

The Gviz User Guide

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1 Introduction

In order to make sense of genomic data one often aims to plot such data in a genome browser, along with a variety of genomic annotation features, such as gene or transcript models, CpG island, repeat regions, and so on. These features may either be extracted from public data bases like ENSEMBL or UCSC, or they may be generated or curated in house. Many of the currently available genome browsers do a reasonable job in displaying these features, and there are options to connect to them from within R (e.g., using the `rtracklayer` package). However, none of these solutions offer the flexibility of the full R graphics system to display large numeric data in a multitude of different ways. The `Gviz` package aims to close this gap by providing a structured visualization framework to plot any type of data along genomic coordinates. It is loosely based on the `GenomeGraphs` package by Steffen Durinck and James Bullard, however the complete class hierarchy as well as all the plotting methods have been restructured in order to increase performance and flexibility. All plotting is done using the grid graphics system, and several specialized annotation classes allow to integrate publicly available genomic annotation data from sources like UCSC or ENSEMBL.

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2 Basic Features

The fundamental concept behind the **Gviz** package is similar to the approach taken by most genome browsers, in that individual types of genomic features or data are represented by separate tracks. Within the package, each track constitutes a single object inheriting from class *gdObject*, and there are constructor functions as well as a broad range of methods to interact with and to plot these tracks. When combining multiple objects, the individual tracks will always share the same genomic coordinate system, thus taking the burden of aligning the plot elements from the user.

It is worth mentioning that tracks in the sense of the **Gviz** package are only defined for a single chromosome on a specific genome, at least during the plotting operation. While the package imposes no fixed structure on the chromosome or on the genome names, it makes sense to stick to a standardized naming paradigm, in particular when fetching additional annotation information from online resources. For the remainder of this vignette, we will make use of the UCSC genome and chromosome identifiers, e.g., the **chr7** chromosome on the mouse **mm9** genome.

The different track classes will be described in more detail in the **Track classes** section further below. For now, let's just take a look at a typical **Gviz** session. We begin our presentation of the available functionality by loading the package:

```
> library(Gviz)
```

The most simple genomic features consists of start and stop coordinates, possibly overlapping each other. CpG islands or microarray probes are real life examples for this class of features. In the Bioconductor world those are most often represented as run-length encoded vectors, for instance in the *IRanges* and *GRanges* classes. To seamlessly integrate with other Bioconductor packages, we can use the same data structures to generate our track objects. A sample set of CpG island coordinates has been saved in the **cpgIslands** object and we can use that for our first annotation track object. The constructor function **AnnotationTrack** is a convenient helper to create the object.

```
> library(IRanges)
> data(cpgIslands)
> chr <- "chr7"
> gen <- "mm9"
> atrack <- AnnotationTrack(cpgIslands, chromosome = chr,
+   genome = gen, name = "CpG")
```

Please note that the **AnnotationTrack** constructor is fairly flexible and can accomodate many different types of inputs. For instance, the start and end coordinates of the annotation features could be passed in as individual arguments **start** and **end**, as a *data.frame* or even as a *GRanges* object. You may want to consult its manual page for more information.

With our first track object being created we may now proceed to the plotting. There is a single function **plotTracks** that handles all of this. As we will learn in the remainder of this vignette, **plotTracks** is quite powerful and has a number of very useful additional arguments. For now we will keep things very simple and just plot the single CpG islands annotation track.

```
> plotTracks(atrack)
```



As you can see, the resulting graph is not particularly spectacular. There is a title region showing the track's name on a gray background on the left side of the plot and a data region showing the seven individual CpG islands on the right. This structure is similar for all the available track objects classes and it somewhat mimicks the layout of the popular UCSC Genome Browser. If you are not happy with the default settings, the *Gviz* package offers a multitude of options to fine-tune the track appearance, which will be shown in the **Plotting Parameters** section.

Appart from the relative distance of the CpG islands, this visualization does not tell us much. One obvious next step would be to indicate the genomic coordinates we are currently looking at to provide some reference. For this purpose, the *Gviz* package offers the *GenomeAxisTrack* class. Object from the class can be created using the constructor function of the same name.

```
> gtrack <- GenomeAxisTrack()
```

Since a *GenomeAxisTrack* object is always relative to the other tracks that are plotted, there is little need for additional arguments. Essentially, the object just tells the `plotTracks` function to add a genomic axis to the plot. Nonetheless, it represent a separate annotation track just as the CpG island track does. We can pass this additional track on to `plotTracks` in the form of a list.

```
> plotTracks(list(gtrack, atrack))
```



You may have realized that the genomic axis does not take up half of the available vertical plotting space, but only uses the space necessary to fit the axis and labels. Also the title region for this track is empty. The *Gviz* package tries to find reasonable defaults for all the parameters controlling the look and feel of a plot so that appealing visualizations can be created without much tinkering. However, all features on the plot including the relative track sizes can also be adjusted manually.

As mentioned before in the beginning of this vignette, a track is defined for a particular chromosome on a particular genome. We can include this information in our plot by means of a chromosome ideogram. An ideogram is a simplified visual representation of a chromosome, with the different chromosomal bands indicated by color, and the centromer (if present) indicated by the shape. The necessary information to produce this visualization is stored in online data repositories, for instance at UCSC. The *Gviz* package offers very convenient connections to some of these repositories, and the *IdeogramTrack* constructor function is one example for such a connection. With just the information about a valid UCSC genome and chromosome, we can directly fetch the chromosome ideogram information and construct a dedicated track object that can be visualized by `plotTracks`. Please not that you will need a working internet connection for this to work, and that fetching data from UCSC can take quite a long time, depending on the server load. The *Gviz* package tries to cache as much data as possible to reduce the bandwidth.

```
> itrack <- IdeogramTrack(genome = gen, chromosome = chr)
```

Similar to the previous examples, we stick the additional track object into a list in order to plot it.

```
> plotTracks(list(itrack, gtrack, atrack))
```



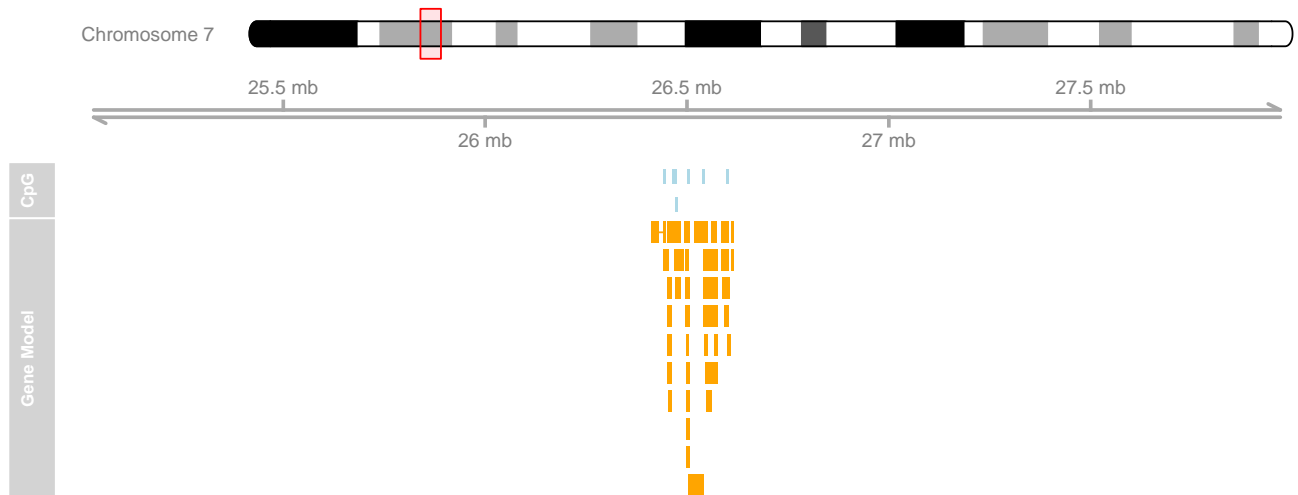
Ideogram tracks are the one exception in all of Gviz's track objects in that they are not really displayed in the same coordinate system like all the other tracks. Instead, the current genomic location is indicated on the chromosome by a red box (or a red line if the width is too small to fit a box). So far we have only looked at very basic annotation features and how to give a point of reference to our plots. Naturally, we also want to be able to handle more complex genomic features, such as gene models. One potential use case would be to utilize gene model information from an existing local source. Alternatively, we could download such data from one of the available online resources like UCSC or ENSEMBL, and there are constructor functions to handle these tasks. For this example we are going to load gene model data from a stored Rclassdata.frame. The track class of choice here is a *GeneRegionTrack* object, which can be constructed via the constructor function of the same name. Similar to the *AnnotationTrack* constructor there are multiple possible ways to pass in the data.

```
> data(geneModels)
> grtrack <- GeneRegionTrack(geneModels, genome = gen,
+   chromosome = chr, name = "Gene Model")
> plotTracks(list(itrack, gtrack, atrack, grtrack))
```



So far the plotted genomic range has been determined by the input tracks. Unless told otherwise, the package will always display the region from the leftmost item to the rightmost item in any of the tracks. Of course such a static view on a chromosomal region is of rather limited use. We often want to zoom in or out on a particular plotting region to see more details or to get a broader overview. To that end, *plotTracks* supports the *from* and *to* arguments that let us choose an arbitrary genomic range to plot.

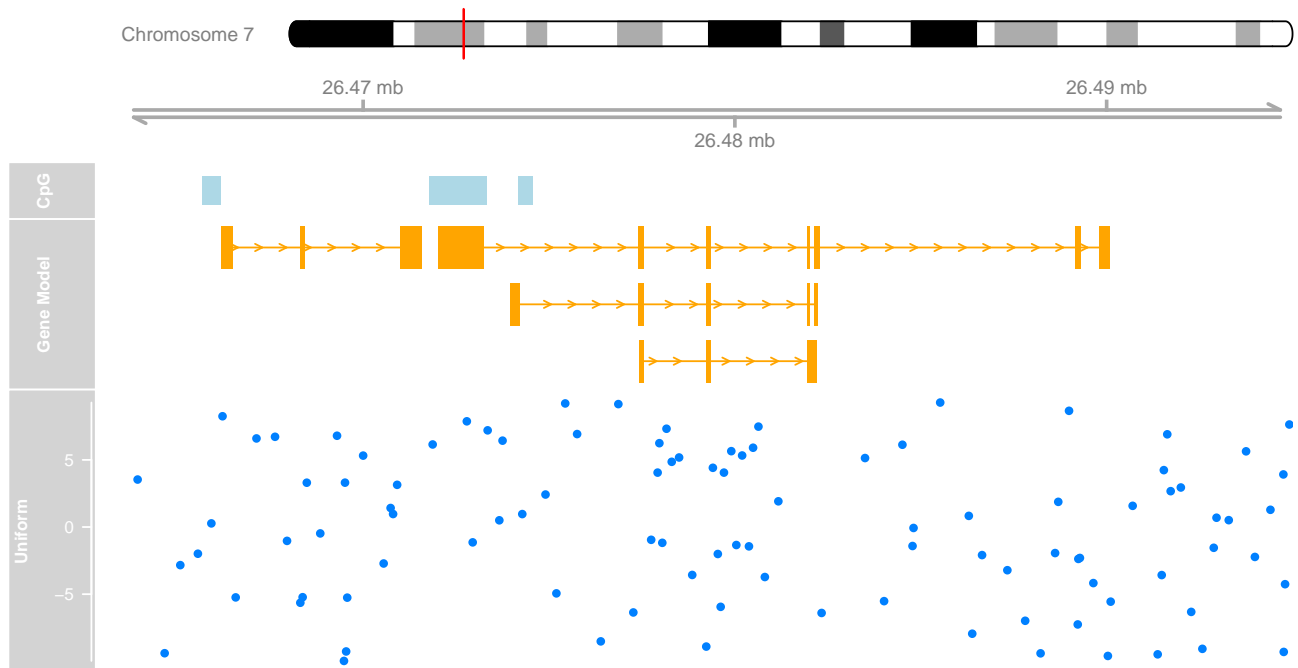
```
> plotTracks(list(itrack, gtrack, atrack, grtrack),
+   from = 2.5e+07, to = 2.8e+07)
```



You may have noticed that the layout of the gene model track has changed depending on the zoom level. This is a feature of the *Gviz* package, which automatically tries to find the optimal visualization settings to make best use of the available space. At the same time, when features on a track are too close together to be plotted as separate items with the current device resolution, the package will try to reasonably merge them in order to avoid overplotting.

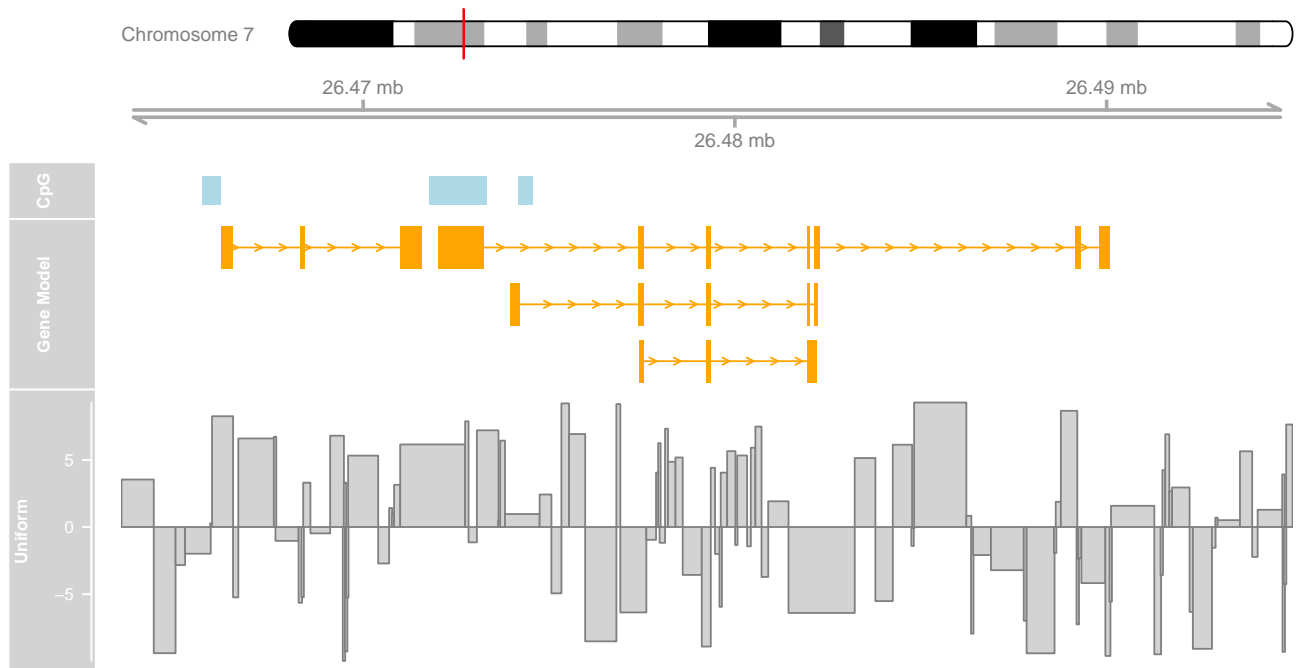
So far we have replicated the features of a whole bunch of other genome browser tools out there. The real power of the package comes with a rather general track type, the *DataTrack*. *DataTrack* objects are essentially run-length encoded numeric vectors or matrices, and we can use them to add all sorts of numeric data to our genomic coordinate plots. There are a whole bunch of different visualization options for these tracks, from dot plots to histograms to box-and-whisker plots. The individual rows in a numeric matrix are considered to be different data groups or samples, and the columns are the raster intervals in the genomic coordinates. Of course, the data points do not have to be evenly spaced; each column is associated to a particular genomic location. For demonstration purposes we can create a simple *DataTrack* object from randomly sampled data.

```
> set.seed(255)
> lim <- c(26463500, 26495000)
> coords <- sort(c(lim[1], sample(seq(from = lim[1],
+   to = lim[2]), 99), lim[2]))
> dat <- runif(100, min = -10, max = 10)
> dtrack <- DataTrack(data = dat, start = coords[-length(coords)],
+   end = coords[-1], chromosome = chr, genome = gen,
+   name = "Uniform")
> plotTracks(list(itrack, gtrack, atrack, grtrack,
+   dtrack), from = lim[1], to = lim[2])
```



The first thing to notice is that the title panel to the right of the plot now contains a y-axis indicating the range of the data track. The default plotting type for numeric vectors is a simple dot plot. This is by far not the only visualization option, and in a sense it is wasting quite a lot of information because the run-length encoded ranges are not immediately apparent. We can change the plot type by supplying the `type` argument to `plotTracks`. A complete description of the available plotting options is given in section [Track classes](#), and a more detailed treatment of the so-called 'display parameters' that control the look and feel of a track is given in the [Plotting Parameters](#) section.

```
> plotTracks(list(itrack, gtrack, atrack, grtrack,
+               dtrack), from = lim[1], to = lim[2], type = "histogram")
```



As we can see, the data values in the numeric vector are indeed matched to the genomic coordinates of the *DataTrack* object. Such a visualization can be particularly helpful when displaying for instance the coverage of NGS reads along a chromosome, or to show the measurement values of mapped probes from a micro array experiment. This concludes our first introduction into the Gviz package. The remainder of this vignette will deal in much more depth with the different concepts and the various track classes and plotting options.

3 Plotting parameters

Although not implicitly told, we have already made use of the plotting parameter facilities in the Gviz package, or, as we will call them from now on, the 'display parameters'. Display parameters are properties of individual track objects (i.e., of any object inheriting from the base *GdObject* class). They can either be set during object instantiation as additional arguments to the constructor functions or, for existing track objects, using the `displayPars` replacement method. In the former case, all named arguments that can not be matched to any of the constructor's formal arguments are considered to be display parameters, regardless of their type or whether they are defined for a particular track class or not. The following code example rebuilds our *GeneRegionTrack* object with a bunch of display parameters set and demonstrates the use of the `displayPars` accessor and replacement methods.

```
> grtrack <- GeneRegionTrack(geneModels, genome = gen,
+   chromosome = chr, name = "Gene Model", showId = TRUE,
+   background.title = "brown")
> head(displayPars(grtrack))
```

```
$fill
[1] "orange"
```

```
$geneSymbols
[1] TRUE
```

```

$showExonId
[1] FALSE

$collapseTranscripts
[1] FALSE

$shape
[1] "smallArrow" "box"

$col
[1] "transparent"

> displayPars(grtrack) <- list(background.panel = "#FFFEDB")
> head(displayPars(grtrack))

$fill
[1] "orange"

$geneSymbols
[1] TRUE

$showExonId
[1] FALSE

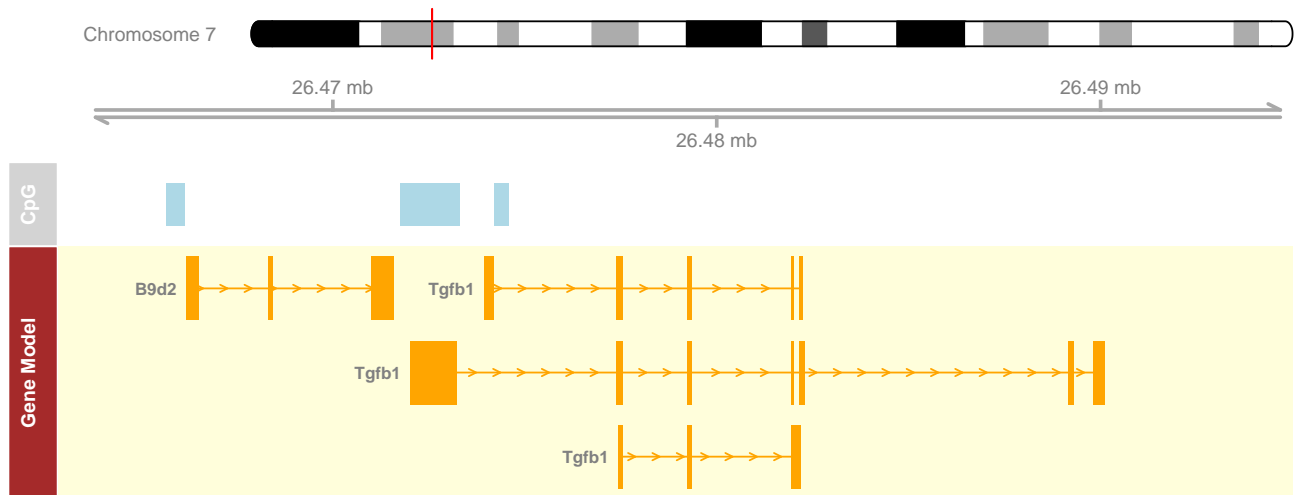
$collapseTranscripts
[1] FALSE

$shape
[1] "smallArrow" "box"

$col
[1] "transparent"

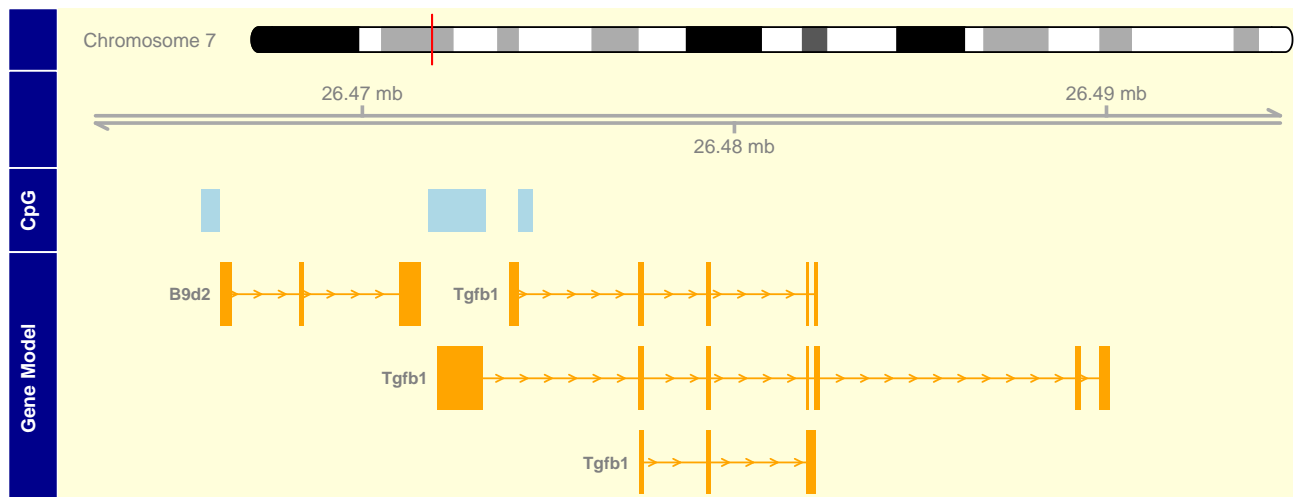
> plotTracks(list(itrack, gtrack, atrack, grtrack),
+           from = lim[1], to = lim[2])

```

For our gene model track we have now added the gene symbols of the different transcripts to the plot and changed the background color of both the title and the data panel. There is a third option to set display parameters for a single plotting operation (rather than the permanent setting in the track object) by passing in additional arguments to the `plotTracks` function. We have already made use of this feature in the previous data plotting type example. It is worth mentioning that all display parameters that are passed along with the `plotTracks` function apply to all track objects in the plot. For some track objects a particular display parameter may not make any sense, and in that case it is simply ignored. Also, the settings only apply for one single plotting operations and will not be retained in the plotted track objects. They do however get precedence over the object-internal parameters. The following line of code exemplifies this behaviour.

```
> plotTracks(list(itrack, gtrack, atrack, grtrack),
+   from = lim[1] - 1000, to = lim[2], background.panel = "#FFEDB",
+   background.title = "darkblue")
```



In order to make full use of the flexible parameter system we need to know which display parameters control which aspect of which track class. The obvious source for this information are the man pages of the respective track classes, which list all available parameters and a short description of their effect and default values in the `Display Parameters` section. Alternatively, we can use the `availableDisplayPars` function, which prints

out the available parameters for a class in a list-like structure. The single argument to the function is either a class name of a track object class, or the object itself, in which case its class is automatically detected.

```
> dp <- availableDisplayPars(grtrack)
> tail(dp)
```

The following display parameters are available for 'GeneRegionTrack' objects: (see ? GeneRegionTrack for details on their usage)

```
min.width (inherited from class 'GdObject'): 1
rotation (inherited from class 'AnnotationTrack'): 0
shape: smallArrow box
showAxis (inherited from class 'GdObject'): TRUE
showExonId: FALSE
showFeatureId (inherited from class 'AnnotationTrack'): FALSE
showId (inherited from class 'AnnotationTrack'): FALSE
showOverplotting (inherited from class 'AnnotationTrack'): FALSE
showTitle (inherited from class 'GdObject'): TRUE
size (inherited from class 'GdObject'): 1
v (inherited from class 'GdObject'): -1
```

As we can see, display parameters can be inherited from parent classes. For the regular user this is not important at all, however it nicely exemplifies the structure of the class hierarchy in the Gviz package.

4 Track classes

In this section we will highlight all of the available annotation track classes in the Gviz package. For the complete reference of all the nuts and bolts, including all the available methods, please see the respective class man pages. We will try to keep this vignette up to date, but in cases of discrepancies between here and the man pages you should assume the latter to be correct.

4.1 GenomeAxisTrack

GenomeAxisTrack objects can be used to add some reference to the currently displayed genomic location to a Gviz plot. In its most basic form it is really just a horizontal axis with genomic coordinate tickmarks. Using the *GenomeAxisTrack* constructor function is the recommended way to instantiate objects from the class. There is no need to know in advance about a particular genomic location when constructing the object. Instead, the displayed coordinates will be determined from the context, e.g., from the *from* and *to* arguments of the *plotTracks* function, or, when plotted together with other track objects, from their genomic locations.

```
> axisTrack <- GenomeAxisTrack()
> plotTracks(axisTrack, from = 1e+06, to = 9e+06)
```



As an optional feature one can highlight particular regions on the axis, for instance to indicated stretches of N nucleotides or gaps in genomic alignments. Such regions have to be supplied to the optional *range* argument of the constructor function as either an *IRanges* or an *IRanges* object.

```
> axisTrack <- GenomeAxisTrack(range = IRanges(start = c(2e+06,
+       4e+06), end = c(3e+06, 7e+06)))
> plotTracks(axisTrack, from = 1e+06, to = 9e+06)
```



Display parameters for GenomeAxisTrack objects

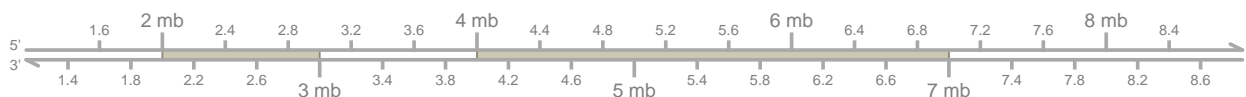
There are a whole bunch of display parameters to alter the appearance of *GenomeAxisTrack* plots. For instance, one could add directional indicators to the axis using the *add53* and *add35* parameters.

```
> plotTracks(axisTrack, from = 1e+06, to = 9e+06, add53 = TRUE,
+       add35 = TRUE)
```



Sometimes the resolution of the tick marks is not sufficient, in which case the *littleTicks* argument can be used to have a more fine-grained axis annotation.

```
> plotTracks(axisTrack, from = 1e+06, to = 9e+06, add53 = TRUE,
+       add35 = TRUE, littleTicks = TRUE)
```



The Gviz package tries to come up with reasonable defaults for the axis annotation. In our previous example, the genomic coordinates are indicated in megabases. We can control this via the *exponent* parameter, which takes an integer value greater than zero. The location of the tick marks are displayed as a fraction of 10^{exponent} .

```
> plotTracks(axisTrack, from = 1e+06, to = 9e+06, exponent = 4)
```



Another useful parameter, *labelPos* controls the arrangement of the tick marks. It takes one of the values *alternating*, *revAlternating*, *above* or *below*. For instance we could align all tick marks underneath the axis.

```
> plotTracks(axisTrack, from = 1e+06, to = 9e+06, labelPos = "below")
```



Sometimes a full-blown axis is just too much, and all we really need in the plot is a small scale indicator. We can change the appearance of the *GenomeAxisTrack* object to such a limited representation by setting the *scale* parameter. Typically, this will be a numeric value between 0 and 1, which is interpreted as the fraction of the plotting region used for the scale. The plotting method will apply some rounding to come up with reasonable and human-readable values. For even more control we can pass in a value larger than 0, which is considered to be an absolute range length. In this case, the user is responsible for the scale to actually fit in the current plotting range.

```
> plotTracks(axisTrack, from = 1e+06, to = 9e+06, scale = 0.5)
```



We still have control over the placement of the label via the *labelPos*, parameter, which now takes the values *above*, *below* and *beside*.

```
> plotTracks(axisTrack, from = 1e+06, to = 9e+06, scale = 0.5,
+   labelPos = "below")
```



For a complete listing of all the available display parameters please see the table below or the man page of the *GenomeAxisTrack* class by typing in `?GenomeAxisTrack` on the R command line.

Display Parameter	Description
<code>add35</code>	Logical scalar. Add 3' to 5' direction indicators.
<code>add53</code>	Logical scalar. Add 5' to 3' direction indicators.
<code>cex</code>	Numeric scalar. The overall font expansion factor for the axis annotation text.
<code>cex.id</code>	Numeric scalar. The text size for the optional range annotation.
<code>col</code>	Character scalar. The color for the axis lines and tickmarks.
<code>col.id</code>	Character scalar. The text color for the optional range annotation.
<code>col.range</code>	Character scalar. The border color for highlighted regions on the axis.
<code>distFromAxis</code>	Numeric scalar. Control the distance of the axis annotation from the tick marks.
<code>exponent</code>	Numeric scalar. The exponent for the axis coordinates, e.g., 3 means mb, 6 means gb, etc. The default is to automatically determine the optimal exponent.
<code>fill.range</code>	Character scalar. The fill color for highlighted regions on the axis.
<code>fontcolor</code>	Character scalar. The font color for the axis annotation text.
<code>fontface</code>	Character scalar. The font face for the axis annotation text.
<code>fontfamily</code>	Character scalar. The font family for the axis annotation text.
<code>fontsize</code>	Numeric scalar. Font size for the axis annotation text in points.
<code>labelPos</code>	Character vector, one in "alternating", "revAlternating", "above" or "below". The vertical positioning of the axis labels. If <code>scale</code> is not NULL, the possible values are "above", "below" and "beside".
<code>littleTicks</code>	Logical scalar. Add more fine-grained tick marks.
<code>lwd</code>	Numeric scalar. The line width for the axis elementes.
<code>scale</code>	Numeric scalar. If not NULL a small scale is drawn instead of the full axis, if the value is between 0 and 1 it is interpreted as a fraction of the current plotting region, otherwise as an absolute length value in genomic coordinates.
<code>showId</code>	Logical scalar. Show the optional range highlighting annotation.

4.2 IdeogramTrack

While a genomic axis provides helpful points of reference to a plot, it is sometimes important to show the currently displayed region in the broader context of a chromosome. Are we looking at distal regions, or somewhere close to the centromere? And how much of the complete chromosome is covered in our plot. To that end the *Gviz* package defines the *IdeogramTrack* class, which is an idealized representation of a single chromosome. When plotted, these track objects will always show the whole chromosome, regardless of the selected genomic region. However, this selection is indicated by a box. The chromosomal data necessary to draw the ideogram is not part of the *Gviz* package itself, but it is rather downloaded from an online source (UCSC). Thus it is important to use both chromosome and genome names that are recognizable in the UCSC data base. You might want to consult their webpage (<http://genome.ucsc.edu/>) or use the `ucscGenomes` function in the *rtracklayer* package for a listing of available genomes.

Assuming the chromosome data are available online, a simple call to the *IdeogramTrack* constructor function including the desired genome and chromosome name are enough to instantiate the object. Since the connection to UCSC can be slow, the package tries to cache data that has already been downloaded for the duration of the R session. If needed, the user can manually clear the cache by calling the `clearSessionCache` function.

```
> ideoTrack <- IdeogramTrack(genome = "hg19", chromosome = "chrX")
> plotTracks(ideoTrack, from = 8.5e+07, to = 1.29e+08)
```



Display parameters for IdeogramTrack objects

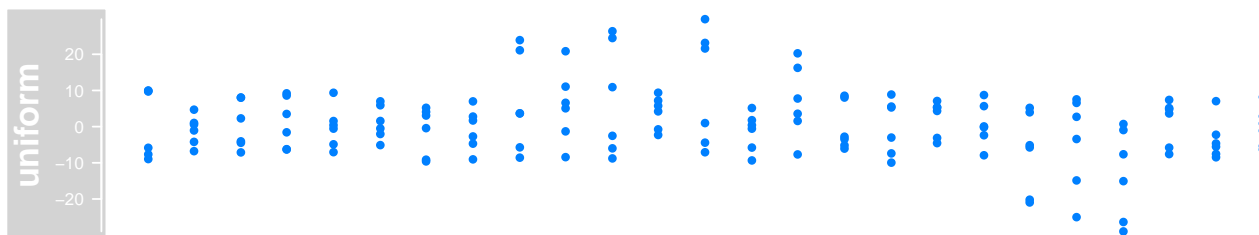
For a complete listing of all the available display parameters please see the table below or the man page of the *IdeogramTrack* class by typing in `?IdeogramTrack` on the R command line.

Display Parameter	Description
bevel	Numeric scalar, between 0 and 1. The level of smoothness for the two ends of the ideogram.
cex	Numeric scalar. The overall font expansion factor for the chromosome name text.
col	Character scalar. The border color used for the highlighting of the currently displayed genomic region.
fill	Character scalar. The fill color used for the highlighting of the currently displayed genomic region.
fontcolor	Character scalar. The font color for the chromosome name text.
fontface	Character scalar. The font face for the chromosome name text.
fontfamily	Character scalar. The font family for the chromosome name text.
fontsize	Numeric scalar. The font size for the chromosome name text.
lty	Character or integer scalar. The line type used for the highlighting of the currently displayed genomic region.
lwd	Numeric scalar. The line width used for the highlighting of the currently displayed genomic region.
showId	Logical scalar. Indicate the chromosome name next to the ideogram.

4.3 DataTrack

Probably the most powerful of all the track classes in the Gviz package are *DataTracks*. Essentially they constitute run-length encoded numeric vectors or matrices, meaning that one or several numeric values are associated to a particular genomic coordinate range. These ranges may even be overlapping, for instance when looking at results from a running window operation. There can be multiple samples in a single data set, in which case the ranges are associated to the columns of a numeric matrix rather than a numeric vector, and the plotting method provides tools to incorporate sample group information. Thus the starting point for creating *DataTrack* objects will always be a set of ranges, either in the form of an *IRanges* or *GRanges* object, or individually as start and end coordinates or widths. The second ingredient is a numeric vector of the same length as the number of ranges, or a numeric matrix with the same number of columns. We can pass this information, along with the genome and the chromosome identifiers, to the **DataTrack** constructor function to instantiate an object. We will load our sample data from an *GRanges* object that comes as part of the Gviz package.

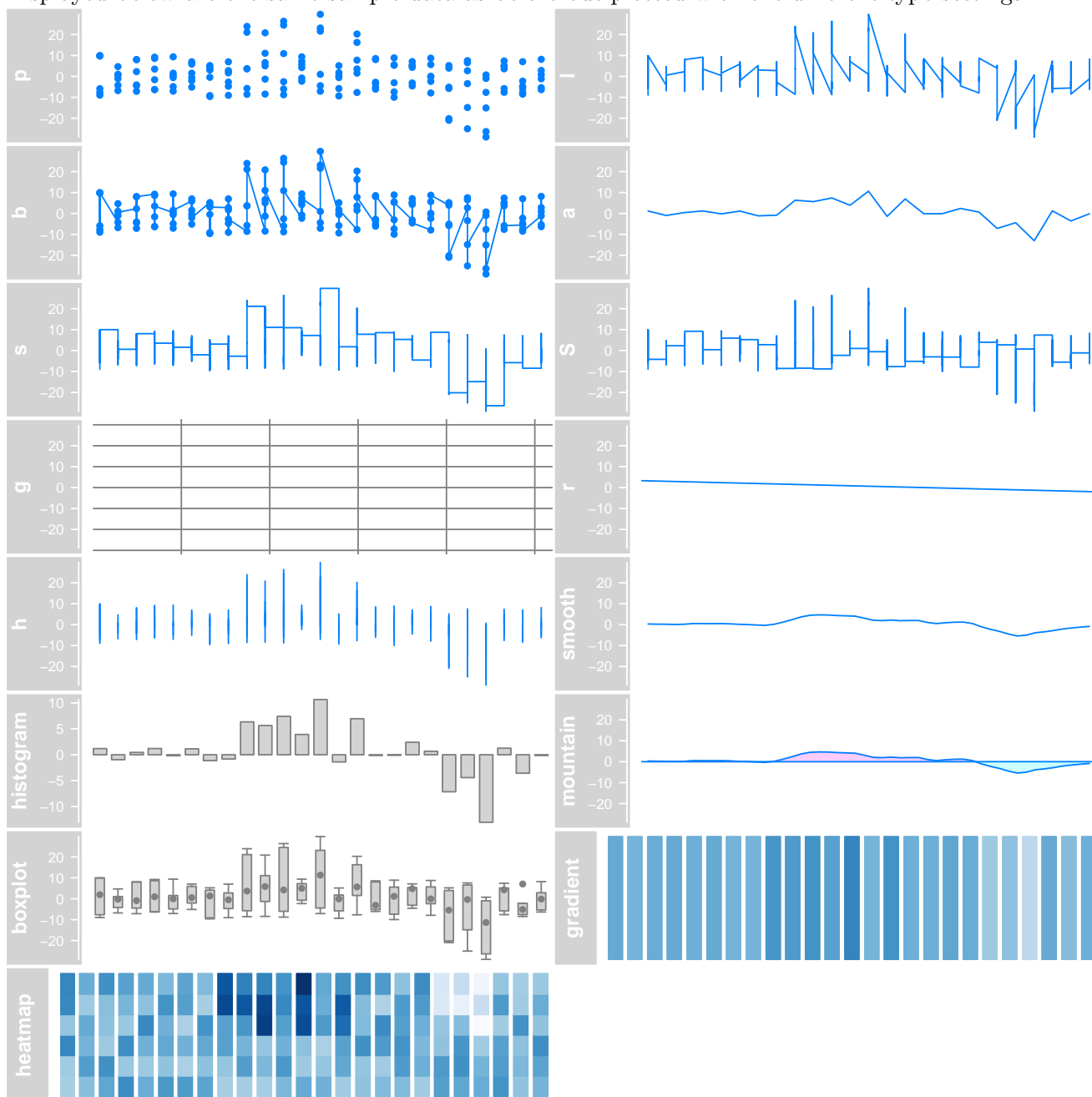
```
> data(twoGroups)
> dTrack <- DataTrack(twoGroups, data = t(as.data.frame(elementMetadata(twoGroups))),
+   genome = "hg19", chromosome = "chrX", name = "uniform")
> plotTracks(dTrack)
```



The default visualization for our very simplistic sample *DataTrack* is a rather uninspiring dot plot. The track comes with a scale to indicate the range of the numeric values on the y-axis, apart from that it looks very much like the previous examples. A whole battery of display parameters is to our disposal to control the track's look and feel. The most important one is the *type* parameter. It determines the type of plot to use and takes one or several of the following values:

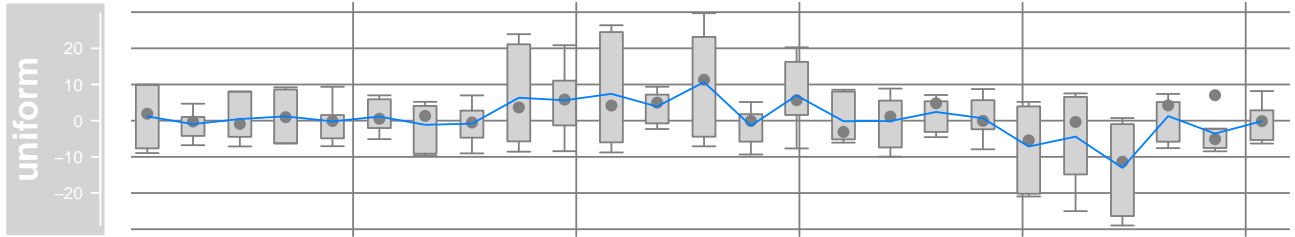
Value	Type
p	dot plot
l	lines plot
b	dot and lines plot
a	lines plot of average (i.e., mean) values
s	stair steps (horizontal first)
S	stair steps (vertical first)
g	add grid lines
r	add linear regression line
h	histogram lines
smooth	add loess curve
histogram	histogram (bar width equal to range with)
mountain	'mountain-type' plot relative to a baseline
boxplot	box and whisker plot
gradient	false color image of the summarized values
heatmap	false color image of the individual values

Displayed below are the same sample data as before but plotted with the different type settings:



You will notice that some of the plot types work better for univariate data while others are clearly designed for multivariate data. The *a* type for instance averages the values at each genomic location before plotting the derived values as a line. The decision for a particular plot type is totally up to the user, and one could even overlay multiple types by supplying a character vector rather than a character scalar as the *(type)* argument. For example, this will combine a boxplot with an average line and a data grid.

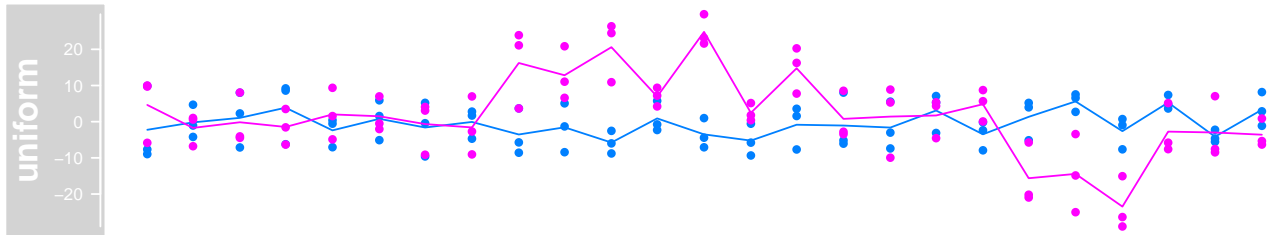
```
> plotTracks(dTrack, type = c("boxplot", "a", "g"))
```



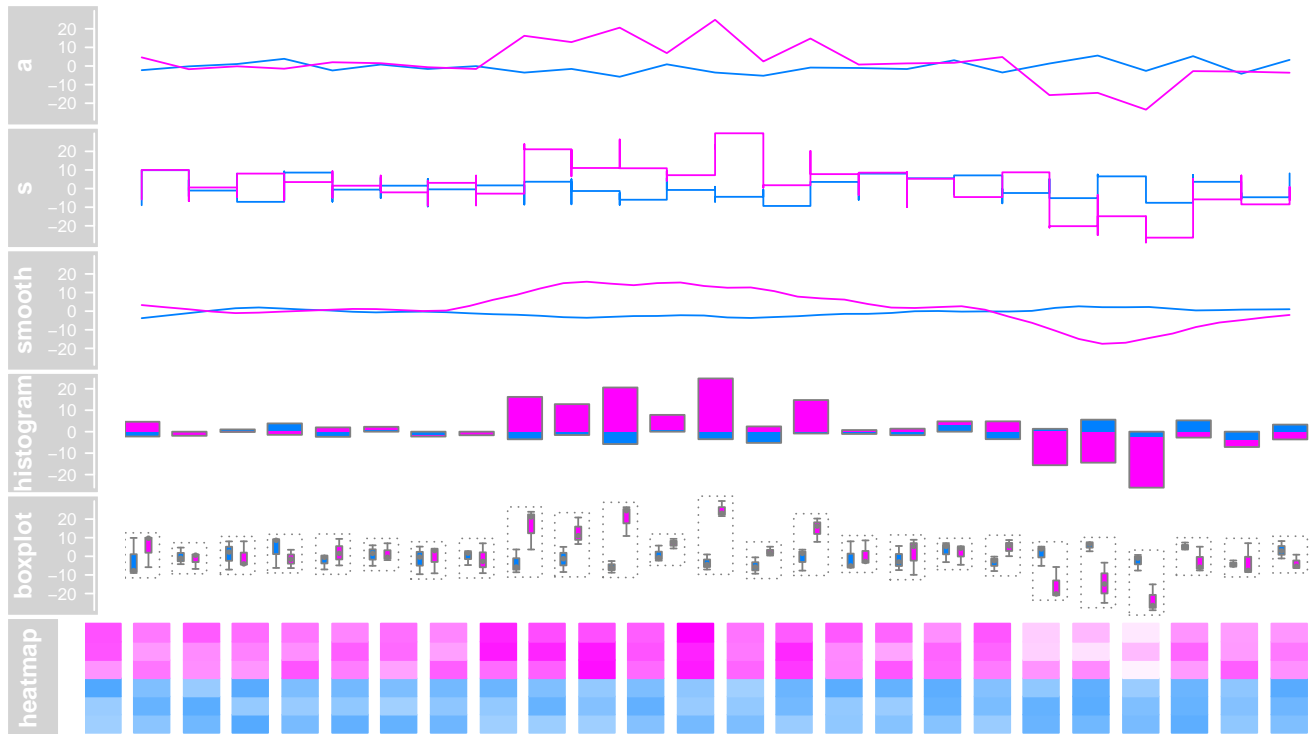
Data Grouping

An additional layer of flexibility is added by making use of `Gviz`'s grouping functionality. The individual samples (i.e., rows in the data matrix) can be grouped together using a factor variable, and, if reasonable, this grouping is reflected in the layout of the respective track types. For instance our example data could be derived from two different sample groups with three replicates each, and we could easily integrate this information into our plot.

```
> plotTracks(dTrack, groups = rep(c("control", "treated"),
+   each = 3), type = c("a", "p"))
```



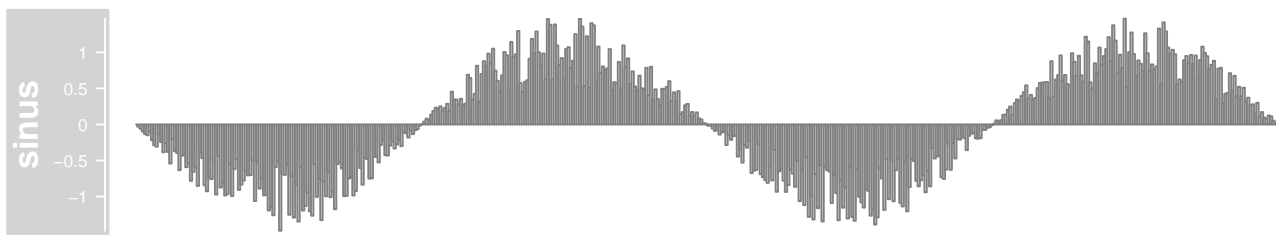
For the dot plot representation the individual group levels are indicated by color coding. For the *a* type, the averages are now computed for each group separately and also indicated by two lines with similar color coding. Grouping is not supported for all plotting types, for example the *mountain* type already uses color coding to convey a different message and for the *gradient* type the data are already collapsed to a single variable. The following gives an overview over some of the other groupable *DataTrack* types. Please note that there are many more display parameters that control the layout of both grouped and of ungrouped *DataTracks*. You may want to check the class' help page for details.



Data transformations

The *Gviz* package offers quite some flexibility to transform data on the fly. This involves both rescaling operations (each data point is transformed on the track's y-axis by a transformation function) as well as summarization and smoothing operations (the values for several genomic locations are summarized into one derived value on the track's x-axis). To illustrate this let's create a significantly bigger *DataTrack* than the one we used before, containing purely syntetic data for only a single sample.

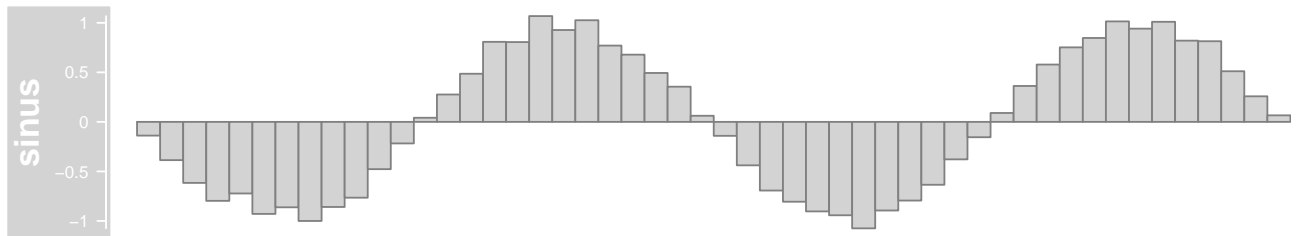
```
> dat <- sin(seq(pi, 10 * pi, len = 500))
> dTrack.big <- DataTrack(start = seq(1, 1e+05, len = 500),
+   width = 15, chromosome = "chrX", genome = "hg19",
+   name = "sinus", data = sin(seq(pi, 5 * pi, len = 500)) *
+   runif(500, 0.5, 1.5))
> plotTracks(dTrack.big, type = "hist")
```



Since the available resolution on our screen is limited we can no longer distinguish between individual coordinate ranges. The *Gviz* package tries to avoid overplotting by collapsing overlapping ranges (assuming the *collapseTracks* is set to `TRUE`). However, it is often desirable to summarize the data, for instance by binning values into a fixed number of windows and subsequent calculation of a summary statistic. This can be

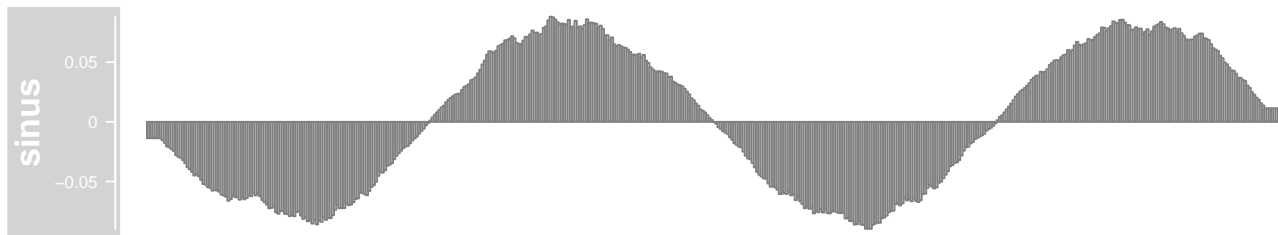
archived by a combination of the *window* and *aggregation* display parameters. The former can be an integer value greater than zero giving the number of evenly-sized bins to aggregate the data in. The latter is supposed to be a user-supplied function that accepts a numeric vector as a single input parameter and returns a single aggregated numerical value. For simplicity, the most obvious aggregation functions can be selected by passing in a character scalar rather than a function. Possible values are `mean`, `median`, `extreme`, `sum`, `min` and `max`. The default is to compute the mean value of all the binned data points.

```
> plotTracks(dTrack.big, type = "hist", window = 50)
```



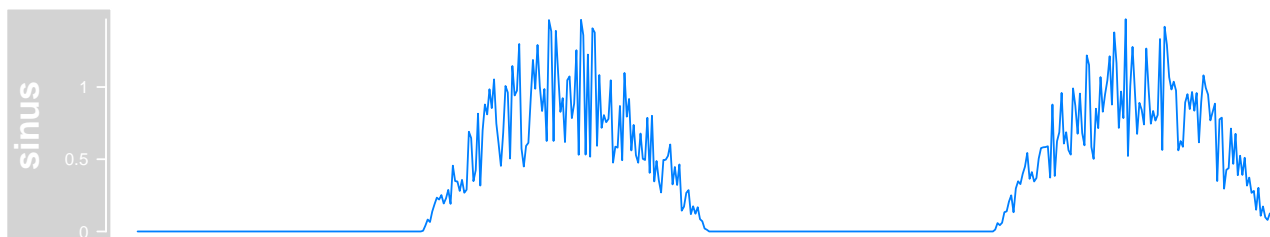
Instead of binning the data in fixed width bins one can also use the *window* parameter to perform more elaborate running window operations. For this to happen the parameter value has to be smaller than zero, and the additional display parameter *windowSize* can be used to control the size of the running window. This operation does not change the number of coordinate ranges on the plot, but instead the original value at a particular position is replaced by the respective sliding window value at the same position. A common use case for sliding windows on genomic ranges is to introduce a certain degree of smoothing to the data.

```
> plotTracks(dTrack.big, type = "hist", window = -1,
+           windowSize = 2500)
```



In addition to transforming the data on the x-axis we can also apply arbitrary transformation functions on the y-axis. One obvious use-case would be to log-transform the data prior to plotting. The framework is flexible enough however to allow arbitrary transformation operations. The mechanism works by providing a function as the *transformation* display parameter, which takes as input a numeric vector and returns a transformed numeric vector of the same length. The following code for instance truncates the plotted data to values greater than zero.

```
> plotTracks(dTrack.big, type = "l", transformation = function(x) {
+   x[x < 0] <- 0
+   x
+ })
```



Display parameters for DataTrack objects

For a complete listing of all the available display parameters please see the table below or the man page of the *DataTrack* class by typing in `?DataTrack` on the R command line.

Display Parameter	Description
aggregation	Function or character scalar. Used to aggregate values in windows or for collapsing overlapping items. The function has to accept a numeric vector as a single input parameter and has to return a numeric scalar with the aggregated value. Alternatively, one of the predefined options mean , median , sum , min , max or extreme can be supplied as a character scalar. Defaults to mean .
alpha	Numeric scalar between 0 and 1. The opacity of the plotting elements, if supported by the device.
amount	Numeric scalar. Amount of jittering in xy-type plots. See <code>panel.xyplot</code> for details.
baseline	Numeric scalar. Y-axis position of an optional baseline. This parameter has a special meaning for mountain-type plots, see the 'Details' section in <i>DataTrack</i> for more information.
box.ratio	Numeric scalar. Parameter controlling the boxplot appearance. See <code>panel.bwplot</code> for details.
box.width	Numeric scalar. Parameter controlling the boxplot appearance. See <code>panel.bwplot</code> for details.
cex	Numeric scalar. The default pixel size for plotting symbols.
cex.legend	Numeric scalar. The size factor for the legend text.
coef	Numeric scalar. Parameter controlling the boxplot appearance. See <code>panel.bwplot</code> for details.
col	Character vector. The base colors to use for all plot types. Unless groups are specified, only the first color in the vector is usually taken.
col	Character or integer scalar. The color used for all line and symbol elements, unless there is a more specific control defined elsewhere.
col.baseline	Character scalar. Color for the optional baseline, defaults to the setting of col .
col.grid	Integer scalar. The line color for grid elements.
col.histogram	Character scalar. Line color in histogram-type plots.
col.line	Character or integer scalar. The color used for line elements. Defaults to the setting of col .
col.mountain	Character scalar. Line color in mountain-type plots, defaults to the setting of col .

col.symbol	Character or integer scalar. The color used for symbol elements. Defaults to the setting of <code>col</code> .
collapse	Logical scalar. Collapse overlapping ranges and aggregate the underlying data.
degree	Numeric scalar. Parameter controlling the loess calculation for smooth and mountain-type plots. See <code>panel.loess</code> for details.
do.out	Logical scalar. Parameter controlling the boxplot appearance. See <code>panel.bwplot</code> for details.
evaluation	Numeric scalar. Parameter controlling the loess calculation for smooth and mountain-type plots. See <code>panel.loess</code> for details.
factor	Numeric scalar. Factor to control amount of jittering in xy-type plots. See <code>panel.xyplot</code> for details.
family	Character scalar. Parameter controlling the loess calculation for smooth and mountain-type plots. See <code>panel.loess</code> for details.
fill	Character scalar. The fill color for area elements, unless there is a more specific control defined elsewhere.
fill.histogram	Character scalar. Fill color in histogram-type plots, defaults to the setting of <code>fill</code> .
fill.mountain	Character vector of length 2. Fill color in mountain-type plots.
fontcolor.legend	Integer or character scalar. The font color for the legend text.
fontface.legend	Integer or character scalar. The font face for the legend text.
fontfamily.legend	Integer or character scalar. The font family for the legend text.
fontsize.legend	Numeric scalar. The pixel size for the legend text.
gradient	Character vector. The base colors for the 'gradient' plotting type.
groups	Vector coercable to a factor. Optional sample grouping. See 'Details' section in <i>DataTrack</i> for further information.
h	Integer scalar. Parameter controlling the number of vertical grid lines, see <code>panel.grid</code> for details.
jitter.x	Logical scalar. Toggle on jittering on the x axis in xy-type plots. See <code>panel.xyplot</code> for details.
jitter.y	Logical scalar. Toggle off jittering on the y axis in xy-type plots. See <code>panel.xyplot</code> for details.
legend	Boolean triggering the addition of a legend to the track to indicate groups. This only has an effect if at least two groups are present.
levels.fos	Numeric scalar. Parameter controlling the boxplot appearance. See <code>panel.bwplot</code> for details.
lineheight.legend	Numeric scalar. The line height for the legend text.
lty	Character or integer scalar. The type for all line elements, unless there is a more specific control defined elsewhere.
lty.baseline	Character or numeric scalar. Line type of the optional baseline, defaults to the setting of <code>lty</code> .
lty.grid	Integer scalar. The line type for grid elements. Defaults to the setting of <code>lty</code> .
lty.mountain	Character or numeric scalar. Line type in mountain-type plots, defaults to the setting of <code>lty</code> .
lwd	Integer scalar. The line width for all line elements, unless there is a more specific control defined elsewhere.

lwd.baseline	Numeric scalar. Line width of the optional baseline, defaults to the setting of <code>lwd</code> .
lwd.grid	Integer scalar. The line width for grid elements. Defaults to the setting of <code>lwd</code> .
lwd.mountain	Numeric scalar. Line width in mountain-type plots, defaults to the setting of <code>lwd</code> .
min.distance	Numeric scalar. The minimum distance in pixel below which to collapse ranges.
na.rm	Boolean controlling whether to discard all NA values when plotting or to keep empty spaces for NAs
ncolor	Integer scalar. The number of colors for the 'gradient' plotting type
notch	Logical scalar. Parameter controlling the boxplot appearance. See <code>panel.bwplot</code> for details.
notch.frac	Numeric scalar. Parameter controlling the boxplot appearance. See <code>panel.bwplot</code> for details.
pch	Integer scalar. The type of glyph used for plotting symbols.
separator	Numeric scalar. Number of pixels used to separate individual samples in heatmap-type plots.
span	Numeric scalar. Parameter controlling the loess calculation for smooth and mountain-type plots. See <code>panel.loess</code> for details.
stackedBars	Logical scalar. When there are several data groups, draw the histogram-type plots as stacked barplots or grouped side by side.
stats	Function. Parameter controlling the boxplot appearance. See <code>panel.bwplot</code> for details.
transformation	Function. Applied to the data matrix prior to plotting or when calling the <code>score</code> method. The function should accept exactly one input argument and its return value needs to be a numeric vector which can be coerced back into a data matrix of identical dimensionality as the input data.
type	Character vector. The plot type, one or several in <code>c("p", "l", "b", "a", "s", "g", "r", "S", "smooth", "histogram", "mountain", "h", "boxplot", "gradient", "heatmap")</code> . See 'Details' section in <i>DataTrack</i> for more information on the individual plotting types.
v	Integer scalar. Parameter controlling the number of vertical grid lines, see <code>panel.grid</code> for details.
varwidth	Logical scalar. Parameter controlling the boxplot appearance. See <code>panel.bwplot</code> for details.
window	Numeric or character scalar. Aggregate the rows values of the data matrix to <code>window</code> equally sized slices on the data range using the method defined in <code>aggregation</code> . If negative, apply a running window of size <code>windowSize</code> using the same aggregation method. Alternatively, the special value <code>auto</code> causes the function to determine the optimal window size to avoid overplotting.
windowSize	Numeric scalar. The size of the running window when the value of <code>window</code> is negative.
ylim	Numeric vector of length 2. The range of the y-axis scale.

4.4 AnnotationTrack

AnnotationTrack objects are the multi-purpose tracks in the *Gviz* package. Essentially they consist of one or several genomic ranges that can be grouped into composite annotation elements if needed. In principle this would be enough to represent everything from CpG islands to complex gene models, however for the latter the package defines the specialized *GeneRegionTrack* class, which will be highlighted in a separate section. Most of the features discussed here will also apply to *GeneRegionTrack* objects, though. As a matter of fact, the *GeneRegionTrack* class inherits directly from class *AnnotationTrack*.

AnnotationTrack objects are easily instantiated using the constructor function of the same name. The necessary building blocks are the range coordinates, a chromosome and a genome identifier. Again we try to be flexible in the way this information can be passed to the function, either in the form of separate function arguments, as *IRanges* or *GRanges* objects. Optionally, we can pass in the strand information for the annotation features and some useful identifiers. For the full details on the constructor function and the accepted arguments see `?AnnotationTrack`.

```
> aTrack <- AnnotationTrack(start = c(10, 40, 120),
+   width = 15, chromosome = "chrX", strand = c("+",
+   "*", "-"), id = c("Huey", "Dewey", "Louie"),
+   genome = "hg19", name = "foo")
> plotTracks(aTrack)
```



The ranges are plotted as simple boxes if no strand information is available, or as arrows to indicate their direction. We can change the range item shapes by setting the *shape* display parameter. It can also be helpful to add the names for the individual features to the plot. This can be achieved by setting the *showFeatureId* parameter to `TRUE`

```
> plotTracks(aTrack, shape = "box", showFeatureId = TRUE)
```



```
> plotTracks(aTrack, shape = "ellipse", showFeatureId = TRUE,
+   fontcolor = "darkblue")
```



In this very simplistic example each annotation feature consisted of a single range. In real life the genomic annotation features that we encounter often consists of several sub-units. We can create such composite *AnnotationTrack* objects by providing a grouping factor to the constructor. It needs to be of similar length as the total number of atomic features in the track, i.e, the number of genomic ranges that are passed to the constructor. The levels of this factor will be used as internal identifiers for the individual composite feature groups, and we can toggle on their printing by setting *showId* to `TRUE`.

```
> aTrack.groups <- AnnotationTrack(start = c(50, 180,
+   260, 460, 860, 1240), width = c(15, 20, 40, 100,
```

```
+ 200, 20), chromosome = "chrX", strand = rep(c("+",
+ "*", "-"), c(1, 3, 2)), group = rep(c("Huey",
+ "Dewey", "Louie"), c(1, 3, 2)), genome = "hg19",
+ name = "foo")
> plotTracks(aTrack.groups, showId = TRUE)
```



Arranging items on the plotting canvas is relatively straight forward as long as there are no overlaps between individual regions or groups of regions. A logical solution to this problem is to stack overlapping items in separate horizontal lines, thus extending the height of the track to accommodate all of them. This involves some optimization, and the Gviz package automatically tries to come up with the most compact arrangement. Let's exemplify this feature with a slightly modified *AnnotationTrack* object.

```
> aTrack.stacked <- AnnotationTrack(start = c(50, 180,
+ 260, 800, 600, 1240), width = c(15, 20, 40, 100,
+ 500, 20), chromosome = "chrX", strand = "*",
+ group = rep(c("Huey", "Dewey", "Louie"), c(1,
+ 3, 2)), genome = "hg19", name = "foo")
> plotTracks(aTrack.stacked, showId = TRUE)
```



We now have our three annotation feature groups distributed over two horizontal lines. One can control the stacking of overlapping items using the *stacking* display parameter. Currently the three values **squish**, **dense** and **hide** are supported. Horizontal stacking is enabled via the **squish** option, which also is the default. **dense** forces overlapping items to be joined in one meta-item and **hide** all together disables the plotting of *AnnotationTrack* items. Please note that adding identifiers to the plot only works for the **squish** option.

```
> plotTracks(aTrack.stacked, stacking = "dense")
```



In addition to annotation groups there is also the notion of a feature type in the Gviz package. Feature types are simply different types of annotation regions (e.g., mRNA transcripts, miRNAs, rRNAs, etc.) that are indicated by different colors. There is no limit on the number of different features, however each element in a grouped annotation item needs to be of the same feature type. We can query and set features using the **feature** and **feature<-** methods.

```
> feature(aTrack.stacked)

[1] "unknown" "unknown" "unknown" "unknown" "unknown" "unknown"

> feature(aTrack.stacked)[1:4] <- c("foo", "bar", "bar",
+ "bar")
```

Unless we tell the **Gviz** package how to deal with the respective feature types they will all be treated similar, i.e., they will be plotted using the default color as defined by the *fill* display paramter. To define colors for individual feature types we simply have to add them as additional display parameters, where the parameter name matches to the feature type and its value is supposed to be a valid R color qualifier. Of course this implies that we can only use type names that are not already taken by other display parameters defined in the package.

```
> plotTracks(aTrack.stacked, showId = TRUE, foo = "darkred",
+           bar = "darkgreen")
```



Stacking of annotation items to avoid overplotting only works as long as there is enough real estate on the plotting canvas to separate all items, i.e., we need all items to be at least a single pixel wide to correctly display them. This limitation is automatically enforced by the **Gviz** package, however it implies that unless neighbouring items are more than one pixel appart we can not distinguish between them and will inevitably introduce a certain amount of overplotting. This means that on a common screen device we can only look at a very limited genomic region of a few kb in full resolution. Given that an average chromosome is in the order of a few gb, we still need a reasonable way to deal with the overplotting problem despite the item stacking functionality. As default, the **Gviz** package will merge all overlapping items into one unified meta-item and only plot that (see 'Collapse' section below for details). In order to indicate the amount of overplotting that was introduced by this process we can use the *showOverplotting* display parameter. It uses a color scale (based on the orginal colors defined for the track), with lighter colors indicating areas of low or no overplotting, and more saturated colors indicating areas of high overplotting density. We exemplify this feature on an *AnnotationTrack* object that represents a good portion of a real human chromosome.

```
> data("denseAnnTrack")
> plotTracks(denseAnnTrack, showOverplotting = TRUE)
```



Collapsing

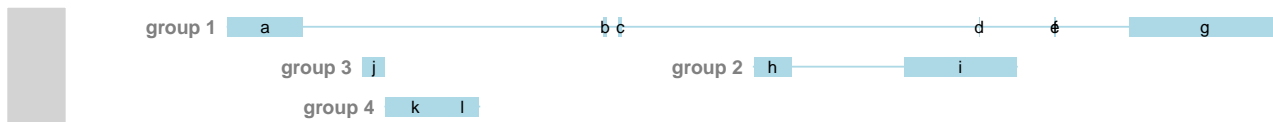
All track types that inherit from class **AnnotationTrack** support the collapsing of overlapping track items, either because they have initially been defined as overlapping coordinates, or because the current device resolution does not allow to sufficiently separate them. For instance, two elements of a feature group may be separated by 100 base pairs on the genomic scale, however when plotted to the screen, those 100 base pairs translate to a distance of less than one pixel. In this case we can no longer show the items as two separate entitites. One solution to this problem would be to allow for arbitrary overplotting, in which case the last one of the overlapping items that is drawn on the device wins. This is not optimal in many ways, and it also poses a significant burden on the graphical engine because a lot of stuff has to be drawn which no one will ever see.

To this end the **Gviz** package provides an infrastructure to reasonably collapse overlappig items, thereby adjusting the information content that can be shown to the available device resolution. By default this feature is turned on, and the user does not have to worry too much about it. However, one should be aware of the

consequences this may have on a given visualization. If you absolutely do not want collapsing to take place, you may completely turn it off by setting the display parameter `collapse` to `FALSE`. Please note that by doing this the `showOverplotting` parameter will also stop working. If you opt in, there is some considerable amount of detailed control to fine tune the collapsing to your needs.

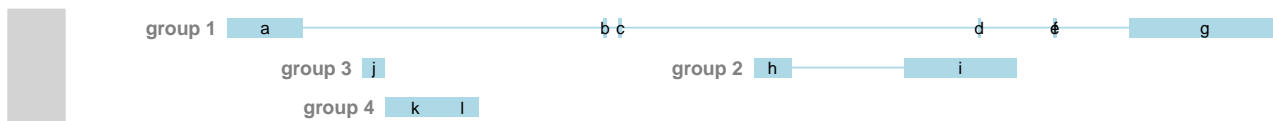
Lets start with a small example track for which element collapsing has been turned off and no adjustments to the ranges have been made. We plot both the item identifiers and the group identifiers to exemplify what is going on.

```
> data(collapseTrack)
> plotTracks(ctrack, extend.left = 1800)
```



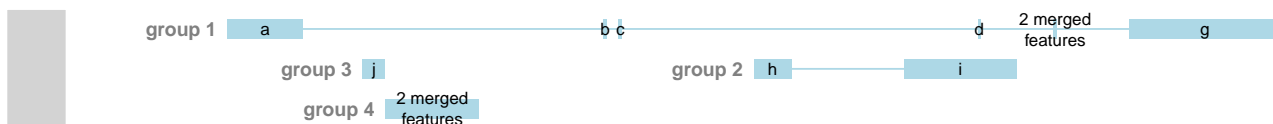
The first thing to notice is that the for item d we do see the item identifier but not the range itself. This is due to the fact that the with of the item is smaller than a single pixel, and hence the graphics system can not display it. There are also the two items e and f which seem to overlay each other completely, and another two items which appear to be one joined item (k and l). Again, this is a resolution issue as their relative distance is smaller than a single pixel, so all we see is a single range and some ugly overplotted identifiers. We can control the first issue by setting the minimum pixel width of a plotted item to be one pixel using the `min.width` display parameter.

```
> plotTracks(ctrack, extend.left = 1800, min.width = 1)
```



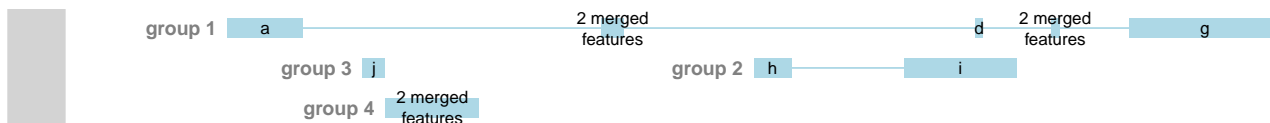
Now the item d has a plotable size and can be drawn to the device. The overplotted items are still rather annoying, but the only way to get rid of those is to turn item collapsing back on.

```
> plotTracks(ctrack, extend.left = 1800, min.width = 1,
+           collapse = TRUE)
```



Now all items that could not be separated by at least one pixel have been merged into a single meta-item, and the software has taken care of the identifiers for you, too. The merging operation is aware of the grouping information, so no two groups were joint together. Sometimes a single pixel width or a single pixel distance is not enough to get a good visualization. In these cases one could decide to enforce even larger values. We can do this not only for the minimum width, but also for the minimum distance by setting the `min.distance` parameter.

```
> plotTracks(ctrack, extend.left = 1800, min.width = 3,
+           min.distance = 5, collapse = TRUE)
```



This time also the two items *b* and *c* have been merged, and all ranges are now at least 3 pixels wide. Depending on the density of items on the plot even this reduction can be insufficient. Because we did not merge complete groups we might still end up with quite a lot of stacks to accomodate all the information. To this end the display parameter `mergeGroups` can be used to disable absolute group separation. Rather than blindly merging all groups (as it is done when `stacking='dense'`) however, the software will only join those overlapping group ranges for which all items are already merged into a single meta item.

```
> plotTracks(ctrack, extend.left = 1800, min.width = 3,
+           min.distance = 5, collapse = TRUE, mergeGroups = TRUE)
```



Display parameters for AnnotationTrack objects

For a complete listing of all the available display parameters please see the table below or the man page of the *AnnotationTrack* class by typing in `?AnnotationTrack` on the R command line.

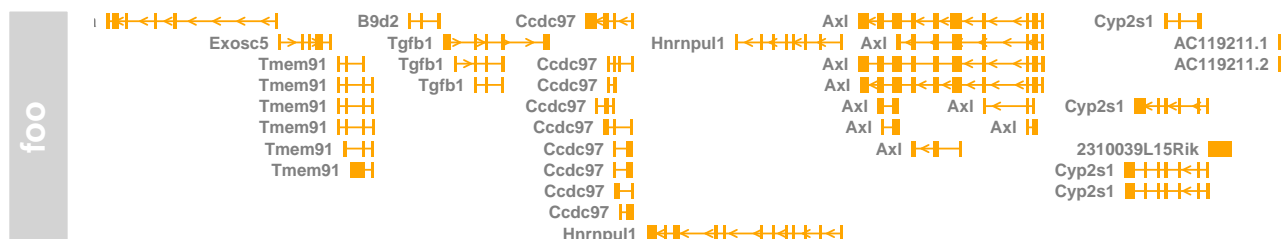
Display Parameter	Description
<code>alpha</code>	Numeric scalar between 0 and 1. The opacity of the plotting elements, if supported by the device.
<code>cex</code>	Numeric scalar. The font expansion factor for item identifiers.
<code>cex.group</code>	Numeric scalar. The font expansion factor for the group-level annotation.
<code>col</code>	Character or integer scalar. The border color for all track items.
<code>fill</code>	Character or integer scalar. The fill color for untyped items. This is also used to connect grouped items. See grouping for details.
<code>fontcolor</code>	Character or integer scalar. The font color for item identifiers.
<code>fontcolor.group</code>	Character or integer scalar. The font color for the group-level annotation.
<code>fontface</code>	Integer scalar. The font face for item identifiers.
<code>fontface.group</code>	Numeric scalar. The font face for the group-level annotation.
<code>fontfamily</code>	Character scalar. The font family for item identifiers.
<code>fontfamily.group</code>	Character scalar. The font family for the group-level annotation.
<code>fontsize</code>	Numeric scalar. The font size for item identifiers.
<code>fontsize.group</code>	Numeric scalar. The font size for the group-level annotation.
<code>lex</code>	Numeric scalar. The line expansion factor for all track items. This is also used to connect grouped items. See grouping for details.
<code>lineheight</code>	Numeric scalar. The font line height for item identifiers.
<code>lty</code>	Character or integer scalar. The line type for all track items. This is also used to connect grouped items. See grouping for details.
<code>lwd</code>	Integer scalar. The line width for all track items. This is also used to connect grouped items. See grouping for details.
<code>mergeGroups</code>	Logical scalar. Merge fully overlapping groups if <code>collapse==TRUE</code> .

min.width	Numeric scalar. The minimum range width in pixels to display. All ranges are expanded to this size in order to avoid rendering issues. See <code>collapsing</code> for details.
rotation	Numeric scalar. The degree of text rotation for item identifiers.
shape	Character scalar. The shape in which to display the track items. Currently only <code>box</code> , <code>arrow</code> , <code>ellipse</code> , and <code>smallArrow</code> are implemented.
showFeatureId	Logical scalar. Control whether to plot the individual track item identifiers.
showId	Logical scalar. Control whether to annotate individual groups.
showOverplotting	Logical scalar. Use a color gradient to show the amount of overplotting for collapsed items. This implies that <code>collapse==TRUE</code>

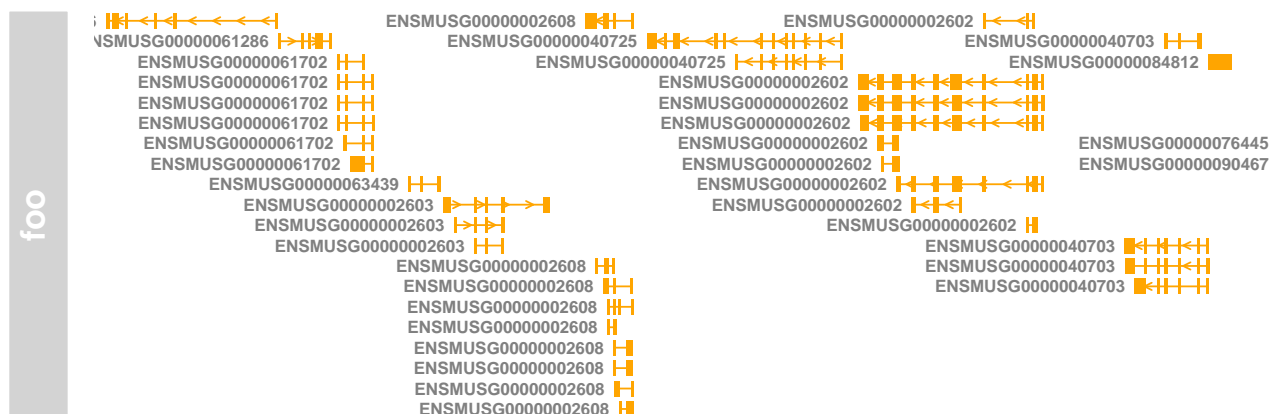
4.5 GeneRegionTrack

GeneRegionTrack objects are in principle very similar to *AnnotationTrack* objects. The only difference is that they are a little more gene/transcript centric, both in terms of plotting layout and user interaction, and that they define a global start and end position. The constructor function of the same name is a convenient tool to instantiate the object from a variety of different sources. In a nutshell we need to pass start and end positions (or the width) of each annotation feature in the track and also supply the exon, transcript and gene identifiers for each item which will be used to create the transcript groupings. For more details about the available options see the class's manual page (`?GeneRegionTrack`). There are a number of accessor methods that make it easy to query and replace for instance exon, transcript or gene assignments. There is also some support for gene aliases or gene symbols which are often times more useful than cryptic data base gene identifiers. The following code that re-uses the *GeneRegionTrack* object from the first section exemplifies some of these features.

```
> data(geneModels)
> grtrack <- GeneRegionTrack(geneModels, genome = gen,
+   chromosome = chr, name = "foo")
> head(gene(grtrack))
> head(transcript(grtrack))
> head(exon(grtrack))
> head(symbol(grtrack))
> plotTracks(grtrack, showId = TRUE)
```



```
> plotTracks(grtrack, showId = TRUE, geneSymbols = FALSE)
```

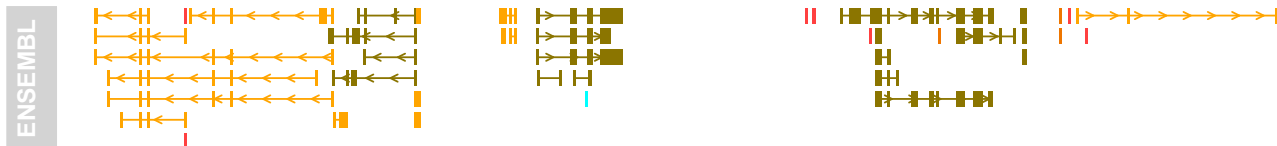


min.width	Numeric scalar. The minimum range width in pixels to display. All ranges are expanded to this size in order to avoid rendering issues. See <code>collapsing</code> for details.
rotation	Numeric scalar. The degree of text rotation for item identifiers.
shape	Character scalar. The shape in which to display the track items. Currently only <code>box</code> , <code>arrow</code> , <code>ellipse</code> , and <code>smallArrow</code> are implemented.
showExonId	Logical scalar. Control whether to plot the individual exon identifiers.
showId	Logical scalar. Control whether to annotate individual groups.
showOverplotting	Logical scalar. Use a color gradient to show the amount of overplotting for collapsed items. This implies that <code>collapse==TRUE</code>

4.6 BiomartGeneRegionTrack

It is often very useful to quickly download gene annotation information from an online repository rather than having to construct it each time from scratch. To this end, the `Gviz` package defines the *BiomartGeneRegionTrack* class, which directly extends *GeneRegionTrack* but provides a direct interface to the ENSEMBL Biomart service (yet another interface to the UCSC data base content is highlighted in the next section). Rather than providing all the bits and pieces for the full gene model, we just enter a genome, chromosome and a start and end position on this chromosome, and the constructor function `BiomartGeneRegionTrack` will automatically contact ENSEMBL, fetch the necessary information and build the gene model on the fly. Please note that you will need an internet connection for this to work, and that contacting Biomart can take a significant amount of time depending on usage and network traffic, and that the results are almost never going to be returned instantaneously.

```
> biomTrack <- BiomartGeneRegionTrack(genome = "hg19",
+   chromosome = chr, start = 2e+07, end = 2.1e+07,
+   name = "ENSEMBL")
> plotTracks(biomTrack)
```



Display parameters for BiomartGeneRegionTrack objects

For a complete listing of all the available display parameters please see the table above in the previous *GeneRegionTrack* section or the man page of the *BiomartGeneRegionTrack* class by typing in `?BiomartGeneRegionTrack` on the R command line.

One additional benefit when fetching the data through Biomart is that we also receive some information about the annotation feature types, which is automatically used for the color coding of the track. The following table shows the available feature types.

Display Parameter	Description	Color
C_segment	Character or integer scalar. Fill color for annotation objects of type 'C_segment'.	burlywood4
D_segment	Character or integer scalar. Fill color for annotation objects of type 'C_segment'.	lightblue

J_segment	Character or integer scalar. Fill color for annotation objects of type 'C_segment'.	dodgerblue2
Mt_rRNA	Character or integer scalar. Fill color for annotation objects of type 'Mt_rRNA'.	yellow
Mt_tRNA	Character or integer scalar. Fill color for annotation objects of type 'Mt_tRNA'.	darkgoldenrod
Mt_tRNA_pseudogene	Character or integer scalar. Fill color for annotation objects of type 'Mt_tRNA_pseudogene'.	darkgoldenrod1
V_segment	Character or integer scalar. Fill color for annotation objects of type 'V_segment'.	aquamarine
miRNA	Character or integer scalar. Fill color for annotation objects of type 'L_segment'.	cornflowerblue
miRNA_pseudogene	Character or integer scalar. Fill color for annotation objects of type 'miRNA_pseudogene'.	cornsilk
misc_RNA	Character or integer scalar. Fill color for annotation objects of type 'misc_RNA'.	cornsilk3
misc_RNA_pseudogene	Character or integer scalar. Fill color for annotation objects of type 'misc_RNA_pseudogene'.	cornsilk4
protein_coding	Character or integer scalar. Fill color for annotation objects of type 'protein_coding'.	gold4
pseudogene	Character or integer scalar. Fill color for annotation objects of type 'pseudogene'.	brown1
rRNA	Character or integer scalar. Fill color for annotation objects of type 'rRNA'.	darkolivegreen1
rRNA_pseudogene	Character or integer scalar. Fill color for annotation objects of type 'rRNA_pseudogene'.	darkolivegreen
retrotransposed	Character or integer scalar. Fill color for annotation objects of type 'retrotransposed'.	blueviolet
scRNA	Character or integer scalar. Fill color for annotation objects of type 'scRNA'.	darkorange
scRNA_pseudogene	Character or integer scalar. Fill color for annotation objects of type 'scRNA_pseudogene'.	darkorange2
snRNA	Character or integer scalar. Fill color for annotation objects of type 'snRNA'.	coral
snRNA_pseudogene	Character or integer scalar. Fill color for annotation objects of type 'snRNA_pseudogene'.	coral3
snoRNA	Character or integer scalar. Fill color for annotation objects of type 'snoRNA'.	cyan
snoRNA_pseudogene	Character or integer scalar. Fill color for annotation objects of type 'snoRNA_pseudogene'.	cyan2
tRNA_pseudogene	Character or integer scalar. Fill color for annotation objects of type 'tRNA_pseudogene'.	antiquewhite3

4.7 DetailsAnnotationTrack

It is sometimes desirable to add more detailed information to particular ranges in an *Gviz* plot for which the notion of genomic coordinates no longer makes sense. For instance, the ranges in an *AnnotationTrack* may represent probe locations on a genome, and for each of these probes a number of measurements from multiple

samples and from different sample groups are available. To this end, the *DetailsAnnotationTrack* provides a flexible interface to further annotate genomic regions with arbitrary additional information. This is achieved by splitting the *AnnotationTrack* plotting region into two horizontal sections: the lower section containing the range data in genomic coordinates, and the upper one containing the additional data for each of the displayed ranges in vertically tiled panels of equal size. The connection between a range item and its details panel is indicated by connecting lines.

The content of the individual details panels has to be filled in by a user-defined plotting function that uses grid (or lattice) plotting commands. This function has to accept a number of mandatory parameters, notably the start, end, strand, chromosome and identifier information for the genomic range, as well as an integer counter indicating the index of the currently plotted details tile. This information can be used to fetch arbitrary details, e.g. from a list, and environment or even from a *GRanges* object which will then be processed and visualized within the plotting function. This may sound rather abstract, and for more details please refer to the class' help page. For now we just want to demonstrate the functionality in a simple little example. We begin by defining a *GRanges* object containing 4 genomic locations. In our example those are considered to be probe locations from a methylation array.

```
> library(GenomicRanges)
> probes <- GRanges(seqnames = "chr7", ranges = IRanges(start = c(2e+06,
+ 2070000, 2100000, 2160000), end = c(2050000,
+ 2130000, 2150000, 2170000)), strand = c("-",
+ "+", "-", "-"))
```

For each of these probes we have methylation measurements from a large number of different samples in a numeric matrix, and within the samples there are two treatment groups. The aim is to compare the distribution of measurement values between these two groups at each probe locus.

```
> methylation <- matrix(c(rgamma(400, 1)), ncol = 100,
+ dimnames = list(paste("probe", 1:4, sep = ""),
+ NULL))
> methylation[, 51:100] <- methylation[, 51:100] +
+ 0:3
> sgroups <- rep(c("grp1", "grp2"), each = 50)
```

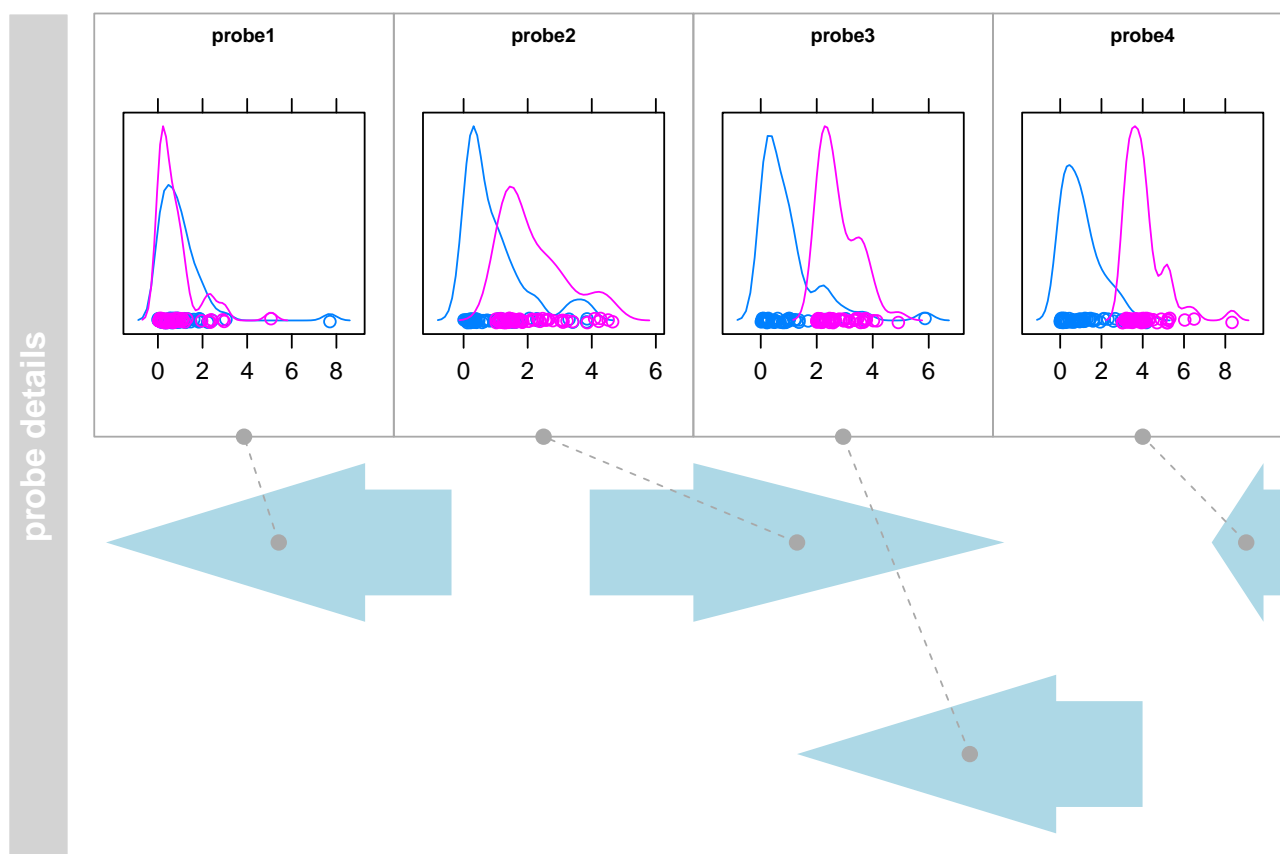
Of course we could use a *DataTrack* with the box-plot representation for this task, however we do have strand-specific data here and some of the probes can be overlapping, so all this information would be lost. We are also interested in the particular shape of the data distribution, so a density plot representation is what we really need. Luckily, the *lattice* package gives us a nice **densityplot** function that supports grouping, so all that's left to do now is to write a little wrapper that handles the extraction of the relevant data from the matrix. This is easily achieved by using the range identifiers, which conveniently map to the row names of the data matrix.

```
> library(lattice)
> details <- function(identifier, ...) {
+   d <- data.frame(signal = methylation[identifier,
+ ], group = sgroups)
+   print(densityplot(~signal, group = group, data = d,
+ main = list(label = identifier, cex = 0.7),
+ scales = list(draw = FALSE, x = list(draw = TRUE)),
+ ylab = "", xlab = "", ), newpage = FALSE,
```

```
+       prefix = "plot")
+ }
```

Finally, it is as simple as calling the *AnnotationTrack* constructor, passing along the wrapper function and calling *plotTracks*.

```
> deTrack <- AnnotationTrack(range = probes, genome = "hg19",
+   chromosome = 7, id = rownames(methylation), name = "probe details",
+   stacking = "squish", fun = details)
> plotTracks(deTrack)
```



It should be noted here that in our little example we rely on the methylation data matrix and the grouping vector to be present in the working environment. This is not necessarily the cleanest solution and one should consider storing additional data in an environment, passing it along using the *detailFunArgs* parameter, or making it part of the details function in form of a closure. The class' help page provides further instructions.

Another use case for the *DetailsAnnotationTrack* class is to deal with the problem of very different feature sizes within a single track. For instance, we may be looking at a rather large genomic region containing one big transcript with many widely spaced exons and a bunch of smaller, more compact transcripts. In this case it would be helpful to provide a zoomed in version of those smaller transcripts. In order to achieve this we can make use of the class' *groupDetails* display parameter, which applies the detail plotting function over each range group rather than over individual range items. First we define a function that selects those groups with a plotted size smaller than 10 pixels. We make use of the unexported function *.pxResolution* here to come up with the mapping between pixel coordinates and genomic coordinates.


```

> selFun <- function(identifier, start, end, track,
+   GdObject, ...) {
+   gcount <- table(group(GdObject))
+   pxRange <- Gviz:::pxResolution(min.width = 20,
+     coord = "x")
+   return((end - start) < pxRange && gcount[identifier] ==
+     1)
+ }

```

The actual detail plotting function is fairly trivial. In the details viewport we simply call `plotTracks` function on the subset of items from each group that has been selected before without plotting the track titles, and also add a scale indicator for some reference. It is worth mentioning however that we need to extract the ranges of the zoomed in track items from the unmodified track object (the `Gdobject.original` argument in the details function) because the object that is plotted in the lower panel contains only the collapsed ranges.

```

> detFun <- function(identifier, GdObject.original,
+   ...) {
+   plotTracks(list(GenomeAxisTrack(scale = 0.3,
+     labelPos = "below", size = 0.2, cex = 0.7),
+     GdObject.original[group(GdObject.original) ==
+       identifier]), add = TRUE, showTitle = FALSE)
+ }

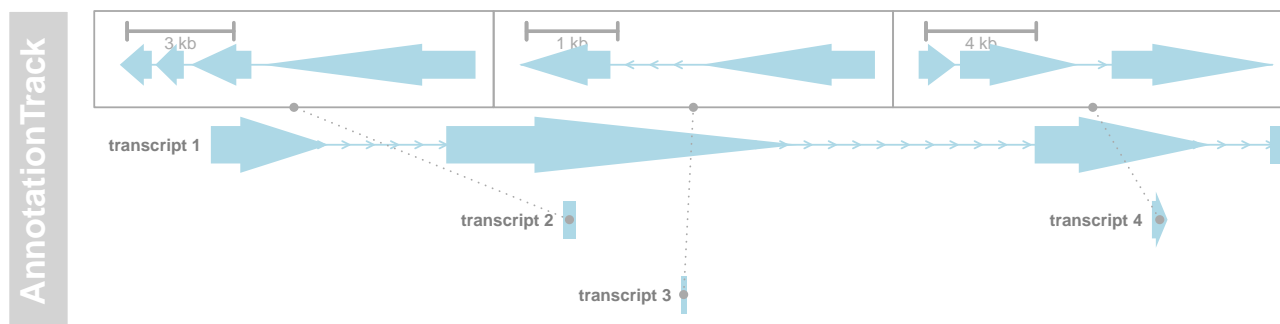
```

Finally, we load some sample data, turn it into a `DetailsAnnotationTrack` object and plot it.

```

> data(geneDetails)
> deTrack2 <- AnnotationTrack(range = geneDetails,
+   chromosome = chr, genome = gen, fun = detFun,
+   selectFun = selFun, groupDetails = TRUE, details.size = 0.3,
+   detailsConnector.cex = 0.5, detailsConnector.lty = "dotted",
+   shape = c("smallArrow", "arrow"), showId = TRUE)
> plotTracks(deTrack2, extend.left = 90000)

```

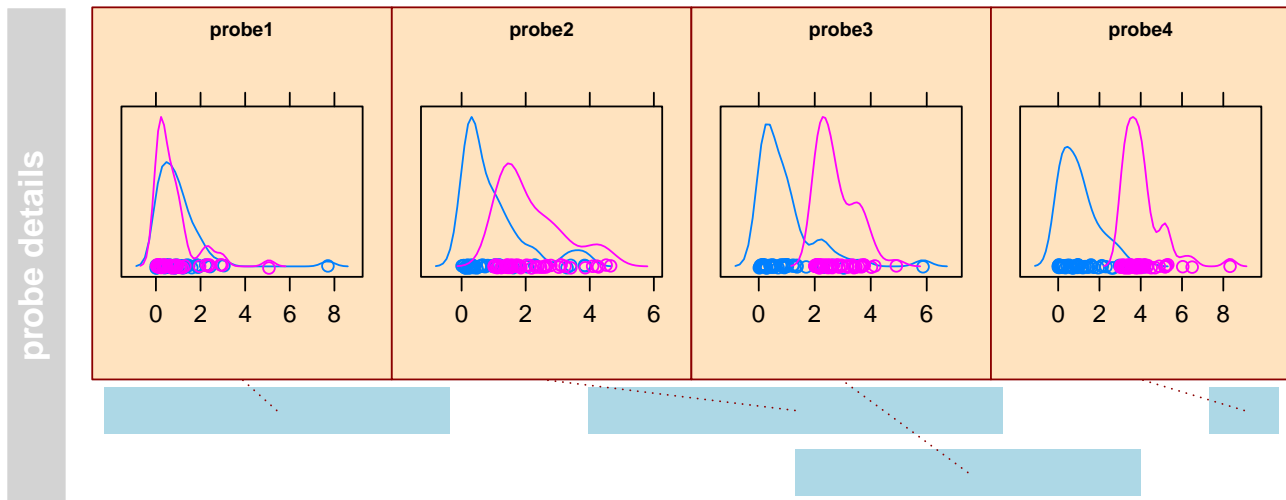


Display parameters for DetailsAnnotationTrack objects

In addition to the display parameters for the *AnnotationTrack* class, some additional parameters can be used to control the look and feel of the details sections. For a complete listing of all the available display

parameters please see the tables below and the one above in the *AnnotationTrack* section or the man page of the *DetailsAnnotationTrack* class by typing in `?DetailsAnnotationTrack` on the R command line.

```
> plotTracks(deTrack, details.size = 0.75, detailsConnector.pch = NA,
+   detailsConnector.col = "darkred", detailsBorder.fill = "#FFE3BF",
+   detailsBorder.col = "darkred", shape = "box",
+   detailsConnector.lty = "dotted")
```



Display Parameter	Description
<code>details.minWidth</code>	Numeric scalar. The minimum width in pixels for a details panel, if less space is available no details are plotted.
<code>details.ratio</code>	Numeric scalar. By default, the plotting method tries to fill all available space of the details panel tiles. Depending on the dimensions of your plot and the number of tiles this may lead to fairly stretched plots. Restricting the ratio of width over height can help to fine tune for somewhat more sane graphics in these cases. Essentially this adds some white space in between individual tiles to force the desired ratio. Together with the <code>size</code> and <code>details.size</code> arguments, which control the vertical extension of the whole track and of the details section, this allows for some fairly generic resizing of the tiles.
<code>details.size</code>	Numeric scalar. The fraction of vertical space of the track used for the details section.
<code>detailsBorder.col</code>	Character or integer scalar. Line color of the border.
<code>detailsBorder.fill</code>	Character or integer scalar. Background color of the border.
<code>detailsBorder.lty</code>	Character or integer scalar. Line type of the border around each details panel.
<code>detailsBorder.lwd</code>	Integer scalar. Line width of the border.
<code>detailsConnector.cex</code>	Numeric scalar. Relative size of the connector's end points.
<code>detailsConnector.col</code>	Character or integer scalar. Color of the line connecting the <code>AnnotationTrack</code> item with its details panel.
<code>detailsConnector.lty</code>	Character or integer scalar. Type of connecting line.
<code>detailsConnector.lwd</code>	Integer scalar. Line width of the connector.
<code>detailsConnector.pch</code>	Integer scalar. Type of the connector's ends.

detailsFunArgs	List. Additional arguments that get passed on the the details plotting function.
groupDetails	Logial scalar. Plot details for feature groups rather than for individual features.

4.8 Creating tracks from UCSC data

The UCSC data bases contain a multitude of genome annotation data for dozens of different organisms. Some of those data are very simple annotations like CpG island locations or SNP locations. Others are more complicated gene models, or even numeric annotations like conservation information. In order to provide a unified interface to all this information, the Gviz package defines a meta-constructor function `UcscTrack`. The idea here is that we can express all of the available UcsC data in one of the package's track types. We use the functionality provided in the `rtracklayer` package to connect to UCSC and to download the relevant information. As a little illustrative example, let's reproduce a view from the famous UCSC genome browser using the Gviz package. As a final result we want to show something similar to Figure 4.8.

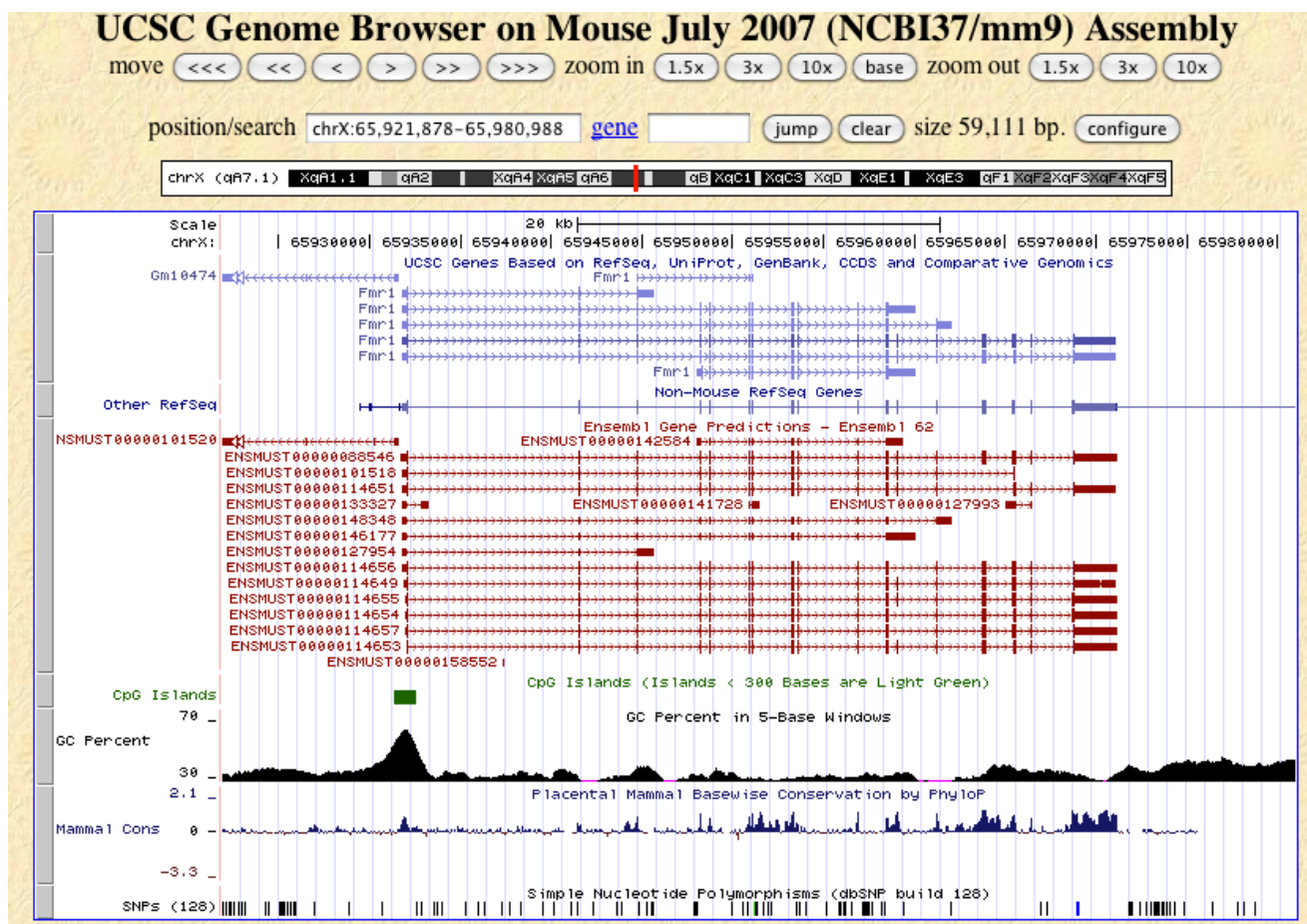


Figure 1: A screen shot of a UCSC genome browser view around the FMR1 locus on the mouse chromosome.

To start we first need to know about the available data in the UCSC data base and about their structure. A good way to do this is to use the table browser on the UCSC web site (<http://genome.ucsc.edu/cgi-bin/hgTables?command=start>). Figure ?? shows the table structure for the first gene model track, the known UCSC genes, in the table browser. We can see that there are multiple fields, some with genomic locations,

other with additional data like labels or identifiers. If we go back to the section about the *GeneRegionTrack* class we remember that we need exactly this type of information for the constructor function. So in order to take the UCSC data and build an object of class *GeneRegionTrack* we need a way to map them to the individual constructor arguments. This is exactly what the *UcscTrack* meta-constructor is supposed to do for us.

Schema for UCSC Genes - UCSC Genes Based on RefSeq, UniProt, GenBank, CCDS and Comparative Genomics				
Database: mm9 Primary Table: knownGene Row Count: 55,419				
Format description: Genes based on RefSeq, GenBank, and UniProt.				
field	example	SQL type	info	description
name	uc007aet.1	varchar(255)	values	Name of gene
chrom	chr1	varchar(255)	values	Reference sequence chromosome or scaffold
strand	-	char(1)	values	+ or - for strand
txStart	3195984	int(10) unsigned	range	Transcription start position
txEnd	3205713	int(10) unsigned	range	Transcription end position
cdsStart	3195984	int(10) unsigned	range	Coding region start
cdsEnd	3195984	int(10) unsigned	range	Coding region end
exonCount	2	int(10) unsigned	range	Number of exons
exonStarts	3195984,3203519	longblob		Exon start positions
exonEnds	3197398,3205713	longblob		Exon end positions
proteinID		varchar(40)	values	UniProt display ID for Known Genes, UniProt accession or RefSeq protein ID for UCSC Genes
alignID	uc007aet.1	varchar(255)	values	Unique identifier for each (known gene, alignment position) pair

Figure 2: A screen shot of a UCSC table browser view on the UCSC Known Genes track.

It needs to know about the track for which to extract the data (and optionally one or several of the tables that make up the collective track data, see *?UcscTrack* for details), about the genomic range including the chromosome for which to extract data, about the type of *Gviz* track that we want to translate this data into, and about the individual track columns and their counterparts in the respective track class constructor. In our example, the track is called *knownGene*, the track type to construct is *GeneRegionTrack*, and the relevant columns are *exonStarts*, *exonEnds*, *name* and *strand*, which we will use as the start and end coordinates of the ranges and for all the exon, transcript and gene identifiers. Here we make use of the high flexibility of the *GeneRegionTrack* constructor in the sense that the exon coordinates actually come in the form of a comma-separated list, combining all the information for one transcript in one row of the table. The function is smart enough to detect this and to split the annotation regions accordingly. The full function call to create the *GeneRegionTrack* from the UCSC data looks like this:

```
> from <- 65921878
> to <- 65980988
> knownGenes <- UcscTrack(genome = "mm9", chromosome = "chrX",
+   track = "knownGene", from = from, to = to, trackType = "GeneRegionTrack",
+   rstarts = "exonStarts", rends = "exonEnds", gene = "name",
+   symbol = "name", transcript = "name", strand = "strand",
+   fill = "#8282d2", name = "UCSC Genes")
```

With a similar approach we can construct the next two gene model tracks based on the *xenoRefGene* and *ensGene* data tables.

```
> refGenes <- UcscTrack(genome = "mm9", chromosome = "chrX",
+   track = "xenoRefGene", from = from, to = to,
+   trackType = "GeneRegionTrack", rstarts = "exonStarts",
+   rends = "exonEnds", gene = "name", symbol = "name2",
```

```

+     transcript = "name", strand = "strand", fill = "#8282d2",
+     stacking = "dense", name = "Other RefSeq")
> ensGenes <- UcscTrack(genome = "mm9", chromosome = "chrX",
+     track = "ensGene", from = from, to = to, trackType = "GeneRegionTrack",
+     rstarts = "exonStarts", rends = "exonEnds", gene = "name",
+     symbol = "name2", transcript = "name", strand = "strand",
+     fill = "#960000", name = "Ensembl Genes")

```

The CpG and SNP tracks are slightly different since a *GeneRegionTrack* representation would not be particularly useful. Instead, we can use *AnnotationTrack* objects as containers. The overall process using the *UcscTrack* meta-constructor remains the same.

```

> cpgIslands <- UcscTrack(genome = "mm9", chromosome = "chrX",
+     track = "cpgIslandExt", from = from, to = to,
+     trackType = "AnnotationTrack", start = "chromStart",
+     end = "chromEnd", id = "name", shape = "box",
+     fill = "#006400", name = "CpG Islands")
> snpLocations <- UcscTrack(genome = "mm9", chromosome = "chrX",
+     track = "snp128", from = from, to = to, trackType = "AnnotationTrack",
+     start = "chromStart", end = "chromEnd", id = "name",
+     feature = "func", strand = "strand", shape = "box",
+     stacking = "dense", fill = "black", name = "SNPs")

```

Most of UCSC's *DataTrack*-like tracks are a little more complex and represent a collection of several sub-tracks, with data originating from multiple tables. To make sure that we get the correct information we have to be a little bit more specific here and also define the particular table on the UCSC data base to use.

```

> conservation <- UcscTrack(genome = "mm9", chromosome = "chrX",
+     track = "Conservation", table = "phyloP30wayPlacental",
+     from = from, to = to, trackType = "DataTrack",
+     start = "start", end = "end", data = "score",
+     type = "hist", window = "auto", col.histogram = "darkblue",
+     fill.histogram = "darkblue", ylim = c(-3.7, 4),
+     name = "Conservation")
> gcContent <- UcscTrack(genome = "mm9", chromosome = "chrX",
+     track = "GC Percent", table = "gc5Base", from = from,
+     to = to, trackType = "DataTrack", start = "start",
+     end = "end", data = "score", type = "hist", window = -1,
+     windowSize = 1500, fill.histogram = "black",
+     col.histogram = "black", ylim = c(30, 70), name = "GC Percent")

```

To add some reference points we also need a genome axis and an *IdeogramTrack* of the x chromosome.

```

> axTrack <- GenomeAxisTrack()
> idxTrack <- IdeogramTrack(genome = "mm9", chromosome = "chrX")

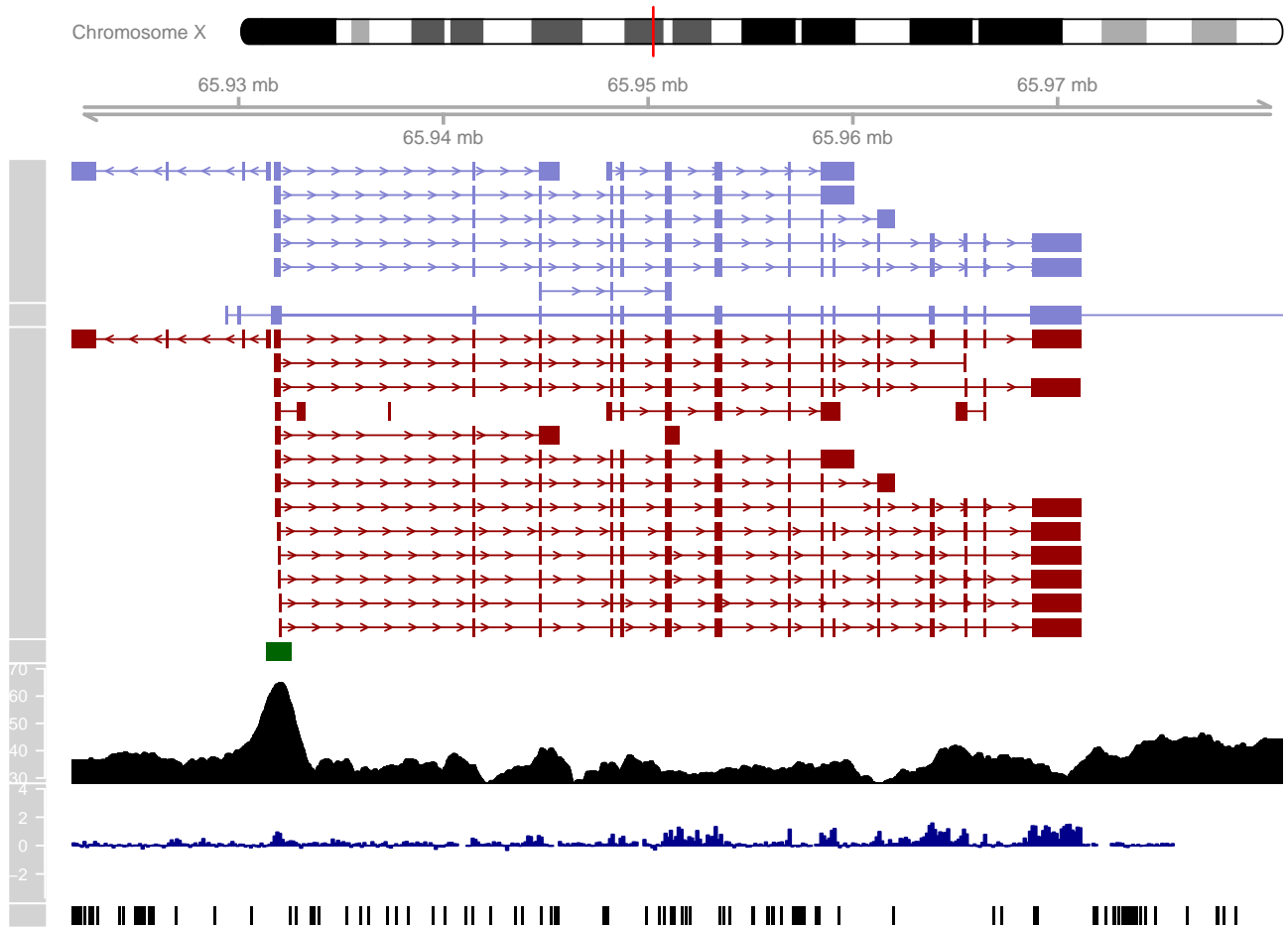
```

And finally we can plot all of our tracks.

```

> plotTracks(list(idxTrack, axTrack, knownGenes, refGenes,
+     ensGenes, cpgIslands, gcContent, conservation,
+     snpLocations), from = from, to = to, showTitle = FALSE)

```



5 Composite plots for multiple chromosomes

As mentioned in the introduction section, a set of Gviz tracks has to share the same chromosome when plotted, i.e., only a single chromosome can be active during a given plotting operation. Consequently, we can not directly create plots for multiple chromosomes in a single call to the `plotTracks` function. However, since the underlying graphical infrastructure of the Gviz package uses grid graphics, we can build our own composite plot using multiple consecutive `plotTracks` calls. All we need to take care of is an adequate layout structure to plot into, and we also need to tell `plotTracks` not to clear the graphics device before plotting, which can be achieved by setting the function's `add` argument to `FALSE`. For details on how to create a layout structure in the grid graphics system, please see the help page at `? grid.layout`).

We start by creating an *AnnotationTrack* objects and a *DataTrack* object which both contain data for several chromosomes.

```
> chroms <- c("chr1", "chr2", "chr3", "chr4")
> maTrack <- AnnotationTrack(range = GRanges(seqnames = chroms,
+   ranges = IRanges(start = 1, width = c(100, 400,
+   200, 1000))), strand = c("+", "+", "-", "+")),
+   genome = "mm9", chromosome = "chr1", name = "foo")
> mdTrack <- DataTrack(range = GRanges(seqnames = rep(chroms,
+   c(10, 40, 20, 100))), ranges = IRanges(start = c(seq(1,
```

```

+     100, len = 10), seq(1, 400, len = 40), seq(1,
+     200, len = 20), seq(1, 1000, len = 100)), width = 9),
+     values = runif(170)), data = "values", chromosome = "chr1",
+     genome = "mm9", name = "bar")

```

Now we also want a genome axis and an *IdeogramTrack* object to indicate the genomic context.

```

> mgTrack <- GenomeAxisTrack(scale = 0.5, labelPos = "below")
> chromosome(itrack) <- "chr1"

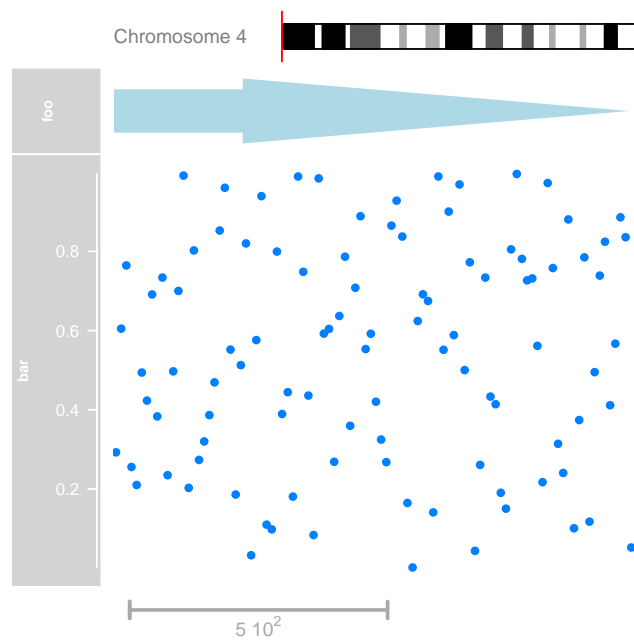
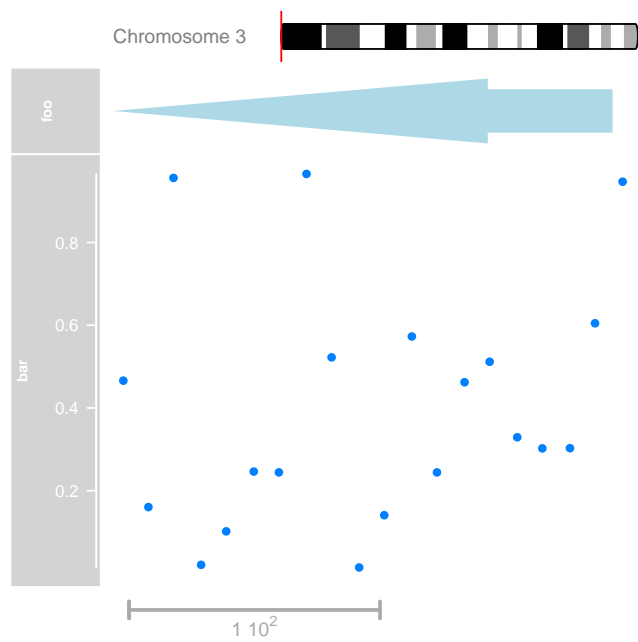
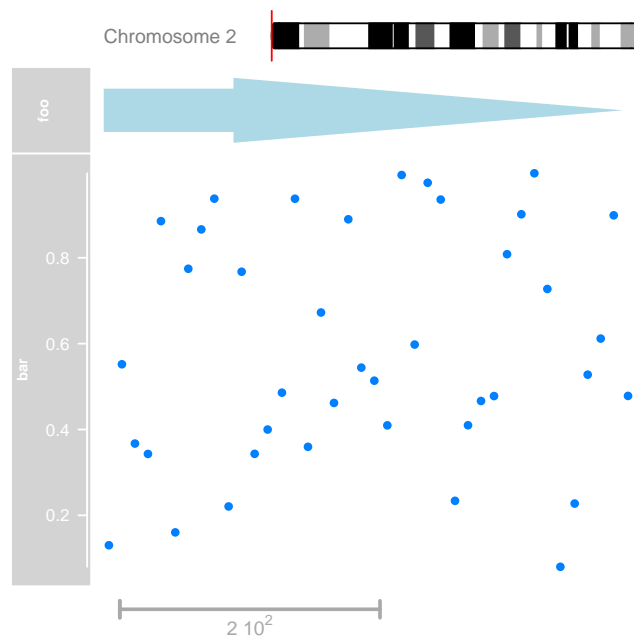
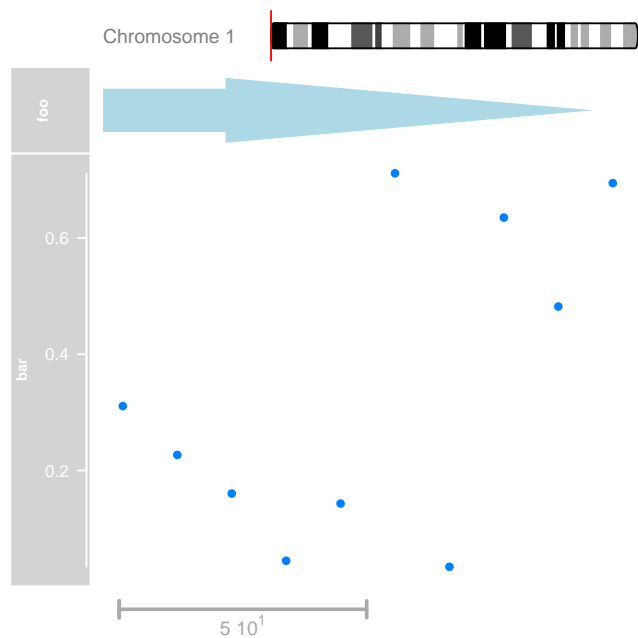
```

Finally, we build a layout in which the plots for each chromosome are placed in a rectangular grid and repeatedly call `plotTracks` for each chromosome.

```

> ncols <- 2
> nrows <- length(chroms)%/%ncols
> grid.newpage()
> pushViewport(viewport(layout = grid.layout(nrows,
+     ncols)))
> for (i in seq_along(chroms)) {
+   pushViewport(viewport(layout.pos.col = ((i -
+     1)%/%ncols) + 1, layout.pos.row = (((i) -
+     1)%/%ncols) + 1))
+   plotTracks(list(itrack, maTrack, mdTrack, mgTrack),
+     chromosome = chroms[i], add = TRUE)
+   popViewport(1)
+ }

```



SessionInfo

The following is the session info that generated this vignette:

```
> sessionInfo()

R version 2.15.0 (2012-03-30)
Platform: i386-apple-darwin9.8.0/i386 (32-bit)

locale:
[1] C

attached base packages:
[1] grid      stats      graphics  grDevices  utils      datasets
[7] methods   base

other attached packages:
[1] lattice_0.20-6      GenomicRanges_1.8.3 IRanges_1.14.2
[4] BiocGenerics_0.2.0  Gviz_1.0.1          xtable_1.7-0

loaded via a namespace (and not attached):
[1] AnnotationDbi_1.18.0 BSgenome_1.24.0
[3] Biobase_2.16.0      Biostrings_2.24.1
[5] DBI_0.2-5           RColorBrewer_1.0-5
[7] RCurl_1.91-1        RSQLite_0.11.1
[9] Rsamtools_1.8.4     XML_3.9-4
[11] biomaRt_2.12.0      bitops_1.0-4.1
[13] rtracklayer_1.16.1  stats4_2.15.0
[15] tools_2.15.0        zlibbioc_1.2.0
```