

deepTools overview

deepTools consists of a set of modules that can be used independently to work with mapped reads. We have subdivided such tasks into *quality controls* (QC), *normalizations* and *visualizations*.

Here's a concise summary of the tools - if you would like more detailed information about the individual tools and example figures, follow the links in the table.

tool	type	input files	main output file(s)	application
bamCorrelate	QC	2 or more BAM	clustered heatmap	Pearson or Spearman correlation between read distributions
bamFingerprint	QC	2 BAM	1 diagnostic plot	assess enrichment strength of a ChIP sample
computeGCbias	QC	1 BAM	2 diagnostic plots	calculate the exp. and obs. GC distribution of reads
correctGCbias	QC	1 BAM, output from computeGCbias	1 GC-corrected BAM	obtain a BAM file with reads distributed according to the genome's GC content
bamCoverage	normalization	BAM	bedGraph or bigWig	obtain the normalized read coverage of a single BAM file
bamCompare	normalization	2 BAM	bedGraph or bigWig	normalize 2 BAM files to each other using a mathematical operation of your choice (e.g. log2ratio, difference)
computeMatrix	visualization	1 bigWig, 1 BED	gzipped table, to be used with heatmapper or profiler	compute the values needed for heatmaps and summary plots
heatmapper	visualization	computeMatrix output	heatmap of read coverages	visualize the read coverages for genomic regions
profiler	visualization	computeMatrix output	summary plot	visualize the average read coverages over a group of genomic regions