

## **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 <a href="http://www.ncbi.nlm.nih.gov/geo/">http://www.ncbi.nlm.nih.gov/geo/</a>. The GCT file format is described at <a href="http://www.broad.mit.edu/cancer/software/genepattern/tutorial/gp\_fileformats.html">http://www.broad.mit.edu/cancer/software/genepattern/tutorial/gp\_fileformats.html</a>.

## 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

## Platform dependencies:

Module type: Preprocess & Utilities

CPU type: any OS: any Language: R