

# Conduct GO Element

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

## Parameters in GUI

Parameter	Description	Default value
<b>Output directory</b>	The directory to store Conduct GO results.	
<b>Title</b>	Title is used to name the output files - so make it meaningful.	Default
<b>Gene Universe</b>	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	in-ann	ann-table-list