Plotting using Genominator and GenomeGraphs (Beta)

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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:

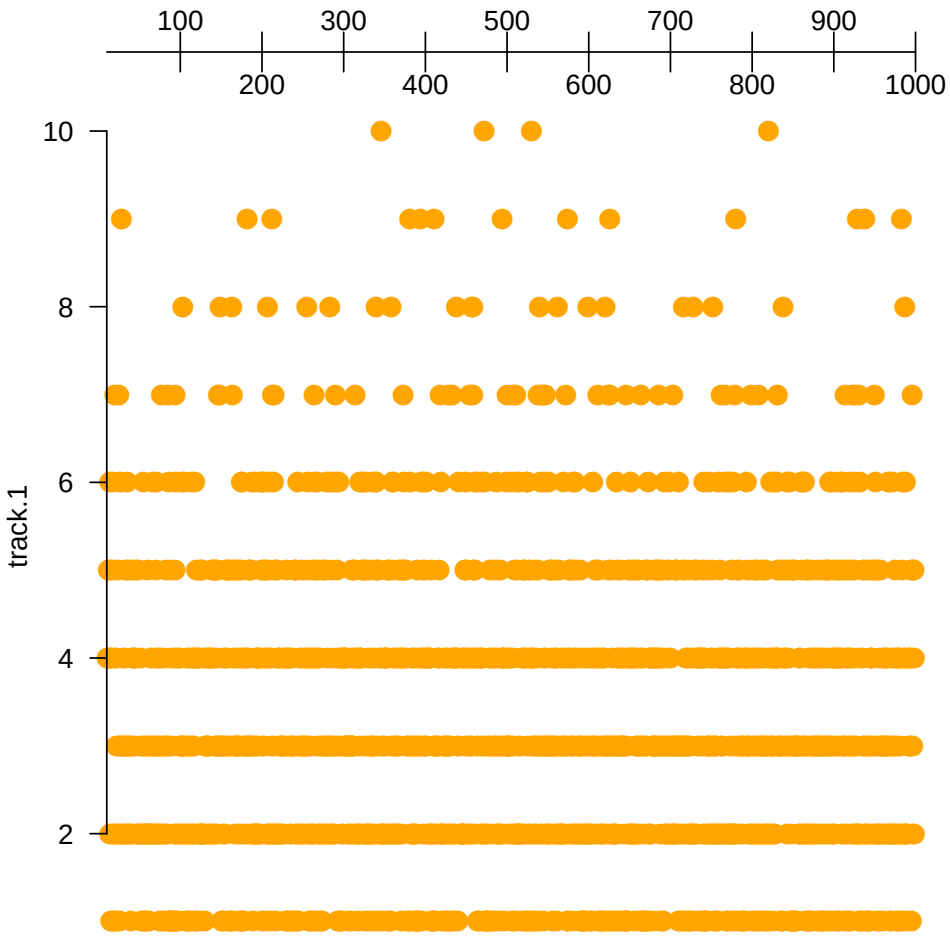
```
> require(Genominator)
> options(verbose = FALSE)
> N <- 100000 # the number of observations.
> K <- 100    # the number of annotation regions, not less than 10
> df <- data.frame(chr = sample(1:16, size = N, replace = TRUE),
+                  location = sample(1:1000, size = N, replace = TRUE),
+                  strand = sample(c(1L,-1L), size = N, replace = TRUE))
> eData <- aggregateExpData(importToExpData(df, dbFilename = "pmy.db", overwrite = TRUE, tablename = "ex
> 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
```

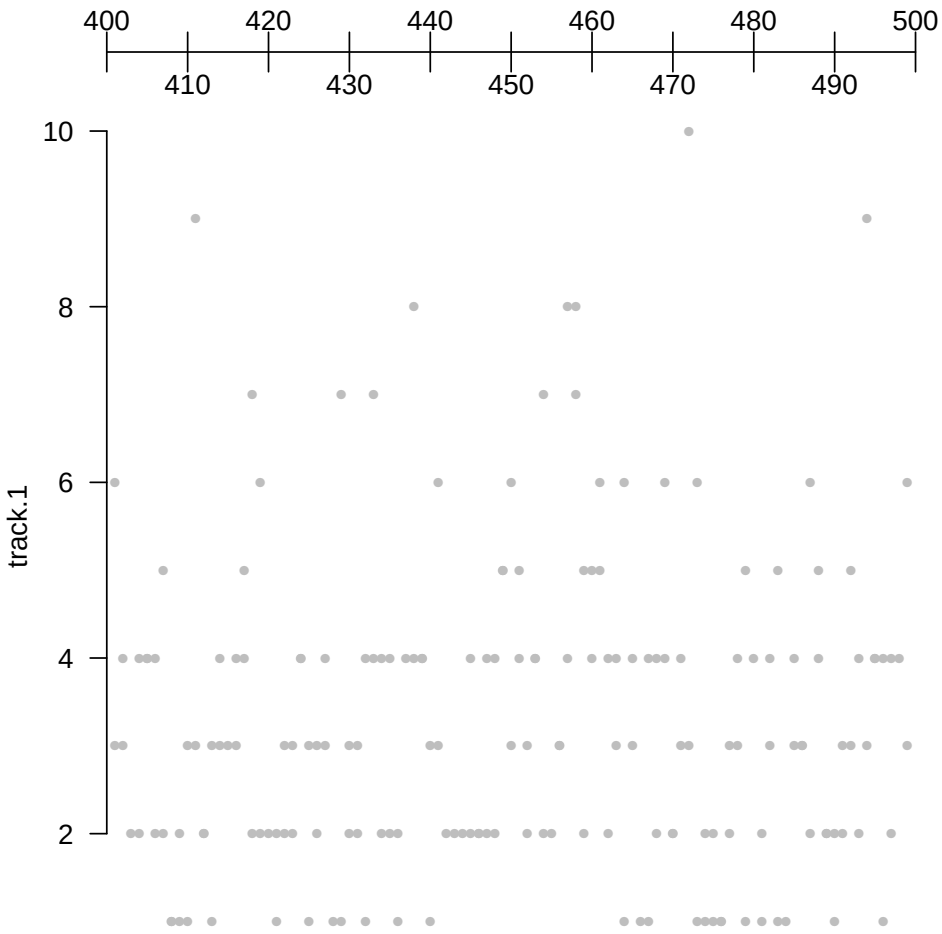
This constructs a function which can be called to view particular pieces of data.

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



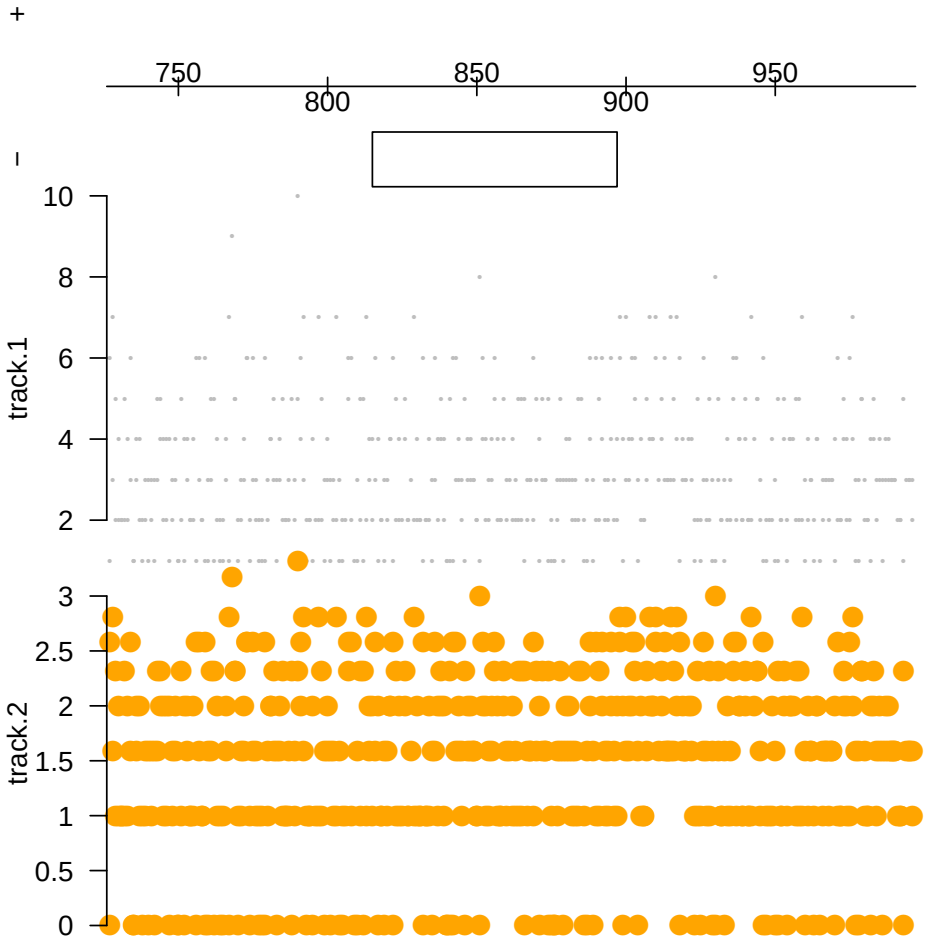
GenomeGraphs provides a wealth of customization options and means of plotting which for the most part are transferable using the list.

```
> 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)
```



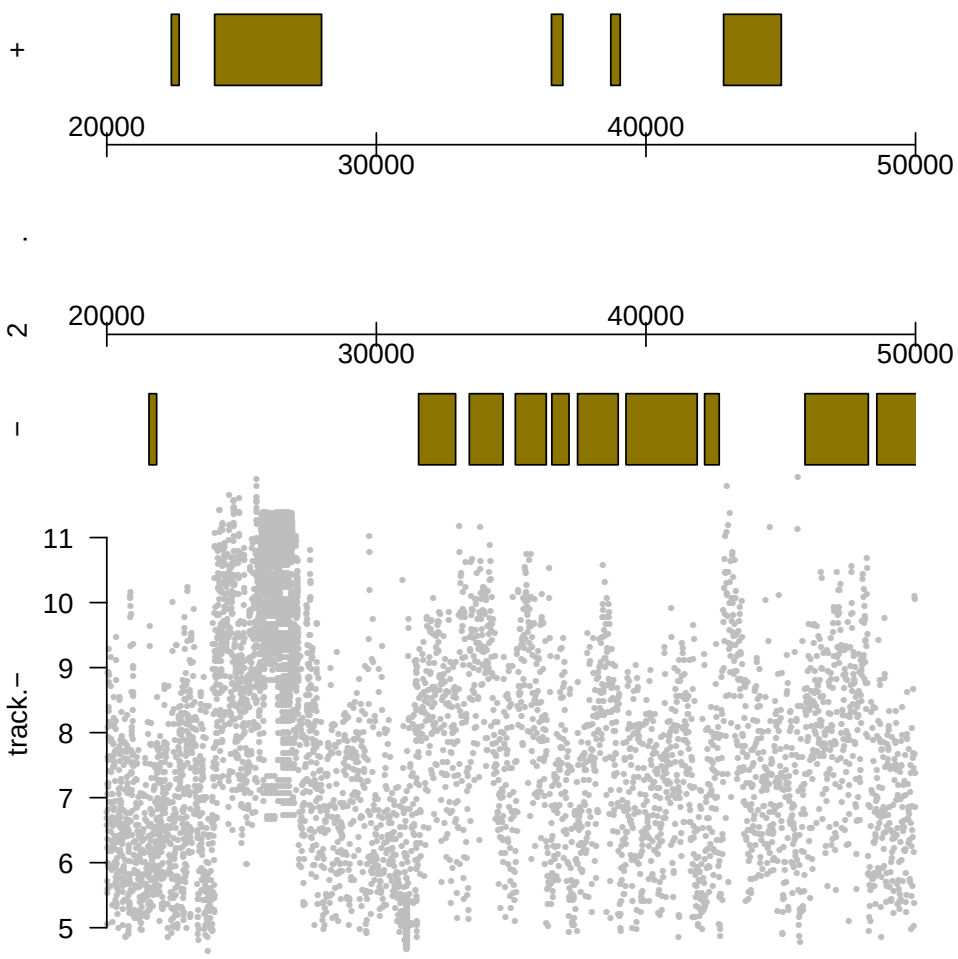
GenomeGraphs also offers a nice way to plot annotation for a given region using data from Ensembl or other sources of annotation - in some cases you have to do a little work because of the way that Biomart indexes the annotation and the way the *Genominator* package works (in this case yeast annotation 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_
+                                            fx = rowMeans, strand = -1,
```

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



SessionInfo

- R version 3.1.1 Patched (2014-09-24 r66678), `i386-w64-mingw32`
- Locale: `LC_COLLATE=C`, `LC_CTYPE=English_United States.1252`, `LC_MONETARY=English_United States.1252`, `LC_NUMERIC=C`, `LC_TIME=English_United States.1252`
- Base packages: base, datasets, grDevices, graphics, grid, methods, parallel, stats, stats4, utils
- Other packages: BiocGenerics 0.12.0, DBI 0.3.1, GenomeGraphs 1.26.0, Genominator 1.20.0, IRanges 2.0.0, RSQLite 0.11.4, S4Vectors 0.4.0, biomaRt 2.22.0
- Loaded via a namespace (and not attached): AnnotationDbi 1.28.0, Biobase 2.26.0, GenomeInfoDb 1.2.0, RCurl 1.95-4.3, XML 3.98-1.1, tools 3.1.1