GenePattern

CopyNumberDivideByNormals Documentation

Description: Determines the copy number of a target SNP
Author: David Twomey and Joshua Gould

Summary

The CopyNumberDivideByNormals module determines the raw copy number of a target SNP. The calculation, which divides the intensity value of the target SNP by the mean intensity value of all normal SNPs, is also called copy number (CN) normalization or normalization with respect to normals.

SNP Input File

The input file is a GenePattern .snp file. Use the SNPFileCreator module to create a GenePattern .snp file from a set of CEL files generated using an Affymetrix SNP chip. The input .snp file must contain both normal and target samples so that CopyNumberDivideByNormals can determine the raw copy number of a target SNP *with respect to normals*.

XCN or CN Output File

CopyNumberDivideByNormals generates an output file that replaces the intensity value of each probe with its raw copy number. The output file can include genotype call information (.xcn file) or not (.cn file). The SNPViewer module requires the genotype call information (.xcn file). The *output file* parameter specifies the name of the output file that is created.

Parameters

Name	Description
snp file	SNP file containing both normal and target samples.
sample info file	Sample information file. This is a tab-delimited file where
	■ The first row contains labels that identify the sample information provided in each column.
	■ Each remaining row provides information for one sample.
	CopyNumberDivideByNormals requires the following columns (column labels are case-sensitive and spacing must be exact), all other columns are ignored:
	■ Sample: contains the sample name
	■ Ploidy(numeric): samples with ploidy=2 are normal samples, all others are target samples.
include genotype calls	Whether the output file should include genotype information:
	■ yes (create xcn file). The output file includes genotype call information. A .xcn file extension is added to the output file name that you specify.
	■ no (create cn file). The output file does not include

output file name   Name of the output file

Output Files

1. .cn or .xcn file containing raw copy number per probe
2. standard output file containing normal and target samples used

Platform Dependencies

Module type: SNP Analysis
CPU type: any
OS: any
Language: Java