

# Genome Coverage Element

Calculates genome coverage using bedtools genomecov.

## 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>Report mode</b>	Histogram () - Compute a histogram of coverage. Per-base (0-based) (-dz) - Compute the depth of feature coverage for each base on each chromosome (0-based). Per-base (1-based) (-d) - Compute the depth of feature coverage for each base on each chromosome (1-based) BEDGRAPH (-bg) - Produces genome-wide coverage output in BEDGRAPH format. BEDGRAPH (including uncovered) (-bga) - Produces genome-wide coverage output in BEDGRAPH format (including uncovered).	Histogram
<b>Split</b>	Treat split BAM or BED12 entries as distinct BED intervals when computing coverage. For BAM files, this uses the CIGAR N and D operations to infer the blocks for computing coverage. For BED12 files, this uses the BlockCount, BlockStarts, and BlockEnds fields (i.e., columns 10,11,12) (-split).	False
<b>Strand</b>	Calculate coverage of intervals from a specific strand. With BED files, requires at least 6 columns (strand is column 6) (-strand).	False
<b>5 prime</b>	Calculate coverage of 5' positions (instead of entire interval) (-5).	False
<b>3 prime</b>	Calculate coverage of 3' positions (instead of entire interval) (-3).	False
<b>Max</b>	Combine all positions with a depth >= max into a single bin in the histogram (-max).	21474836 47
<b>Scale</b>	Scale the coverage by a constant factor. Each coverage value is multiplied by this factor before being reported. Useful for normalizing coverage by, e.g., reads per million (RPM). Default is 1.0; i.e., unscaled (-scale).	1.00000
<b>Trackline</b>	Adds a UCSC/Genome-Browser track line definition in the first line of the output (-trackline).	False
<b>Trackopts</b>	Writes additional track line definition parameters in the first line (-trackopts).	

## Parameters in Workflow File

Type: genomecov

Parameter	Parameter in the GUI	Type
out-mode	Output directory	numeric
custom-dir	Custom directory	string
out-name	Output file name	string
genome	Genome	string
mode-id	Report mode	numeric
split-id	Split	boolean
strand-id	Strand	boolean
prime5-id	5 prime	boolean
prime3-id	3 prime	boolean
max-id	Max	numeric
scale-id	Scale	numeric
trackline-id	Trackline	boolean
trackopts-id	Trackopts	string

## 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