

Gene-by-gene approach report

Output a table of genes found in a reference sequence.

Element type: genebygene-report-id

Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
Output file	File to store a report.		output-file	string
Annotation name	Annotation name used to compare genes and reference genomes.	blast-result	annotation_name	string
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	existing	string
Identity cutoff	Identity between gene sequence length and annotation length in percent. BLAST identity (if specified) is checked after	90.0000%	identity	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