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	i**n-ann**	*ann-table-list*