Local BLAST+ Search Element

Finds annotations for DNA sequence in a local BLAST database.

BLAST+ is a newer version of the BLAST package and is recommended to use by the NCBI.

BLAST+ is used as an external tool from UGENE and it must be installed on your system. To learn more about the external tools, please, read main UGENE User Manual.

Parameters in GUI

Parameter	Description	Default value
Search type	Selects the type of the BLAST searches.	blastn
Database path	Path to the database files.	
Database name	Base name for BLAST DB files.	
Tool path	Path to the BLAST executable.	default
Temporary directory	Directory for temporary files.	default
Expected value	Expectation threshold value.	10
Culling limit	If the query range of a hit is enveloped by that of at least this many higher-scoring hits, delete the hit	0
Annotate as	Name of the result annotations.	blast_result
Gapped alignment	Perform gapped alignment.	use
Gap costs	Cost to create and extend a gap in an alignment.	2 2
Match scores	Reward and penalty for matching and mismatching bases.	1 -3
BLAST output	Location of BLAST output file.	
BLAST output type	Type of BLAST output file.	XML (-outfmt 5)

Parameters in Workflow File

Type: blast-plus

Parameter	Parameter in the GUI	Type
blast-type	**Search type**	*string* Available values are: • blastn • blastp • blastx • tblastn • tblastx
db-path	**Database path**	*string*
db-name	**Database name**	*string*
tool-path	**Tool path**	*string*
temp-dir	**Temporary directory**	*string*
e-val	**Expected value**	*numeric*
max-hits	**Culling limit**	*numeric*
result-name	**Annotate as**	*string*

gapped-aln	**Gapped alignment**	*boolean*
gap-costs	**Gap costs**	*string*
match-scores	**Match scores**	*string*
blast-output	**BLAST output**	*string*
type-output	**BLAST output type**	*string*

Input/Output Ports

The element has 1 *input port*:

Name in GUI: *Input sequence*

Name in Workflow File: in-sequence

Slots:

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

And 1 *output port*:

Name in GUI: *Annotations*

Name in Workflow File: out-annotations

Slots:

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