JMP Genomics, Version 9.0 - Release Notes

This document describes changes and enhancements from JMP Genomics, Version 8.2 to JMP Genomics, Version 9.0. Processes are described in the order in which they first appear in the JMP Genomics menu[1].

General Features

SAS Platform Updates

JMP Genomics 9.0 is built on the latest SAS release, SAS 9.4M4. 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 9.0 is built on the latest JMP release, JMP v13.2. 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 updated to reflect all new and updated software features.

1. **Note**: If you have a suggestion, comment, or encounter a bug in JMP Genomics 9.0, 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.

Import

Import VCF Files

This import engine is now able to incorporate raw read depth information from the "INFO" column in VCF files generated using Samtools and SNVer, in addition to the "FORMAT" column generated by BOWTIE or other NGS software.

The number of variants that can be stored in a single data file has been increased to 10,000,000, allowing users to store chromosome data in one large file rather than split among multiple files.

Finally, this process now includes an option for excluding sex chromosomes and mitochondrial variants from the output.

Workflows

Basic RNA-Seq Workflow

An option to enable **TPM Normalization**, which takes reads per kilobase (RPK) and adjusts per million scaling factor for each sample, has been added.

Genetics

Several new processes have been added. In addition, a number of enhancements to existing analytical procedure for facilitating genetic analyses have been added to JMP Genomics 9.0.

Impute Missing Genotypes *New!*

This new process imputes numeric missing marker genotypes (0, 1, or 2) for diploid organisms using the *k*-nearest neighbor imputation (*kNNi*) or the linkage disequilibrium *k*-nearest neighbor imputation (*LD-kNNi*) methods.

Collapse Multiallelic Genotypes *New!*

This new process creates an output data set containing one column per marker from an input data set that contains one column per each marker allele. This process assumes a diploid organism, which implies that only two alleles are allowed for every individual.

Genomic Heritability *New!*

This new process (located under the *Other Association Testing* submenu) estimates the genetic variance explained by marker variables using a mixed model framework[2]. This analysis allows you to determine the estimated genetic influence to a trait based on the SNP data matrix instead of using a formal experimental design.

Cross Evaluation *and* Progeny Simulation

Several new output enhancements have been made to more easily explore and filter the crosses and simulated progeny in a crop improvement breeding experiment.

Cross IDs can now be used to color-code graphical output in both processes.

Means plots for RIL + Multi-Generation crosses are color-coded by Cross IDs.

A heat map of predicted trait values versus Cross ID, color-coded for the frequency/counts of progeny that have that specific trait values for that cross, has been added to **Progeny Simulation**.

Q-K Model Fitness *and* Q-K Mixed Model

Both **Q-K Model Fitness** and **Q-K Mixed Model** now verify that variables specified as class variables are also included as either fixed or random effects.

Predictive Modeling

Genomics BLUP

An option to generate a plot of progeny means by cross has been added.

An option for specifying an ID Variable has been added. This option enables the process to use the ID variable to either impute missing values in the cross ID variable or to generate a new variable identifying the crosses when one does not already exist.

2. Yang J, Benyamin B, McEvoy BP, Gordon S, Henders AK, Nyholt DR, *et al*. 2010. Common SNPs explain a large proportion of the heritability for human height. *Nature Genetics* **42**: 565-569.