Verification and Configuration Instructions

JMP® Genomics 3.1 for SAS® 9.1.3

Required Verification and Configuration Steps

Once you have successfully completed the installation of the SAS® 9.1.3 Foundation and JMP® Genomics 3.1 as described in the Roadmap, continue with the verification, customization and configuration instructions as described in this document.

Verification

After you follow Steps 1 -4 in the Road Map for JMP Genomics 3.1 for SAS 9.1.3, launch JMP Genomics. Verify that the splash screen says **JMP Genomics 3.1**.

When JMP 7 is started for the first time, you will need to use the SAS Installation Data (SID) file name `jmp70_xxxxxx.txt` (in which *xxxxxx* is your JMP Genomics Software Order). You should have received this file attached to an e-mail. The `jmp70_xxxxxx.txt` file should be saved in the `C:\Program Files\SAS\JMP7` directory.

If you did not receive this file, please contact the SAS Contracts Department. In the U.S and Puerto Rico, call (800) 727-0025, and press option 3. For Contracts support outside the U.S. and Puerto Rico, please refer to http://support.sas.com/adminservices/contact.html for e-mail contact information.

Note: *When you open JMP Genomics for the first time, you may be prompted to merge menus. Click* **No** *whenever you are prompted to merge menus! Attempting to merge customized menus from prior versions of JMP or JMP Genomics is strongly discouraged. See* Customizing JMP Genomics Menus *on page 8 of this document for more information and instructions.*

Verify that the Genomics menu item is present on the top tool bar, as shown in Figure 1.

Figure 1: The JMP Genomics menu bar

Verify that all of the Genomics submenus are present under the main genomics menu, as shown in Figure 2.
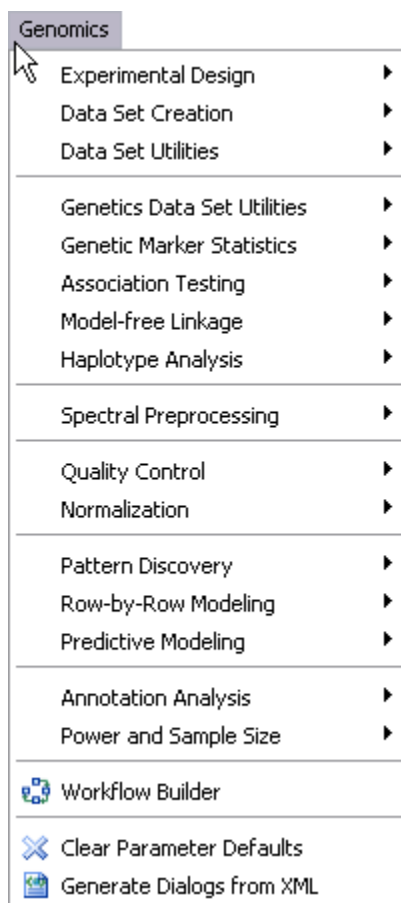
Figure 2: The JMP Genomics submenus.

If the Genomics menu is missing or you do not see all of the submenus shown in Figure 2, you must activate the new menus.

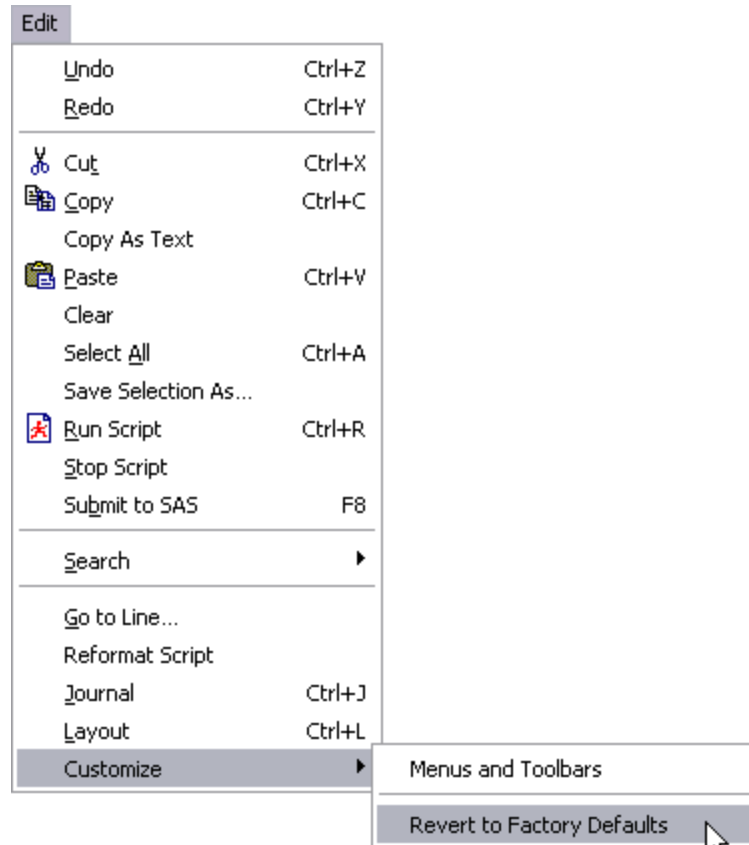Select **Edit** > **Customize** > **Revert to Factory Defaults**, as shown in Figure 3.

Figure 3: Activation of new menus.

If the shortcut icons on the desktop do not display properly after you install JMP Genomics 3.1, right-click anywhere in the desktop and select **Refresh**.

Set Preferences

To upload external data files correctly using analytical processes, JMP Genomics requires that certain preferences are set. These preferences should automatically set when you open JMP Genomics 3.1 for the first time.

However, some users, particularly beta-testers for JMP 7 or JMP Genomics 3.1, may need to reset these preferences. You may set these preferences upon opening JMP Genomics for the first time (or if one or more of these preferences is changed accidentally) by selecting **File** > **Set Genomics Preferences**.

Please note that there will be no visible sign that the preferences have been reset. You should therefore complete the following steps to verify that the preferences have been reset:

1. Select **File** > **Preferences**.

   The Preference Settings window opens, as shown in Figure 4.

2. Verify that the **Save Text files as Unicode** box is not checked. The unchecked box should appear as shown in Figure 5.

   You may choose to select or deselect additional preferences by checking or unchecking the appropriate box(es).
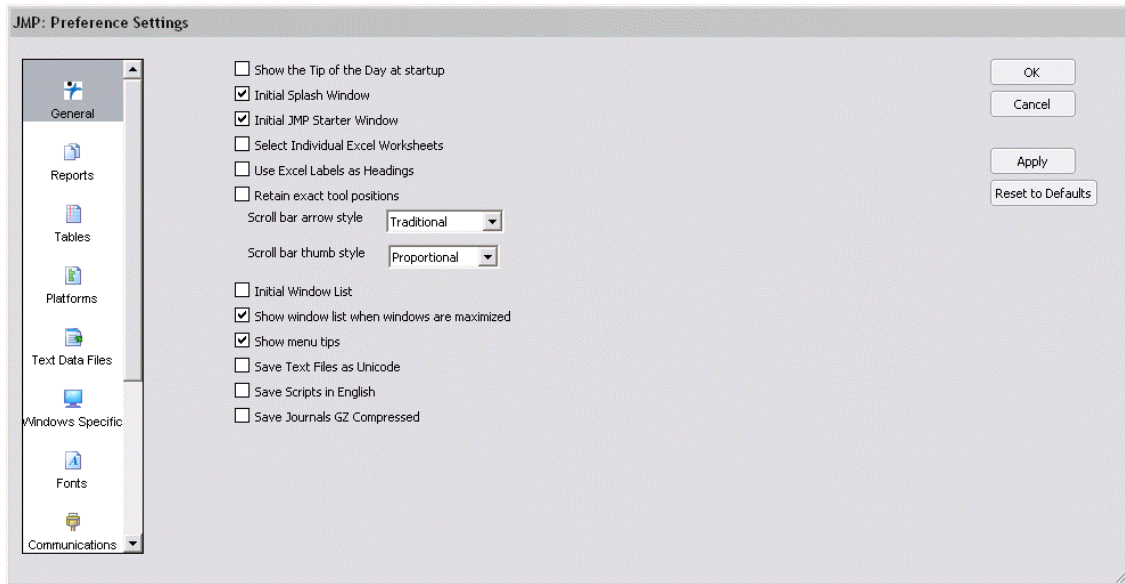
Figure 4: The General tab of the Preference Settings window has been set correctly.
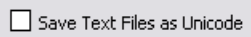

Figure 5: The unchecked Save Text files as Unicode box

3. Click on the Text Data Files icon on the left-hand side of the window.

4. In Import Settings, verify that the **Comma** box is not checked.

5. In Export Settings, verify that the **Tab** option **End of Field** box is selected.
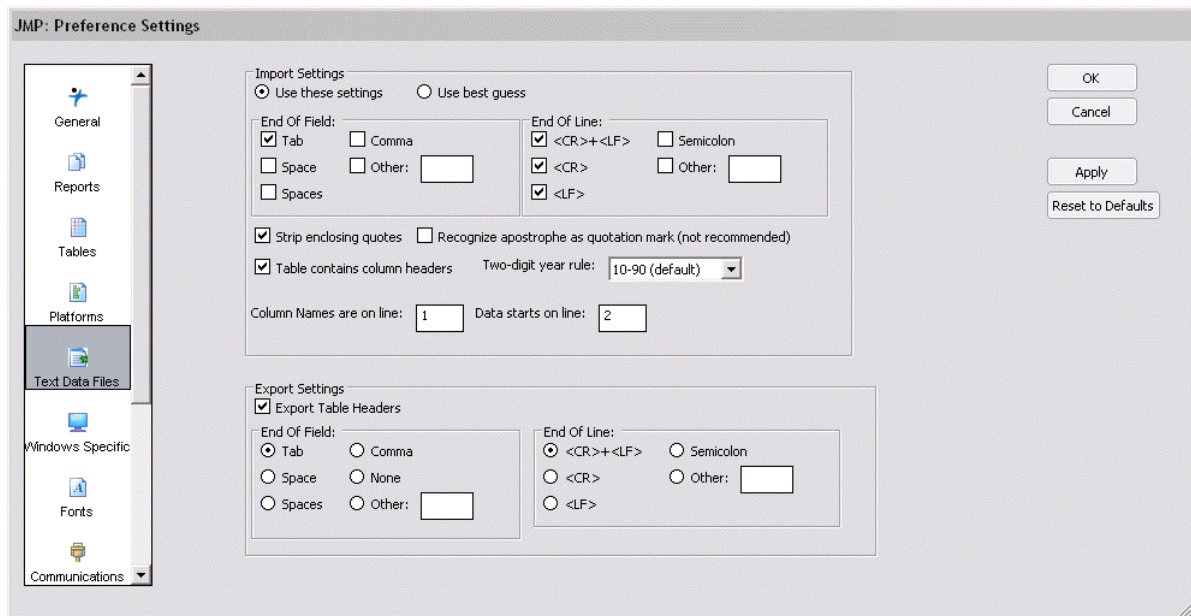

Figure 6: The Text Data Files tab of the Preference Settings window has been set correctly.

Generate Dialogs

JMP Genomics requires the generation of JSL dialogs from XML specifications. Both the JSL dialogs and the XML specifications are stored in the ProcessLibrary folder. The dialogs should automatically be generated when JMP Genomics 3.1 is opened for the first time.

However, some users, particularly beta-testers for JMP 7 and JMP Genomics 3.1 and users who may have accidentally deleted one or more JSL dialogs will need to regenerate the dialogs. To do this, select **Genomics** > **Generate Dialogs from XML**.

Upgrade SAS 9.1.3 with Service Pack 4 (including JRE 1.4.2_09)

If you installed JMP Genomics 3.1 by upgrading JMP Genomics 2.x, please verify whether you have upgraded to SAS 9.1.3 with Service Pack 4 (SP4). Launch SAS. Select **Help** > **About SAS 9**. If you do not have SP4 installed with your SAS 9.1.3, please install Service Pack 4 for SAS Foundation for your operating system from

```
http://ftp.sas.com/techsup/download/hotfix/e9_sbcs_prod_list.html#e9h004
```

SP4 on Windows requires JRE Version 1.4.2_09. This JRE is included in your SAS 9.1.3 SP4 and should be installed on your machine. You can easily check the status of the JRE as follows:

1. Start SAS 9.

2. From a Program Editor, submit the following code:

```
Proc JavaInfo; Run;
```

3. Check the SAS Log for the value of `java.version` and `java.vm.version`.

Apply Hot Fixes for Genetics Processes

To run the most up-to-date versions of the SAS/Genetics procedures for the Genetics processes, download and install the latest SAS/Genetics Hot Fix from this location:

```
http://ftp.sas.com/techsup/download/hotfix/e9_win_sbcs.html#gn
```

This link is also available from your main JMP Genomics menu by selecting **Help** > **JMP Genomics Web Links**.

Install PROC GLIMMIX for Marker-Trait Association and Radial Basis Machine Processes

To run the Marker-Trait Association and Radial Basis Machine processes in JMP Genomics, you must first install SAS/STAT PROC GLIMMIX from
`http://support.sas.com/rnd/app/da/glimmix.html`. This link is available from your main JMP Genomics menu by clicking **Help** > **JMP Genomics Web Links**.

Install PROC GLMSELECT for General Linear Model Selection Process

To run the General Linear Model Selection process, you must first install SAS/STAT PROC GLMSELECT from `http://support.sas.com/rnd/app/da/glmselect.html`. This link is available from your main JMP Genomics menu by clicking **Help** > **JMP Genomics Web Links**.

Getting Started

The main components of JMP Genomics are now operational. See the configuration steps below to set up the optional processes and to optimize memory settings. Additional information is available from

the *JMP Genomics User Guide* and the *JMP Genomics User Guide Supplement* which are available from the main JMP Genomics Help menu (**Help** > **Books** > **JMP Genomics User Guide**).

Note: *This guide is in .pdf format, so you will need Acrobat Reader to open it. Reader can be downloaded free of charge at the Adobe website:* `www.adobe.com.`

Read and follow the guidelines in Chapter 1 of the *JMP Genomics User Guide*, then proceed to other chapters and the supplement according to your interests. Updates will be made available periodically. Please check `http://www.jmp.com/software/genomics/index.shtml` for updates to the *User's Guide*.

Optional Configuration Steps

Microsoft Windows

Increase Memory Limits and Eliminate Error Messages in Triplicate

If you are running Windows OS, you might want to edit your `SASV9.cfg` file to increase memory limits and prevent SAS ERROR messages from appearing in triplicate. The typical location for this file in is: `C:\Program Files\SAS\SAS 9.1\nls\en\SASV9.cfg`.

The operating system may use additional amounts of memory. The memory used by SAS includes virtual memory and is therefore not limited to RAM. If `MEMSIZE` is set to a value that is too low and could cause performance problems, the value of `MEMSIZE` is determined by SAS.

MEMSIZE Parameter

For the Windows OS, the operating system will most likely use virtual memory. The memory used by SAS includes virtual memory and is therefore not limited to RAM. If `MEMSIZE` is set to a value that is too low, it could cause performance problems. The value of `MEMSIZE` can be specified by SAS.

For optimal performance, use the default value of '0' for MEMSIZE

SASV9.cfg File

For the Windows OS, you may wish to edit the `SASV9.cfg` file.

To edit the `SASV9.cfg` file, follow these steps:

1. Close all SAS and JMP Genomics sessions.

2. Use a text editor to open the `SASV9.cfg` file.

3. Add the following lines to this file:

   ```
   -MEMSIZE 0
   -MVARSIZE MAX
   -MSYMTABMAX MAX
   -NOOVP
   ```

   If any of these options already exist, you may replace them with the new values.

4. Save the `SASV9.cfg` file.

All subsequent invocations of SAS will use these changes.

SORTSIZE parameter

The `SORTSIZE` parameter specifies the amount of machine memory available to SAS for sorting large data files.

1. Close all SAS and JMP Genomics sessions.

2. Use a text editor to open the `SASV9.cfg` file.

3. Add the following line to this file:

   ```
   -SORTSIZE X
   ```

   in which *X* indicates the amount of memory to be assigned to SAS for sorting large data files.

A `SORTSIZE` value set at '0' assigns all available memory to SAS. This option is not recommended since it will affect the performance of other applications.

One recommended approach is to specify half the available memory on your machine. For example, if your machine has 1GB of memory, type

```
-SORTSIZE 512m
```

Save the `SASV9.cfg` file. All subsequent invocations of SAS will use these changes.

Set Web Access via a Proxy Server for KEGG Pathway Search and Color Processes

A proxy server is a server that sits between a Web browser and an external server on the Web to filter requests, improve performance, and share connections. If your computer accesses the Internet through a proxy server, you need to specify your proxy server name and port number to enable the system to search KEGG Pathways data through the Web. If your computer does not access the Internet through a proxy server, skip this configuration step.

To specify the proxy server, select **Genomics** > **Annotation Analysis** > **Configure Proxy Settings**. The Configure Proxy Settings window opens, as shown in Figure 7.
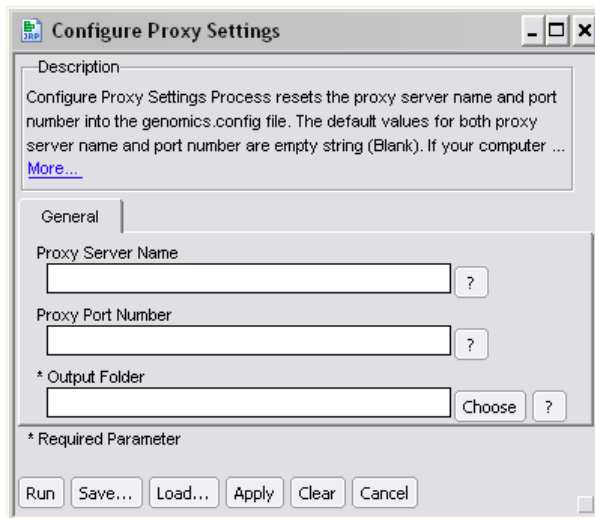
Figure 7: The Configure Proxy Settings window

1. Type the proxy server name (in the form *servername.domain.com*) in the Proxy Server Name field.

2. Type the proxy port number (commonly `80`) in the Proxy Port Number field.

3. Click the **Choose** button to select the Output Folder.

4. Click the **Run** button. A SAS Message displays when Configure Proxy Settings is completed.

If you are not sure what values to specify, you may be able to find this information in your Web browser settings.

For example, in Internet Explorer, select **Tools** > **Internet Options** > **Connections** tab > **LAN Settings** button > **Use a proxy server** check box > **Advanced** button.

The Proxy Settings window opens and displays your HTTP proxy name and port number. Your IT Administrator may also be able to provide the values.

Install Affymetrix GeneChip Bioconductor Expresso Process

To run the Affymetrix GeneChip Bioconductor Expresso process in JMP Genomics, you must first install R and the Affy package from `http://www.bioconductor.org/`.

Note: *You must also install the packages specific to your Affymetrix chip.*

Customizing JMP Genomics Menus

The menu customization system has changed considerably in JMP Genomics 3.1, so merging menu customizations from a prior JMP Genomics version is not easily accomplished and is strongly discouraged. When asked if you would like to merge menus from an earlier version of JMP Genomics, click **No**.

If you accidentally select **Yes** to merge your menus from a previous version and encounter an error message, complete the following steps to reset the menus:

1. Close JMP Genomics (from the Windows Task Manager if necessary).

2. Relaunch JMP Genomics.

3. When prompted to merge menus, select **No**.

4. Select **Edit** > **Customize** > **Revert to Factory Defaults** to restore the factory menus.

If you had customized menus in previous version of JMP or JMP Genomics, and would like to replicate the customization in JMP Genomics 3.1, complete the following steps:

1. Select **Edit** > **Customize** > **Menus and Toolbars**. A menu tree browser appears in the left of your JMP Genomics window, as shown in Figure 8.
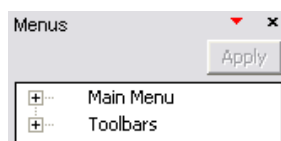

Figure 8: The menu tree browser

2. Click on the plus signs to open menu subsections, and right-click to insert or modify items as needed to complete your customization.

3. Click **Apply** to save your changes.