

Mouse Infinium methylation data processing with RnBeads

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Introduction The goal is to display some key data frame structures and visuals that you can expect to get from running the code in RnBeads_with_RepeatMasker.R

Using RnBeads dev version (Müller et al. 2019).

Setup¹² What should RepeatMasker table and \$SAMPLE.csv file look like? `sample.table` was created solely for demonstration purposes; it's not needed to run the code.

```
head(tab.rmsk)
```

```
head(sample.table,14)
```

Interesting but confusing functions `get.table()` returns a useful, unsorted data frame of statistics for each \$ANNOTATION probe(rows) from `diffmeth.$ANNOTATION` S4 object. `annotation()` returns row-matching annotation for each probe in `tab.$ANNOTATION`.

```
diffmeth.rmsk <- rnb.execute.computeDiffMeth(rnb.set, cmp.cols, region.types="rmsk")
tab.rmsk <- get.table(diffmeth.rmsk,comparison, region.type="rmsk",return.data.frame=T)
aa.rmsk <- annotation(rnb.set,type="rmsk")
```

```
head(tab.rmsk)
```

```
head(aa.rmsk)
```

These two data frames are bound together.

```
annotated.tab.rmsk <- data.frame(tab.rmsk,aa.rmsk, row.names=NULL)
head(annotated.tab.rmsk)
```

Order the rows by “combinedRank”. The rownames of the `annotated.tab.$ANNOTATION.order` data frame refers to the original row numbers of the `annotated.tab.sites` data frame, which is not ordered.

```
annotated.tab.rmsk.order <- annotated.tab.rmsk[order(annotated.tab.rmsk[, "combinedRank"]),]
head(annotated.tab.rmsk.order,3)
```

¹Run `rmarkdown::render("RnBeads_with_RepeatMasker.Rmd")` in the same workspace as .R to avoid worrying about global environment.

²`rnb.set` object is not stored well in the global environment. If there are errors, re-run the script from top to bottom (remove output folders “result” and “resultFull”). There is a way to write theses objects to disk instead of RAM, but I didn't want to lose any disk space.

```
rownames(annotated.tab.rmsk.order)[1:10]
```

```
## [1] "12842" "2839" "22365" "24294" "6831" "20269" "17342"  
## [8] "17343" "7604" "8467"
```

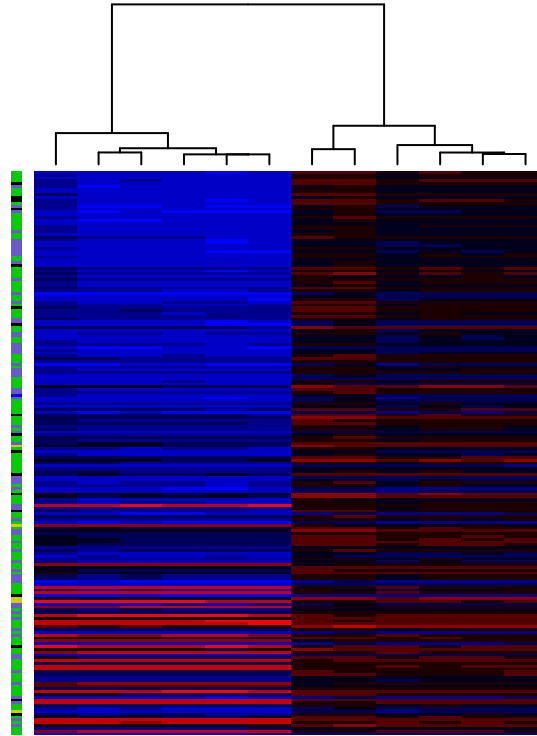
annotated.tab.\\$ANNOTATION.order data frame does not contain any information about beta values. These are extracted from rnb.set using `meth()`, annotation name, and row index from annotated.tab.\\$ANNOTATION.order.

```
topDiffBeta.rmsk.full <- meth(rnb.set.full, type="rmsk")[as.integer(rownames(annotated.tab.rmsk.order))]
```

Heatmap(s) Differentially methylated probes annotated with RepeatMasker

```
colSide <- annotated.tab.rmsk.order$name  
  
colSide <- gsub("LTR", "slateblue3", colSide)  
colSide <- gsub("LINE", "green3", colSide)  
colSide <- gsub("SINE", "green3", colSide)  
colSide <- gsub("DNA", "black", colSide)  
colSide <- gsub("Simple_repeat", "yellow3", colSide)  
colSide <- gsub("Other", "blue", colSide)  
colSide <- gsub("Unknown", "blue", colSide)  
  
par(font=2, font.axis=2, font.lab=2, cex.lab=1.5, cex.axis=1.5, lty=1)  
heatmap.2(topDiffBeta.rmsk.full[1:200, c(1, 5, 9, 2, 6, 10, 3, 7, 11, 4, 8, 12)],  
          col=colfunc(10), scale="none", Rowv=F, Colv=T,  
          cexCol=1, labCol=NA, labRow=NA, srtCol=0, adjCol=c(0.5, 0),  
          density.info = "none", trace="none", dendrogram = "column",  
          symkey=FALSE, symbreaks=F, revC = FALSE, RowSideColors = colSide[1:200],  
          breaks=c(0.0, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1),  
          lmat=rbind(c(5, 0, 4), c(3, 1, 2)),  
          lhei=c(1, 4),  
          lwid=c(1.75, 0.1, 3.5), margins=c(5, 12), cexRow=1.2)
```

```
## Error in plot.new(): figure margins too large
```



Müller, Fabian, Michael Scherer, Yassen Assenov, Pavlo Lutsik, Jörn Walter, Thomas Lengauer, and Christoph Bock. 2019. “RnBeads 2.0: Comprehensive Analysis of DNA Methylation Data.” *Genome Biology* 20 (1): 55. <https://doi.org/10.1186/s13059-019-1664-9>.