JMP Genomics

Whether you're working in agriculture, pharmacogenomics, biotechnology, or other areas of genomic research, JMP Genomics provides tools to analyze rare and common variants, detect differential expression patterns, find signals in next-generation sequencing data, discover reliable biomarker profiles, and visualize patterns through integrated genomics data analysis workflows.

JMP Genomics combines the industry-leading power of SAS® Analytics with the graphical flexibility of JMP, providing a unique visual exploration interface tailored to understanding the complexity in OMICS data and employing appropriate advanced statistical techniques.

Genetic Marker Analysis for Crop Improvement

The need for innovative, sustainable agricultural practices is one of the world’s most pressing concerns. JMP Genomics allows plant breeders and crop bioscientists to drive the selection of healthier crops by modeling genetic variability, optimizing breeding choices, simulating multiple-trait breeding programs and balancing trade-offs across key desirable traits.

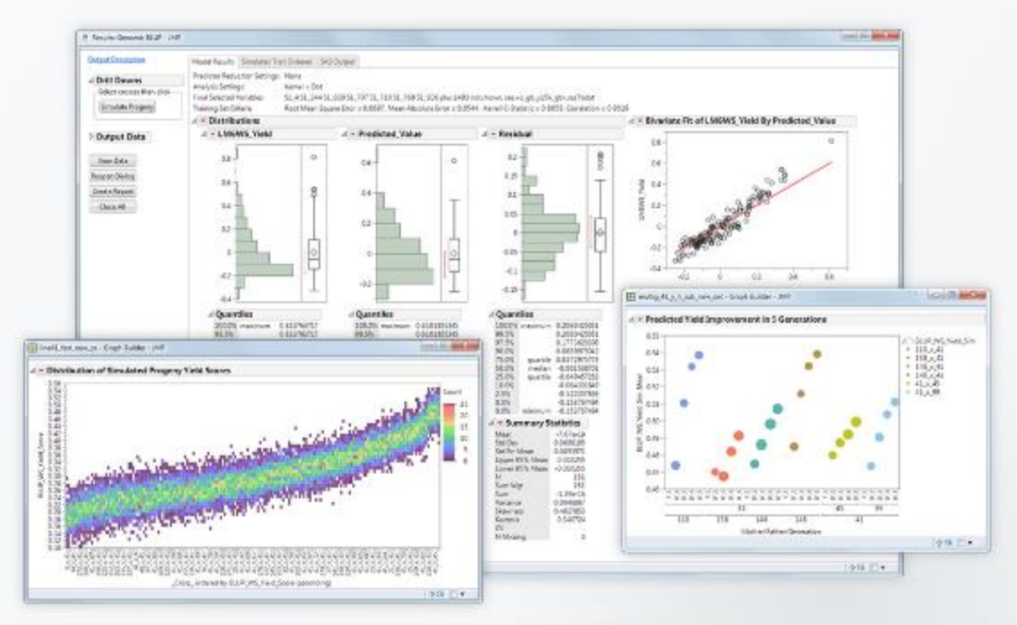
Genomic Selection Analysis Workflow Overview

Employ pre-built analysis workflows for marker quality and association or use individual analysis reports to assess quality, filter markers and prepare (imputation/recode etc.) your data for predictive modeling analysis via the Predictive Modeling Review or Genomic-BLUP report options. Marker scores from predictive models are used for each trait in the Cross Evaluation and Progeny Simulation reports using genomic predictions to assess simulations of multi-year iterative selection breeding programs.

Overview of JMP Genomics Analysis Report Capabilities for Crop Science

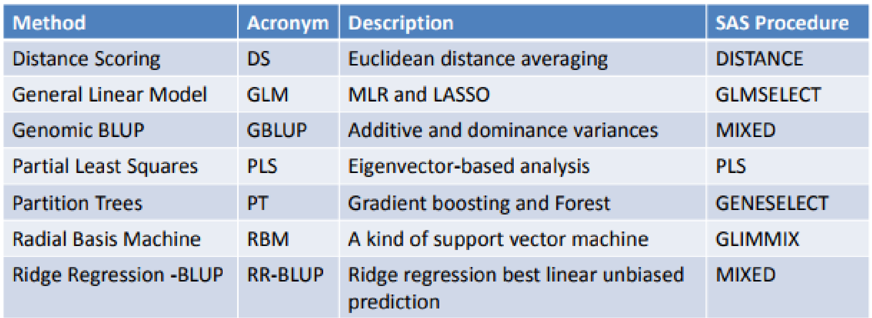
- Genetic Marker Utilities
    - Quality Assessment and Marker Filtering
    - Recode and Imputation
    - Linkage Disequilibrium, tag-SNP selection
- Genetic Marker Association
    - Relationship Matrix estimation and PCA analysis for population structure
    - Simple and Complex single-marker and multi-marker models
        - SNP-Trait association, Q-K Mixed Models, SNP Interaction Models
            - Binary, Nominal, Ordinal and Continuous Trait Support

- Breeding Analysis
    - GxE Interaction models to support Multi-environment (MET) produce stability measures, AMMI models
    - Cross Evaluation and Progeny Simulation
        - Analytically derive potential cross outcomes using Genomic Selection prediction algorithms and simulate multi-year progeny sets based on multi-trait selection
        - Utilizes score programs from the JMP Genomics Predictive Modeling Review



- Predictive Modeling for Genomic Selection
    - The Predictive Modeling Review Tool
        - Build templates of predictive model libraries
        - Employ advanced predictor filtering and marker-selection
        - Perform Cross-validation and model comparison
        - Fit multiple models and evaluate multiple traits simultaneously

Examples of popular prediction algorithms supported



Method	Acronym	Description	SAS Procedure
Distance Scoring	DS	Euclidean distance averaging	DISTANCE
General Linear Model	GLM	MLR and LASSO	GLMSELECT
Genomic BLUP	GBLUP	Additive and dominance variances	MIXED
Partial Least Squares	PLS	Eigenvector-based analysis	PLS
Partition Trees	PT	Gradient boosting and Forest	GENESELECT
Radial Basis Machine	RBM	A kind of support vector machine	GLIMMIX
Ridge Regression -BLUP	RR-BLUP	Ridge regression best linear unbiased prediction	MIXED

- Experimental Population (Biparental) Analysis Support
    - Build, compare and create consensus Linkage Maps
    - IM/CIM/MIM QTL Analysis