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/
Docker image: jupyter/datascience-notebook:r-4.0.3

Version	Comment
5.2	Updated for new NCBI FTP paths. Upgraded to R 4.0.3