

Run Multiple Genotype Association Tests

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Overview

This script runs genotypic association tests on multiple dependent phenotype columns. All applicable genotype association tests can be run simultaneously for binary, integer-valued and real-valued dependent columns.

If the False Discovery Rate (FDR) option is chosen, additional FDR results according to two different FDR algorithms, "BH" (Benjamini-Hochberg) and "BY" (Benjamini-Yekutieli), are presented.

Note: This script **DOES NOT** run Multivariate Association tests.

Recommended Directory Location

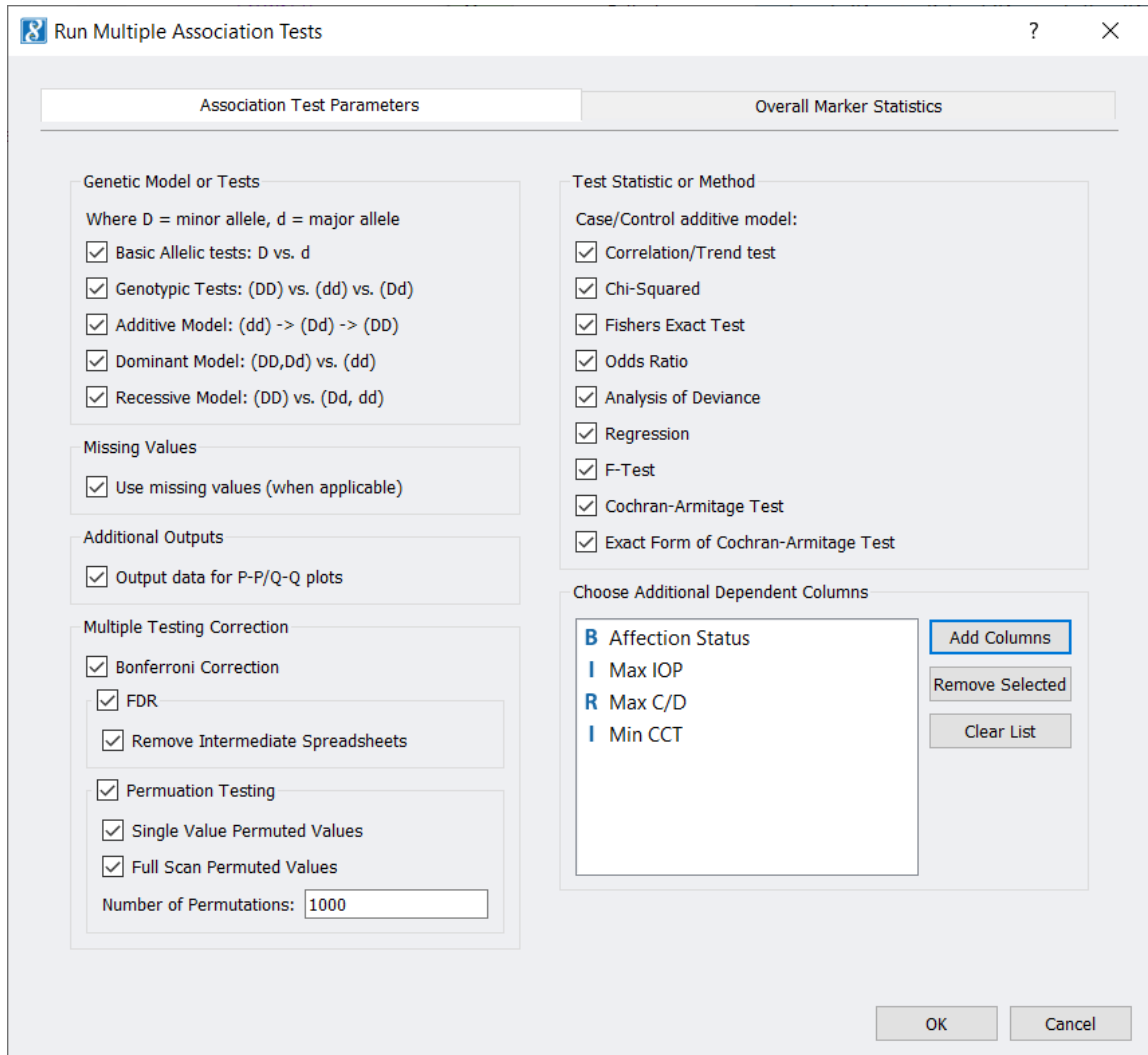
Save the script to the following directory:

***..\Application Data\Golden Helix SVS\UserScripts\Spreadsheet\Genotype**

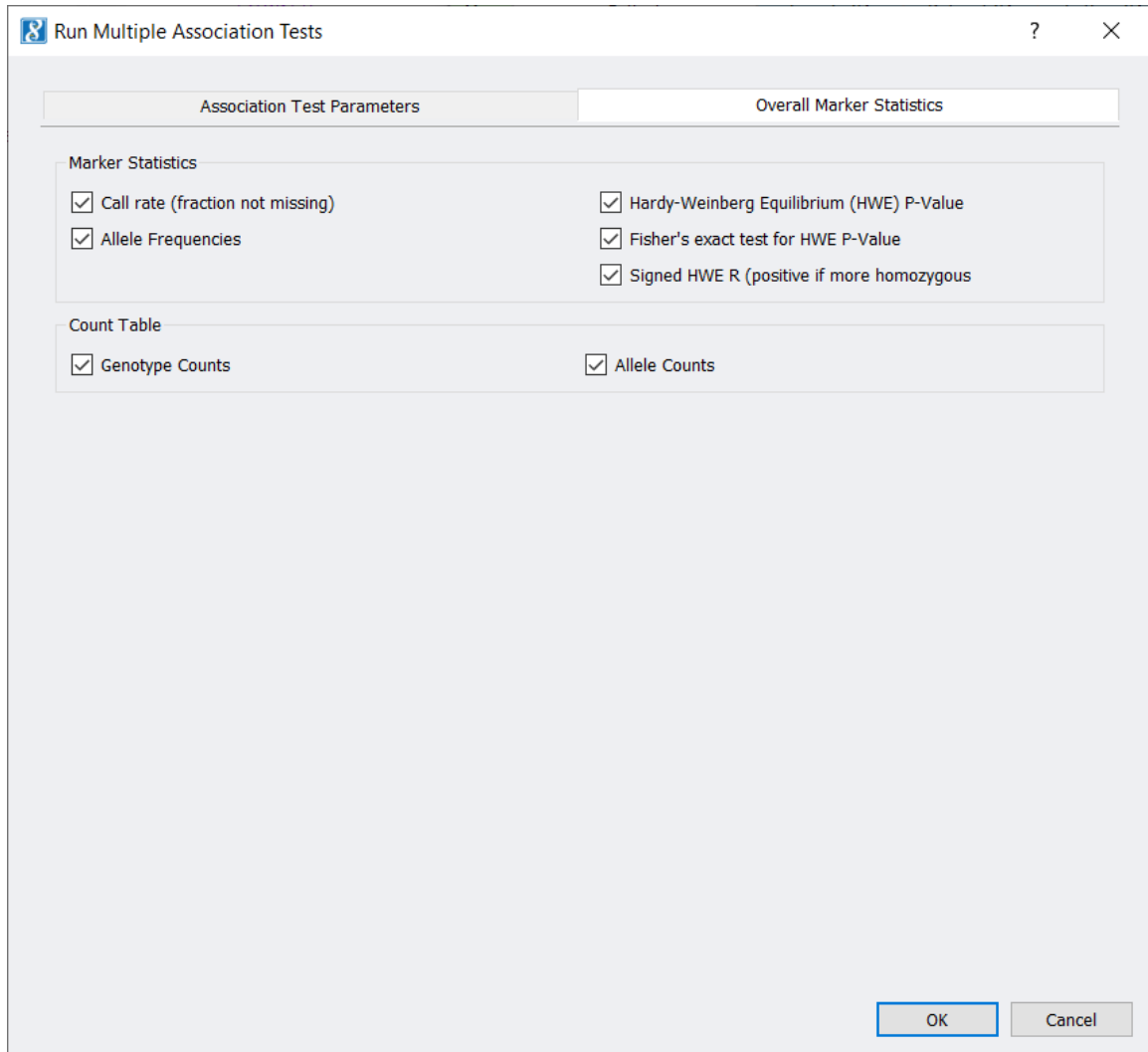
Note: The **Application Data** folder is a hidden folder on Windows operating systems and its location varies between XP and Vista. The easiest way to locate this directory on your computer is to open SVS and go to **Tools > Open Folder > UserScripts Folder**. If saved to the proper folder, this script will be accessible from the spreadsheet **Genotype** menu.

Using the Script

- 1) From a spreadsheet with several binary or numeric phenotypes and several genotype columns, choose **Genotype > Run Multiple Genotype Association Tests**.



- 2) Select the Genetic Models, Test Statistics, and output options in the window. Also choose any binary or numeric dependent columns with which you wish to perform association tests. These will be used in addition to any columns that were already marked as “dependent” (magenta color) in the spreadsheet.
- 3) The next tab has additional output options, similar to the genotype association tests window. Select the appropriate options and click **OK**.



- 4) The applicable tests are performed according to the type of dependent and the options selected. The resultant spreadsheets, which may be accessed through the Project Navigator Window, are named according to the genetic model and the phenotype used.