

Genome Coverage Element

Calculates genome coverage using bedtools genomecov.

Element type: genomecov

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	<i>numeric</i>
Custom directory	Specify the output directory.		custom-dir	<i>string</i>
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.		out-name	<i>string</i>
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	<i>string</i>
Report mode	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	mode-id	<i>numeric</i>
Split	Treat split BAM or BED12 entries as distinct BED intervals when computing coverage. For BAM files, this uses the CIGAR $\backslash N$ and $\backslash D$ 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	split-id	<i>boolean</i>
Strand	Calculate coverage of intervals from a specific strand. With BED files, requires at least 6 columns (strand is column 6) (-strand).	False	strand-id	<i>boolean</i>
5 prime	Calculate coverage of 5' positions (instead of entire interval) (-5).	False	prime5-id	<i>boolean</i>
3 prime	Calculate coverage of 3' positions (instead of entire interval) (-3).	False	prime3-id	<i>boolean</i>
Max	Combine all positions with a depth \geq max into a single bin in the histogram (-max).	21474836 47	max-id	<i>numeric</i>
Scale	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	scale-id	<i>numeric</i>
Trackline	Adds a UCSC/Genome-Browser track line definition in the first line of the output (-trackline).	False	trackline-id	<i>boolean</i>
Trackopts	Writes additional track line definition parameters in the first line (-trackopts).		trackopts-id	<i>string</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>