

# Export Univariate Segment Means to Wiggle Files

**Author: James Grover, Golden Helix, Inc.**

## Overview

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

## Recommended Directory Location

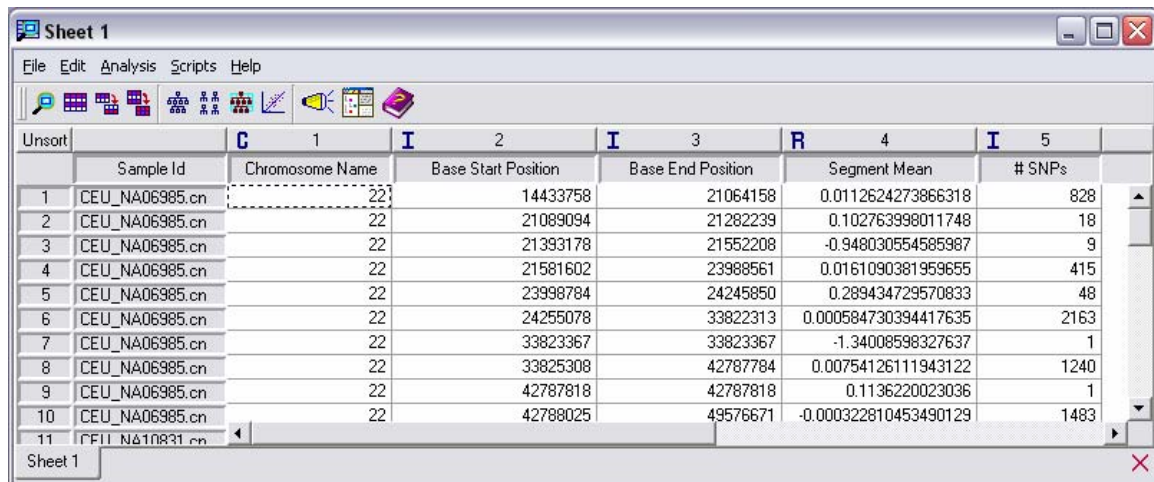
A good directory location for saving this script would be:  
**C:/HelixTree/scriptsHT/user/Spreadsheet/Scripts/.**

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 univariate 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](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).



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	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	CFII_NA10831.cn									

Figure 1. Segment means spreadsheet.

Open the segment means spreadsheet and select the Export Univariate 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 choose a directory to store the Wiggle files. A Wiggle file will be created for each sample in the data set. Choose a directory and click Save. These Wiggle files can now be loaded in a supported genome browser.