

## computeMatrix

computeMatrix (version 1.0.3)

regions to plots

regions to plot 1

Regions to plot:

1: UCSC Main on D. melanogaster: flyBaseGene (genome)

File, in BED format, containing the regions to plot.

Label:

genes

Label to use in the output.

Remove regions to plot 1

regions to plot 2

Regions to plot:

82: (as bed) bamCompare on data 62 and data 63: ratio

File, in BED format, containing the regions to plot.

Label:

Label to use in the output.

Remove regions to plot 2

Add new regions to plot

Score file:

53: log2ratio\_PolII\_Input.bigwig (SES)

Should be a bigWig file (containing a score, usually covering the whole genome). You can generate a bigWig file either from a bedGraph or WIG file using UCSC tools or from a BAM file using the deepTool bamCoverage.

computeMatrix has two main output options:

reference-point

In the scale-regions mode, all regions in the BED file are stretched or shrunk to the same length (bp) that is indicated by the user. Reference-point refers to a position within the BED regions (e.g. start of region). In the reference-point mode only those genomic positions before (downstream) and/or after (upstream) the reference point will be plotted.

The reference point for the plotting:

beginning of region (e.g. TSS)

Discard any values after the region end:

☐

This is useful to visualize the region end when not using the scale-regions mode and when the reference-point is set to the TSS.

Distance upstream of the start site of the regions defined in the region file:

500

If the regions are genes, this would be the distance upstream of the transcription start site.

Distance downstream of the end site of the given regions:

5000

If the regions are genes, this would be the distance downstream of the transcription end site.

Show advanced output settings:

yes

Save the matrix of values underlying the heatmap:

☐

Save the data underlying the average profile:

☐

Save the regions after skipping zeros or min/max threshold values:

☐

The order of the regions in the file follows the sorting order selected. This is useful, for example, to generate other heatmaps keeping the sorting of the first heatmap.

Show advanced options:

yes

Length, in base pairs, of the non-overlapping bin for averaging the score over the regions length:

50

Sort regions:

no ordering

Whether the output file should present the regions sorted.

**Method used for sorting.:**

mean

The value is computed for each row.

**Define the type of statistic that should be displayed.:**

mean

The value is computed for each bin.

**Indicate missing data as zero:**



Set to "yes", if missing data should be indicated as zeros. Default is to ignore such cases which will be depicted as black areas in the heatmap. (see "Missing data color" options of the heatmapper for additional options).

**Skip zeros:**



Whether regions with only scores of zero should be included or not. Default is to include them.

**Minimum threshold:**

**Skip zeros:**



Whether regions with only scores of zero should be included or not. Default is to include them.

**Minimum threshold:**

Any region containing a value that is equal or less than this numeric value will be skipped. This is useful to skip, for example, genes where the read count is zero for any of the bins. This could be the result of unmappable areas and can bias the overall results.

**Maximum threshold:**

Any region containing a value that is equal or higher than this numeric value will be skipped. The max threshold is useful to skip those few regions with very high read counts (e.g. major satellites) that may bias the average values.

**Scale:**

If set, all values are multiplied by this number.

Execute