

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 |