

---

# Plotting using Genominator and GenomeGraphs (Beta)

James Bullard

Kasper Daniel Hansen

Modified: April 18, 2010, Compiled: April 16, 2015

This vignette is preliminary, and should be viewed as subject to change. A number of the functions are not directly exported by the package – there is a reason for that.

In this vignette we demonstrate how to visualize data using the *GenomeGraphs* package. The main idea is that we want to build a plotting function which we can use to plot regions. The simplest case is the following:

First, we make a database:

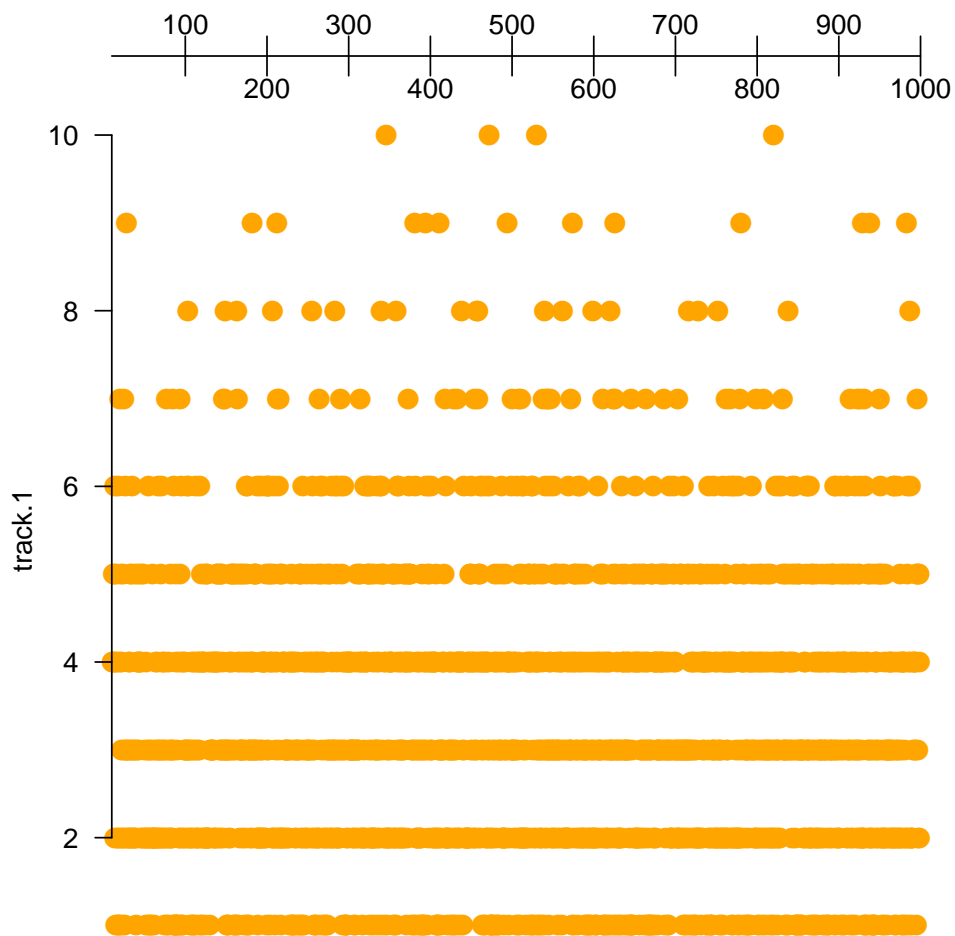
```
> require(Genominator)
> options(verbose = FALSE)
> N <- 100000 # the number of observations.
> K <- 100    # the number of annotation regions, not less than 10
> df <- data.frame(chr = sample(1:16, size = N, replace = TRUE),
+                 location = sample(1:1000, size = N, replace = TRUE),
+                 strand = sample(c(1L,-1L), size = N, replace = TRUE))
> eData <- aggregateExpData(importToExpData(df, dbFilename = "pmy.db", overwrite = TRUE, tablename = "e"),
+                           by = "chr", FUN = function(x) {
+                             counts = matrix(0, nrow = 1000, ncol = 2)
+                             for (i in 1:nrow(x)) {
+                               counts[i, x[i, "strand"]] = x[i, "location"]
+                             }
+                             counts
+                           })
> annoData <- data.frame(chr = sample(1:16, size = K, replace = TRUE),
+                        strand = sample(c(1, -1), size = K, replace = TRUE),
+                        start = (st <- sample(1:1000, size = K, replace = TRUE)),
+                        end = st + rpois(K, 75),
+                        feature = c("gene", "intergenic")[sample(1:2, size = K, replace = TRUE)])
> rownames(annoData) <- paste("elt", 1:K, sep = ".")

> rp <- Genominator:::makeRegionPlotter(list("track.1" = list(expData = eData, what = "counts")))
> args(rp)

function (chr, start, end, overlays = NULL, title = NULL, ...)
NULL
```

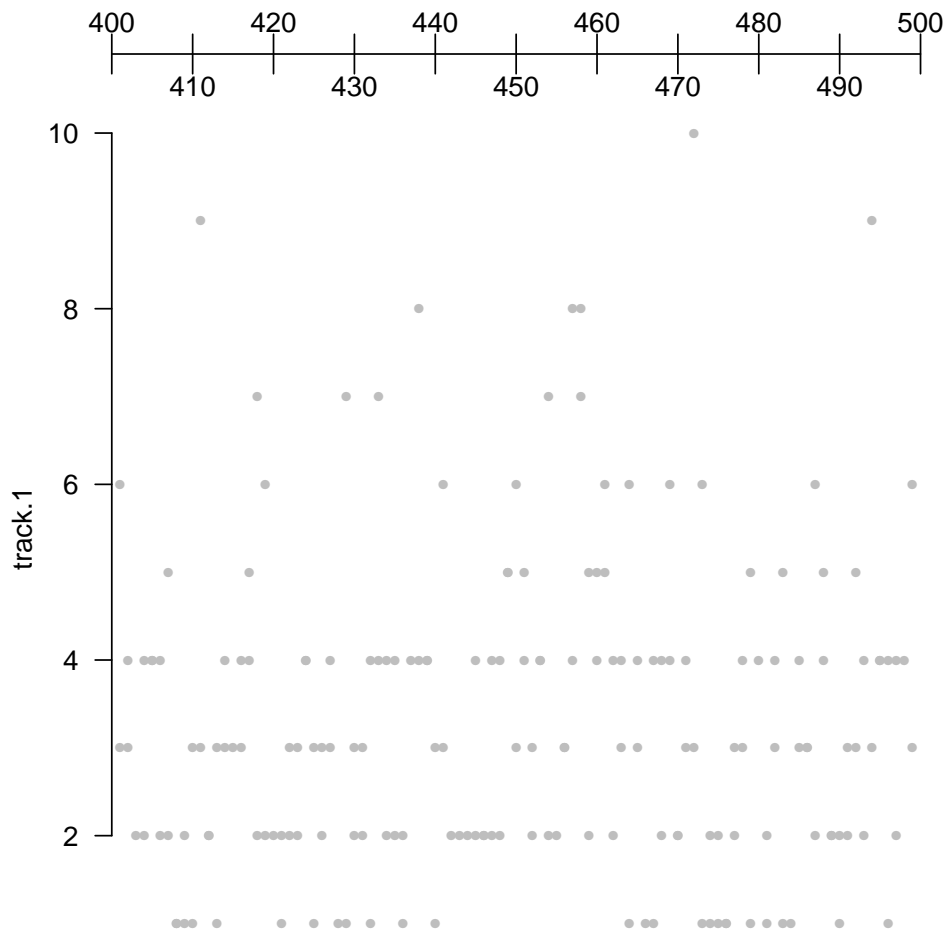
This constructs a function which can be called to view particular pieces of data.

```
> rp(1, 10, 1000)
```



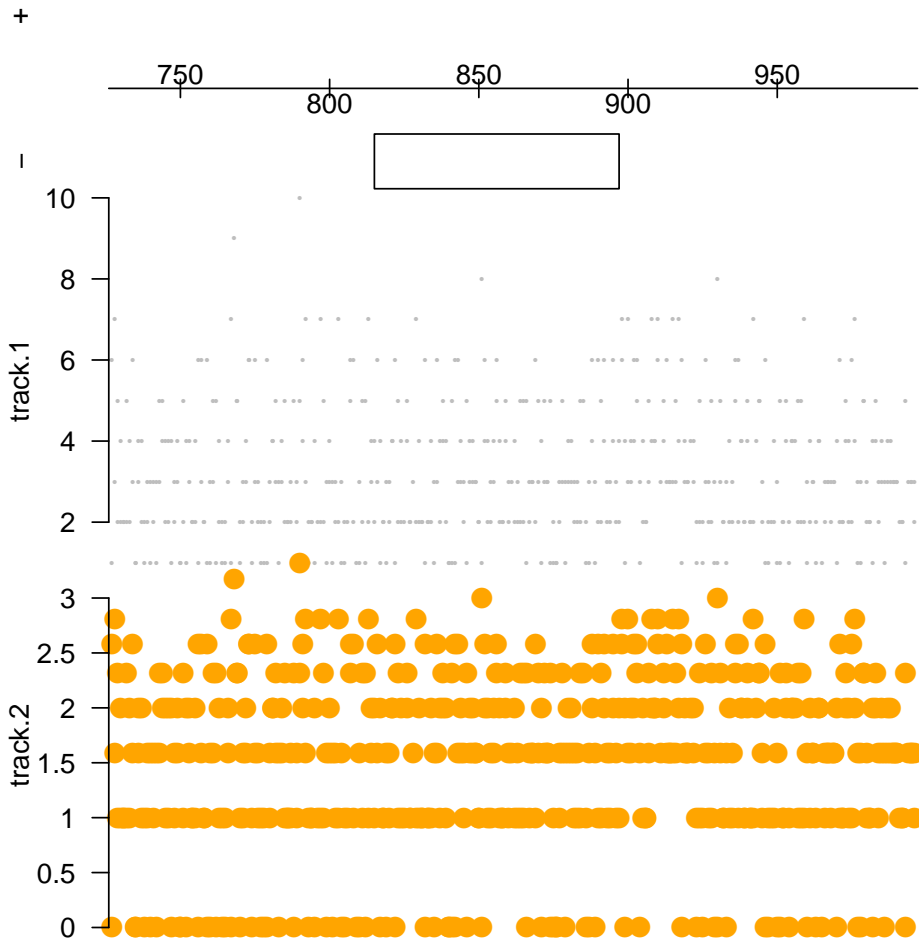
*GenomeGraphs* provides a wealth of customization options and means of plotting which for the most part are transferable using the list.

```
> rp <- Genominator:::makeRegionPlotter(list("track.1" = list(expData = eData, what = "counts",
+                                                              dp = DisplayPars(lwd = .45, color = "grey"))))
> rp(1, 400, 500)
```



Here we can plot our annotation using the annotation factory construct. This is probably a little advanced. An easier thing is to use Ensembl to do the plotting of the annotation. Often, however, you will want to augment the annotation produced by Ensembl.

```
> annoFactory <- Genominator:::makeAnnoFactory(annoData, featureColumnName = "feature",
+                                             groupColumnName = NULL, idColumnName = NULL,
+                                             dp = DisplayPars("gene" = "blue",
+                                             "intergenic" = "green"))
> rp <- Genominator:::makeRegionPlotter(list("track.1" = list(expData = eData, what = "counts",
+                                             dp = DisplayPars(lwd=.2, color = "grey")),
+                                             "track.2" = list(expData = eData, what = "counts",
+                                             fx = log2, DisplayPars(lwd=.3, color = "black"))),
+                                       annoFactory = annoFactory)
> rp(annoData[1,"chr"], annoData[1, "start"] - 100, annoData[1, "end"] + 100)
```



*GenomeGraphs* also offers a nice way to plot annotation for a given region using data from Ensembl or other sources of annotation - in some cases you have to do a little work because of the way that Biomart indexes the annotation and the way the *Genominator* package works (in this case yeast annotation is stored with Roman numerals denoting the chromosomes).

```
> require("biomaRt")
> mart <- useMart("ensembl", dataset = "scerevisiae_gene_ensembl")
> annoFactory <- Genominator::makeAnnoFactory(mart, chrFunction = function(chr) as.roman(chr))
> load(system.file("data", "chr1_yeast.rda", package = "Genominator"))
> head(chr1_yeast)
```

	chr	location	strand	mRNA_1	mRNA_2
1	1	1	-1	9.038919	8.614710
2	1	1	-1	9.172428	8.558421
3	1	2	-1	9.422065	9.131857
4	1	2	-1	8.679480	8.442943
5	1	2	-1	8.546894	8.794416
6	1	2	-1	8.784635	8.918863

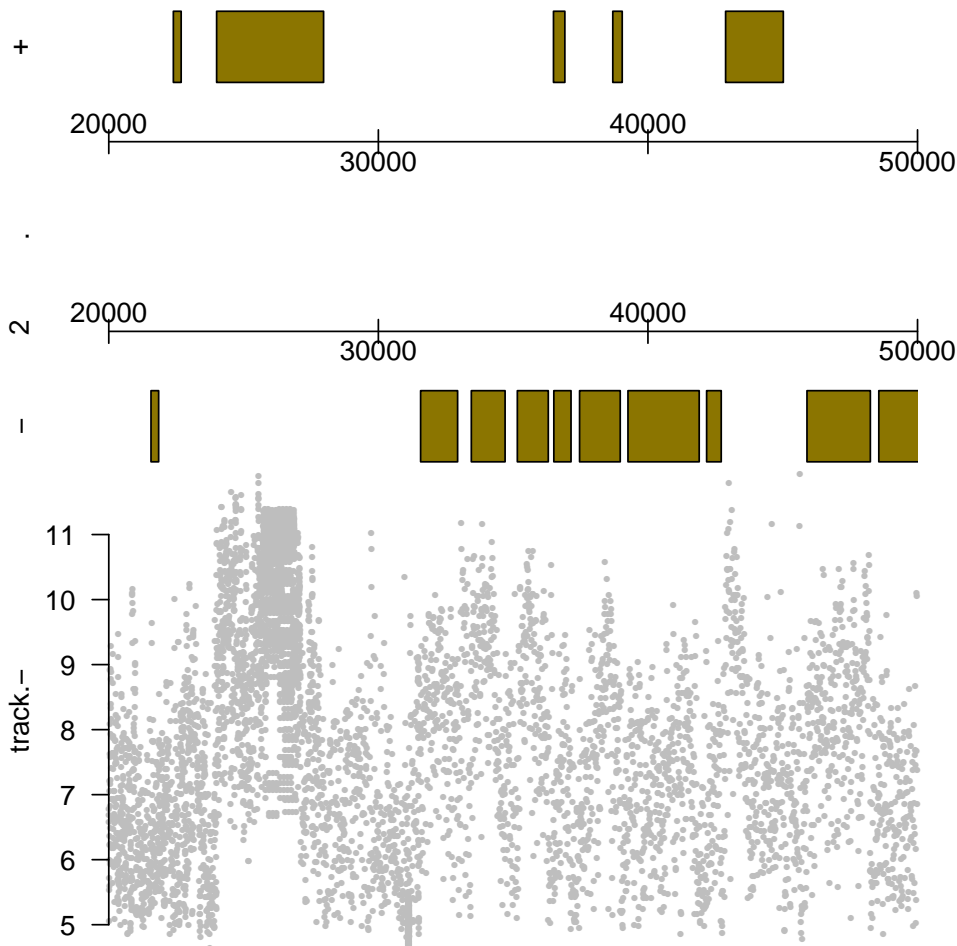
```
> yData <- importToExpData(chr1_yeast, dbFilename = "my.db", tablename = "yeast",
+                           overwrite = TRUE)
> rp <- Genominator::makeRegionPlotter(list("track.-" = list(expData = yData, what = c("mRNA_1", "mRNA_2"),
+                           fx = rowMeans, strand = -1,
```

---

```

+                                     dp = DisplayPars(lwd=.3, color = "grey")),
+                                     annoFactory = annoFactory)
> rp(1, 20000, 50000)

```



## SessionInfo

- R version 3.2.0 RC (2015-04-08 r68161), x86\_64-apple-darwin10.8.0
- Locale: en\_US.UTF-8/en\_US.UTF-8/en\_US.UTF-8/C/en\_US.UTF-8/en\_US.UTF-8
- Base packages: base, datasets, graphics, grDevices, grid, methods, parallel, stats, stats4, utils
- Other packages: BiocGenerics 0.14.0, biomaRt 2.24.0, DBI 0.3.1, GenomeGraphs 1.28.0, Genominator 1.22.0, IRanges 2.2.0, RSQLite 1.0.0, S4Vectors 0.6.0
- Loaded via a namespace (and not attached): AnnotationDbi 1.30.0, Biobase 2.28.0, bitops 1.0-6, GenomeInfoDb 1.4.0, RCurl 1.95-4.5, tools 3.2.0, XML 3.98-1.1