Write Sequence Element

The element gets message(s) with sequence data and, optionally, associated annotations data and saves the data to the specified file(s) in one of the appropriate formats (GenBank, FASTA, etc.).

Element type: write-sequence

Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
Data storage	Place to store workflow results: local file system or a database.		**data-storage**	*string*
Output file	Location of the output data file. If this attribute is set, then the “Location” slot is not taken into account.		**url-out**	*string*
Output file suffix	This suffix will be used for generating the output file name.		**url-suffix**	*string*
Existing file	If a target file already exists, you can specify how it should be handled: either overwritten, renamed or appended (if supported by file format).	Rename	**write-mode**	*numeric* Available values are: • 0 - for overwrite • 1 - for append • 2 - for rename
Document format	Format of the output file.	fasta	**document-format**	*string* Available values are: • fasta • fastq • genbank • raw
Accumulate objects	Accumulates all incoming data in one file or creates separate files for each input. In the latter case, an incremental numerical suffix is added to a file name.	True	**accumulate**	*boolean*
Split sequence	Split each incoming sequence on several parts.	1	**split**	*numeric*

Input/Output Ports

The element has 1 *input port*:

Name in GUI: *Sequence*

Name in Workflow File: in-sequence

Slots:

Slot In GUI	Slot in Workflow File	Type
Sequence	**sequence**	*sequence*
Location	**url**	*string*
Set of annotations	**annotations**	*annotation-table-list*