

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)
```

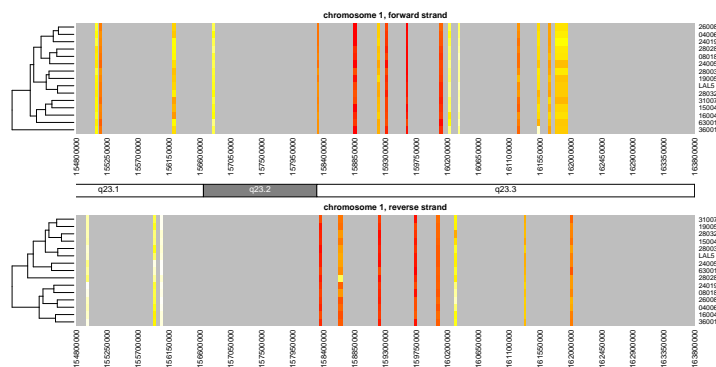
ChrMapPlot

Number of features plotted: 157



Chromosomes can be subsetting 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=50000, 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 4.5.0 (2025-04-11 ucrt)
Platform: x86_64-w64-mingw32/x64
Running under: Windows Server 2022 x64 (build 20348)
```

```
Matrix products: default
LAPACK version 3.12.1
```

```
locale:
[1] LC_COLLATE=C
```

```
[2] LC_CTYPE=English_United States.utf8
[3] LC_MONETARY=English_United States.utf8
[4] LC_NUMERIC=C
[5] LC_TIME=English_United States.utf8
```

```
time zone: America/New_York
tzcode source: internal
```

```
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_3.21.0    ChromHeatMap_1.63.0
[4] annotate_1.87.0       XML_3.99-0.18          AnnotationDbi_1.71.0
[7] IRanges_2.43.0       S4Vectors_0.47.0      ALL_1.51.0
[10] Biobase_2.69.0       BiocGenerics_0.55.0   generics_0.1.4
```

```
loaded via a namespace (and not attached):
```

```
[1] SparseArray_1.9.0      bitops_1.0-9
[3] RSQLite_2.4.0          lattice_0.22-7
[5] grid_4.5.0             fastmap_1.2.0
[7] blob_1.2.4             jsonlite_2.0.0
[9] Matrix_1.7-3           restfulr_0.0.15
[11] GenomeInfoDb_1.45.4    DBI_1.2.3
[13] httr_1.4.7             UCSC.utils_1.5.0
[15] Biostrings_2.77.1      codetools_0.2-20
[17] abind_1.4-8            cli_3.6.5
[19] rlang_1.1.6            crayon_1.5.3
[21] XVector_0.49.0         bit64_4.6.0-1
[23] cachem_1.1.0           DelayedArray_0.35.1
[25] yaml_2.3.10            S4Arrays_1.9.1
[27] tools_4.5.0            parallel_4.5.0
[29] BiocParallel_1.43.3    memoise_2.0.1
[31] Rsamtools_2.25.0       SummarizedExperiment_1.39.0
[33] curl_6.2.3             vctrs_0.6.5
[35] R6_2.6.1              png_0.1-8
[37] BiocIO_1.19.0          matrixStats_1.5.0
[39] rtracklayer_1.69.0     KEGGREST_1.49.0
[41] bit_4.6.0              pkgconfig_2.0.3
[43] GenomicRanges_1.61.0   GenomicAlignments_1.45.0
[45] MatrixGenerics_1.21.0  xtable_1.8-4
[47] rjson_0.2.23           compiler_4.5.0
[49] RCurl_1.98-1.17
```