

# 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        |
|----------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------|
| <b>Substitution Matrix</b>             | Describes the rate at which one character in a sequence changes to other character states over time.                                                              | Auto                 |
| <b>Algorithm</b>                       | 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               |
| <b>Filter Results</b>                  | Specifies either to filter the intersected results or to return all the results.                                                                                  | filter-intersections |
| <b>Min Score</b>                       | Minimal percent similarity between a sequence and a pattern.                                                                                                      | 90%                  |
| <b>Search in</b>                       | Specifies which strands should be searched: direct, complementary or both.                                                                                        | both strands         |
| <b>Search in Translation</b>           | Translates a supplied nucleotide sequence to protein and searches in the translated sequence.                                                                     | False                |
| <b>Gap Open Score</b>                  | Penalty for opening a gap.                                                                                                                                        | -10.0                |
| <b>Gap Extension Score</b>             | Penalty for extending a gap.                                                                                                                                      | -1.0                 |
| <b>Use Pattern Names</b>               | Use a pattern name as an annotation name.                                                                                                                         | True                 |
| <b>Annotate as</b>                     | Name of the result annotations.                                                                                                                                   | misc_feature         |
| <b>Qualifier name for pattern name</b> | 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                                                                                                                                                                                       |
|------------------------|----------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>matrix</b>          | <b>Substitution Matrix</b> | <i>string</i><br><br>Available values are: <ul style="list-style-type: none"><li>• Auto - for auto detecting matrix</li><li>• blosum60</li><li>• dna</li><li>• rna</li><li>• ...</li></ul> |
| <b>algorithm</b>       | <b>Algorithm</b>           | <i>string</i><br><br>Available values are: <ul style="list-style-type: none"><li>• Classic 2</li><li>• SSE2</li><li>• OpenCL</li><li>• CUDA</li></ul>                                      |
| <b>filter-strategy</b> | <b>Filter Results</b>      | <i>string</i><br><br>Available values are: <ul style="list-style-type: none"><li>• filter-intersections</li><li>• none</li></ul>                                                           |

|                          |                                        |                                                                                                                                                                                                                                   |
|--------------------------|----------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>min-score</b>         | <b>Min Score</b>                       | <i>numeric</i>                                                                                                                                                                                                                    |
| <b>strand</b>            | <b>Search in</b>                       | <i>numeric</i><br><br>Available values are: <ul style="list-style-type: none"> <li>• 0 - for searching in both strands</li> <li>• 1 - for searching in direct strand</li> <li>• 2 - for searching in complement strand</li> </ul> |
| <b>amino</b>             | <b>Search in Translation</b>           | <i>boolean</i>                                                                                                                                                                                                                    |
| <b>gap-open-score</b>    | <b>Gap Open Score</b>                  | <i>numeric</i>                                                                                                                                                                                                                    |
| <b>gap-ext-score</b>     | <b>Gap Extension Score</b>             | <i>numeric</i>                                                                                                                                                                                                                    |
| <b>use-names</b>         | <b>Use Pattern Names</b>               | <i>boolean</i>                                                                                                                                                                                                                    |
| <b>result-name</b>       | <b>Annotate as</b>                     | <i>string</i>                                                                                                                                                                                                                     |
| <b>pattern-name-qual</b> | <b>Qualifier name for pattern name</b> | <i>string</i>                                                                                                                                                                                                                     |

## 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            |
|-----------------|-----------------------|-----------------|
| <b>Sequence</b> | <b>sequence</b>       | <i>sequence</i> |

The second input port:

**Name in GUI:** *Pattern data*

**Name in Workflow File:** pattern

**Slots:**

| Slot In GUI     | Slot in Workflow File | Type            |
|-----------------|-----------------------|-----------------|
| <b>Sequence</b> | <b>sequence</b>       | <i>sequence</i> |

And 1 *output port*:

**Name in GUI:** *Pattern annotations*

**Name in Workflow File:** out-annotations

**Slots:**

| Slot In GUI               | Slot in Workflow File | Type                    |
|---------------------------|-----------------------|-------------------------|
| <b>Set of annotations</b> | <b>annotations</b>    | <i>annotation-table</i> |