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:

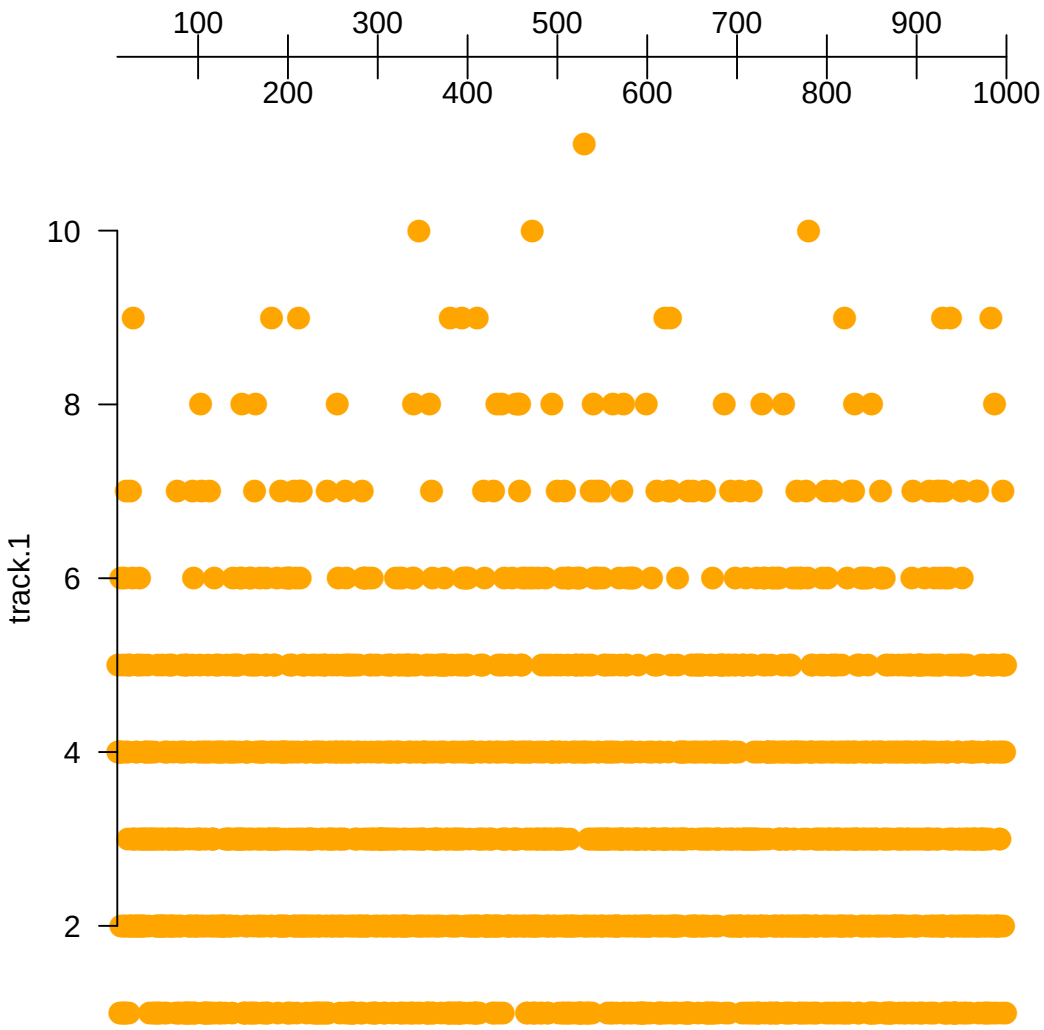
```
> require(Genominator)
> options(verbose = FALSE)
> N <- 1e+05
> K <- 100
> df <- data.frame(chr = sample(1:16, size = N, replace = TRUE),
+     location = sample(1:1000, size = N, replace = TRUE),
+     strand = sample(c(1L, -1L), size = N, replace = TRUE))
> eData <- aggregateExpData(importToExpData(df, filename = "pmy.db",
+     overwrite = TRUE, tablename = "ex_tbl"))
> 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
```

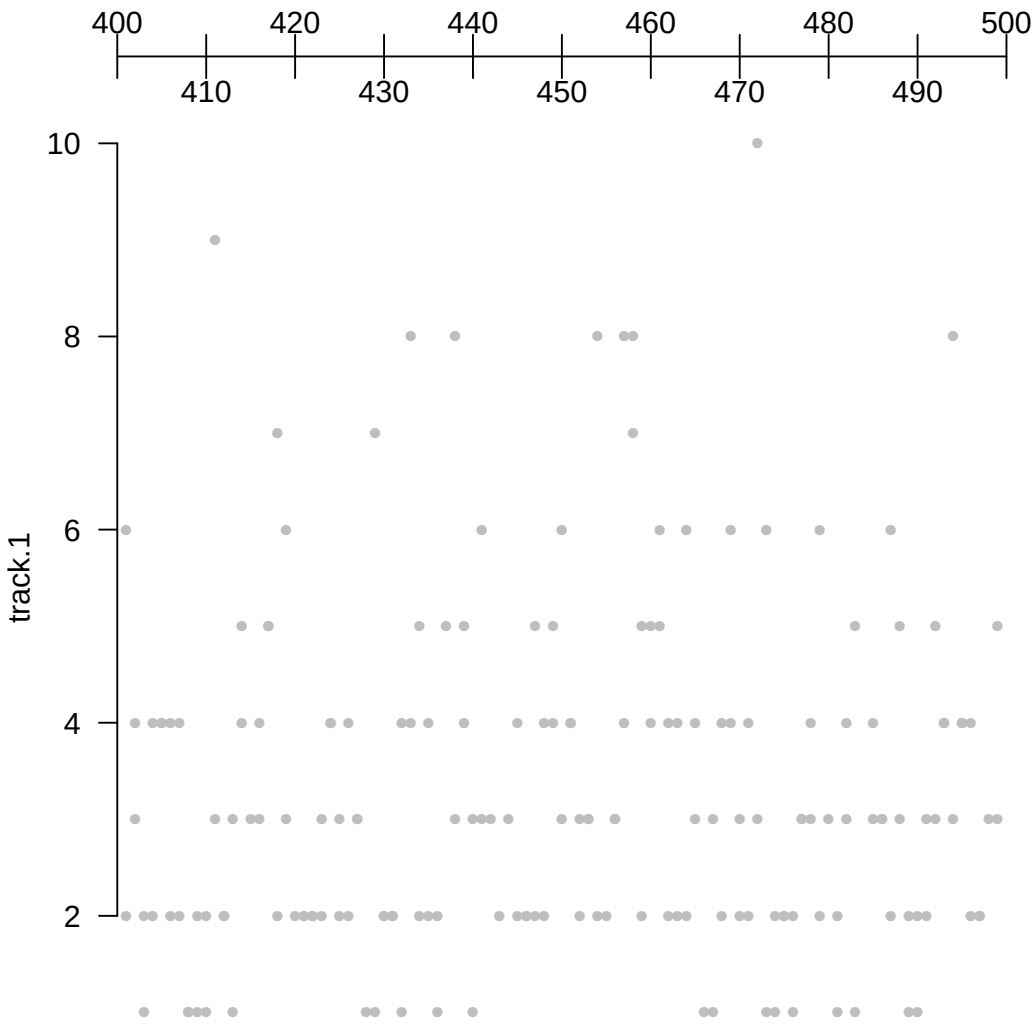
This constructs a function which can be called to view particular pieces of data.

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



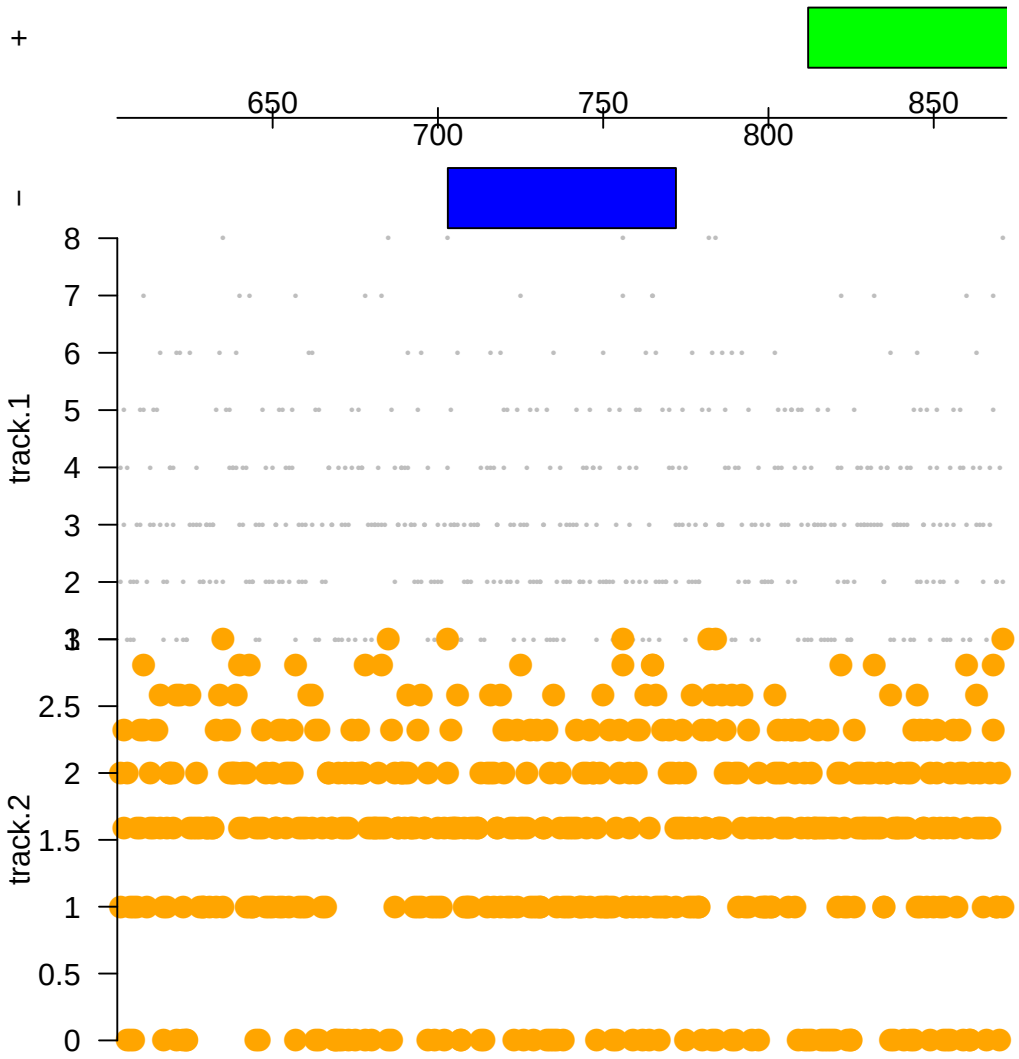
GenomeGraphs provides a wealth of customization options and means of plotting which for the most part are transferable using the list.

```
> rp <- Genominator:::makeRegionPlotter(list(track.1 = list(expData = eData,
+     what = "counts", dp = DisplayPars(lwd = 0.45, 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(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 = 0.2, color = "grey")),
+     track.2 = list(expData = eData, what = "counts",
+         fx = log2, DisplayPars(lwd = 0.3, 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.Biomart(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   I        1     -1 9.038919 8.614710
2   I        1     -1 9.172428 8.558421
3   I        2     -1 9.422065 9.131857
4   I        2     -1 8.679480 8.442943
5   I        2     -1 8.546894 8.794416
6   I        2     -1 8.784635 8.918863
```

```
> yData <- importToExpData(chr1_yeast, filename = "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 = 0.3, color = "grey"))), annoFactory = annoFactory)
> rp(1, 20000, 50000)
```