Gene-by-gene approach report

Output a table of genes found in a reference sequence.

Parameters in GUI

Parameter	Description	Default value
Output file	File to store a report.	
Annotation name	Annotation name used to compare genes and reference genomes..	blast-result
Existing file	If a target report already exists you should specify how to handle that. Merge two table in one. Overwrite or Rename existing file..	Merge
Identity cutoff	Identity between gene sequence length and annotation length in per cent. BLAST identity (if specified) is checked after	90.0000%

Parameters in Workflow File

Type: genebygene-report-id

Parameter	Parameter in the GUI	Type
output-file	**Output file**	*string*
annotation_name	**Annotation name**	*string*
existing	**Existing file**	*string*
identity	**Identity cutoff**	*numeric*

Input/Output Ports

The element has 1 *input port*:

Name in GUI: Gene by gene report data

Name in Workflow File: in-data

Slots:

Slot In GUI	Slot in Workflow File	Type
Input annotations	**gene-ann**	*ann-table-list*
Input sequences	**gene-seq**	*seq*