Slopbed Element

Increases the size of each feature in files using bedtools slop.

Element type: slopbed

Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
Output directory	Select an output directory. Custom - specify the output directory in the 'Custom directory' parameter. Workflow - internal workflow directory. Input file - the directory of the input file.	Input file	**out-mode**	*numeric*
Custom directory	Specify the output directory.		**custom-dir**	*string*
Output file name	A name of an output file. If default of empty value is provided the output name is the name of the first file with additional extention.		**out-name**	*string*
Genome	In order to prevent the extension of intervals beyond chromosome boundaries, bedtools slop requires a genome file defining the length of each chromosome or contig (-g).	human. hg18	**genome-id**	*string*
Each direction increase	Increase the BED/GFF/VCF entry by the same number base pairs in each direction. If this parameter is used -l and -l are ignored. Enter 0 to disable (-b).	0	**b-id**	*numeric*
Substract from start	The number of base pairs to subtract from the start coordinate. Enter 0 to disable (-l).	0	**l-id**	*numeric*
Add to end	The number of base pairs to add to the end coordinate. Enter 0 to disable (-r).	0	**r-id**	*numeric*
Strand-based	Define -l and -r based on strand. For example. if used, -l 500 for a negative-stranded feature, it will add 500 bp to the end coordinate (-s).	False	**s-id**	*boolean*
As fraction	Define -l and -r as a fraction of the featureâs length. E.g. if used on a 1000bp feature, -l 0.50, will add 500 bp âupstreamâ (-pct).	False	**pct-id**	*boolean*
Print header	Print the header from the input file prior to results (-header).	False	**header-id**	*boolean*

Input/Output Ports

The element has 1 *input port*:

Name in GUI: Input File

Name in Workflow File: in-file

Slots:

Slot In GUI	Slot in Workflow File	Type
Source URL	**url**	*string*

And 1 *output port*:

Name in GUI: Output File

Name in Workflow File: out-file

Slots:

Slot In GUI	Slot in Workflow File	Type
Source URL	**url**	*string*