Find Pattern Element

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

Parameters in GUI

Parameter	Description	Default value
Annotate as	Name of the result annotation.	misc_feature
Pattern(s)	Semicolon-separated list of patterns to search for.	
Pattern file	Load pattern from file in any sequence format or in newline-delimited format.	
Use pattern name	If patterns are loaded from a file, use names of pattern sequences as annotation names. The name from the parameters is used by default.	False
Max Mismatches	Maximum number of mismatches between a substring and a pattern.	0
Search in	Specifies which strands should be searched: direct, complementary or both.	both strands
Allow Insertions /Deletions	Takes into account possibility of insertions/deletions when searching. By default substitutions are only considered.	False
Support ambiguous bases	Performs correct handling of ambiguous bases. When this option is activated insertions and deletions are not considered.	False
Search in Translation	Translates a supplied nucleotide sequence to protein and searches in the translated sequence.	False
Qualifier name for pattern name	Name of qualifier in result annotations which is containing a pattern name.	pattern_name

Parameters in Workflow File

Type: search

Parameter	Parameter in the GUI	Type
result-name	**Annotate as**	*string*
pattern	**Pattern(s)**	*string*
pattern_file	**Pattern file**	*string*
use-names	**Use pattern name**	*boolean*
max-mismatches-num	**Max Mismatches**	*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
allow-ins-del	**Allow Insertions/Deletions**	*boolean*
ambiguous	**Support ambiguous bases**	*boolean*
amino	**Search in Translation**	*boolean*
pattern-name-qual	**Qualifier name for pattern name**	*string*

Input/Output Ports

The element has 1 *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*
Plain text	**text**	*string*

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*