

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')
```

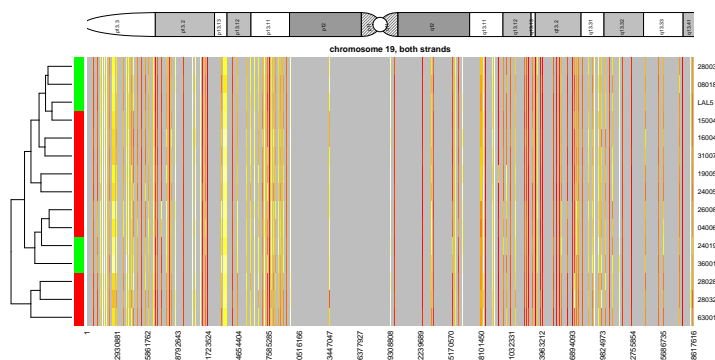
The output *chrdata* object here contains the expression data indexed by coordinate. Note that the `makeChrStrandData` function is based on the `Makesense` function in the `geneplotter` package, removing the internal call to `lowess` to avoid smoothing the data (which is undesirable in this case). The `makeChrStrandData` function is used specifically because it incorporates information on both the start and end chromosome coordinates for each locus. This allows the `plotChrMap` function to accurately represent target widths on the chromosome plot.

3 Plotting the heat map

Once the data has been prepared, a single call to `plotChrMap` will generate the chromosome heat map. There are many options available for this plot, and only a couple of them are illustrated here. Here we generate a whole-chromosome plot (chromosome 19), with both strands combined into a single heat map:

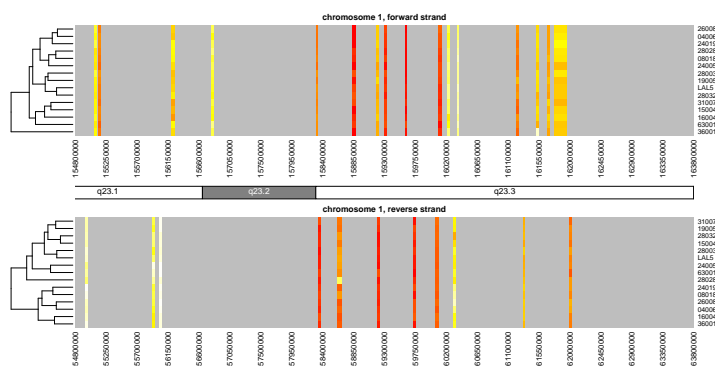
```
> groupcol <- ifelse( ALLs$mol.biol == 'ALL1/AF4', 'red', 'green' )
> plotChrMap(chrdata, 19, strands='both', RowSideColors=groupcol)
```

```
ChrMapPlot
Number of features plotted: 157
```



Chromosomes can be subsetted by cytoband or start/end coordinates along the chromosome. The following illustrates how one might plot the strands separately (this is the default behavior):

```
> plotmap<-plotChrMap(chrdata, 1, cytoband='q23', interval=5000, srtCyto=0, cexCyto=1.2)
```



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 4.4.1 (2024-06-14)
Platform: x86_64-pc-linux-gnu
Running under: Ubuntu 24.04.1 LTS
```

```
Matrix products: default
BLAS: /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3
LAPACK: /usr/lib/x86_64-linux-gnu/openblas-pthread/libopenblas-r0.3.26.so; LAPACK versio
```

```
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
```

```
time zone: Etc/UTC
tzcode source: system (glibc)
```

attached base packages:

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

other attached packages:

```
[1] hgu95av2.db_3.13.0      org.Hs.eg.db_3.19.1  ChromHeatMap_1.59.0
[4] annotate_1.83.0          XML_3.99-0.17        AnnotationDbi_1.67.0
[7] IRanges_2.39.2          S4Vectors_0.43.2    ALL_1.47.0
[10] Biobase_2.65.1          BiocGenerics_0.51.0
```

loaded via a namespace (and not attached):

```
[1] SparseArray_1.5.31      bitops_1.0-8
[3] lattice_0.22-6          RSQlite_2.3.7
[5] grid_4.4.1              fastmap_1.2.0
[7] blob_1.2.4              Matrix_1.7-0
[9] jsonlite_1.8.8          restfulr_0.0.15
[11] GenomeInfoDb_1.41.1     DBI_1.2.3
[13] httr_1.4.7              UCSC.utils_1.1.0
[15] Biostrings_2.73.1       codetools_0.2-20
[17] abind_1.4-5             cli_3.6.3
[19] rlang_1.1.4             crayon_1.5.3
[21] XVector_0.45.0          bit64_4.0.5
[23] DelayedArray_0.31.11    cachem_1.1.0
[25] yaml_2.3.10             S4Arrays_1.5.7
[27] tools_4.4.1             parallel_4.4.1
[29] BiocParallel_1.39.0     memoise_2.0.1
[31] GenomeInfoDbData_1.2.12 Rsamtools_2.21.1
[33] SummarizedExperiment_1.35.1 curl_5.2.2
[35] buildtools_1.0.0        vctrs_0.6.5
[37] R6_2.5.1                png_0.1-8
[39] matrixStats_1.3.0       BiocIO_1.15.2
[41] rtracklayer_1.65.0      zlibbioc_1.51.1
[43] KEGGREST_1.45.1         bit_4.0.5
[45] pkgconfig_2.0.3         xfun_0.47
[47] GenomicRanges_1.57.1    GenomicAlignments_1.41.0
[49] MatrixGenerics_1.17.0   sys_3.4.2
[51] knitr_1.48              xtable_1.8-4
[53] rjson_0.2.22            maketools_1.3.0
[55] compiler_4.4.1          RCurl_1.98-1.16
```