Package 'LinkageMapView'

October 12, 2022

Type Package

Title Plot Linkage Group Maps with Quantitative Trait Loci

Version 2.1.2

Description Produces high resolution, publication ready linkage maps and quantitative trait loci maps. Input can be output from 'R/qtl', simple text or comma delimited files. Output is currently a portable document file.

Depends R(>= 2.10)

URL https://github.com/louellette/LinkageMapView

BugReports https://github.com/louellette/LinkageMapView/issues

License GPL-3

LazyData TRUE

Imports qtl (>= 1.39-5), plotrix (>= 3.6-3), grDevices, graphics, utils, RColorBrewer

Suggests rmarkdown, testthat, knitr

RoxygenNote 6.0.1

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

Date/Publication 2018-01-21 15:00:11 UTC

R topics documented:

`carrot` *a carrot comparative linkage map data frame kindly provided by Massimo Iorizzo: Cavagnaro et al. BMC Genomics 2014, 15:1118*

Description

Contains the following columns:

1. group - This will be the title for the linkage group unless overridden.
2. position - must be in numerical order ascending within linkage group name.
3. locus - marker name at this position.

Usage

```
carrot
```

Format

An object of class `data.frame` with 126 rows and 3 columns.

`LinkageMapView` *LinkageMapView: A package for plotting linkage group maps and QTLs*

Description

LinkageMapView produces high resolution, publication ready linkage maps and QTL maps.

Details

There are many optional parameters to format the output pdf. Please see the help for function lmv.linkage.plot for a full description of each parameter and examples.

`lmv.linkage.plot` *LinkageMapView plotting function*

Description

lmv.linkage.plot is the main function to produce linkage group maps and has many parameters to customize the pdf output.

Usage

```
lmv.linkage.plot(mapthis, outfile, mapthese = NULL, at.axis = NULL,
  autoconnadj = TRUE, cex.axis = par("cex.axis"),
  cex.lgtitle = par("cex.main"), cex.main = par("cex.main"),
  col.axis = par("col.axis"), col.lgtitle = par("col.main"),
  col.main = par("col.main"), conndf = NULL, denmap = FALSE,
  dupnbr = FALSE, font.axis = par("font.axis"),
  font.lgtitle = par("font.main"), font.main = par("font.main"),
  header = TRUE, labdist = 0.3, labels.axis = TRUE, lcex = par("cex"),
  lcol = par("col"), lfont = par("font"), lgperrow = NULL,
  lgtitles = NULL, lgw = 0.25, lg.col = NULL, lg.lwd = par("lwd"),
  lty.axis = "solid", lwd.axis = 1, lwd.ticks.axis = lwd.axis,
  main = NULL, markerformatlist = NULL, maxnbrcolsfordups = 3,
  pdf.bg = "transparent", pdf.family = "Helvetica", pdf.fg = "black",
  pdf.width = NULL, pdf.height = NULL, pdf.pointsize = 12,
  pdf.title = "LinkageMapView R output", posonleft = NULL,
  prtlgtitles = TRUE, qtldf = NULL, revthese = NULL, rcex = par("cex"),
  rcol = par("col"), rfont = par("font"), roundpos = 1, rsegcol = TRUE,
  ruler = FALSE, sectcoldf = NULL, segcol = NULL, qtlscanone = NULL,
  showonly = NULL, units = "cM", ylab = units)
```

Arguments

`mapthis`	Required, either a 'cross' object from r/qtl, a csv or txt file or a data frame with the following 3 columns in this order: 1. Required, linkage group name. This will be the title for the linkage group unless overridden - see lgtitles. 2. Required, position - must be in numerical order ascending within linkage group name. 3. Required, locus - marker name at this position. 4. Optional, segcol - color for the line across the chromosome at this marker. See also segcol parameter.
`outfile`	Required, name for the output pdf file.
`mapthese`	Optional vector of linkage group names to print. The default, NULL, will print all linkage groups in mapthis.

`at.axis` Optional. The points at which tick-marks are to be drawn on the ruler. Non-finite (infinite, NaN or NA) values are omitted. By default (when NULL) tickmark locations are computed. #' @seealso `axis`

`autoconnadj` If TRUE (the default), locus with the same name (homologs) on adjacent linkage groups will be connected with a line.

`cex.axis` The magnification to be used for axis (ruler) text. The default is par("cex.axis").

`cex.lgtitle` The magnification to be used for linkage group titles. The default is par("cex.main").

`cex.main` The magnification to be used for main title. The default is par("cex.main").

`col.axis` The color to be used for axis (ruler) text. Defaults to par("col.axis").

`col.lgtitle` The color to be used for linkage group titles. Defaults to par("col.main").

`col.main` The color to be used for the main title. Defaults to par("col.main").

`conndf` An optional data frame containing markers to be connected with lines (homologs). If autoconnadj = TRUE, these lines will appear as well as those with the same name in adjacent linkage groups. Required columns:

- fromchr Linkage group for the line start.
- fromlocus Locus name for the line start.
- tochr Linkage group for the line end.
- tolocus Locus name for the line end.

`denmap` If TRUE, you are requesting a density map which means no locus or position labels will be printed and the following parameters are set: ruler = TRUE autoconndf = FALSE conndf = NULL See also sectcoldf parameter

`dupnbr` If TRUE, only the first marker name at a position will print with (## more) afterwards indicating the number of duplicate markers at that position. dupnbr should be left to the default, FALSE, if showonly provided.

`font.axis` An integer which specifies which font to use for the axis (ruler) text. The default is par("font.axis"). 1 is plain text. 2 is bold. 3 is italic. 4 is bold italic.

`font.lgtitle` An integer which specifies which font to use for the linkage group titles text. The default is par("font.main"). 1 is plain text. 2 is bold. 3 is italic. 4 is bold italic.

`font.main` An integer which specifies which font to use for title text. The default is par("font.main"). 1 is plain text. 2 is bold. 3 is italic. 4 is bold italic.

`header` A boolean indicating if the input file has a header row. Default is TRUE.

`labdist` Distance in inches from the chromosome to the position and locus labels. The default is 0.3 inches.

`labels.axis` Optional. This can either be a logical value specifying whether (numerical) annotations are to be made at the tickmarks on the ruler, or a character or expression vector of labels to be placed at the tickpoints. If this is not logical, at should also be supplied and of the same length. The default is TRUE.

`lcex` A numerical value giving the amount by which position labels should be magnified. The default is par("cex"). See also rcex for locus labels.

`lcol` The color for the position labels. The default is par("col"). See also rcol for locus labels.

`lfont` An integer which specifies which font to use for the position labels. The default is par("font"). See also rfont for locus labels.

`lgperrow` An integer specifying how many linkage groups to plot in one row. As many rows as needed to plot all requested linkage groups will be plotted.

`lgtitles` Optional vector of titles for the linkage groups. These will override the default, which is that the linkage group names in the input print as titles. This may be useful if in mapthese you have indicated to print the same linkage group more than once for the purpose of showing homologous markers without having lines cross. See also cex.lgtitle, col.lgtitle, font.lgtitle

`lgw` Width of chromosome in inches. Default is 0.25 inches.

`lg.col` Linkage group color. The color of the chromosomes. The default is the background color (pdf.bg).

`lg.lwd` Linkage group linewidth. The width of the line around the chromosome. Defaults to par("lwd").

`lty.axis` Optional. Line type for both the axis line and the tick marks.

`lwd.axis` Optional. Line width for the axis line. The default is 1.

`lwd.ticks.axis` Optional. Line width for the axis tick marks. Default is lwd.axis

`main` An optional title for the linkage group map. See also cex.main, col.main, and font.main.

`markerformatlist`
An optional list containing the following vectors:

- locus Required. A vector of loci for which the following should be applied.
- col Optional. The color for these locus labels. This color will override rcol. See also rsegcol.
- cex Optional. A numerical vlue giving the amount by which these locus labels should be magnified. This value will override rcex.
- font Optional. An integer which specifies which font to use for these locus labels. This value will override rfont.

`maxnbrcolsfordups`
Indicates the number of columns across the page for locus labels appearing at duplicate positions. The default is 3.

`pdf.bg` Background color for the pdf. Default is "transparent".

`pdf.family` Font family for all text. Default is "Helvetica".

`pdf.fg` Foreground color for the pdf. Default is black.

`pdf.width` Width of the output file in inches. Defaults to the size necessary to fit all linkage groups with other options specified.

`pdf.height` Height of the output file in inches. Defaults to the size necessary to fit all linkage groups with other options specified.

`pdf.pointsize` The default point size to be used. Defaults to 12.

`pdf.title` Title to be passed to pdf as metadata. This title does not appear except in the pdf metadata. Defaults to "LinkageMapView R output".

`posonleft` A vector of boolean (TRUE or FALSE) the length of the number of linkage groups to be plotted. If FALSE, print positions on right hand side of linkage group and locus names on left hand side of linkage group. Default is TRUE.

`prtlgtitles` If FALSE do not print linkage group titles. Default is TRUE.

`qtldf` An optional data frame containing QTL information for plotting. The data frame, if provided, must contain:

- chr Linkage group name for QTL.
- qtl Name (label) for QTL.
- so Start of outer interval. Numeric.
- si Start of inner interval. Numeric.
- ei End of inner interval. Numeric.
- eo End of outer interval. Numeric.
- col Color for QTL.

`revthese` Optional vector of linkage group names to reverse. The end position becomes position 0 and position 0 becomes the end position.

`rcex` A numerical value giving the amount by which locus labels should be magnified. The default is par("cex"). See also lcex for position labels.

`rcol` The color for the locus labels. The default is par("col"). See also lcol for position labels.

`rfont` An integer which specifies which font to use for the locus labels. The default is par("font"). See also lfont for position labels.

`roundpos` Number of positions after the decimal point to print for positions. Default is 1

`rsegcol` Color of the segments across the chromosome and to the label. TRUE, the default, indicates the color should be the same as the label.

`ruler` A single boolean (TRUE OR FALSE). If TRUE, an axis is drawn on the left hand side of the page and the position labels are not printed on any linkage group. The default is FALSE.

`sectcoldf` Optional data frame containing the following named columns indicating sections of the chromosome to be colored:

- Required, chr - matches from input file or cross object linkage group name
- Required, s - start position in cM
- Required, e - end position in cM
- Required, col - color for section
- Optional, dens - a numeric cm / marker value used to print the density map legend.

For a density map, use the lmvdencolor function to populate sectcoldf. When denmap = TRUE and no sectcoldf parameter is supplied, lmvdencolor is called with defaults fully populating the sectcoldf data frame. See also the denmap parameter.

@seealso `lmvdencolor`

`segcol` Optional. Name of the column in mapthis that contains colors for the line segments across the chromosome. If specified, this overrides rsegcol.

qtlscanone	Optional scanone data frame from package r/qtl. If provided, all QTLs in the dataframe will be drawn by calculating their start and end with the r/qtl function bayesint with defaults.
showonly	Optional vector of marker names. If provided, only these marker names will be printed.
units	Units of the position values supplied in mapthis. The default value is cM (centimorgan) but any value can be provided. The value provided is only used for a ruler (y axis) title and the density map legend text.
ylab	Optional. Title for the y-axis (ruler). The default value is units. See units parameter.

Examples

```
## take a cross object from r/qtl and produce linkage map
## on chr 1,4,6,15

library(qtl)
data(hyper)
outfile = file.path(tempdir(), "hyper.pdf")
lmv.linkage.plot(hyper,outfile,mapthese=c(1,4,6,15))

## color some of the markers for emphasis

library(qtl)
data(hyper)

# make a list to pass label options
flist <- list()
locus <- c("D1Mit123","D1Mit105","D6Mit273","D15Mit56","D15Mit156")
col   <- c("red")
flist[[1]] <- list(locus=locus,col=col)

outfile = file.path(tempdir(), "hyperred.pdf")
lmv.linkage.plot(hyper,outfile,mapthese=c(1,4,6,15),markerformatlist=flist)

## change some of the pdf options and chromosome color
## changing linkage group title color (col.lgtitle) to same as
## foreground pdf color

library(qtl)
data(hyper)

outfile = file.path(tempdir(), "hyperlg.pdf")
lmv.linkage.plot(hyper,outfile,
mapthese=c(1,4,6,15),
pdf.bg="black",pdf.fg="white",col.lgtitle="white",
pdf.height=8,pdf.title="myhyper",lg.col="tan")

## change all label colors and fonts
```

```
library(qtl)
data(hyper)

outfile = file.path(tempdir(), "hypercol.pdf")
lmv.linkage.plot(hyper,outfile,mapthese=c(1,4,6,15),
lcol="blue",lfont=2,lcex=1.2,rcol="red",rfont=3,rcex=2)

## make a dataframe to pass sections of chr to col
## use a ruler instead of printing positions as labels
## only allow one column for duplicate markers at same position
## (default is 3)

library(qtl)
data(hyper)

chr = c(1, 4, 6, 15)
s = c(82,35,9.8,7.7)
e = c(94,47,21.9,13.1)
col = c("pink","blue","blue","green")
sectcoldf <-  data.frame(chr, s, e, col,stringsAsFactors = FALSE)

outfile = file.path(tempdir(), "hyperruler.pdf")
lmv.linkage.plot(hyper,outfile,mapthese=c(1,4,6,15),
ruler=TRUE,maxnbrcolsfordups = 1, sectcoldf=sectcoldf)

## plot qtls also out of a r/qtl scanone object
## plot marker names on left (instead of right) of chr 4 and 7

library(qtl)
data(hyper)

# create scanone df for testing
hyper <-
 calc.genoprob(hyper,
               step = 2.0,
               map.function = "haldane",
               stepwidth = "fixed")
hyper.scanone <- scanone(hyper)

outfile = file.path(tempdir(), "testrqtlhyper2.pdf")
lmv.linkage.plot(hyper,
   outfile, mapthese=c(1,4,6,7,15),
   qtlscanone = hyper.scanone,
   posonleft = c(TRUE,FALSE,TRUE,FALSE,TRUE))

## Not run:
## plot a carrot comparative linkage map
## kindly provided by Massimo Iorizzo:
## Cavagnaro et al. BMC Genomics 2014, 15:1118

# make a df to pass qtl info
qtldf <- data.frame(
  chr = character(),
```

```
  qtl = character(),
  so = numeric(),
  si = numeric(),
  ei = numeric(),
  eo = numeric(),
  col = character(),
  stringsAsFactors = FALSE
)
qtldf <- rbind(qtldf,
               data.frame(
                 chr = "70349LG3",
                 qtl = "RTPE-Q1",
                 so = 36.6,
                 si = 37,
                 ei = 37,
                 eo = 38,
                 col="red"
               ))
# make a list to pass label options
flist <- list()
locus <- c("BSSR-094", "K0149", "K0627", "K2161", "ESSR-087", "ESSR-057")
font  <- c(2)   #bold
flist[[1]] <- list(locus = locus, font = font)
locus <- c("F3H", "FLS1")
font  <- c(4)   #bold italic
flist[[2]] <- list(locus = locus, font = font)
locus <- c("P3", "P1", "Raa1")
font  <- c(3)   #italic
col <- c("red")
flist[[3]] <- list(locus = locus, font = font, col = col)
filename <- system.file("extdata", "Carrot.csv", package="LinkageMapView")
outfile = file.path(tempdir(), "carrot.pdf")
lmv.linkage.plot(
  mapthis = filename,
  outfile = outfile,
  ruler = TRUE,
  lgtitle = c("2170", "70349", "10117"),
  maxnbrcolsfordups = 1,
  markerformatlist = flist,
  lg.col = "lightblue1",
  pdf.width =10,
  revthese = c("70349LG3"),
  qtldf=qtldf
)

## End(Not run)

## do a density map with default colors
data(oat)

outfile = file.path(tempdir(), "oat_Mrg01.pdf")
lmv.linkage.plot(oat,outfile,mapthese=c("Mrg01","Mrg02"),denmap=TRUE)
```

```
## Not run:
## do a density map and provide your own colors with lmvdencolor helper
data(oat)
##
outfile = file.path(tempdir(), "oat_Mrg01_YlGn.pdf")

sectcoldf <- lmvdencolor(oat,colorin =
colorRampPalette(RColorBrewer::brewer.pal(8, "YlGn"))(5))

lmv.linkage.plot(oat,outfile,denmap=TRUE,sectcoldf=sectcoldf)

## End(Not run)
```

`lmvdencolor` *LinkageMapView density color function*

Description

lmvdencolor is a helper function which you can use to create a data frame of colors to be used as the sectcoldf input parameter on the lmv.linkage.plot command. The colors will be used to color the linkage group based on the density of position/marker.This function is called with default values when the denmap = TRUE parameter is specified for lmv.linkage.plot and no sectcoldf parameter is found.

Usage

```
lmvdencolor(df, wsize = 30, bias = 5,
  colorin = colorRampPalette(RColorBrewer::brewer.pal(8, "Spectral"))(25))
```

Arguments

`df`	Required, a data frame with the first two columns in this order: 1. Linkage group name. 2. Position - must be in numerical order ascending within linkage group name. If the maximum position in any linkage group is < 1000, the density will be calculated for each position. Otherwise the number of positions included for each density calculation will be: ceiling(maximum position of an linkage group/1000)
`wsize`	Optional, default = 30. # of postions in the sliding window for calculating postitions/marker. If the maximum position in any linkage group is >= 1000, the default sliding window size will be adjusted by the same ratio as the number of positions included for each density calculate.
`bias`	Optional, default = 5. a positive number. Higher values give more widely spaced colors at the high end.
`colorin`	Optional, a vector of colors to use where the first value is the color for the lowest density and the last value is the color for the highest density. Default is: rev(colorRampPalette(RColorBrewer::brewer.pal(8, "Spectral"))(25))

Value

a data frame that can be used as sectcoldf input on the lmv.linkage.plot function to color the chromosome for a density map.

See Also

colorRamp

lmv.linkage.plot

Examples

```
# add a column to a linkage group data frame to specify colors for
# line segments in lmv.linkage.plot using default colors from RColorBrewer
# Spectral palette.  Then just plot the returned colors out to see how
# they look.

data(oat)

sectcoldf <- lmvdencolor(oat)

# see colors produced

image(seq_along(oat[,2]), 1, as.matrix(seq_along(oat[,2])),
 col=sectcoldf$col, axes=FALSE, xlab="", ylab="")
```

---

oat *oat consensus map data frame*

Description

Chaffin, A. S., Y. Huang, S. Smith, W. A. Bekele, E. Babiker, B. N. Gnanesh, B. J. Foresman, S. G. Blanchard, J. J. Jay, R. W. Reid, C. P. Wight, S. Chao, R. Oliver, E. Islamovic, F. L. Kolb, C. McCartney, J. W. Mitchell Fetch, A. D. Beattie, ?. Bjornstad, J. M. Bonman, T. Langdon, C. J. Howarth, C. R. Brouwer, E. N. Jellen, K. E. Klos, J. A. Poland, T. Hsieh, R. Brown, E. Jackson, J. A. Schlueter, and N. A. Tinker. 2016. A Consensus Map in Cultivated Hexaploid Oat Reveals Conserved Grass Synteny with Substantial Subgenome Rearrangement. Plant Genome 9. doi:10.3835/plantgenome2015.10.0102

Usage

```
oat
```

Format

An object of class `data.frame` with 16668 rows and 3 columns.

Details

Contains the following columns:

1. Group - This will be the title for the linkage group unless overridden.
2. Position - must be in numerical order ascending within linkage group name.
3. Locus - marker name at this position.

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