GLAD Documentation

Description: Gain and Loss Analysis of DNA
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Summary

The GLAD module detects the altered regions in the genomic pattern and assigns a status (normal, gained, or lost) to each chromosomal region.

- The input file is a GenePattern .cn file that contains sorted SNPs and raw copy numbers. Use the SNPFileCreator and CopyNumberDivideByNormals modules to create the input file.

- The output file is a text file that describes each altered region: start, end, number of SNPs, and smoothed copy number.

References

1. Hupé, P., Stransky, N., Thiery, J. P., Radvanyi, F., and Barillot, E. (2004). Analysis of array CGH data: from signal ratio to gain and loss of DNA regions. Bioinformatics, 20:3413–3422.

2. BioConductor GLAD package, http://bioconductor.org/.

Parameters

Name	Description
copy.number.input.file	cn file that contains sorted SNPs and raw copy number value per probe. (note: data should not be in log2)
output.filename	Name of the output file

Output Files

1. GLAD output file (GLAD status per probe)

Platform Dependencies

Module type: SNP Analysis
CPU type: any
OS: any
Language: R 2.5.0