

Export Multivariate Segment Means to Wiggle Files

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Overview

This script exports the segment means spreadsheet (created upon running Copy Number Segmentation in CNAM having selected the multivariate segmenting algorithm) as a single Wiggle file that can be opened and viewed in supported genome browsers.

Note: This script only works with SVS 6.4 or later.

Recommended Directory Location

A good directory location for saving this script would be:

C:/HelixTree/scriptsHT/user/Spreadsheet/Scripts/.

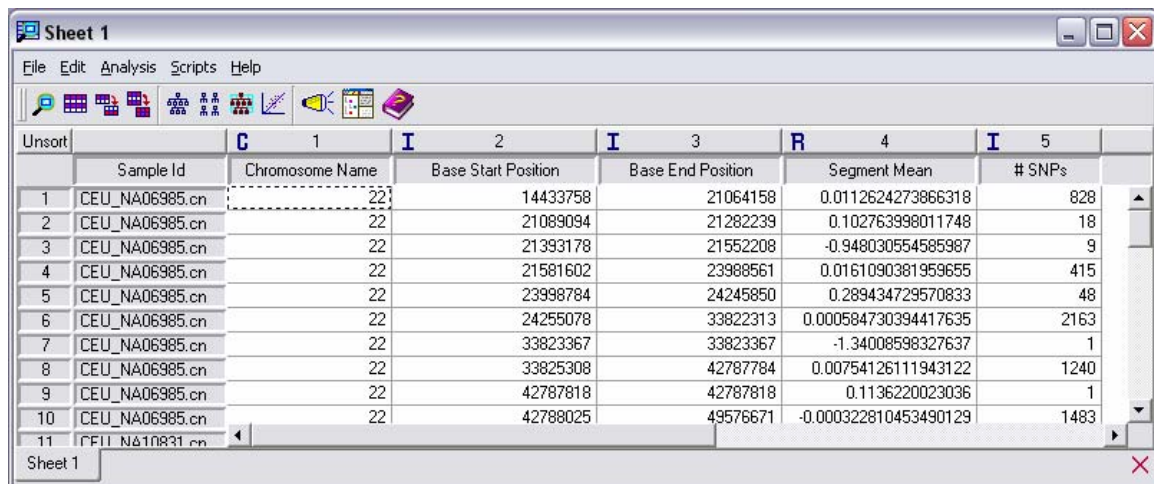
When saved to this folder, the script will be accessible from the spreadsheet **Scripts** menu.

Using the Script

To use this script, first run Copy Number Segmentation from the CNAM menu choosing the multivariate segmenting algorithm. (For more information on running copy number segmentation see:

http://www.goldenhelix.com/SNP_Variation/Manual/using_the_copy_number_analysis_segmentation_tool.html).

The result will be two spreadsheets, a segment covariate spreadsheet and a segment means spreadsheet (Figure 1).



Unsort	Sample Id	Chromosome Name	Base Start Position	Base End Position	Segment Mean	# SNPs
1	CEU_NA06985.cn	22	14433758	21064158	0.0112624273866318	828
2	CEU_NA06985.cn	22	21089094	21282239	0.102763998011748	18
3	CEU_NA06985.cn	22	21393178	21552208	-0.948030554585987	9
4	CEU_NA06985.cn	22	21581602	23988561	0.0161090381959655	415
5	CEU_NA06985.cn	22	23998784	24245850	0.289434729570833	48
6	CEU_NA06985.cn	22	24255078	33822313	0.000584730394417635	2163
7	CEU_NA06985.cn	22	33823367	33823367	-1.34008598327637	1
8	CEU_NA06985.cn	22	33825308	42787784	0.00754126111943122	1240
9	CEU_NA06985.cn	22	42787818	42787818	0.1136220023036	1
10	CEU_NA06985.cn	22	42788025	49576671	-0.000322810453490129	1483
11	CHB_NA10831.cn					

Figure 1. Segment means spreadsheet.

Open the segment means spreadsheet and select the Export Multivariate Segment Means to Wiggle Files script from the spreadsheet menu location where it was stored. Or, from the project viewer, select **Tools->Run Script** to open a dialog to browse for the script location.

Running this script will prompt you to save a single Wiggle file. Give it a name and click Save. This Wiggle file can now be loaded in a supported genome browser.