

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 ideogram 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.

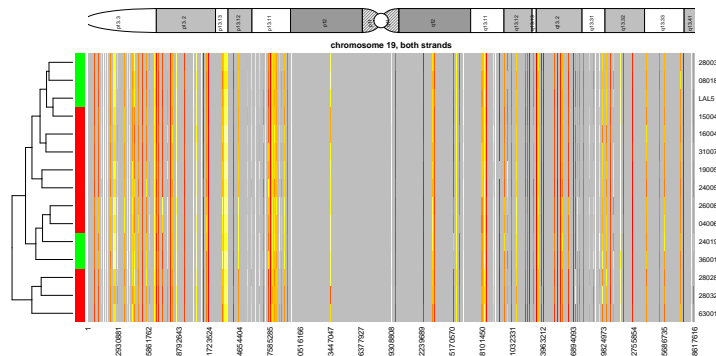
3 Plotting the heat map

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



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 4.5.2 (2025-10-31)
Platform: x86_64-pc-linux-gnu
Running under: Ubuntu 24.04.3 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-p0.3.26.so; LAPACK version 3.11.0

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 [4] LC_COLLATE=en_US.UTF-8
 [5] LC_MONETARY=en_US.UTF-8
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 [7] LC_PAPER=en_US.UTF-8
 [8] LC_NAME=en_US.UTF-8
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```

```

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[7] LC_PAPER=en_US.UTF-8      LC_NAME=C
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[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_3.22.0      ChromHeatMap_1.65.0
[4] annotate_1.89.0          XML_3.99-0.20            AnnotationDbi_1.73.0
[7] IRanges_2.45.0          S4Vectors_0.49.0        ALL_1.53.0
[10] Biobase_2.71.0          BiocGenerics_0.57.0     generics_0.1.4

```

loaded via a namespace (and not attached):

```

[1] SparseArray_1.11.10      bitops_1.0-9
[3] lattice_0.22-7           RSQLite_2.4.5
[5] grid_4.5.2               evaluate_1.0.5
[7] fastmap_1.2.0            blob_1.3.0
[9] Matrix_1.7-4             cigarillo_1.1.0
[11] restfulr_0.0.16          DBI_1.2.3
[13] httr_1.4.7               Biostings_2.79.4
[15] codetools_0.2-20         abind_1.4-8
[17] cli_3.6.5                rlang_1.1.7
[19] crayon_1.5.3             XVector_0.51.0
[21] bit64_4.6.0-1            DelayedArray_0.37.0
[23] cachem_1.1.0             yaml_2.3.12
[25] S4Arrays_1.11.1          tools_4.5.2
[27] parallel_4.5.2           BiocParallel_1.45.0
[29] memoise_2.0.1            Rsamtools_2.27.0
[31] SummarizedExperiment_1.41.0 curl_7.0.0
[33] buildtools_1.0.0         vctrs_0.7.1
[35] R6_2.6.1                 png_0.1-8
[37] matrixStats_1.5.0        BiocIO_1.21.0
[39] rtracklayer_1.71.3       KEGGREST_1.51.1
[41] Seqinfo_1.1.0           bit_4.6.0
[43] pkgconfig_2.0.3          xfun_0.56
[45] GenomicRanges_1.63.1     GenomicAlignments_1.47.0
[47] MatrixGenerics_1.23.0    sys_3.4.3
[49] knitr_1.51              xtable_1.8-4
[51] rjson_0.2.23            maketools_1.3.2
[53] compiler_4.5.2          RCurl_1.98-1.17

```