

Sloped Element

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

Parameters in GUI

Parameter	Description	Default value
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
Custom directory	Specify the output directory.	
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 extension.	
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
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
Subtract from start	The number of base pairs to subtract from the start coordinate. Enter 0 to disable (-l).	0
Add to end	The number of base pairs to add to the end coordinate. Enter 0 to disable (-r).	0
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
As fraction	Define -l and -r as a fraction of the feature's length. E.g. if used on a 1000bp feature, -l 0.50, will add 500 bp â upstreamâ (-pct).	False
Print header	Print the header from the input file prior to results (-header).	False

Parameters in Workflow File

Type: slopped

Parameter	Parameter in the GUI	Type
out-mode	Output directory	<i>numeric</i>
custom-dir	Custom directory	<i>string</i>
out-name	Output file name	<i>string</i>
genome-id	Genome	<i>string</i>
b-id	Each direction increase	<i>numeric</i>
l-id	Subtract from start	<i>numeric</i>
r-id	Add to end	<i>numeric</i>
s-id	Strand-based	<i>boolean</i>
pct-id	As fraction	<i>boolean</i>
header-id	Print header	<i>boolean</i>

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	<i>string</i>

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	<i>string</i>