

# The lodplot Package

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**Type** Package

**Title** Plot a genome scan

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**Depends** R ( $\geq 0.99$ ), grid, graphics, stats

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**Description** Assorted plots of location score versus genetic map position

**License** GPL

**URL** <http://www.qimr.edu.au/davidD>

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`chrom.bands`*Dataset of human chromosomes and their banding patterns*

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### Description

Dataset used to produce human chromosomal ideograms for plotting purposes.

### Usage

```
data(chrom.bands)
```

### Format

A data frame with 4068 observations on the following 12 variables.

**chr** a character vector

**arm** a character vector

**band** a character vector

**ISCN.top** a numeric vector

**ISCN.bot** a numeric vector

**bases.top** a numeric vector

**bases.bot** a numeric vector

**stain** a character vector

**cM.top** a numeric vector

**cM.bot** a numeric vector

**n.markers** a numeric vector

**p.markers** a numeric vector

### Details

The original file gives only the physical map positions. The genetic map positions are interpolated from the Rutgers linkage map (Kong et al 2004).

### Source

[ftp://ftp.ncbi.nlm.nih.gov/genomes/H\\_sapiens/maps/mapview/BUILD.35.1/ideogram.gz](ftp://ftp.ncbi.nlm.nih.gov/genomes/H_sapiens/maps/mapview/BUILD.35.1/ideogram.gz).

### References

Kong X, Murphy K, Raj T, He C, White PS, Matise TC. 2004. A Combined Linkage-Physical Map of the Human Genome. *American Journal of Human Genetics*, 75(6):1143-8.

---

```
chromosome.viewlinkage
```

*Produce a viewport with the chromosome along the top and a pendant lod score plot*

---

## Description

Pretty plot of location score versus genetic map position on one (human) chromosome

## Usage

```
chromosome.viewlinkage(x, chrom, statistic = "lod", pheno.names = NULL,
  min.stat = 0, max.stat = 4, col = 1:6, lwd = 2, lty = 1,
  hpos = 0.85, width = 0.05, chromname.cex=1.5,
  units = "cM", bands = "major", xticdist=50,
  show.y.axis = FALSE, new = FALSE, ...)
```

## Arguments

<code>x</code>	is a data.frame containing variables <code>chr</code> (indicating the chromosome 1..X), <code>pos</code> (the map position, usually in cM), and the statistics to be plotted.
<code>chrom</code>	is the chromosome to be plotted.
<code>statistic</code>	is the vector of test statistics to be plotted, defaulting to "lod".
<code>pheno.names</code>	gives a long name for the statistics, defaulting to the statistic name.
<code>min.stat</code>	is the minimum plottable value of the statistic.
<code>max.stat</code>	is the maximum plottable value of the statistic.
<code>col</code>	is a vector of colours for the lod curve.
<code>lty</code>	is a vector of line types for the lod curve.
<code>lwd</code>	is a vector of line widths for the lod curve.
<code>chromname.cex</code>	is relative font size for the chromosome label.
<code>units</code>	are the map units, defaulting to "cM".
<code>hpos</code>	is the Y coordinate for the chromosome ideogram
<code>width</code>	is the width of the chromosome ideogram
<code>bands</code>	is which chromosomal bands to display on the ideogram.
<code>xticdist</code>	is the spacing of the X axis tickmarks, defaulting to 50.
<code>show.y.axis</code>	determines whether the Y axis should be shown.
<code>new</code>	indicates whether addition to existing plot.
<code>...</code>	are other graphical parameters to be passed to <code>plot.default</code> .

**Details**

Given a set of genetic location scores and chromosomal positions, `chromosome.viewlinkage` produces a plot for chromosome `chrom`. A chromosome ideogram is drawn at the top of the plot, with band locations expressed on the same scale as the map positions (cM).

**Value**

A grid graphical object.

**Author(s)**

David L Duffy

---

```
chromosome.viewsequence
```

*Produce a viewport with the chromosome along the top and a pendant lod score plot*

---

**Description**

Pretty plot of location score versus sequence map position on one (human) chromosome

**Usage**

```
chromosome.viewsequence(x, chrom, statistic = "lod", pheno.names = NULL,
  min.stat = 0, max.stat = 4, col = 1:6, lwd = 2, lty = 1,
  hpos = 0.85, width = 0.05, chromname.cex=1.5,
  units = "bp", bands = "major", xticdist=5e7,
  show.y.axis = FALSE, new = FALSE, ...)
```

**Arguments**

<code>x</code>	is a data.frame containing variables <code>chr</code> (indicating the chromosome 1..X), <code>pos</code> (the map position, in base pairs), and the statistics to be plotted.
<code>chrom</code>	is the chromosome to be plotted.
<code>statistic</code>	is the vector of test statistics to be plotted, defaulting to "lod".
<code>pheno.names</code>	gives a long name for the statistics, defaulting to the statistic name.
<code>min.stat</code>	is the minimum plottable value of the statistic.
<code>max.stat</code>	is the maximum plottable value of the statistic.
<code>col</code>	is a vector of colours for the lod curve.
<code>lty</code>	is a vector of line types for the lod curve.
<code>lwd</code>	is a vector of line widths for the lod curve.
<code>chromname.cex</code>	is relative font size for the chromosome label.

units	are the map units, defaulting to "bp".
hpos	is the Y coordinate for the chromosome ideogram
width	is the width of the chromosome ideogram
bands	is which chromosomal bands to display on the ideogram.
xticdist	is the spacing of the X axis tickmarks, defaulting to 5e7.
show.y.axis	determines whether the Y axis should be shown.
new	indicates whether addition to existing plot.
...	are other graphical parameters to be passed to plot.default.

### Details

Given a set of genetic location scores and chromosomal positions, `chromosome.viewsequence` produces a plot for chromosome `chrom`. A chromosome ideogram is drawn at the top of the plot, with band locations expressed on the same scale as the map positions (bp).

### Value

A grid graphical object.

### Author(s)

David L Duffy

---

`grid.semicircle`     *Draws a semicircle*

---

### Description

Using grid graphical commands, draws a semicircle (including the base).

### Usage

```
grid.semicircle(base.x, base.y, base.length, height = base.length,
  side = 1, orientation = NULL, col = NULL)
```

### Arguments

<code>base.x</code>	is X coordinate of base
<code>base.y</code>	is Y coordinate of base
<code>base.length</code>	is length of base of semicircle
<code>height</code>	is height of semicircle
<code>side</code>	is orientation of semicircle, one of four cardinal directions
<code>orientation</code>	is orientation, in degrees
<code>col</code>	is line colour used to draw the semicircle

**Details**

Draw a semicircle either oriented to the four cardinal points (side 1=below 2=left 3=above, 4=right), in which case `base.x` and `base.y` determine the bottom left point of base, or an angle, when `base.x` and `base.y` are the midpoint of the base.

**Value**

A grid graphical object.

**Author(s)**

David L Duffy

---

halfsibscan

*Simulation of affected half-sib pair genome scan*

---

**Description**

Generate results from an affected half-sib pair genome scan

**Usage**

```
halfsibscan(N = 100, grid = 1)
```

**Arguments**

<code>N</code>	is the number of affected half-sib pair families
<code>grid</code>	the distance between the (perfectly informative) scan markers

**Details**

Carried out the appropriate random walk on each chromosome to generate lod scores that would result if there were no trait loci segregating in the pedigrees sampled.

**Value**

A data frame, containing:

```
this-is-escaped-codenormal-bracket12bracket-normal
  the chromosome (1..22, X)
this-is-escaped-codenormal-bracket15bracket-normal
  the genetic map position on the chromosome
this-is-escaped-codenormal-bracket18bracket-normal
  the simulated lod score.
```

**Author(s)**

David L Duffy

**See Also**

plot.scan

**Examples**

```
#  
# Plot one simulated scan  
#  
plot.scan(halfsibscan(), with.X=TRUE)
```

---

my.xtics                      *Set tic length for axis in grid graphical plot*

---

**Description**

Sets the tic length for axis in grid graphical plot.

**Usage**

```
my.xtics(at, length = 0.5)
```

**Arguments**

at                      gives locations of tics  
length                  gives length of tics

**Details**

Simple wrapper for grid.segments.

**Value**

Grid graphical object.

**Author(s)**

David L Duffy

---

`paint.chromosome`     *Draw a chromosome ideogram*

---

### Description

Produce an ideogram of a specified human chromosome, using base graphics. Usually for addition to a plot of linkage analysis results, so the chromosome length is in genetic map units (usually cM).

### Usage

```
paint.chromosome(chrom, pos = 0, units = "cM", width = 0.4, bands = "major")
```

### Arguments

<code>chrom</code>	is the chromosome (1..X).
<code>pos</code>	is the Y position.
<code>units</code>	is the user X axis units, usually "cM" or "M".
<code>width</code>	is the width of the ideogram.
<code>bands</code>	is which chromosomal bands to display on the ideogram.

### Value

A base graphics plot.

### Author(s)

David L Duffy

---

`plot.scan`     *Plot results of a linkage genome scan*

---

### Description

Produces several types of plot of the lod score (or other test statistic) versus genetic map position (cM) on each of 22 human autosomal chromosomes along with the X chromosome if requested. Decorates with a chromosome ideogram if appropriate.

### Usage

```
plot.scan(x, type = "layout", statistic = "lod", with.X = TRUE,  
min.stat = 0, max.stat = 4, pheno.names = NULL, units = "cM",  
col = 1:6, lty = 1, lwd = 2, chromname.cex=0.9, ...)
```

**Arguments**

<code>x</code>	is a data.frame containing variables <code>chr</code> (indicating the chromosome 1..X), <code>pos</code> (the map position, usually in cM), and the statistics to be plotted.
<code>type</code>	is the type of plot: "layout", "linear", "overwrite", or "histogram", defaulting to "layout".
<code>statistic</code>	is the test statistic to be plotted, defaulting to "lod".
<code>with.X</code>	flags whether the X chromosome is to be included in the plot.
<code>min.stat</code>	is the minimum plottable value of the statistic.
<code>max.stat</code>	is the maximum plottable value of the statistic.
<code>pheno.names</code>	gives a long name for the statistics, defaulting to the statistic name.
<code>units</code>	are the map units, defaulting to "cM".
<code>col</code>	is a vector of colours for the lod curve.
<code>lty</code>	is a vector of line types for the lod curve.
<code>lwd</code>	is a vector of line widths for the lod curve.
<code>chromname.cex</code>	is the relative font size for the chromosome label.
<code>...</code>	are other graphical parameters to be passed to <code>plot.default</code> .

**Details**

Given a set of genetic location scores and chromosomal positions, `plot.scan` defaults to producing an array of plots ("layout"), one per chromosome, with each scaled to the chromosome length. A chromosome ideogram is drawn at the top of each plot, with band locations expressed on the same scale as the map positions (usually cM).

Alternatively, the "linear" option plots the entire genome on one graph, with divisions between the chromosomes. Chromosome ideograms are not added. The "overwrite" option overwrites the curves for each chromosome onto one graph, and the "histogram" option gives the distribution of lod scores over the entire sample.

The function uses the grid library. The ideogram band genetic map positions were interpolated from the physical positions of the bands estimated from the Build 35.1 human sequence for the NCBI Map Viewer.

**Value**

A grid type graphical object.

**Author(s)**

David L Duffy

**References**

Human chromosome ideograms. [ftp://ftp.ncbi.nlm.nih.gov/genomes/H\\_sapiens/maps/mapview/BUILD.35.1/ideogram.gz](ftp://ftp.ncbi.nlm.nih.gov/genomes/H_sapiens/maps/mapview/BUILD.35.1/ideogram.gz). Accessed September 2005.

**Examples**

```
# Plot one simulated scan
plot.scan(halfsibscan(), col="red", with.X=TRUE)
# plot a genome scan
## Not run: x <-read.table("nfr.lod", h=T, na=".")
## Not run:
plot.scan(x, statistic=c("flat.vc","flat.sqt1"),
  col=c("red","blue"),with.X=TRUE)
## End(Not run)
```

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