

PcIToGct Documentation

Module name: PclToGct

Description: Converts files in Stanford's pcl format to GenePattern's gct

format

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Summary: The pcl and gct file formats are very similar. The key difference is that pcl files support 'weights', while gct files are unweighted. The conversion from pcl to gct provides three options for handling weights:

Ignore the weights in the pcl file

Multiply values by weights (altering biological data)

• Print an error if any weight in the pcl file is not equal to one

In addition, the converter ensures that each row is the same length by adding the appropriate number of "empty" columns. (This is needed for some imputation modules that expect a fixed number of columns in each row.)

While a gct file supports empty cells, most GenePattern modules require all cells to have values. Thus, it will usually be necessary to run a missing value imputation module (e.g. ImputeMissingValuesKNN) after converting a .pcl file to a .gct file.

To convert a .gct file to a .pcl file, use the GctToPcl module.

References:

- 1. Stanford pcl file format: http://genome-www5.stanford.edu/help/formats.shtml#pcl
- 2. Broad GCT file format: http://genepattern.org/tutorial/gp_fileformats.html?gct

Parameters:

Name Description Choices

input.filename: Source pcl file to convert to gct file

output.filename: Name of gct file to output

weight.handling How to handle manually edited Ignore weights;

weights in the pcl file Multiply values by weights (altering

biological data);

Print error if weights not equal to 1

present:

Return Value:



output filename

Platform dependencies:

Task type: Data Format Conversion

CPU type: any
OS: any
Java JVM level: n/a
Language: Perl

Support files: pclToGct.pl