Genome Coverage Element

Calculates genome coverage using bedtools genomecov.

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 extention.	
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
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 uncoveded) (-bga) - Produces genome-wide coverage output in BEDGRAPH format (including uncovered).	Histogram
Split	Treat âsplitâ BAM or BED12 entries as distinct BED intervals when computing coverage. For BAM files, this uses the CIGAR âNâ and âDâ 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
Strand	Calculate coverage of intervals from a specific strand. With BED files, requires at least 6 columns (strand is column 6) (-strand).	False
5 prime	Calculate coverage of 5â positions (instead of entire interval) (-5).	False
3 prime	Calculate coverage of 3â positions (instead of entire interval) (-3).	False
Max	Combine all positions with a depth >= max into a single bin in the histogram (-max).	2147483647
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
Trackline	Adds a UCSC/Genome-Browser track line definition in the first line of the output (-trackline).	False
Trackopts	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*