ChIP-Seq Coverage

The workflow sample, described below, prepare ChIP-Seq processed data (with BedTools and bedGraphToBigWig) for visualization in a genome browser. For input BED-file produces BigWig file.

How to Use This Sample

If you haven't used the workflow samples in UGENE before, look at the "How to Use Sample Workflows" section of the documentation.

Workflow Sample Location

The workflow sample "ChIP-Seq Coverage" can be found in the "NGS" section of the Workflow Designer samples.

Workflow Image

The opened workflow looks as follows:

| File List | Slopbed | Output File | Genome Coverage | Output File | Convert bedGraph Files to bigWig |
|---------------|----------------------|-------------|---------------------------|-------------|-------------------------------------|
| Gets paths of | Increases the size | 0 29 | Produces genome-wide | 9 -9 | |
| files: unset. | of each feature in | | coverage output in | | Converts bedGraph files |
| | files from from File | | BEDGRAPH format. from | | to bigWig from Genome |
| | List with bedtool | | from Slopbed with bedtool | | Coverage with |
| | slop. | | genomecov. | | bedGraphToBigWig. |

Workflow Wizard

The wizard has 3 pages.

1. Input data Page: On this page you must input BED file with ChIP-Seq tags.

| ChIP-Seq Coverage Wizard | | | 5 × |
|--------------------------|-----------------------------|----------|---------------|
| | Input data ChIP-Seq Tags | | |
| | BED File | Required | |
| Defaults | | | Next > Cancel |

2. <u>Parameters Page:</u> Here you can optionally modify parameters that should be used for the Slopbed, Genome Coverage and BedGraphToBigWig elements.

| U ChIP-Seq Coverage Wizard | 8 × |
|----------------------------|---|
| | Slopbed Genome /Users/pro/Documents/ugene/trunk/installer/macosx/debug. V |
| | Slopbed Advanced Show slopbed advancedparameters + |
| | Genome Coverage Genome //Users/pro/Documents/ugene/trunk/installer/macosx/debug, Report mode BEDGRAPH |
| | Genome Coverage Advanced Show genome coverage advancedparameters |
| | BedGraphToBigWig Genome (/Users/pro/Documents/ugene/trunk/installer/macosx/debug, |
| | BedGraphToBigWig Advanced Show bedgraphtobigwig advancedparameters + |
| | |
| Defaults | < Back Next > Cancel |

The following parameters are available:

| Gen ome | 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. The format of the file is: (-g). |
|---|---|
| Eac h dire ction incr ease | Increase the BED/GFF/VCF entry by the same number base pairs in each direction. If this parameter is used -I and -I are ignored. Enter 0 to disable. (-b) |
| Sub stra ct from start | The number of base pairs to subtract from the start coordinate. Enter 0 to disable. (-I) |
| Add to end | The number of base pairs to add to the end coordinate. Enter 0 to disable. (-r) |
| Stra nd- bas ed | Define -I and -r based on strand. For example. if used, -I 500 for a negative-stranded feature, it will add 500 bp to the end coordinate. (-s) |
| As fract ion | Define -I and -r as a fraction of the feature's length. E.g. if used on a 1000bp feature, -I 0.50, will add 500 bp upstream. (-pct) |
| Print hea der | Print the header from the input file prior to results. (-header) |
| Filte r start >en d fields | Remove lines with start postion greater than end position |
| Rep ort 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). |
| mode | |

| Stra Calculate coverage of intervals from a specific strand. With BED files, requires at least 6 columns (strand is column 6). (-strand) 5 prine Calculate coverage of 5' positions (instead of entire interval). (-5) 3 min Calculate coverage of 3' positions (instead of entire interval). (-3) Max Combine all positions with a depth >= max into a single bin in the histogram. (-max) 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) Trac Adds a UCSC/Genome-Browser track line definition in the first line of the output. (-trackline) Rtine Writes additional track line definition parameters in the first line. (-trackopts) Bock size Number of items to bundle in r-tree (-blockSize). Items Scale the coverages of (-unc). Gest If set, do not use compression (-unc). | Split | Treat BAM or BED12 entries as distinct BED intervals when computing coverage. For BAM files, this uses the CIGAR and 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) |
|--|-------------------|---|
| prime constraint 3 prime Calculate coverage of 3' positions (instead of entire interval). (-3) Max Combine all positions with a depth >= max into a single bin in the histogram. (-max) 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) Trac Adds a UCSC/Genome-Browser track line definition in the first line of the output. (-trackline) Trac Writes additional track line definition parameters in the first line. (-trackopts) Rops Number of items to bundle in r-tree (-blockSize). size Number of data points bundled at lowest level (-itemsPerSlot). sper slot If set, do not use compression (-unc). | | Calculate coverage of intervals from a specific strand. With BED files, requires at least 6 columns (strand is column 6). (-strand) |
| prime Control of the second secon | - | Calculate coverage of 5' positions (instead of entire interval). (-5) |
| 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) Trac kline Adds a UCSC/Genome-Browser track line definition in the first line of the output. (-trackline) Trac kline Writes additional track line definition parameters in the first line. (-trackopts) Bloc k size Number of items to bundle in r-tree (-blockSize). k size Number of data points bundled at lowest level (-itemsPerSlot). s per slot If set, do not use compression (-unc). | - | Calculate coverage of 3' positions (instead of entire interval). (-3) |
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| s per slot Unc omp ress If set, do not use compression (-unc). | k | Number of items to bundle in r-tree (-blockSize). |
| omp ress | s per | Number of data points bundled at lowest level (-itemsPerSlot). |
| Output Files Bases On this name you can calent an autput directory. | omp ress ed | |

3. <u>Output Files Page:</u> On this page you can select an output directory:

| ChIP-Seq Coverage Wizard | | | | 8 × |
|--------------------------|---|------------|-------|------------|
| | Output data Output folders Output directory Custom directory | Input file | | • |
| | | | | |
| | | (Pode | Ambre | |
| Defaults | | < Back | Apply | Run Cancel |