Search for TFBS with Weight Matrix Element

Searches each input sequence for transcription factor binding sites significantly similar to specified weight matrices. In case several profiles were supplied, searches with all profiles one by one and outputs merged set of annotations for each sequence.

Parameters in GUI

Parameter	Description	Default value
Result annotation	Name of the result annotations.	misc_feature
Search in	Specifies which strands should be searched: direct, complement or both.	both strands
Min score	Minimum score to detect transcription factor binding site in percents.	85

Parameters in Workflow File

Type: wmatrix-search

Parameter	Parameter in the GUI	Type
result-name	**Result annotation**	*string*
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
min-score	**Min score**	*numeric*

Input/Output Ports

The element has 2 *input ports*. The first port:

Name in GUI: *Sequence*

Name in Workflow File: in-sequence

Slots:

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

The second input port gets the SITECON model:

Name in GUI: *Weight matrix*

Name in Workflow File: in-wmatrix

Slots:

Slot In GUI	Slot in Workflow File	Type
Weight matrix	**wmatrix**	*wmatrix*

And there is 1 *output port*:

Name in GUI: *Weight matrix annotations*

Name in Workflow File: out-annotations

Slots:

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