JMP Genomics, Version 9.1 - Release Notes

This document describes changes and enhancements from JMP Genomics, Version 9.0 to JMP Genomics, Version 9.1, which is being released via the SAS Hotfix Mechanism. In addition to general maintenance updates, several new enhancements to analytical processes were made. Processes are described in the order in which they first appear in the JMP Genomics menu[1].

The JMP Genomics 9.1 hotfix can be downloaded from http://ftp.sas.com/techsup/download/hotfix/HF2/C9X.html#C9X004.

Genetics

A number of enhancements to existing analytical procedures for facilitating genetic analyses have been added to JMP Genomics 9.1.

Cross Evaluation *and* Progeny Simulation

A new option to *Compute Selection Index* allows the computation of a linear combination of multiple trait values into a single value

It is now possible to simulate multiple generations for outcrossed (non-selfing) individuals. Previously this was only available for back-cross and selfing populations.

Trait means are now added into the report results data filter in order to explore crosses/progeny by trait mean thresholds.

A smaller usability change now allows Chromosomes to be specified using character as well as numeric values. Values no longer need to be sorted but the levels must be grouped appropriately.

In **Cross Evaluation**, new options enable automatic selection of best progenies using trait threshold values, a selection Index cut-off selection, or a percentage. Additionally, this report can now be used to evaluate individuals without making crosses.

1. **Note**: If you have a suggestion, comment, or encounter a bug in JMP Genomics 9.1, 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.

Pattern Discovery

A *Covariates for Partial Correlations* option that allows the specification of numerical covariates has been added to **Cross Correlation**. This option allows integrative analyses, for example eQTL, to adjust all correlations by specified covariates to control in a more formal model.

Predictive Modeling

Partition Trees

A new file output (with suffix ptr_mod.sas7bdat) is created that can be used as a score file to enable scoring tree-based models in **Cross Evaluation** and **Progeny Simulation**.

Genomics BLUP

Chromosomes can now be specified using character as well as numeric values. Values no longer need to be sorted but the levels must be grouped.

Predictive Modeling Review

Several enhancements have been made that allow for multiple runs of cross-validation across multiple traits. A new add-in is available that takes the results of a predictive modeling review and allows quick selection, refitting and model averaging (building an ensemble) for each trait.

Utilities

Register Add-Ins *New!*

This new utility provides a convenient method to install and update newly created add-ins that leverage either open-source packages (such as R) or extend the functionality of JMP Genomics. These add-ins are now shipped with the product and are available on the JMP Community.

Add-Ins

Genomic Bayesian Regression *New!*

This add-in serves as a wrapper around the BGLR R package for genomic prediction using Bayesian methods. This process can be used in the **Cross Validation Model Comparison**, **Test Set Model Comparison**, and **Learning Curves Model Comparison** processes to extend modeling options in JMP Genomics to include these increasingly common Bayesian methods.

Predictive Modeling Summary *New!*

This add-in is used to summarize results of **Predictive Modeling Review**. It can help select and refit the best models, and perform model ensembling and data merging.