

# Introduction to the plotAlongChrom function

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April 15, 2025

## 1 Introduction to the example data

The purpose of this vignette is to demonstrate some of the functionalities of the `plotAlongChrom` in the *tilingArray* package. We use a small subset data from an expression profiling paper [1]; The data only include the region from 35000bp to 50000bp in yeast chromosome one. Expression profiling is done in YPE and YPD conditions, 3 replicates each. Further information about the experimental design can be found at the paper website <http://steinmetzlab.embl.de/NFRsharing/>.

```
> library("grid")
> library("RColorBrewer")
> library("tilingArray")

> data("segnf")
> class(segnf)

[1] "environment"

> ls(segnf)

[1] "1.+" "1.-"

> segnf$"1.+"

Object of class 'segmentation':
Data matrix: 1775 x 6
Change point estimates for number of segments S = 1:17
Confidence intervals for 1 fits from S = 17 to 17
Selected S = 17

> head(segnf$"1.+"@y)

      YPE1  YPE2  YPE3  YPD1  YPD2  YPD3
[1,] -1.55 -2.70 -2.52 -4.78 -6.66 -4.62
[2,] -1.95 -4.20 -3.55 -3.93 -4.75 -4.74
[3,] -2.24 -2.24 -1.86 -6.15 -4.74 -3.82
[4,] -2.59 -2.52 -2.39 -4.31 -4.44 -4.40
[5,] -2.62 -3.91 -4.41 -4.94 -5.19 -4.65
[6,] -4.30 -4.82 -4.61 -5.62 -5.14 -5.60

> dim(segnf$"1.+"@y)

[1] 1775    6
```

```

> head(segnf$"1."@x)
[1] 35001 35009 35017 35025 35033 35041
> length(segnf$"1."@x)
[1] 1775
> segnf$"1."@logLik
[1] -Inf -5136 -4772 -4627 -4562 -4498 -4428 -4372 -4314 -4280 -4235 -4198
[13] -4148 -4106 -4082 -4059 -4045
> segnf$"1."@nrSegments
[1] 17
> head(segnf$"1."@breakpoints[[segnf$"1."@nrSegments]])
  lower estimate upper
1    13         13    13
2   158        158   158
3   177        177   177
4   242        242   242
5   258        259   260
6   273        273   273

```

The **segnf** object is an environment which contains two objects of class *segmentation*. **segnf** is the output of the **segChrom** in the *tilingArray* package. The *segmentation* object in **segnf** stores the probe expression information in the slot **y**. As can be seen, it contains 1775 probes and 6 array hybes in two conditions. The genomic coordinates where the probes aligned to is stored in the slot **x**. The order of the slot **x** is the same as the probe row order in slot **y**. The segment boundary information is stored in the slot **breakpoints** which is a list that contains all the optimal placement of 1 segment to the designate number(here in this data set is 17) of segments for this data. A log likelihood score for each placement is stored in slot **logLik** from which the best one is choosen and stored in the slot **nrSegments**. Further information about how the segmentation algorithm works, please read the vignette segmentation demo.

```

> data(gffSub)
> head(gffSub)
  id chr start  end strand source  feature  Name orf_classification
41 41  1 35156 36304      +   SGD      gene   YAL060W      Verified
42 42  1 35156 36304      +   SGD      CDS    YAL060W      Verified
43 43  1 36497 36919      -   SGD      gene   YAL059C-A      Dubious
44 44  1 36497 36919      -   SGD CDS_dubious YAL059C-A      Dubious
45 45  1 36510 37148      +   SGD      gene   YAL059W      Verified
46 46  1 36510 37148      +   SGD      CDS    YAL059W      Verified
  gene
41 BDH1
42 BDH1
43 <NA>
44 <NA>
45 ECM1
46 ECM1

```

The **gffSub** object is a data frame that contains the SGD annotated features of the region 35000bp-50000bp for yeast chromosome one.

## 2 Visualizing the expression profiling with the plotAlongChrom function

The function `plotAlongChrom` accepts an environment as its first argument, which is expected to contain objects of class *segmentation* with names given by `paste(chr, c("+", "-"), sep=".")`, where `chr` is the chromosome identifier.

The following code generates Figure 1, a dot plot that averaged across all hybes.

```
> grid.newpage()
> plotAlongChrom(segnf, chr=1, coord=c(35000, 50000), what="dots", gff=gffSub)
```



Figure 1: Along-chromosome dot plot of the averaged value across all hybes.

We could also make separate dot plot for different hybes by setting the parameter `sepPlot` as `TRUE`. The following code generates Figure 2 that plots the expression separately for the two conditions.

```
> segObj = new.env(parent = baseenv())
> nmLabel = colnames(segnf$"1."+@"y")
> lab = gsub("\\d", "", nmLabel)
> for(nm in paste(1, c("+", "-"), sep=".")){
+   s = get(nm, env = segnf)
+   rpY = tapply(1:length(lab), lab, function(i) rowMeans(s@y[,i]))
+   s@y = do.call(cbind, rpY)
+   assign(nm, s, segObj)
+ }
> grid.newpage()
> plotAlongChrom(segObj, chr=1, coord=c(35000, 50000), what="dots", gff=gffSub, sepPlot = T)
```

However, with the number of hybes increases, it is very hard to see the difference in dot plots in a normal screen. Thus, if the number of hybes is more than 4, the function will force to take the average. A better alternative of displaying multiple hybes is to use the heatmap. The following code generates Figure 3 that makes the heatmap plot.

```
> grid.newpage()
> plotAlongChrom(segnf, chr=1, coord=c(35000, 50000), what="heatmap", gff=gffSub,
+   rowNamesHeatmap=nmLabel, makeRasterImage=FALSE)
```



Figure 2: Along-chromosome dot plot of the averaged value among different replicates for YPD and YPE condition.

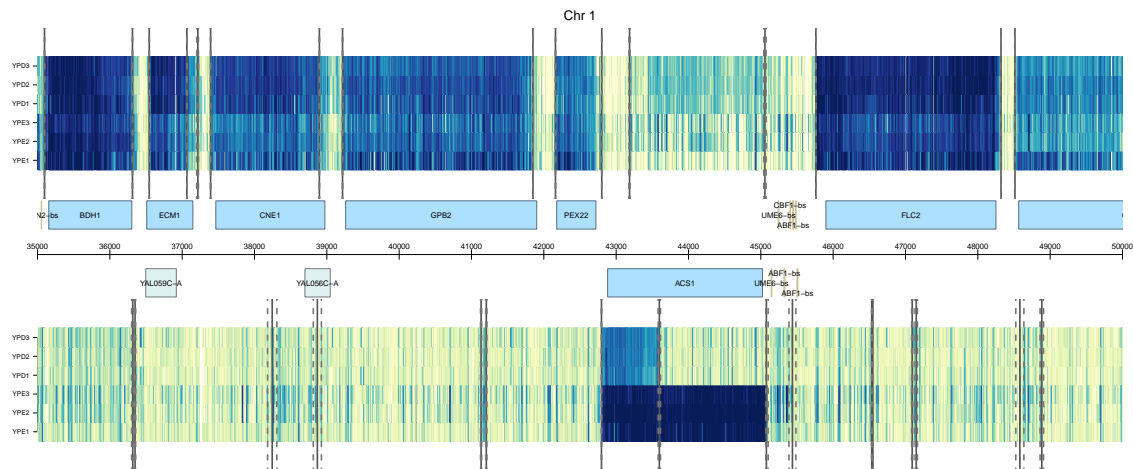


Figure 3: Along-chromosome heatmap plot of all the replicates in YPD and YPE condition.

Start with R 2.11.0, the *grid* package introduced the raster array image function `grid.raster` which is a faster and efficient way of generating heatmap images. From R 2.11.0, The *tilingArray* package will use the `grid.raster` function as default to make heatmap images replacing the previous `grid.rect` function. The choice between the two drawing functions can be changed by the parameter *makeRasterImage*. The following code generates Figure 4 that makes the raster heatmap plot.

```
> grid.newpage()
> plotAlongChrom(segnf,chr=1, coord=c(35000,50000),what="heatmap", gff=gffSub,
+               rowNamesHeatmap=nmLabel,makeRasterImage=TRUE)
```

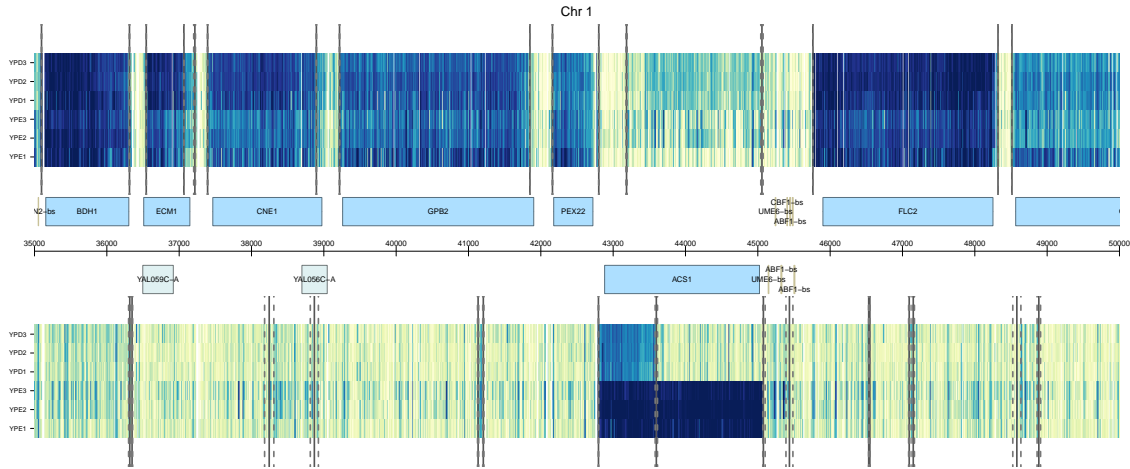


Figure 4: Along-chromosome raster heatmap plot of all the replicates in YPD and YPE condition.

The color gradient of the heatmap could be changed by the parameter *colHeatmap*. The following code generates Figure 5 that makes the raster heatmap plot using a blue color gradient.

```
> grid.newpage()
> plotAlongChrom(segnf,chr=1, coord=c(35000,50000),what="heatmap", gff=gffSub,
+               rowNamesHeatmap=nmLabel,makeRasterImage=TRUE,
+               colHeatmap = colorRamp(brewer.pal(9, "Blues")))
```

## References

- [1] Zhenyu Xu, Wu Wei, Julien Gagneur, Fabiana Perocchi, Sandra Clauder-Munster, Jurgi Camblong, Elisa Guffanti, Francoise Stutz, Wolfgang Huber and Lars M. Steinmetz Bidirectional promoters generate pervasive transcription in yeast. *Nature*, 2009. [1](#)



Figure 5: Along-chromosome raster heatmap plot of all the replicates in YPD and YPE condition with a blue color gradient.