

GenePattern

GEOImporter Documentation

Description: Imports data from the Gene Expression Omnibus (GEO)
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Summary: Creates a gct file from a GEO series record or a GEO Dataset. For more information about GEO, see <http://www.ncbi.nlm.nih.gov/geo/>. The GCT file format is described at <https://www.genepattern.org/file-formats-guide#GCT>.

Parameters:

Name	Description
GEO.accession	GEO Series record (GSExxx) or a GEO Dataset (GDSxxx). Either a GEO accession or a GEO SOFT file must be given.
GEO.SOFT.filename	GEO SOFT file. Either a GEO SOFT file or a GEO accession must be given.
Drop.NA.Rows	For GSExxx series GEO datasets, omit rows that contain all "NA" values. TRUE/FALSE.
data.column.name	The name of the column that contains the expression values if input is a GEO series
output.file	The name of the output file

Output Files:
gct file

Module Language: R 4.0.3

Source Repository: <https://github.com/genepattern/GEOImporter/releases/tag/v6>

Docker image: genepattern/geoimporter:1

Dockerfile: <https://github.com/genepattern/GEOImporter/blob/v6/Dockerfile>

Version	Comment
6	Added support omitting rows containing all "NA" values. Updated to use R-4.0.3 in a GEOImporter specific Docker container.
5.2	Updated for new NCBI FTP paths. Upgraded to R 4.0.3 - Beta