GenomeGraphs
An introduction

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**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
“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):

```r
> 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

```r
> 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

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

![Graph showing the comparison between axTrack and gnTrack, highlighted regions indicating specific intervals, and a legend for YDR418W.](image)
Session Info

- R version 2.14.0 Under development (unstable) (2011-06-20 r56188), x86_64-apple-darwin10.7.4
- 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