

ChromHeatMap

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1 Introduction

The **ChromHeatMap** package provides functions for visualising expression data in a genomic context, by generating heat map images in which data is plotted along a given chromosome for all the samples in a data matrix.

These functions rely on the existence of a suitable **AnnotationDbi** package which provides chromosome location information for the probe- or gene-level identifiers used in your data set. The data themselves must be in either an `ExpressionSet`, or a data matrix with row names corresponding to probe or gene identifiers and columns corresponding to samples. While the **ChromHeatMap** package was originally designed for use with microarray data, given an appropriate **AnnotationDbi** package it can also be used to visualise data from next-generation sequencing experiments.

The output heatmap can include sample clustering, and data can either be plotted for each strand separately, or both strands combined onto a single heat map. An idiogram showing the cytogenetic banding pattern of the chromosome will be plotted for supported organisms (at the time of writing: *Homo sapiens*, *Mus musculus* and *Rattus norvegicus*; please contact the maintainer to request additions).

Once a heat map has been plotted, probes or genes of interest can be identified interactively. These identifiers may then be mapped back to gene symbols and other annotation via the **AnnotationDbi** package.

2 Data preparation

Expression data in the form of a data matrix must initially be mapped onto its corresponding chromosome coordinates. This is done using the `makeChrStrandData`:

```
> library('ALL')
> data('ALL')
> selSamples <- ALL$mol.biol %in% c('ALL1/AF4', 'E2A/PBX1')
> ALLs <- ALL[, selSamples]
> library('ChromHeatMap')
> chrdata <- makeChrStrandData(exprs(ALLs), lib='hgu95av2')
```


Other options include subsetting of samples, adding a color key to indicate sample subsets, deactivating the sample-based clustering and so on. See the help pages for `plotChrMap` and `drawMapDendro` for details.

Note that the default colors provided by the `heat.colors` function are not especially attractive or informative; consider using custom-defined colors, for example by using the **RColorBrewer** package.

The output of the `plotChrMap` function can be subsequently used with the `grabChrMapProbes` function which enables the user to identify the probes or genes responsible for heatmap bands of interest.

Note that the `layout` and `par` options for the current graphics device are *not* reset following generation of the image. This is so that the `grabChrMapProbes` function can accurately identify the region of interest when the user interactively clicks on the diagram.

4 Interactive probe/gene identification

Often it will be of interest to determine exactly which probes or genes are shown to be up- or down-regulated by the `plotChrMap` heat map. This can be done using the `grabChrMapProbes` function. This takes the output of the `plotChrMap` function, asks the user to mouse-click the heatmap on either side of the bands of interest and returns a character vector of the locus identifiers in that region. These can then be passed to the **AnnotationDbi** function `mget` to identify which genes are being differentially expressed.

```
> probes <- grabChrMapProbes( plotmap )
> genes <- unlist(mget(probes, envir=hgu95av2SYMBOL, ifnotfound=NA))
```

Note that due to the way the expression values are plotted, genes which lie very close to each other on the chromosome may have been averaged to give a signal that could be usefully plotted at screen resolution. In such cases the locus identifiers will be returned concatenated, separated by semicolons (e.g. “37687_i_at;37688_f_at;37689_s_at”). Typically this is easily solved by zooming in on a region of interest, using either the “cytoband” or “start” and “end” options to `plotChrMap`. See also the “interval” option for another approach to this problem.

5 Session information

The version number of R and packages loaded for generating the vignette were:

```
R version 3.2.2 (2015-08-14)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 14.04.3 LTS
```

locale:

```
[1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
[3] LC_TIME=en_US.UTF-8      LC_COLLATE=C
[5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
[7] LC_PAPER=en_US.UTF-8     LC_NAME=C
```

```
[9] LC_ADDRESS=C                LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
```

attached base packages:

```
[1] stats4    parallel  stats      graphics  grDevices  utils      datasets
[8] methods   base
```

other attached packages:

```
[1] hgu95av2.db_3.2.2    org.Hs.eg.db_3.2.3    RSQLite_1.0.0
[4] DBI_0.3.1            ChromHeatMap_1.24.0  annotate_1.48.0
[7] XML_3.98-1.3         AnnotationDbi_1.32.0 IRanges_2.4.0
[10] S4Vectors_0.8.0     ALL_1.11.0           Biobase_2.30.0
[13] BiocGenerics_0.16.0
```

loaded via a namespace (and not attached):

```
[1] XVector_0.10.0        GenomicRanges_1.22.0
[3] zlibbioc_1.16.0      GenomicAlignments_1.6.0
[5] BiocParallel_1.4.0   xtable_1.7-4
[7] GenomeInfoDb_1.6.0   tools_3.2.2
[9] SummarizedExperiment_1.0.0 lambda.r_1.1.7
[11] futile.logger_1.4.1   rtracklayer_1.30.0
[13] futile.options_1.0.0 bitops_1.0-6
[15] RCurl_1.95-4.7       Biostings_2.38.0
[17] Rsamtools_1.22.0
```