

# Sloped Element

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

**Element type:** sloped

## Parameters

| Parameter                      | Description  | Default value  | Parameter in Workflow File | Type           |
|--------------------------------|--|----------------|----------------------------|----------------|
| <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>out-mode</b>            | <i>numeric</i> |
| <b>Custom directory</b>        | Specify the output directory.  |                | <b>custom-dir</b>          | <i>string</i>  |
| <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 extention.   |                | <b>out-name</b>            | <i>string</i>  |
| <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.<br>hg18 | <b>genome-id</b>           | <i>string</i>  |
| <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>b-id</b>                | <i>numeric</i> |
| <b>Subtract from start</b>     | The number of base pairs to subtract from the start coordinate. Enter 0 to disable (-l).   | 0              | <b>l-id</b>                | <i>numeric</i> |
| <b>Add to end</b>              | The number of base pairs to add to the end coordinate. Enter 0 to disable (-r).  | 0              | <b>r-id</b>                | <i>numeric</i> |
| <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>s-id</b>                | <i>boolean</i> |
| <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 upstream (-pct).  | False          | <b>pct-id</b>              | <i>boolean</i> |
| <b>Print header</b>            | Print the header from the input file prior to results (-header).   | False          | <b>header-id</b>           | <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> |