

Germinate 2: A platform for Illumina SNP genotyping and high volume phenotypic data.



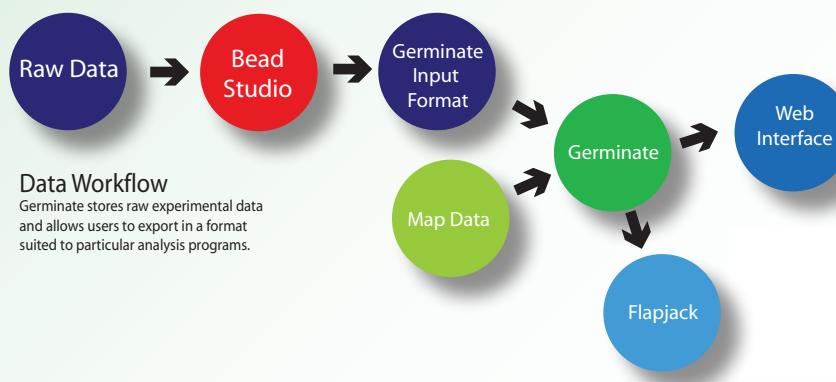
Paul Shaw, Iain Milne, Linda Cardle, Andy Flavell, Robbie Waugh and David Marshall
Scottish Crop Research Institute, Invergowrie, Dundee, Scotland DD2 5DA.



Introduction

Germinate 2 is a generic plant data management platform designed to hold phenotypic, genotypic and passport data and was developed at SCRI. We have recently added components to the system specifically developed and optimised to deal with high throughput genotyping technologies and large scale field trial experiments.

Germinate allows the integration of different data types into a number of export formats suitable for external analysis tools.

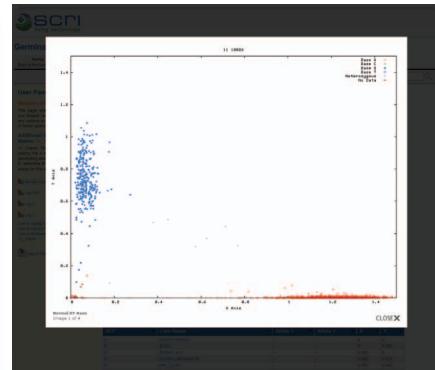


Data Pooling

Information sources for markers are brought together in one place including both internal and external data sources.

Phenotypic Data

The use of interactive Flash based charts is used to display phenotypic data held in the database.



Generated X/Y Signal Plot

In order to determine the quality of called genotypes Germinate can generate scatter plots on the fly from raw experimental data.



Data Export Options

Germinate facilitates the export of data in a number of formats. Data is grouped into experiments and datasets and data is exported using a marker and line grouping which allows the intersection of 2 groups to be exported. In this way complex groupings can be easily defined. The use of these logical groupings also means that if multiple datasets exist on the same genotyping plate they can be distinguished and treated separately for analysis.

Data exported to our genotype visualization application Flapjack (see poster 815) contains embedded information to allow data to be retrieved from the Germinate database from which it was exported.

Additional data export options include the ability to restrict exported data based on data quality filters. The cut-off levels for these filters can be user defined.

Line Passport and Additional Information

All information including annotations on a particular line are available on a single line profile page.



The authors gratefully acknowledge the financial support of the BBSRC and RERAD