MLM with Multiple Phenotypes

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Overview

This script runs the equivalent of **Spreadsheet > Genotype > Mixed Linear Model Analysis** on multiple dependent phenotype columns, one column at a time. All possible **Mixed Linear Model Analysis** tests can be run on each of your dependent columns, which may be binary, integer-valued or real-valued columns.

Note: This script DOES NOT run <u>Multivariate</u> Analysis. Each dependent variable/column is used individually for all MLM 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) Start with a spreadsheet with (1) the binary or numeric columns that need to be phenotypes for this feature, and (2) mapped genotypic data or mapped numerically recoded genotypic data.
2) Make the binary or numeric columns that you wish to have as phenotypes for this feature "dependent".
3) Choose **Genotype > MLM with Multiple Phenotypes**.
4) A dialog that looks just like the dialog for **Spreadsheet > Genotype > Mixed Linear Model Analysis** will appear. Fill in this dialog with the tests you wish to perform on each phenotype and click **OK**. **NOTE:** To save output spreadsheets, you may wish to use a *Pre-Computed Kinship Matrix*. Otherwise, an IBS kinship matrix will be redundantly computed for every phenotype.
5) The processing will occur, one phenotype at a time, and output spreadsheet(s) will be generated for each phenotype.
6) The title of each output spreadsheet will be preceded by the name, in parentheses, of the tested phenotype from which that output resulted.