Tablet, Flapjack, CurlyWhirly and Strudel : SCRI Visualization Tools To Support SNP Discovery, Genotype Analysis & Comparative Mapping

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Tablet: NGS Assembly Visualization

- High-performance visualization and data navigation
- Display of reads in both packed and stacked formats
- File format support for ACE, AFG, MAQ, and SOAP, with experimental SAM
- Import GFF3 features and quickly find/highlight them
- Search and locate reads by name across entire data sets
- Entire-contig overviews, showing data layout or coverage information
- Simple install routine via auto-updating graphical installers
- Support for Windows, Apple OS X, Linux and Solaris, in 32 and 64-bit
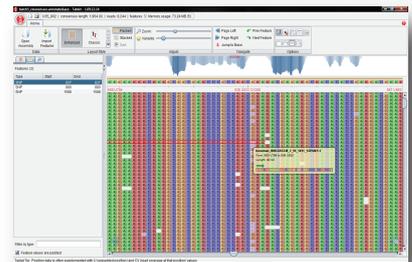
Flapjack: High Density Graphical Genotyping

- Visualizations are rendered in real-time
- Simple formats for map, genotype, trait and QTL data
- Individual alleles coloured by state, frequency or similarity to a given standard line.
- Real time moving of lines or markers, insertions or deletions of data
- Sorting by genotype similarity to other lines, or by trait scores.
- Map based information e.g. QTL positions can be aligned against graphical genotypes
- XML-based project format and export of raw data or image files, Germinate compatibility
- Flapjack readily handles data sets approaching 1 billion (10^9) genotypes in size
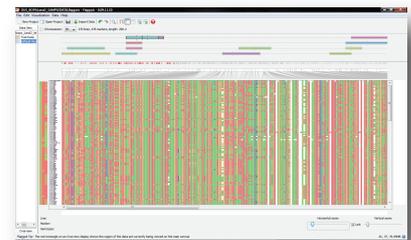

CurlyWhirly : Facile Exploration of 3D Ordination Data

- X,Y,Z data such as PCO or PCA
- Load any kind of numerical data and any number of variables
- Reorient graph to any position for inspection of data
- Zoom graph in and out
- Select which combination of variables to display
- Highlight data points according to category to selectively view data from one or more categories only
- Choose from several background colours
- Display data label with mouseover on data points
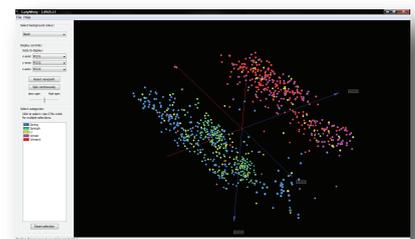
Strudel : Comparative inference across multiple genomes

- Visualize multiple genomes and thousands of homologies interactively and in real time
- Continuous zoom ranging from entire genome views to singles features
- Explore intervals such as QTLs and list annotation for features
- Search for features by name
- Filter homologies on display by BLAST e-value
- Single genome mode also supported
- Ships with example dataset to facilitate familiarization with the software
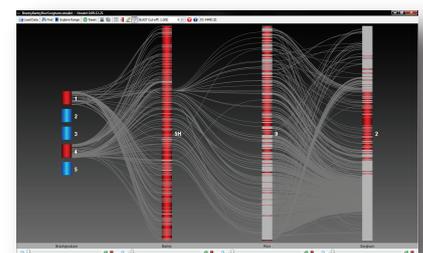
Acknowledgements

See us at:

Allele Mining and Genomic Diversity Workshop 5:40 pm on Saturday
Computer Demos of these tools at 3:10 pm on Wednesday
Posters 323, 029 and 829 (the Germinate 2 Database),
The Barley Workshop 1:50 Saturday, Plant Genome DB Outreach Consortium