Conduct GO Element

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

Parameters in GUI

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

Parameters in Workflow File

Type: conduct-go-id

Parameter	Parameter in the GUI	Type
output-dir	**Output directory**	*string*
title	**Title**	*string*
gene-universe	**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*