Breeding View – what it is?

- Simple graphical interface to conduct statistical analysis of phenotypic and genotypic data
- Can access procedures in Genstat or R-scripts and allows analyses to be configured
- Integrated into the IBP Breeding Management System (BMS)

Breeding View – Rationale for development

- Existing packages are complex
  - Many features that are not relevant
  - Steep learning curve
  - Focus on publication ready graphics
- Majority of Breeders have specific, routine requirements
  - Standard set of analyses
  - Push lots of data quickly
- BV provides a choice of statistical engine (Genstat or R)

Current analysis pipelines

Statistical Analysis of Phenotyping Data

- Single site analysis is available for complete and incomplete block designs as well as row-column designs and spatial analysis.
  - New designs are being added at each update,
  - Analyses can be run in batches over environments and traits,
- Two-stage multi-site analysis is available for GxE and stability analysis with or without grouping of environments,
  - Single pass meta analysis of unbalanced site by season data is being incorporated.
Statistical analysis of Genotyping Data

- Single trait linkage analysis (QTL)
  - Quality control phenotypes (summary statistics)
  - Quality control marker data
  - QTL detection – genome wide scan using single and composite IM
  - Output includes profile plots and tables
  - Results available for automatic viewing in Flapjack
  - HTML report of QTL results

- Multiple trait & environment sequential analysis
  - QTL results for each trait combined
  - Single Flapjack view for all traits

Accessing BV from the BMS
Accessing BV from the BMS

Running an analysis in BV

Output from BV

Saving output to the BMS

To Come

- Ongoing updates to the Genstat and R scripts to support new field designs and analysis types as they are added to the BMS
  - Additional field designs (e.g., Augmented, P-rep)
  - Line x Tester analysis
- All pipelines fully integrated in BMS
- Addition of new pipelines (e.g., multi-site/multi-year analysis)
- Incremental improvements to output and reports
- Improved documentation for all pipelines

To Come

- Ability to add user/community developed R-scripts to BV
- Want to know more? [www.integratedbreeding.net](http://www.integratedbreeding.net)
- Questions about licensing? [s.andrews@cgiar.org](mailto:s.andrews@cgiar.org)
Thanks!