

# Read Sequence Element

Reads sequences and annotations if any from local or remote files.

## Parameters in GUI

| Parameter                   | Description                                                                                                                                                              | Default value |
|-----------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------|
| <b>Input files</b>          | Semicolon-separated list of datasets to the input files.                                                                                                                 |               |
| <b>Mode</b>                 | If the file contains more than one sequence, "split" mode sends them as is to output, while "merge" appends all the sequences and outputs the merged sequence.           | Split         |
| <b>Merging gap</b>          | In the "merge" mode, inserts the specified number of gaps between the original sequences. This is helpful e.g. to avoid finding false positives at the merge boundaries. | 10            |
| <b>Sequence count limit</b> | Split mode only. Read only first N sequences from each file. Set 0 value for reading all sequences.                                                                      | 0             |
| <b>Accession filter</b>     | Only reports a sequence with the specified accession (id).                                                                                                               |               |

## Parameters in Workflow File

Type: read-sequence

| Parameter                   | Parameter in the GUI        | Type                                                                                                                                      |
|-----------------------------|-----------------------------|-------------------------------------------------------------------------------------------------------------------------------------------|
| <b>url-in</b>               | <b>Input files</b>          | <i>string</i>                                                                                                                             |
| <b>mode</b>                 | <b>Mode</b>                 | <i>numeric</i><br>Available values are: <ul style="list-style-type: none"><li>• 0 - for split mode</li><li>• 1 - for merge mode</li></ul> |
| <b>merge-gap</b>            | <b>Merging gap</b>          | <i>numeric</i>                                                                                                                            |
| <b>sequence-count-limit</b> | <b>Sequence count limit</b> | <i>numeric</i>                                                                                                                            |
| <b>accept-accession</b>     | <b>Accession filter</b>     | <i>string</i>                                                                                                                             |

## Input/Output Ports

The element has 1 *output port*:

**Name in GUI:** *Sequence*

**Name in Workflow File:** out-sequence

**Slots:**

| Slot In GUI               | Slot in Workflow File | Type                    |
|---------------------------|-----------------------|-------------------------|
| <b>Sequence</b>           | <b>sequence</b>       | <i>sequence</i>         |
| <b>Set of annotations</b> | <b>annotations</b>    | <i>annotation-table</i> |
| <b>Source URL</b>         | <b>url</b>            | <i>string</i>           |