Remote BLAST Element

Finds annotations for the supplied DNA sequence in the NCBI remote database.

Parameters in GUI

Parameter	Description	Default value
Database	Selects the database to search through. Available databases are blastn, blastp and cdd.	ncbi-blastn
Database	Select the database to search through.	
Expected value	This parameter specifies the statistical significance threshold of reporting matches against the database sequences.	10
Max hits	Maximum number of hits. The maximum available number is 5000.	10
Megablast	Use megablast.	False
Short sequence	Optimizes search for short sequences.	False
Entrez query	Enter an Entrez query to limit search.	
Annotate as	Name of the result annotations.	
BLAST output	Location of the BLAST output file. This parameter insignificant for cdd search.	
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

Parameters in Workflow File

Type: blast-ncbi

Parameter	Parameter in the GUI	Type
db	**Database**	*string* Available values are: • ncbi-blastn • ncbi-blastp • ncbi-cdd
db	**Database**	*string*
e-val	**Expected value**	*string*
max-hits	**Max hits**	*numeric*
megablast	**Megablast**	*boolean*
short-sequence	**Short sequence**	*boolean*
entrez-query	**Entrez query**	*string*
result-name	**Annotate as**	*string*
blast-output	**BLAST output**	*string*
gap-costs	**Gap costs**	*string*
match-scores	**Match scores**	*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*