

# Bioinformatics Resources at the Scottish Crop Research Institute



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## Introduction

The Plant Bioinformatics Group at SCRI are actively involved in the development of tools to aid cereal researchers. These range from database infrastructure to genotype visualization tools. All of our applications are freely available to the cereals research community. For more information visit our website at <http://bioinf.scri.ac.uk>.

## Germinate - Database Infrastructure Platform

Germinate is a generic plant data management platform implemented in MySQL and is designed to act as a scaffolding on which complex web-based applications can be developed to leverage information from experimentally derived data. Germinate currently handles phenotypic, genotypic and passport data. The system offers users with a standard set of interfaces for interrogation, browsing and displaying of a number of data types and can be easily expanded to add custom functionality depending on the application being developed. It is hoped that Germinate can grow into a stable set of tools on which diverse datasets can be seamlessly integrated using the common platform making interrogation of data from disparate or diverse datasets simpler.



## Hordeum Relator - Linking Barley Data & Resources

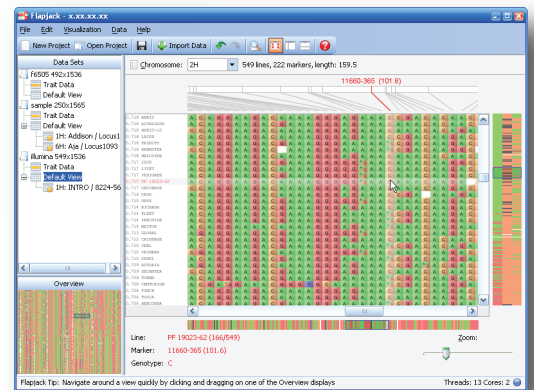
For Hordeum species several different unigene sets have been developed, based on different combinations of ESTs, different software tools and different assembly parameters, many which have been used as a basis for the design of genomics resources. As a result there is a growing need to provide a cross-referencing framework for data integration both within species and to other crop and model organism genomes.

The Hordeum Relator database and website has been developed to meet this need and have been implemented to support barley projects at SCRI. The basis of the application is a cross-referencing database implemented in MySQL which holds the results of regularly updated reciprocal BLAST analysis of the key unigene assemblies together with the EST content of the resulting contigs. In addition, it contains, as appropriate, the results reciprocal blast analyses of these assemblies with the rice and Brachypodium genomes

## Flapjack - Genotype Visualization

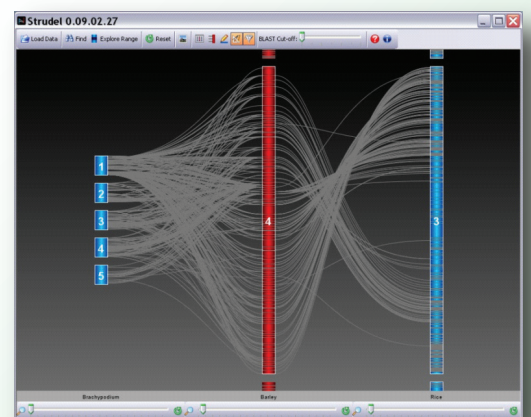
New software tools for graphical genotyping and haplotype visualization are required that can routinely handle the large data volumes generated by the high throughput Illumina SNP platform and comparable genotyping technologies. Flapjack is a visualization tool to facilitate analysis of these data types. Its visualizations are rendered in real-time allowing for rapid navigation and comparisons between lines, markers and chromosomes.

Flapjack provides a number of alternative graphical genotype views with individual alleles coloured by state, frequency or similarity to a given standard line.



## Strudel - Comparative Map Viewer

Strudel is our new graphical tool for visualizing genetic and physical maps of genomes for comparative purposes. The application aims to let the user examine their data at a variety of different levels of resolution, from entire maps to individual markers, and explore syntenic relationships between genomes. All browsing and interaction with Strudel happens in real-time - there is no need to wait while the maps are generated.



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