

Average Markers by Gene

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Overview

This script calculates the average of all quantitative columns by gene regions defined by a gene annotation track.

Recommended Directory Location

Save the script to the following directory:

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

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 select **Tools > Open Folder > UserScripts Folder**. If saved to the proper folder, this script will be accessible from the spreadsheet **Numeric** menu.

Using the Script

1. Open a marker mapped spreadsheet containing real or integer valued columns.
2. Select **Numeric > Average Markers by Gene**
3. Choose an appropriate gene annotation track and optionally choose to expand the gene regions by a given distance in bp.

The resulting spreadsheet contains an average value for each gene region/sample found in the original spreadsheet. Missing values are skipped.