



CBSWrapperPipeline Documentation

Description: A one step pipeline that runs CBS.

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Help Forum: genepattern.org/help

Summary

This pipeline is a one step pipeline which runs CBS. It is only meant to be used as a scatter step for the ParallelCBS scatter-gather pipeline.

Parameters

Name	Description
input file	A file containing copy number data in CN format
sample name	The name of the sample to use in analysis. Leave this blank to use the first sample in the input file.
permutations	Number of permutations used for p-value computation
significance level	The significance level for the test to accept change-points
output prefix	The prefix to use for the output file name

Output Files

1. <output.prefix>.cbs.txt

A tab delimited text file with six columns: the sample id, the chromosome number, map position of the start of the segment, the map position of the end of the segment, the number of markers in the segment, and the average value in the segment.

Platform Dependencies

Module type: pipeline

CPU type: any

OS: any

GenePattern

Language: R

GenePattern Module Version Notes

Date	Version	Description
9/7/2012	1	Initial version.
3/26/2019	2	Updated to use CBS v3