JMP Genomics, Version 10.1 - Release Notes

This document describes changes and enhancements from JMP Genomics, Version 10.0 to JMP Genomics, Version 10.1. In addition to general maintenance updates, several enhancements to analytical processes were made. Processes are described in the order in which they first appear in the JMP Genomics menu[1].

General Features

JMP Genomics is an integrated solution built with JMP and SAS capabilities to deliver dedicated analysis workflows for genomic and biological data experiments.

SAS Platform Updates

JMP Genomics 10.1 is built on the latest shipping SAS release, currently this is SAS 9.4M7. For more information about the enhancements to SAS analytical software that are included in this release, please see the What's New in SAS 9.4 web page.

JMP Platform Updates

JMP Genomics 10.1 is built on JMP version 15.1. JMP Genomics 10.1 now includes JMP PRO capabilities. For more information about the enhancements to JMP software that are included in this release, please see the New in JMP web page.

Software Documentation Updates

The User Guide has been restructured and updated to reflect all new and updated software features.

General Enhancements

This update includes numerous bug fixes and updates to enhance compatibility with third party software packages

Import

Import VCF Files

New option for specifying a subset of chromosomes to import from the VCF files.

Reference Gene Normalization

Probe normalization options originally located in the Nanostring Input Engine are now located here. Control Gene normalization now includes both positive and negative control methods.

---

[1] **Note**: If you have a suggestion, comment, or encounter a bug in JMP Genomics 10.1, please click **Send a Comment or a Feature Request** under **Genomics > Documentation and Help** or email details to Genomics@jmp.com. For bugs, it is especially helpful if you can attach a settings file for the JMP Genomics process in which you encountered the problem, along with a subset of your data that can be used to reproduce the error. If you cannot share a subset of your own data but can reproduce the problem with one of our sample data sets, please send us a settings file for this so that we can replicate the error. We make every effort to address the issue promptly.

Workflows

Basic miRNA/miRNA-Seq Workflow
Option for modeling either count data or continuous data has been added.

Basic Single Cell RNA-Seq Workflow
A new option for specifying the number of principal components to use for clustering.
Ability to specify clustering method has been added. Users specify the range of clusters expected and the workflow selects the optimum number and uses it for subsequent analyses.
A new option enables you to select a subset of genes based on their importance in the table and view the selected genes on the GTEx Portal.
A suite of options for analyzing selected genes using either the t-SNE or UMAP R packages have been added.
A 3-dimensional scatter plot has been added to enhance SVD analysis.
Scatter plots are optimized to the output dimension for t-SNE and UMAP
Options for excluding and recovering excluded cells have been added to output tabs.
Local data filters have been added to select output tabs.
Options for removing ribosomal and mitochondrial genes from the analysis have been added.
Output now includes dot plots and ridgeline plots for further analyzing gene expression levels in each cluster and across clusters.
Several updates to improve the VST method have been made to improve consistency.
New ability to split graphs based on conditions specified in the Experimental Design File (EDF)

Genetics

Multiple APs
Information on multiple testing corrections and *p*-value adjustments previously shown in output graph legends have been consolidated and moved to text boxes above the graphs.
An option for specifying ploidy level has been added to **Recode Genotypes**, **Impute Missing Genotypes**, and **Marker Properties**.

Relationship Matrix
New option to specify the color theme of the Heat map.

Q-K Model Fitness
Minimum and maximum values in the Model Fitting Information Plots have been set.
Separate graphs are generated when fitting non-continuous variables into 3 categories (likelihood-based, pseudo-likelihood-based, and *chi*-square-based).

Haplotype Estimation
A new *LD P-Value Plot* output tab showing linkage disequilibrium among haplotype alleles is generated when testing for allelic association for LD.

Linkage Map Order
Multiple code updates have been made to match updates to the Onemap R package.

QTL Single Marker Analysis
Process updated to include continuous and class cofactor analysis.

QTL IM, CIM and MIM Analysis
Controls for adjusting frame size of output graphics have been added.
Process updated to include continuous and class cofactor variables along with functionalities in the MIM method to add/delete Cofactors and their interactions with QTLs

Expression

Correlation and Principal Variance Components Analysis
User can now specify individual principal components to use.
A local data filter has been added to the Variance Components charts.

Predictive Modeling

Multiple Models
All predictive models now include the Matthews Correlation Coefficient as part of the training set criteria.

Predictive Modeling Review
A new *Folder of Review* field allows the user to specify a folder that contains reviews.
Genomic BLUP, **Genomic Bayesian Regression**, and **XGBoost Regression** have been added to the list of models that can be fitted.

Data Set Utilities

Concatenate Data *New!*
This new process stacks rows of two or more SAS data sets into a single data set containing rows of all the input files.

General Utilities

R Package Manager
Additional R packages have been added.

Applying the Hot Fix

JMP Genomics, Version 10.1 is being released as a Hot Fix on May 10, 2021. It is available for download from the SAS Hot Fixes web page. You must have JMP Genomics, version 10.0, installed before applying the Hot Fix.

To apply the Hot Fix:

- Navigate to the Hot Fix download site (https://tshf.sas.com/techsup/download/hotfix/HF2/K1Q.html#K1Q001 and download the K1Q001x6.zip hot fix file.
- Copy the downloaded zip file into the C:\Program Files\SASHome\InstallMisc\HotFixes\New directory (this assumes you installed JMP Genomics 10.0 in the default location).
- Click **Starter>SAS>SAS Deployment Manager 9.4** and select **Apply Hot Fix** and follow the prompts.

If you order and install JMP Genomics after May 10, 2021, the hotfix has already been applied.