

GenePattern

ExtractRowNames Documentation

Module name: ExtractRowNames
Description: Extracts the features (e.g. gene accessions) from a dataset into a separate text file
Author: Joshua Gould, gp-help@broad.mit.edu

Summary: The ExtractRowNames module extracts the row names (i.e. the “features”), which are usually gene accession names, from a .res, .gct. or .odf file and writes them to a text file.

Parameters:

Name	Description
input.filename:	.res, .gct, .odf, file from the row names are extracted
output.file:	output filename containing the row names - .txt

Platform dependencies:

Task type: Preprocess & Utilities
CPU type: any
OS: any
Java JVM level: 1.4
Language: Java

Return Value:

1. a .txt file containing the extracted row names

Release Information

Renamed from ExtractFeatureListRows