

Conduct GO Element

Given a list of genes, using Bioconductor (GO, GOSTats) and DAVID at NIH.

Element type: conduct-go-id

Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
Output directory	The directory to store Conduct GO results.		output-dir	string
Title	Title is used to name the output files - so make it meaningful.	Default	title	string
Gene Universe	Select a gene universe.	hgu133a.db	gene-universe	string

Input/Output Ports

The element has 1 *input port*:

Name in GUI: Conduct GO data

Name in Workflow File: in-data

Slots:

Slot In GUI	Slot in Workflow File	Type
Target genes	in-ann	ann-table-list