



XChromosomeCorrect Documentation

Description: Corrects SNP values on the X chromosome for samples from male donors
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Summary

For each sample from a male donor, the XChromosomeCorrect module doubles the intensity value for each SNP on the X chromosome.

- 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. **Note:** XChromosomeCorrect accepts only non-allele-specific .snp files (.snp files that contain one intensity value per probe).
- The output file is a GenePattern .snp file that contains the corrected intensity values.

Parameters

Name	Description
snp filename	GenePattern .snp file (non-allele-specific) that contains one intensity value per probe.
sample info filename	Name of a sample information file (for example, a dChip format sample information file). This is a tab-delimited file where <ul style="list-style-type: none">▪ The first row contains labels identifying the content of each column.▪ Each remaining row describes one sample. XChromosomeCorrect requires columns with the following labels (label names are case-sensitive and spacing must be exact), all other columns are ignored: <ul style="list-style-type: none">▪ Sample: contains the sample name▪ Gender: contains a value of M or F for each sample
output file	Name of the output file. By default, the output file is named <i>input-file.xcorrected.snp</i> .

Output Files

1. .snp file (with corrected intensity values)

Platform Dependencies

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