

# Sloped Element

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

## Parameters in GUI

Parameter	Description	Default value
<b>Output directory</b>	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
<b>Custom directory</b>	Specify the output directory.	
<b>Output file name</b>	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.	
<b>Genome</b>	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
<b>Each direction increase</b>	Increase the BED/GFF/VCF entry by the same number base pairs in each direction. If this parameter is used -l and -r are ignored. Enter 0 to disable (-b).	0
<b>Subtract from start</b>	The number of base pairs to subtract from the start coordinate. Enter 0 to disable (-l).	0
<b>Add to end</b>	The number of base pairs to add to the end coordinate. Enter 0 to disable (-r).	0
<b>Strand-based</b>	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
<b>As fraction</b>	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 to upstream (-pct).	False
<b>Print header</b>	Print the header from the input file prior to results (-header).	False

## Parameters in Workflow File

Type: slopbed

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