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*