

Average Markers by Gene

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Overview

This script calculates an average value for each row over each region as defined by a gene annotation track or a string marker map field. This script requires a marker mapped spreadsheet with several quantitative columns.

Recommended Directory Location

Save the script to the following directory:

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

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's **Analysis** menu.

Using the Script

1. Open a spreadsheet containing several mapped quantitative columns.
2. Choose **Analysis >Average Markers by Gene**.
3. Optionally choose to **Define regions with Annotation Track**:
 - a) Choose an appropriate track
 - b) Choose either gene or transcript to use.
4. Or **Define regions with Marker Map**:
 - a) Choose appropriate string field.
5. Optionally extend regions by a given distance in bp.
6. Click **OK**.

The resulting spreadsheet is created as a child node of the original spreadsheet and contains the average values based on the above selections.