

Collect Motifs with SeqPos Element

Finds motifs enriched in a set of regions.

Element type: seqpos-id

Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
Output directory	The directory to store seqpos results.		output-dir	<i>string</i>
Genome assembly version	UCSC database version (GENOME).	hg19	assembly	<i>string</i>
Output file name	Name of the output file which stores new motifs found during a de novo search (-n).	Default	out_name	<i>string</i>
De novo motifs	Run de novo motif search (-d).	False	de_novo	<i>boolean</i>
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	motif_db	<i>string</i>
Region width	Width of the region to be scanned for motifs; depends on a resolution of assay (-w).	600	reg_width	<i>numeric</i>
Pvalue cutoff	Pvalue cutoff for the motif significance (-p).	0.001	p_val	<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>