Get Sequences by Annotations Element

Extracts annotated regions from input sequence.

Parameters in GUI

Parameter	Description	Default value
Annotation names (required)	List of annotation names which will be accepted or filtered. Use space as the separator.	
Accept of filter	Selects the name filter: accept specified names or accept all except specified.	Accept
Complement	Complements the annotated regions if the corresponding annotation is located on the complement strand.	True
Translate	Translates the annotated regions if the corresponding annotation marks a protein subsequence.	True
Extend left	Extends the resulted regions to left.	0
Extend right	Extends the resulted regions to right.	0
Gap length	Inserts a gap of a specified length between the merged locations of the annotation.	1

Parameters in Workflow File

Type: extract-annotated-sequence

Parameter	Parameter in the GUI	Type
annotation-names	**Annotation names**	*string*
accept-or-filter	**Accept or filter**	*boolean* Available values are: • true - for accept • false - for filter
complement	**Complement**	*boolean*
translate	**Translate**	*boolean*
extend-left	**Extend left**	*numeric*
extend-right	**Extend right**	*numeric*
merge-gap-length	**Gap length**	*numeric*

Input/Output Ports

The element has 1 *input port*:

Name in GUI: *Input sequence*

Name in Workflow File: in-sequence

Slots:

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

And 1 *output port*:

Name in GUI: *Annotated regions*

Name in Workflow File: out-sequence

Slots:

Slot In GUI	Slot in Workflow File	Type

Sequence	**sequence**	*sequence*
Set of annotations	**annotations**	*annotation-table*