Read Sequence Element

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

Parameters in GUI

Parameter	Description	Default value
Input files	Semicolon-separated list of datasets to the input files.	
Mode	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
Merging gap	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
Sequence count limit	Split mode only. Read only first N sequences from each file. Set 0 value for reading all sequences.	0
Accession filter	Only reports a sequence with the specified accession (id).	

Parameters in Workflow File

Type: read-sequence

Parameter	Parameter in the GUI	Туре
url-in	Input files	string
mode	Mode	numeric
		Available values are:
		0 - for split mode 1 - for merge mode
merge-gap	Merging gap	numeric
sequence-count-limit	Sequence count limit	numeric
accept-accession	Accession filter	string

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	Туре
Sequence	sequence	sequence
Set of annotations	annotations	annotation-table
Source URL	url	string