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**	*string*
Genome assembly version	UCSC database version (GENOME).	hg19	**assembly**	*string*
Output file name	Name of the output file which stores new motifs found during a de novo search (-n).	Default	**out_name**	*string*
De novo motifs	Run de novo motif search (-d).	False	**de_novo**	*boolean*
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**	*string*
Region width	Width of the region to be scanned for motifs; depends on a resolution of assay (-w).	600	**reg_width**	*numeric*
Pvalue cutoff	Pvalue cutoff for the motif significance (-p).	0.001	**p_val**	*numeric*

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**	*ann-table-list*