Chi-Squared Test with Continuity Correction
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Overview

This script performs a Chi-squared test on a spreadsheet with a binary dependent and genotypic data. The output will contain results for the traditional test as well as results with the Yates continuity correction applied. The following genetic models are available; Basic Allelic, Dominant, or Recessive.

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 operating systems. The easiest way to locate this directory on your computer is to open SVS and go to **Tools > Open > Open UserScripts Folder** and save the script in the **\Spreadsheet\Genotype** 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 a binary dependent column and several genotypic columns, select **Genotype > Chi-Squared Test with Continuity Correction**.
2. Choose the appropriate genetic model and click **OK**.

The resulting spreadsheet contains the X^2 Statistic values, P-values and –log 10 P-values for both the standard chi-squared test and the test with the Yates continuity correction applied. The spreadsheet also contains the cell counts that are used to calculate the test statistic.

References

http://en.wikipedia.org/wiki/Yates's_correction_for_continuity