

heatmap

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Version: 2v1

Title: heatmap

Description: Generates a high resolution heatmap with easy options for manipulating color annotation bars and other plotting parameters.

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Depends R (v3.4.3)

Imports: png, som, stats, graphics, grDevices, utils, datasets, methods, base

Suggests: compiler

Git url: <https://github.com/cdschar/heatmap>

heatmap Usage:

Requires the heatmap3.R package and using a manifest file with sample group annotations can subset a data file of various formats, normalize the data, and output a heatmap.

Files:

heatmap3.R – R library containing the functions to make the heatmap. Some of the text overlaps margins and future versions will fix this. The pdf can be opened in Adobe Illustrator or other similar programs for modifications and tweaks to create a final version.

plot.Heatmap.zscore.R – Driver script that generates the plots using Z-score normalization of data by rows. Requires the sample manifest file and data file. Various options are annotated to control the display of the heatmap.

Sample.manifest.txt – Manifest file that contains a sample column of unique sample IDs and group annotations for each sample. Column headers are fixed and are required for subsetting the data. Other custom columns can be added in addition to the three required columns.

Column description and functions

1. **x** – Numbering column for of all samples.
2. **sample** – TRUE/FALSE to determine if region should be plotted.
3. **group** – chromosome name for region to plot.

Data Files – The function is designed to plot RNA-seq or ATAC-seq data and requires that each data column have a title that contains the unique sample ID. The current version assumes data columns have unique sample names that match the manifest file with any one of the following extensions: “.rpm, .rpkm, .fpkm, .rppm”. Additional extensions can be added to the script.