Search for TFBS with SITECON Element

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

Element type: sitecon-search

Parameters

Parameter	Description	Default value	Parameter in Workflow File	Туре
Result annotation	Name of the result annotations.	misc_featu re	result-name	string
Search in	Specifies which strands should be searched: direct, complement or both.	both strands	strand	numeric Available values are: • 0 - for searchin g in both strands • 1 - for searchin g in direct strand • 2 - for searchin g in comple ment strand
Min score	Recognition quality threshold, should be less than 100%. Choosing too low threshold will lead to recognition of too many TFBS recognised with too low trustworthiness. Choosing too high threshold may result in no TFBS recognised.	85	min-score	numeric
Min err1	Alternative setting for filtering results, minimal value of Error type I. Note that all thresholds (by score, by err1 and by err2) are applied when filtering results.	0.0	err1	numeric
Max err2	Alternative setting for filtering results, max value of Error type II. Note that all thresholds (by score, by err1 and by err2) are applied when filtering results.	0.001	err2	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	Туре
Sequence	sequence	sequence

The second input port gets the SITECON model:

Name in GUI: Sitecon model

Name in Workflow File: in-sitecon

Slots:

Slot In GUI	Slot in Workflow File	Туре
Sitecon model	sitecon-model	sitecon-model

And there is 1 output port:

Name in GUI: Sitecon annotations

Name in Workflow File: out-annotations

Slots:

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