Statistical Discovery.™ From SAS.

JMP® Genomics

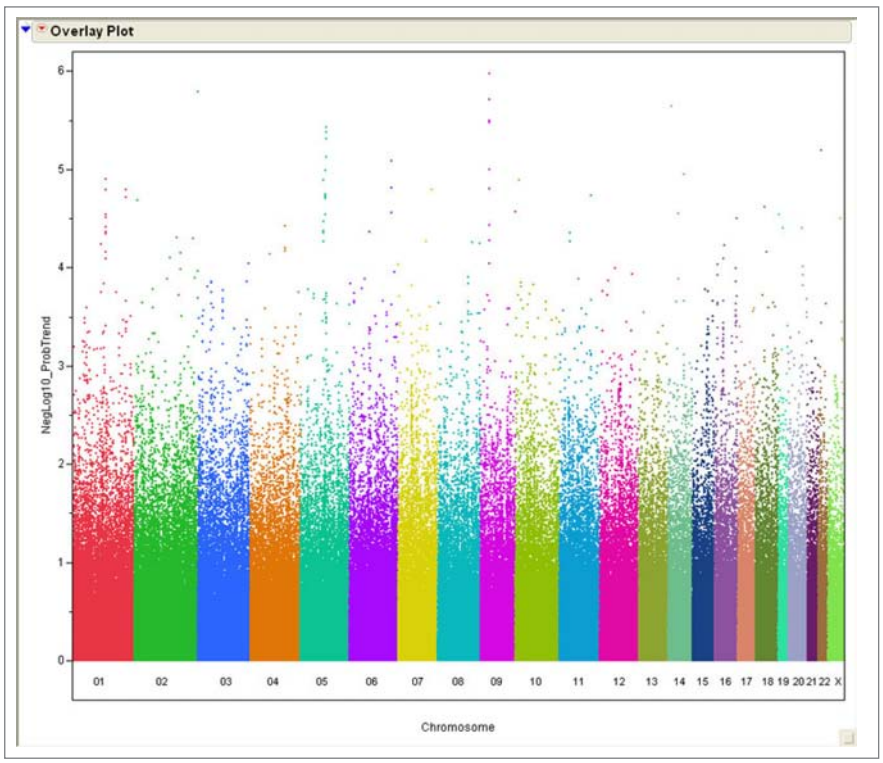
See and explore genomic data related to agriculture, pharmacogenomics, biotechnology and more.

JMP Genomics software from SAS combines interactive JMP graphics and robust SAS® Analytics, allowing researchers to see and explore genomic data from every angle, understand it and share analysis with colleagues.

Even students new to genomic analysis quickly begin to discover important trends and outliers in their data, thanks to simplified dialogs and customized workflows that eliminate the need for programming skills or advanced statistical training.

Whether you're working with next-generation sequencing studies or microarrays, in agriculture or pharma-cogenomics, JMP Genomics provides the tools you need to analyze rare and common variants, detect differential expression patterns, understand NGS data, discover reliable biomarker profiles, and incorporate pathway information into your analysis workflows. With capabilities for integration with R, Excel and other tools, JMP Genomics becomes your analytic hub.

With the JMP Genomics Starter, a customizable home window, new and existing users can quickly access the tools that fit their analytic needs. The JMP Genomics Wizard guides you through the import of sample information and data sets from popular genomics data platforms and text formats.



Conduct genomewide association studies (GWAS) in humans, animal models or plants, and then visualize results with Manhattan plots or other advanced graphics.

Beyond its rich library of prebuilt graphics, JMP Genomics includes full access to the extensive analysis and graphical features offered by the JMP platform. Tools like the drag-and-drop Graph Builder and interactive Data Filter provide the flexibility for all users to create customized views of their data.

In JMP Genomics 7 you'll find substantial capabilities for genomic selection in agriculture and biomarker discovery in pharmacogenomics. Linkage mapping, QTL analysis, and genomic selection functionalities guide crop and livestock breeding strategies, uncovering markers for increased yield or resistance to disease, pests and extreme weather conditions.

Multitrait predictive modeling reviews coupled with cross-evaluation and progeny simulation transform crop improvement programs, helping breeders quickly identify optimal lines for future breeding cycles. Extensive capabilities for expression analysis and genetic association studies simplify molecular marker discovery for disease prognosis or treatment response, identifying sources of patient variability

and providing clinically useful results in pharmacogenomics applications.

Genomic selection for crop improvement

JMP Genomics serves as your experimental design and analysis platform for crop breeding programs. Biologists and breeders can employ linkage mapping and QTL analysis for experimental populations, and complex association methods for diversity populations to identify markers for pest and pathogen resistance.

Comprehensive predictive modeling reviews perform genomic selection with multiple traits of interest to improve breeding selection and accuracy, allowing insights that aren't possible with classical phenotypic selection. These genomic selection tools uncover optimal combinations of markers to produce desirable traits, which in turn can be used to design and evaluate future crosses to produce healthier foods.

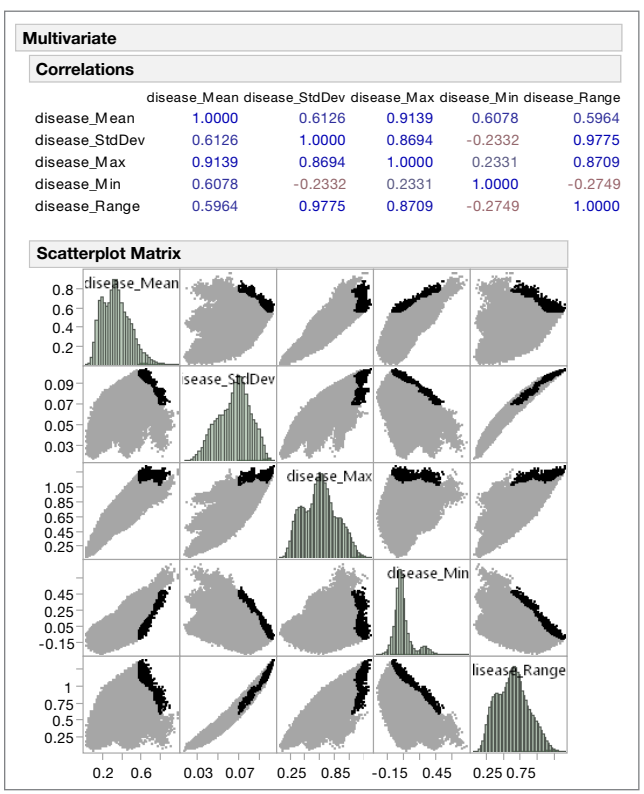
Pharmacogenomics

Patient variability in pharmacokinetics or pharmacodynamics may be a function of underlying genetic variation, causing inherent differences in treatment response or disease prognosis. With the rising influence of genomic data in medical and pharmaceutical applications, JMP Genomics allows users to make the most of their biomedical research data and uncover clinically relevant results.

Using variant data from standard genotyping arrays or next-gen studies, JMP Genomics lets you perform large GWAS with clinical outcomes using common or rare variants. Subgroup analyses identify populations that will benefit most from a specific treatment and save others valuable time and resources on low efficacy treatments.

Biologists, biostatisticians and clinicians can discover molecular markers that predict survival outcomes, gaining biological insight as well as prognosis information. Comprehensive SNP and copy number analysis capabilities uncover variants in tumor cells that may serve as targets for cancer therapies.

JMP Genomics streamlines your translational research pipelines, helping you quickly identify biomarkers for various clinical outcomes and build test panels that can be translated into practice.



Identify ideal sequence candidates for breeding with the Pareto Frontier tool.

Expression

Easy-to-use basic and intermediate workflows simplify analysis of expression intensities and read counts from RNA-seq studies. JMP Genomics 7 offers a range of normalization and analysis options for both array data and summaries from next-gen studies. Point-and-click workflows simplify gene and exon expression, and RNA-seq analysis for new users.

JMP Genomics also supports more complex expression analyses, such as screening for allele-specific expression, filtering intensities or counts, performing batch normalization, and applying sample and gene filters to quickly reanalyze subsets of your data.

Genetics

JMP Genomics provides exceptional tools for statistical geneticists, from

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simple case-control association and linkage disequilibrium analyses to complex linear models supporting covariates, interactions and random effects. The software seamlessly imports variant data sets from VCF files, CLCbio SNP and indel reports, summary files from Complete Genomics, PLINK text and binary files, and common output formats from SNP arrays.

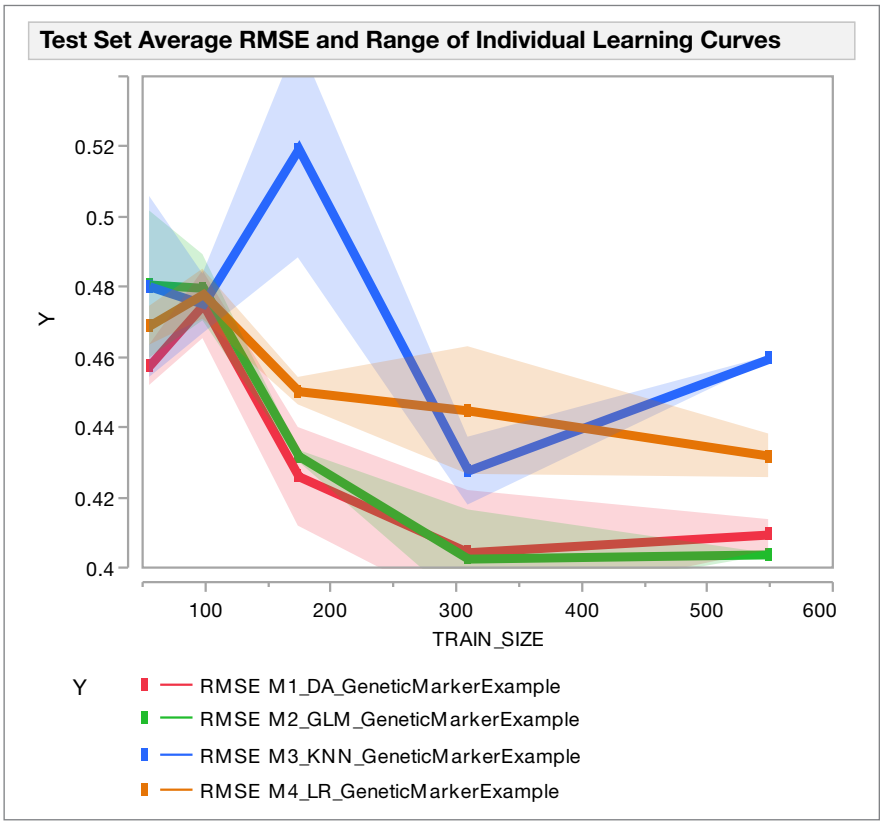
With comprehensive GWAS capabilities, JMP Genomics lets you examine associations between SNPs and multiple continuous traits, correct for population structure, and explore SNP-SNP interactions. Select from an extensive set of rare variant association methods to group rare SNP variants within genes, pathways or positional groups, and find identical by state genomic regions between related or unrelated individuals.

Point-and-click Q-K mixed model analysis simplifies the creation, compression and integration of relationship matrices into association tests, making it easy to simultaneously correct for population structure and relatedness.

Next-generation sequencing

Next-generation sequencing experiments yield a vast amount of information, from variant genotypes to RNA expression levels. JMP Genomics provides downstream statistical analysis capabilities for aligned reads from state-of-the-art sequence analysis pipelines.

Import counts from text formats, or summarize counts from SAM and BAM files to take advantage of normalization and generalized linear modeling methods tailored for count data. Basic workflows



Use Learning Curves to identify optimal predictive models in your clinical genomics data.

for RNA-seq and miRNA-seq streamline steps in statistical analysis.

Load genotypes directly from a variety of text formats or VCF files, or call variants from a set of BAM files using a reference genome. JMP Genomics supports a wide range of methods for association analysis of rare and common SNP variants and can identify regions identical by state (IBS) between related or unrelated individuals.

JMP Genomics lets researchers take advantage of the rich information within sequencing experiments by screening for significant correlations between different data types. The JMP Genomics Browser provides comprehensive views of next-gen data, showing counts or statistical analysis results, and overlaying histogram and heat plot tracks with individual- or group-level summaries to complement known SNP and gene tracks.

Linkage mapping and QTL analysis

JMP Genomics provides a suite of interactive processes for the construction, optimization, and visualization of genetic marker linkage maps used to improve agronomic crops and guide animal breeding efforts.

Geneticists can identify linkage groups automatically or interactively using genetic distance, recombination fraction, or genotypes from experimental inbred crosses. JMP Genomics includes

advanced optimization algorithms to order markers within linkage groups, with options to designate consensus groups and framework markers.

Intuitive graphics let you visualize and filter newly created or imported marker maps, or create high-quality multichromosome views.

New algorithms introduced in JMP Genomics 7 allow larger marker data sets in linkage mapping analysis. Additional support for outcrossing populations is also available, both in linkage mapping and downstream QTL analysis.

Newly constructed marker maps let you explore genotype-environment interactions in multienvironment trials, summarize phenotype information with interactive graphics, and perform QTL analysis. Haley-Knott regression and permutation options expand capabilities for interval and composite interval mapping of QTLs. Also, new multiple interval mapping methods allow more extensive QTL analyses, including the identification of epistatic relationships.

Copy number

Easily explore copy number and loss of heterozygosity (LOH) data between groups or within individuals using JMP Genomics. Data quality assessment functions identify outlier samples and data points, and fast circular binary segmentation (CBS) performs partition analysis to visualize shared patterns across samples. Built-in functions allow you to easily adjust copy number or LOH data sets using paired or grouped reference samples.

ANOVA-based approaches are also available to find statistically significant differences between experimental groups, or to compare individual samples to a reference group. Interactive graphical displays and the JMP Genomics Browser make it simple to identify shared regions of interest as well as unique variations in copy number.

Predictive modeling

JMP Genomics excels at predictive modeling, offering a broad and robust array of methods, as well as options for predictor filtering, predictor lock-in and cross-validation. The software guides biologists and biostatisticians through comprehensive exploratory analyses of separate and paired data types and allows combining multiple predictor types to build, test and cross-validate biomarker signatures with a choice of hold-out methods. Replication and iteration strategies seek to reduce bias, with honest cross-validation approaches that can accurately assess the relative performance of hundreds of different models at a time.

JMP Genomics 7 provides improvements in computational speed with high-performance logistic regression. Predictive modeling capabilities now include ridge regression, elastic net regularization, and additional methods for predictor optimization and variable selection – a significant advantage for high-dimensional genomics data. The new predictive modeling review tool allows users to easily build and compare multiple models for multiple traits.

Pathways

Uncover biological meaning in your analysis results by linking pathway information with JMP Genomics. With a few simple clicks, upload gene lists to partner tool Ingenuity Pathways Analysis to view and color pathways, and add IPA information to analysis data sets to perform gene set enrichment tests. JMP Genomics offers gene set scoring, which summarizes individual measurements of gene expression at the pathway level to detect related but heterogeneous patterns of differential expression.

Researchers can also incorporate gene set and pathway information from MSigDB into analysis data sets, group genes by cytoband, or create custom annotation groups using positional information.

Corporate, government and academic licenses for JMP Genomics are available by annual subscription. JMP Genomics is supported on most 32- and 64-bit business versions of Windows 7 and Windows 8 desktop and server operating systems.

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