



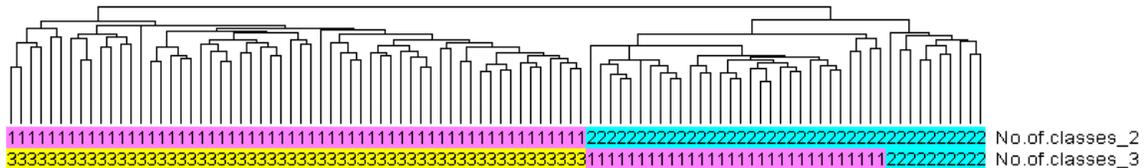
ClusteringToCls Documentation

Description: Generate .cls file(s) from a hierarchical clustering result

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Summary

ClusteringToCls module generates .cls file(s) based on an agglomerative hierarchical clustering (HC) result [1]. Subclass splitting is traced from the root of the dendrogram generated by HC, and a sample cluster that contains at least “min.sample” samples is allowed to form a subclass.



References

1. M.B. Eisen, et al. "Cluster Analysis and Display of Genome-Wide Expression Patterns," PNAS, 14863-14868 (1998)

Links

.atr file format

http://www.broadinstitute.org/cancer/software/genepattern/gp_guides/file-formats/sections/atr

Parameters

Name	Description
input filename	Hierarchical clustering result (output of Hierarchical Clustering module, .atr)
output file	Prefix of output files, Default: ClusteringToCls
min sample	Minimum number of samples allowed to form a cluster, Default: 10



cls start from	Class label as ordinal numbers start from "1" (default) or "0" in output .cls files, Default: start from 1
search depth	Depth of tree search, Default: 30
sample info	Output class label for each sample in tab-delimited text? (can be opened in Excel, samples in the same order with .gct used for clustering), Default: no

Input Files

1. input filename
See .atr file format

Output Files

1. ~.cls
Sample class labels in .cls format.
2. ~.txt
Sample class labels in tab-delimited text

Example Data

ClusteringToCls_example_dataset.atr

Platform Dependencies

Module type: Preprocess & Utilities
CPU type: Any
OS: Any
Language: R