Smith-Waterman Search Element

Searches regions in a sequence similar to a pattern sequence. Outputs a set of annotations.

Under the hood is the well-known Smith-Waterman algorithm for performing local sequence alignment.

Element type: ssearch

Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
Substitution Matrix	Describes the rate at which one character in a sequence changes to other character states over time.	Auto	**matrix**	*string* Available values are: • Auto - for auto detecting matrix • blosum60 • dna • rna • ...
Algorithm	Version of the Smith-Waterman algorithm. You can use the optimized versions of the algorithm (SSE, CUDA and OpenCL) if your hardware supports these capabilities.	OPENCL	**algorithm**	*string* Available values are: • Classic 2 • SSE2 • OpenCL • CUDA
Filter Results	Specifies either to filter the intersected results or to return all the results.	filter-intersections	**filter-strategy**	*string* Available values are: • filter-intersections • none
Min Score	Minimal percent similarity between a sequence and a pattern.	90%	**min-score**	*numeric*
Search in	Specifies which strands should be searched: direct, complementary or both.	both strands	**strand**	*numeric* Available values are: • 0 - for searching in both strands • 1 - for searching in direct strand • 2 - for searching in complement strand
Search in Translation	Translates a supplied nucleotide sequence to protein and searches in the translated sequence.	False	**amino**	*boolean*
Gap Open Score	Penalty for opening a gap.	-10.0	**gap-open-score**	*numeric*
Gap Extension Score	Penalty for extending a gap.	-1.0	**gap-ext-score**	*numeric*
Use Pattern Names	Use a pattern name as an annotation name.	True	**use-names**	*boolean*
Annotate as	Name of the result annotations.	misc_feature	**result-name**	*string*
Qualifier name for pattern name	Name of qualifier in result annotations which is containing a pattern name.	pattern name	**pattern-name-qual**	*string*

Input/Output Ports

The element has 2 *input ports.* The first input port:

Name in GUI: *Input data*

Name in Workflow File: in-sequence

Slots:

Slot In GUI	Slot in Workflow File	Type
Sequence	**sequence**	*sequence*

The second input port:

Name in GUI: *Pattern data*

Name in Workflow File: pattern

Slots:

Slot In GUI	Slot in Workflow File	Type
Sequence	**sequence**	*sequence*

And 1 *output port*:

Name in GUI: *Pattern annotations*

Name in Workflow File: out-annotations

Slots:

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