



## 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.
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](https://jupyter/datascience-notebook:r-4.0.3)

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