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.

Parameters in GUI

Parameter	Description	Default value
Substitution Matrix	Describes the rate at which one character in a sequence changes to other character states over time.	Auto
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
Filter Results	Specifies either to filter the intersected results or to return all the results.	filter-intersections
Min Score	Minimal percent similarity between a sequence and a pattern.	90%
Search in	Specifies which strands should be searched: direct, complementary or both.	both strands
Search in Translation	Translates a supplied nucleotide sequence to protein and searches in the translated sequence.	False
Gap Open Score	Penalty for opening a gap.	-10.0
Gap Extension Score	Penalty for extending a gap.	-1.0
Use Pattern Names	Use a pattern name as an annotation name.	True
Annotate as	Name of the result annotations.	misc_feature
Qualifier name for pattern name	Name of qualifier in result annotations which is containing a pattern name.	pattern name

Parameters in Workflow File

Type: ssearch

Parameter	Parameter in the GUI	Type
matrix	**Substitution Matrix**	*string* Available values are: • Auto - for auto detecting matrix • blosum60 • dna • rna • ...
algorithm	**Algorithm**	*string* Available values are: • Classic 2 • SSE2 • OpenCL • CUDA
filter-strategy	**Filter Results**	*string* Available values are: • filter-intersections • none

min-score	**Min Score**	*numeric*
strand	**Search in**	*numeric* Available values are: • 0 - for searching in both strands • 1 - for searching in direct strand • 2 - for searching in complement strand
amino	**Search in Translation**	*boolean*
gap-open-score	**Gap Open Score**	*numeric*
gap-ext-score	**Gap Extension Score**	*numeric*
use-names	**Use Pattern Names**	*boolean*
result-name	**Annotate as**	*string*
pattern-name-qual	**Qualifier name for pattern name**	*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*