

# Managing of Elements Parameters

The parameters values can be edited for the both *algorithm* and *constraint* elements.

When you select an *element* on the *Scene*, it's description and parameters appear in the *Property Editor*.

Property Editor

Element Name

Annotate As

Direction

**Smith-Waterman** : Finds regions of similarity to the specified pattern in each input sequence (nucleotide or protein one).  
Under the hood is the Smith-Waterman algorithm for performing local sequence alignment.  
To configure the algorithm element parameters go to the "Parameters" area below.

Parameters

Name	Value
Pattern	
Scoring matrix	Auto
Algorithm	Classic 2
Filter results	filter-intersections
Min score	90%
Search i...nslation	False
Gap open score	-10.00
Gap ext score	-1.00

**Pattern** : A subsequence pattern to look for.

There are some common parameters:

- *Element Name* sets the name of the current element.
- *Annotate As* sets the name of the result annotations.
- *Direction* specifies the direction of the current element relatively to other elements in the schema (i.e. either the result must be searched in the current strand of the input sequence or in the reverse complementary strand). To learn more read [Managing Strands](#).

Other parameters can be found in the *Parameters* area. Depending on the parameter in question, the value is selected either from a drop-down list or a spinbox, etc.