GenomeGraphs
An introduction

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GenomeGraphs

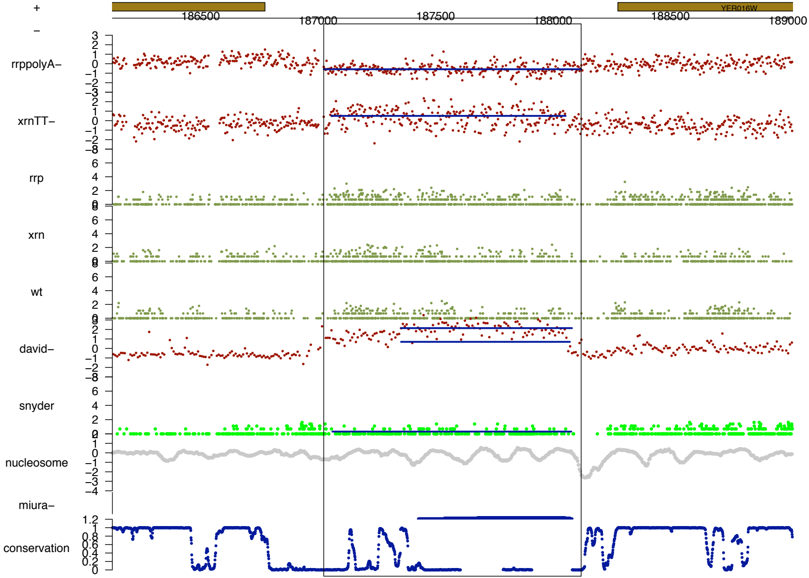
GenomeGraphs is a package for visualizing data along genomic coordinates – a bit like a browser.

It uses *biomaRt* to obtain annotation on genomic intervals from Ensembl.

An example

An example from Lee *et al.*, PLoS Genetics 2008, 4 (12) e1000299.

An example



mcl.9, chr: 5

Concepts

"Tracks" are made by a number of constructors, like `makeGeneRegion`, `makeIdeogram`, `makeGenomeAxis` and `makeBaseTrack`.

Each function constructs an object of a certain class, and typically has an argument `dp` of the form `dp = DisplayPars(color = "blue")`. Use `showDisplayOptions` to get a list of possible values (with defaults):

```
> showDisplayOptions("BaseTrack")
```

```
alpha  =  1
color  =  orange
lty  =  solid
lwd  =  1
size  =  5
type  =  p
```

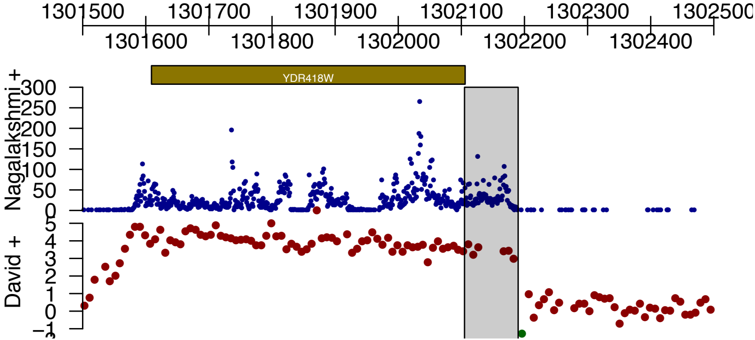
Tracks are put together in a standard `list` and plotted using `gdPlot`.

An example

```
> data("seqDataEx", package = "GenomeGraphs")
> str = seqDataEx$david[,"strand"] == 1
> biomart = useMart("ensembl", "scerevisiae_gene_ensembl")
> axTrack <- makeGenomeAxis(dp = DisplayPars(size = 3))
> gnTrack <- makeGeneRegion(chromosome = "IV", start = 1300000,
+                           end = 1310000,
+                           strand = "+", biomart = biomart,
+                           dp = DisplayPars(plotId = TRUE,
+                           idRotation = 0, cex = .5))
> nagTrack <- makeBaseTrack(base = seqDataEx$snyder[, "location"
+                           value = seqDataEx$snyder[, "counts"]
+                           dp = DisplayPars(lwd = .3,
+                           color = "darkblue", ylim = c(0,300))
> dTrack <- makeGenericArray(probeStart = seqDataEx$david[str,
+                                 "location"],
+                            intensity = seqDataEx$david[str,
+                                 "expr", drop=FALSE],
+                            dp = DisplayPars(pointSize = .5))
```

An example

```
> gdPlot(list(axTrack, "+" = gnTrack, "Nagalakhsmi" = nagTrack,
+             "David +" = dTrack),
+        minBase = 1301500, maxBase = 1302500)
```



Session Info

- R version 2.14.0 Under development (unstable) (2011-06-20 r56188), `x86_64-apple-darwin10.7.4`
- 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, stats, utils
- Other packages: biomaRt 2.9.2, GenomeGraphs 1.13.0
- Loaded via a namespace (and not attached): RCurl 1.6-6, tools 2.14.0, XML 3.4-0