

Collect Motifs with SeqPos Element

Finds motifs enriched in a set of regions.

Parameters in GUI

Parameter	Description	Default value
Output directory	The directory to store seqpos results.	
Genome assembly version	UCSC database version (GENOME).	hg19
Output file name	Name of the output file which stores new motifs found during a de novo search (-n).	Default
De novo motifs	Run de novo motif search (-d).	False
Motif database	Known motif collections. (-m). Warning: computation time increases with selecting additional databases. It is recommended to use cistrome.xml. It is a comprehensive collection of motifs from the other databases with similar motifs deleted.	cistrome.xml
Region width	Width of the region to be scanned for motifs; depends on a resolution of assay (-w).	600
Pvalue cutoff	Pvalue cutoff for the motif significance (-p).	0.001

Parameters in Workflow File

Type: seqpos-id

Parameter	Parameter in the GUI	Type
output-dir	Output directory	<i>string</i>
assembly	Genome assembly version	<i>string</i>
out_name	Output file name	<i>string</i>
de_novo	De novo motifs	<i>boolean</i>
motif_db	Motif database	<i>string</i>
reg_width	Region width	<i>numeric</i>
p_val	Pvalue cutoff	<i>numeric</i>

Input/Output Ports

The element has 1 *input port*.

Name in GUI: SeqPos data

Name in Workflow File: in-data

Slots:

Slot In GUI	Slot in Workflow File	Type
Input regions	cp_treat-ann	<i>ann-table-list</i>