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, integervalued 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

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

Association Test Parameters	Overall Marker Statistics
Genetic Model or Tests Where D = minor allele, d = major allele Genotypic Tests: D vs. d Additive Model: (DD) vs. (dd) vs. (Dd) Characteristic (dd) -> (Dd) -> (DD) Characteristic (DD,Dd) vs. (dd) Recessive Model: (DD) vs. (Dd, dd) Missing Values Use missing values (when applicable) Additional Outputs Coutput data for P-P/Q-Q plots	Test Statistic or Method Case/Control additive model: Correlation/Trend test Chi-Squared Fishers Exact Test Odds Ratio Analysis of Deviance Regression F-Test Cochran-Armitage Test Exact Form of Cochran-Armitage Test Choose Additional Dependent Columns
Multiple Testing Correction Bonferroni Correction FDR Remove Intermediate Spreadsheets Permuation Testing Single Value Permuted Values Full Scan Permuted Values Number of Permutations:	B Affection Status I Max IOP R Max C/D I Min CCT Add Columns Remove Selected Clear List

- 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**.

Run Multiple Association Tests		?	>
Association Test Parameters	Overall Marker Statistics		
Marker Statistics			
Call rate (fraction not missing)	✓ Hardy-Weinberg Equilibrium (HWE) P-Value		
Allele Frequencies	Fisher's exact test for HWE P-Value		
	Signed HWE R (positive if more homozygous		
Count Table			
Genotype Counts	Allele Counts		
	ОК	Can	

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.