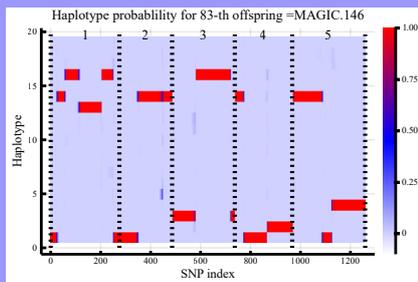
BrAPI compatible

Our pipeline can interoperate with plant breeding data bases, facilitating a smooth access to the phenotypic and genotypic data for the analysis

Intuitive interfaces to powerful analyses

Access standard and advanced methods for single and multi-trial phenotypic analyses with easy to use interfaces such as Shiny, customizable to suit your needs.

Select trials

DRIP05

Select trait

yield

Select model design

row column

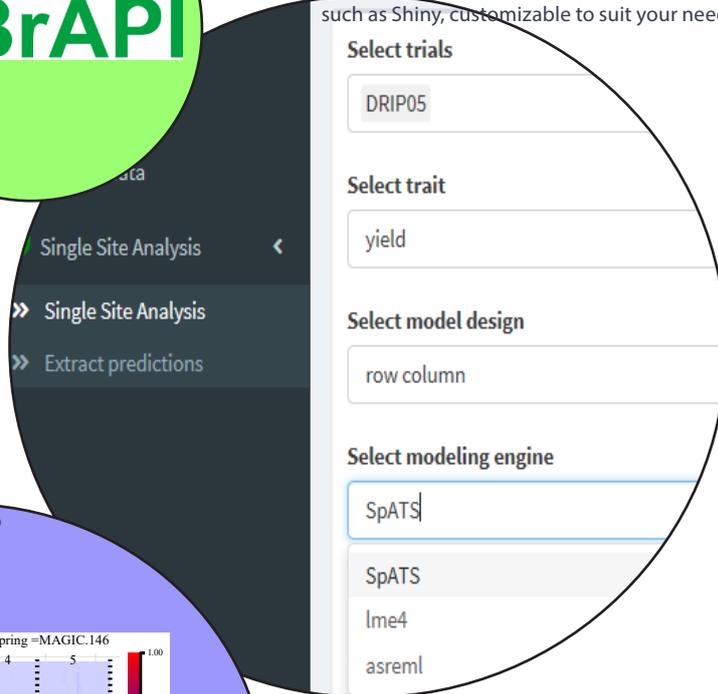**Select modeling engine**

SpATS

SpATS

lme4

asreml

Novel methods for map construction, imputation and calculation of IBD probabilities for traditional and new types of breeding populations

The Reconstructing Ancestral Blocks BIT by bit algorithm uses a continuous time Markov process to trace ancestral history of DNA segments and is at the heart of a set of algorithms for universal genetic map construction and QTL mapping (in combination with mixed model technology).

Flexible procedures for calculating spatially adjusted means for field and phenotyping platform experiments

The pipeline offers several modelling approaches to correct phenotypic data for spatial effects. These approaches range from the traditional mixed models with ARxAR processes to spatial adjustment with 2-dimensional p-splines.

Fast procedures for single and multi-trait / environment QTL analysis

A general and fast mixed model based approach identifies QTLs in bi- and multi-parental populations and diversity panels. Unique facilities for analyzing and visualizing GxE and QTLxE patterns.