Installation Instructions for the Outcross Linkage Map Analyses Add-In

These instructions describe the process for downloading and installing the **Outcross Linkage Map Analyses** Add-In to JMP Genomics on your Windows desktop machine. These instructions include three major sections:

1 **Software Download and Installation**

Lists directions for downloading and installing the three components (the **Outcross Linkage Map Analyses** Add-In, the R software, and the OneMap package) and for configuring SAS to work with the download software.

2 **Analyses Supported in JMP Genomics**

Description of JMP Genomics input engines and analytical processes used for analysis of outcross data

3 **Getting Started with Outcross Data Analysis in JMP Genomics**

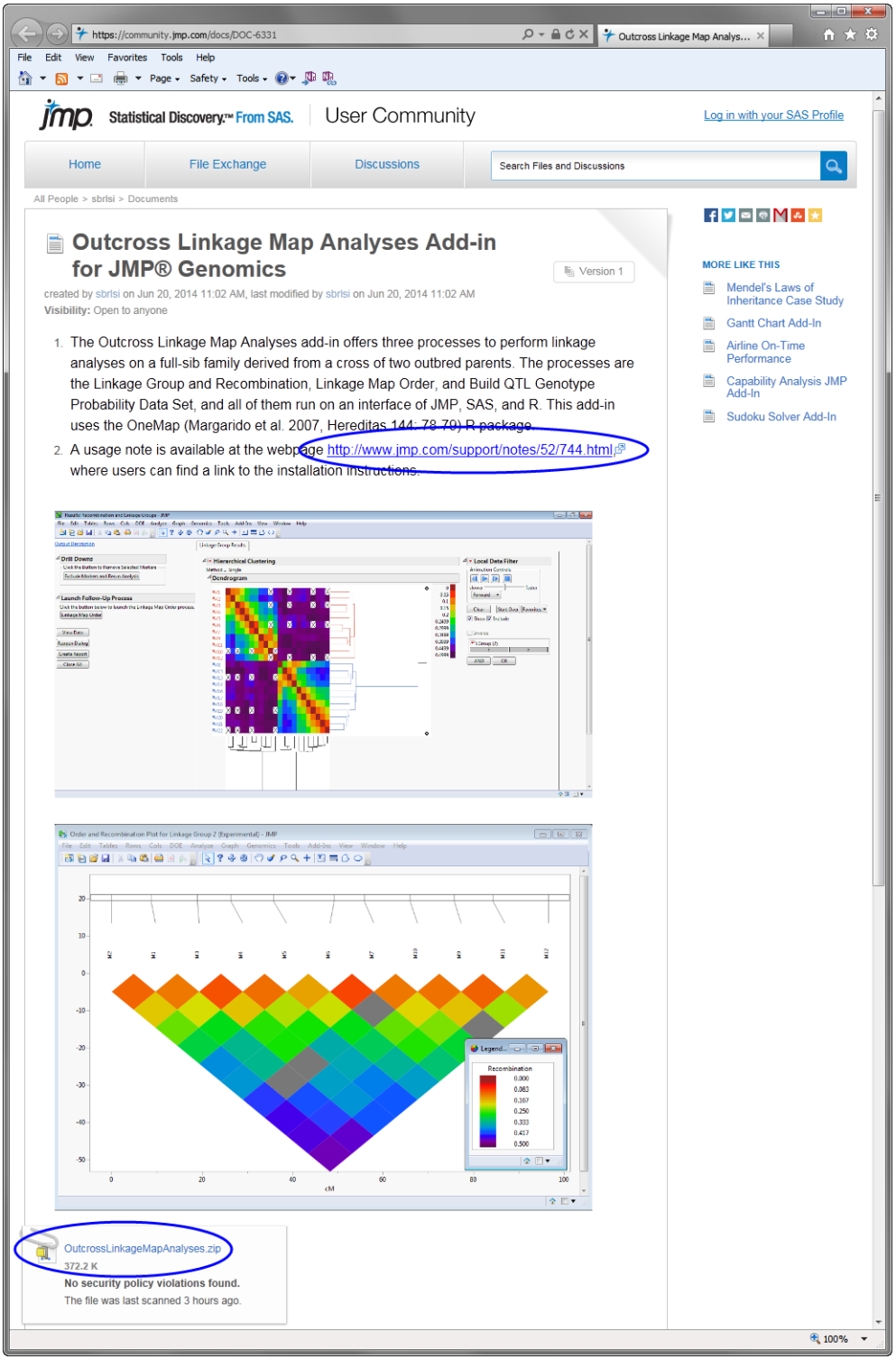
Description of the sample settings and data sets that come with the **Outcross Linkage Map Analyses** Add-In and exemplify the types of analyses that can be performed.

Software Download and Installation

The Outcross Linkage Map Analyses Add-In

The **Outcross Linkage Map Analyses** Add-In can be downloaded from the JMP File Exchange website.

Open a browser and navigate to https://community.jmp.com/docs/DOC-6331.


https://community.jmp.com/docs/DOC-6331
Outcross Linkage Map Analys...
File Edit View Favorites Tools Help
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Statistical Discovery.™ From SAS.
User Community
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File Exchange
Discussions
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All People > sbrisi > Documents
Outcross Linkage Map Analyses Add-in for JMP® Genomics
Version 1
created by sbrisi on Jun 20, 2014 11:02 AM, last modified by sbrisi on Jun 20, 2014 11:02 AM
Visibility: Open to anyone
1. The Outcross Linkage Map Analyses add-in offers three processes to perform linkage analyses on a full-sib family derived from a cross of two outbred parents. The processes are the Linkage Group and Recombination, Linkage Map Order, and Build QTL Genotype Probability Data Set, and all of them run on an interface of JMP, SAS, and R. This add-in uses the OneMap (Margarido et al. 2007, Hereditas 144: 78-79) R package.
2. A usage note is available at the webpage http://www.jmp.com/support/notes/52/744.html where users can find a link to the installation instructions.
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OutcrossLinkageMapAnalyses.zip
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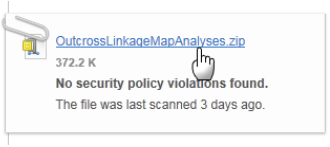
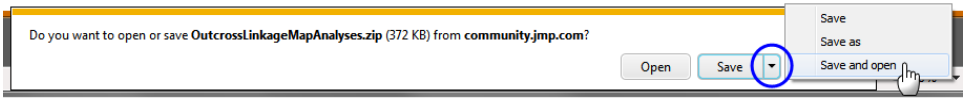
There are two links on this page: one link to an information page and the second for downloading the add-in

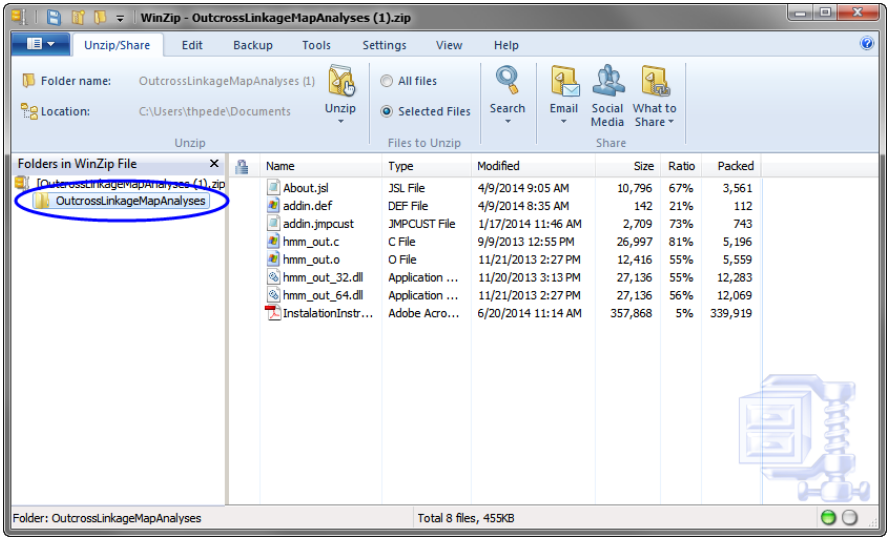
- Click **OutcrossLinkageMapAnalysis.zip** (as shown below) to download the ZIP file containing the add-in.



- Click the **Save** arrow (circled below) to to open a pop-up menu and then click **Save and open** to download the ZIP files containing the **Outcross Linkage Map Analyses** Add-In.

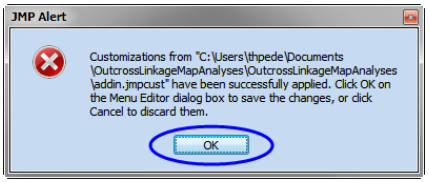


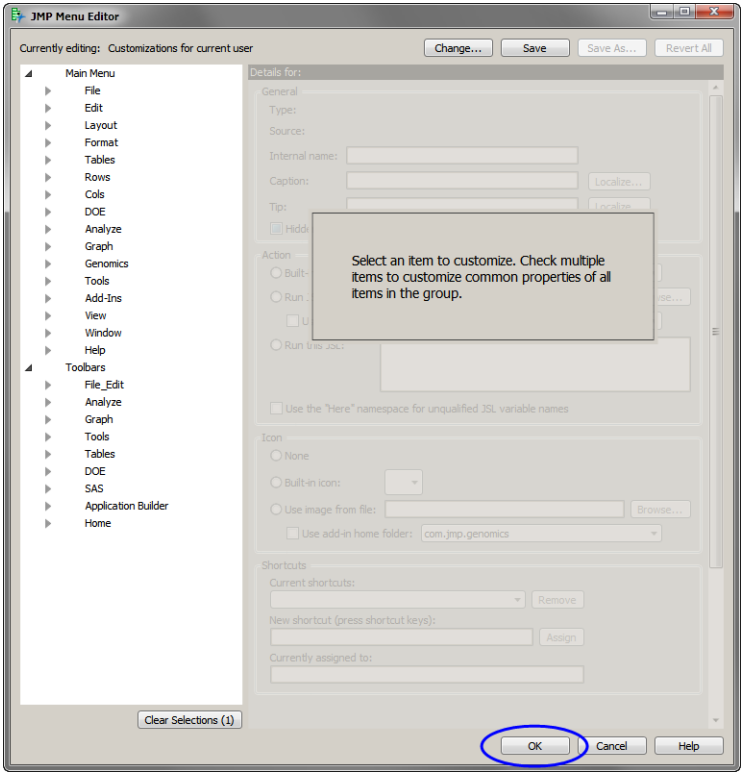
- Click **Unzip** to unzip the file to your machine.
- Click the **OutcrossLinkageMapAnalysis** folder (circled below) to open the folder containing the unzipped Add-In files.



- Launch JMP Genomics.
- Drag the **addin.def** and **addin.jmpcust** files onto the JMP Genomics window.

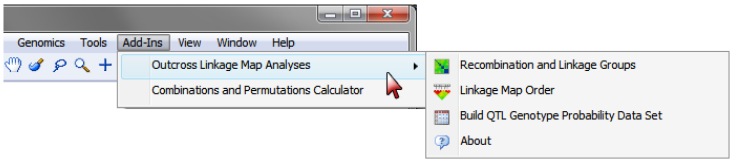
A **JMP Alert** window and the **JMP Menu Editor** appear.





Click **OK** in both windows to install the Add-In and modify the JMP Menu.

A new **Add-Ins** menu is added to the Menu bar. The three APs used for analysis of outcross data can be accessed from this menu.



The R Software Application

The R software application can be downloaded from the Comprehensive R Archive Network website. (http://cran.r-project.org/bin/windows/base/). You must use R version 3.0.1 or higher, as these are the only versions supported for integration with SAS 9.4M1.

- Click the Download link to download the R package to your Windows machine.
- You should follow the Installation and other instructions listed on the R website to install the software..

Note: The R software application must be downloaded and installed before you can proceed to the next step.

The OneMap Software Application

There are two methods that you can use to install the OneMap software application.

Installation of the OneMap Package Directly from the R Console

- Launch the R software;
- Click Packages, on the main menu
- Click Install Package(s)…;
- Choose a CRAN mirror and click **OK**;
- Scroll down to the onemap package, select it, and click **OK** to install the package.

Download the onemap ZIP file onto your computer from the R Project website

- Navigate to http://www.r-project.org.
- Click the CRAN link and select a CRAN Mirror. Click on the link to open the download page.
- Click the packages link to open the Contributed Packages page (shown below).
- Click the Table of Available Packages, sorted by name link.
- Scroll down to the onemap link.
- Click on the onemap_2.0-4.tar.gz link to download the Package source file. Save the file in a known location on your machine.
- Launch the R software;
- Click **Packages** on the main menu.
- Click **Install Package(s) from ZIP files…**
- Navigate to folder where you placed the OneMap package ZIP file, selected it, and click Open to install the package.

Modify the sasv9.cfg File to Include the -RLANG Option in the SAS System

File.

You must set this option or you will encounter error messages when attempting to use this Add-In.

- Navigate to the location of the sasv9.cfg file on your computer. Typically, this file is located in th C:\Program Files\SASHome\SASFoundation\9.4\nls\en\ directory.
- Open the file with a text editor.
- Type `-RLANG` in the first line of the file.
- Save and close the sasv9.cfg file.

Refer to the RLANG System Option page (http://support.sas.com/documentation/cdl/en/imlug/63541/HTML/default/viewer.htm#imlug_r_sect003.htm) for more information.

Outcross Analyses Supported in JMP Genomics

File Conversion:

The JMP Genomics OneMap Import and Export Engine is used to translate OneMap input text-formatted files into SAS Data Sets that are used in JMP Genomics analyses. Click Import > Other Genetics > OneMap to access this process from the JMP Genomics Starter.

Note: SAS Data Sets can also be translated into OneMap input text file format using the same process.

JMP Genomics Outcross processes use the same marker coding as OneMap, which was proposed by Wu and Ma, 2002[1]. OneMap has a tutorial that can be used as a guide on how to code markers.

Linkage Map Analyses:

Three JMP Genomics Outcross processes (Linkage Group and Recombination, Linkage Map Order, and Build QTL Genotype Probability Data Set) are run on an interface of SAS and R to perform linkage analysis on outcrossed lines. Every analyses that is submitted to these processes starts with SAS commands that send the required information to OneMap functions that run within the R environment, then all results are sent back to a SAS environment.

Click Add-Ins > Outcross Linkage Map Analysis to access these processes from the JMP Genomics Starter.

1. Wu, R. and C-H Ma. 2002. Simultaneous maximum likelihood estimation of linkage and linkage phases in outcrossing species. *Theor. Pop. Biol.* **61**:349-363.

QTL MAPPING:

Once the Linkage Map Analyses have been performed, the appropriate output files can be loaded into the QTL IM, CIM and MIM Analysis process for standard QTL mapping analyses.

Getting Started with Analysis of Outcross Data in JMP Genomics

Settings

JMP Genomics comes with sample settings that were built to exemplify the types of analyses that the software supports. A description of each sample setting available for the different outcross processes are described below:

File Conversion

The **simuf1txttosas** setting is designed to exemplify the conversion of an input text file in the format used by OneMap into SAS Data Sets that are properly formatted for JMP Genomics analyses.

The **simuf1sastotxt** setting is designed to exemplify the conversion SAS Data Sets into an input text file suitable for OneMap.

Linkage Group and Recombination

The **simuf1_min** setting is designed to exemplify the analysis of recombination and linkage group in full-sibs, and it has two data sets: an input SAS Data Set (simuf1.sas7bdat), and an Annotation SAS Data Set (simuf1_anno.sas7bdat).

Linkage Map Order

The **simuf1_min_lgr** setting was designed to exemplify the analysis of marker ordering without the use of a framework map, and it has two data sets: an input SAS Data Set (simuf1_min_lgr.sas7bdat) and a Genotype SAS Data Set (simuf1.sas7bdat).

The **simuf1_frame** setting is designed to exemplify the analysis of marker ordering with the use of a framework map, and it has two data sets: an input SAS Data Set simuf1_min_frame.sas7bdat and a Genotype SAS Data Set (simuf1.sas7bdat).

The **simuf1_order** setting is designed to exemplify the analysis of marker ordering with the use of an order variable that pre-specify the order of markers on which genetic distances must be computed, and it has three data sets: an input SAS Data Set (simuf1_min_frame.sas7bdat), a Genotype SAS Data Set (simuf1.sas7bdat), and an Order SAS Data Set (simuf1_min_order.sas7bdat).

Build QTL Genotype Probability Data Set

The **simuf1_min_sr** setting is designed to exemplify the computation of prior conditional probabilities of putative QTL in full-sibs, and it has two data sets: an input SAS Data Set (simuf1_min_sr.sas7bdat) and an Annotation SAS Data Set (simuf1_min_lgr_lmo_sr.sas7bdat).

QTL IM, CIM and MIM Analysis

The **simuf1_IM** setting is designed to exemplify the procedure of QTL mapping in full-sibs, and it has three data sets: an input SAS Data Set (simuf1_min_sr.sas7bdat), an Annotation SAS Data Set (simuf1_min_lgr_lmo_sr.sas7bdat), and a Genotype Probability Data Set (simuf1_min_sr_gp.sas7bdat).

Data Sets

simuf1.txt:

This data set is in the text format used by OneMap. It contains phenotypes of 22 markers distributed along two linkage groups and measurements on two quantitative traits of a simulated full-sib family with 300 individuals derived from a bi-parental cross of two simulated outbred parents. Of the two traits, one has only noise without any QTL effect, and the other has some QTL effects.

simuf1.sas7bdat:

This data set is the simuf1.txt text file converted to a SAS Data Set.

simuf1_anno.sas7bdat:

This data set contains marker types and marker names of all 22 markers found in the simuf1.sas7bdat data set.

simuf1_min_lgr.sas7bdat:

This data set is the output of the Linkage Group and Recombination Analyses process run using the simuf1.sas7bdat data set as input. It contains, the estimated pairwise recombination fraction matrix between all markers, and preliminary linkage groups.

simuf1_min_frame.sas7bdat:

This data set is the output of the Linkage Group and Recombination Analyses run using the simuf1.sas7bdat data set as input. It contains the estimated pairwise recombination fraction matrix between all markers, and preliminary linkage groups. In addition, it contains, a framework map variable (frame_Order) that was artificially introduced into the data set.

simuf1_min_order.sas7bdat:

This data set is the output of the Linkage Group and Recombination Analyses process run using simuf1.sas7bdat data set as input. This data set contains, among other things, an order variable (cM_Kosambi) that pre-specify the order of markers on which genetic distances must be computed.

simuf1_min_sr.sas7bdat:

This data set is the simuf1.sas7bdat data set in which the markers have been reordered to match their positions in the linkage groups.

simuf1_min_tps.sas7bdat:

This data set contains the elements of the lower triangle matrix of pairwise recombination fraction between all markers in the simuf1.sas7bdat data set, as well as the elements of the lower triangle matrix of pairwise *LOD* values, for all four possible linkage phases for a cross of two outbred parents.

simuf1_min_lgr_lmo_sr.sas7bdat:

This data set is the output of the Linkage Map Order process run using the simuf1.sas7bdat data set as input. It contains linkage groups, markers ordered within each linkage group, genetic distance between markers, marker types, and linkage phases.

simuf1_min_sr_gp.sas7bdat:

This data set is the output from the conditional probability analysis of the simuf1.sas7bdat data set. It contains prior conditional probabilities of putative QTL in full-sibs.