Package ‘idiogramFISH’

August 22, 2023

Title Shiny App. Idiograms with Marks and Karyotype Indices
Version 2.0.13
Date 2023-08-21

Description
Plot idiograms of karyotypes, plasmids, circular chr. having a set of data.frames for chromosome data and optionally mark data. Two styles of chromosomes can be used: without or with visible chromatids. Supports micrometers, cM and Mb or any unit. Three styles of centromeres are available: triangle, rounded and inProtein; and six styles of marks are available: square (squareLeft), dots, cM (cMLeft), cenStyle, upArrow (downArrow), exProtein (inProtein); its legend (label) can be drawn inline or to the right of karyotypes. Idiograms can also be plotted in concentric circles. It is possible to calculate chromosome indices by Levan et al. (1964) <doi:10.1111/j.1601-5223.1964.tb01953.x>, karyotype indices of Watanabe et al. (1999) <doi:10.1007/PL00013869> and Romero-Zarco (1986) <doi:10.2307/1221906> and classify chromosomes by morphology Guerra (1986) and Levan et al. (1964).

Depends R (>= 3.5)
Imports rlang, crayon, plyr, dplyr, tidyr, scales
License GPL (>= 2)
Encoding UTF-8
LazyData true
Suggests rentrez, ggplot2, ggpubr, ggtree, phytools, treeio, rmdformats, knitr, kableExtra, rvcheck, badger, rmarkdown, RCurl, shiny, shinydashboard, rhtmlsontable, gtools, rclipboard, clipr, shinyjs
VignetteBuilder rmdformats, knitr, kableExtra, rmarkdown, RCurl, rvcheck, badger, rentrez
SystemRequirements pandoc (>= 2.0)
BugReports https://gitlab.com/ferroao/idiogramFISH/-/issues
RoxygenNote 7.2.3
Description

armRatioCI: reads a data.frame and produces AR (arm ratio), CI (centromeric index), Guerra and Levan classifications.

swapChrRegionDfSizeAndMarks: reads data.frames to swap arms

Usage

armRatioCI(dfChrSize, rnumeric = FALSE)

swapChrRegionDfSizeAndMarks(dfChrSize, dfMarkPos, chrNamesToSwap)
**asymmetry**

**Arguments**

- `dfChrSize` name of data.frame with columns: shortArmSize, longArmSize
- `numeric` boolean, returns only numeric AR, CI
- `dfMarkPos` name of data.frame of marks
- `chrNamesToSwap` name of chr. names to swap arms

**Value**

data.frame (armRatioCI)
list of data.frames (swapChrRegionDfSizeAndMarks)

**References**

LEVAN A, FREDGA K, SANDBERG AA (1964) NOMENCLATURE FOR CENTROMERIC POSITION ON CHROMOSOMES. Hereditas 52:201-220.


**See Also**

chrbasicdatamono

**Examples**

armRatioCI(dfOfChrSize)
armRatioCI(bigdfOfChrSize)
swapChrRegionDfSizeAndMarks(dfOfChrSize, dfOfMarks, "1")

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**asymmetry**

FUNCTIONS *asymmetry* and *asymmetryA2*.

**Description**

asymmetry: calculates karyotype asymmetry A and A2.
asymmetryA2: calculates karyotype asymmetry A2

This functions read a data.frame with columns: shortArmSize and longArmSize
If several species present, use column OTU.
It returns a list with the A and A2 indices

\[
A = \frac{\sum_{i=1}^{n} \frac{longArm_i - shortArm_i}{CI_i}}{n}
\]
A: Watanabe et al. (1999) asymmetry of karyotype ranging from 0 (symmetric) to 1 (asymmetric)

\[ A_2 = \frac{sCL}{xCL} \]

(s = std dev, CL = chr. length, x = mean) (Romero-Zarco 1986)

related to:

\[ CV_{CL} = A_2 * 100 \]

(CV = coeff. var.) (Paszko 2006)

Usage

```r
asymmetry(dfChrSize, asDf = FALSE)
asymmetryA2(dfChrSize)
```

Arguments

- `dfChrSize` name of data.frame
- `asDf` boolean, return d.f. instead of list

Value

list

References


See Also

- `chrbasicdatamono`
- `chrbasicdatamono`
- `chrbasicdataHolo`

Examples

```r
asymmetry(dfOfChrSize)
myAlist <- asymmetry(bigdfOfChrSize)
as.data.frame(myAlist)
asymmetryA2(dfOfChrSize)
as.data.frame(asymmetryA2(bigdfOfChrSize))
asymmetryA2(dfChrSizeHolo)
as.data.frame(asymmetryA2(bigdfChrSizeHolo))
```
chrbasicdataHolo

chrbasicdataHolo    Chr. basic data Holo.

Description

dfChrSizeHolo: Example data for holocentrics for 1 species
bigdfChrSizeHolo: Example data for holocentrics for several species, OTU
parentalAndHybHoloChrSize: Example data for holocentrics for several species, OTU
bigdfOfChrSize3Mb: Example data in Mb without chr. arms for three species, OTU

Usage

dfChrSizeHolo
bigdfChrSizeHolo
parentalAndHybHoloChrSize
bigdfOfChrSize3Mb

Format

data.frame with columns:

OTU grouping OTU (species), optional if only one OTU
chrName name of chromosome
chrSize size of chromosome, micrometers or Mb
group chromosome group, optional
chrNameUp optional name over kar.
Mbp optional name to show size in Mbp, use only when chrSize is not in Mbp

An object of class data.frame with 12 rows and 3 columns.
An object of class data.frame with 13 rows and 3 columns.
An object of class data.frame with 14 rows and 3 columns.

See Also

asymmetryA2
plotIdiograms
markdataholo
chrbasicdatamono

Chr. basic data Monocen.

Description

dfOfChrSize: Example data for monocentrics
bigdfOfChrSize: Example data for monocentrics for several species, OTU
humChr: Data for human karyotype, measured from Adler (1994)
allChrSizeSample: Example data for monocentrics for several species, OTU
parentalAndHybChrSize: Example data for monocentrics for GISH
traspadf: Example data for Tradescantia (Rhoeo) spathacea (Golczyk et al. 2005)

Usage

dfOfChrSize
bigdfOfChrSize
humChr
allChrSizeSample
parentalAndHybChrSize
traspadf

Format

data.frame with columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>OTU</td>
<td>OTU, species, optional if only one OTU (species)</td>
</tr>
<tr>
<td>chrName</td>
<td>name of chromosome</td>
</tr>
<tr>
<td>shortArmSize</td>
<td>size of short arm, micrometers</td>
</tr>
<tr>
<td>longArmSize</td>
<td>size of long arm, micrometers</td>
</tr>
<tr>
<td>group</td>
<td>chr group, optional</td>
</tr>
<tr>
<td>chrNameUp</td>
<td>optional name over kar.</td>
</tr>
<tr>
<td>Mbp</td>
<td>optional name to show size in Mbp, use only when shortArmSize is not in Mbp</td>
</tr>
</tbody>
</table>

An object of class data.frame with 50 rows and 4 columns.
An object of class data.frame with 24 rows and 4 columns.
An object of class data.frame with 75 rows and 4 columns.
An object of class data.frame with 13 rows and 4 columns.
An object of class data.frame with 12 rows and 4 columns.
citrusSize

Source
http://www.pathology.washington.edu/research/cytopages/idiograms/human/

References

See Also
plotIdiograms
armRatioCI
asymmetry
markposDFs

Functions: citrusSize, citrusMarkPos, markOverCMA

description
Helper function to create data.frames with chr. size and mark size data for Citrus based on categories in Carvalho et al. (2005)
Special behaviour while plotting: normally you will get chr. names as: B_1, B_2, etc. to remove _, use chrIdPatternRem='_*' in plotIdiograms. However, for FL+ and FL0, this conversion is automatic. So, in plot you will never see FL0_1, FL0_2, for example.

Usage
citrusSize( A = 0, B = 0, C = 0, D = 0, E = 0, F = 0, FL = 0, FL0 = 0, G = 0, shortArm = 1.2, longArm = 1.7, shortArmFL = 1.3, longArmFL = 1.8, OTU = "OTU 1"
)
citrusMarkPos( chrSizeDf, mSizePter = 0.25, mSizeQter = 0.35, mSizePprox = 0.35, mOther = 0.25, markName = "CMA"
)
markOverCMA(
  citrusMarkPosDF,
  chrType = "B", chrName, chrRegion = "p", markName = "45S", shrinkMark = TRUE
)
Arguments

A  number of A to calculate (citrusSize)
B  number of B to calculate (citrusSize)
C  number of C to calculate (citrusSize)
D  number of D to calculate (citrusSize)
E  number of E to calculate (citrusSize)
F  number of F to calculate (citrusSize)
FL number of FL+ to calculate (citrusSize)
FLØ number of FLØ to calculate (citrusSize)
G  number of G to calculate (citrusSize)
shortArm for A to G (not FL) (citrusSize)
longArm for A to G (not FL) (citrusSize)
shortArmFL for FL (citrusSize)
longArmFL for FL (citrusSize)
OTU name of species (citrusSize)
chrSizeDf data.frame created with citrusSize function (citrusMarkPos)
mSizePter numeric, default size for P(short) ter (terminal) bands. 0.25 (default) (citrusMarkPos)
mSizeQter numeric, default size for Q(long) ter (terminal) bands. 0.35 (default) (citrusMarkPos)
mSizePprox numeric, default size for P prox (proximal) bands. 0.35 (default) (citrusMarkPos)
mOther numeric, default size for other bands. 0.25 (default) (citrusMarkPos)
markName character, default name of mark "CMA", or "45S", respectively. (citrusMarkPos,markOverCMA)
citrusMarkPosDF data.frame, with CMA marks (markOverCMA)
chrType character, defaults to "B", chr. type to duplicate mark (markOverCMA)
chrName character, defaults to "B", chr. name(s) to duplicate mark (markOverCMA)
chrRegion character, arm, defaults to "p". for mark duplication (markOverCMA)
shrinkMark boolean, shrink new mark to be created (markOverCMA)

Value

data.frame
data.frame
data.frame
References

Examples

citrusSizeDF <- citrusSize(B = 1, D = 11, F = 4, FL0 = 2, OTU = "C. jambhiri")
suppressMessages(
  plotIdiograms(citrusSizeDF,
  indexIdTextSize = .4, # font size
  rulerNumberSize = .4, # font size
  rulerTitleSize = .4, # font size
  rulerPos = -.5, # ruler pos.
  xPosRulerTitle = 1.5, # ruler title pos.
  orderChr = "original" # order of chr. as in d.f.
  )
)
citrusSizeDF2 <- citrusSize(
  B = 2, D = 10, F = 4, FL0 = 1,
  FL = 1, # equivalent to FL+
  OTU = "C. limettioides"
  )
suppressMessages(
  plotIdiograms(citrusSizeDF2, # FL^NA error corrected in 1.15.4
  indexIdTextSize = .4, # font size
  rulerNumberSize = .4, # font size
  rulerTitleSize = .4, # font size
  rulerPos = -.5, # ruler pos.
  xPosRulerTitle = 1.5, # ruler title pos.
  orderChr = "original" # order of chr. as in d.f.
  )
)
citrusMarkPosDF <- citrusMarkPos(citrusSizeDF)
suppressMessages(
  plotIdiograms(
    dfChrSize = citrusSizeDF, # chr. size data.frame
    dfMarkPos = citrusMarkPosDF, # mark position data.frame (inc. cen.)
    ruler = FALSE, # remove
    chrIndex = FALSE, # remove
    morpho = FALSE, # remove
    karIndex = FALSE, # remove
    indexIdTextSize = .4, # font size
    xlimRightMod = 4, # xlim mod.
    orderChr = "original", # order chr. as in d.f.
    chrColor = "blue", # chr. color
    legendHeight = 3 # legend item height
    )
)
citrusMarkPosDF45S <- markOverview(citrusMarkPosDF, chrType = "B", chrRegion = "p", markName = "45S")
suppressMessages(
  plotIdiograms(
    dfChrSize = citrusSizeDF, # chr. size data.frame
    dfMarkPos = citrusMarkPosDF45S, # mark position data.frame (inc. cen.)
    ruler = FALSE, # remove ruler
    chrIndex = FALSE, # remove index
    morpho = FALSE, # remove morphol.
    karIndex = FALSE, # remove
    indexIdTextSize = .4, # font size chr.
    xlimRightMod = 4, # modify xlim
    orderChr = "original", # as in d.f.
    chrColor = "blue",
    legendHeight = 5, # height of legend item
    colorBorderMark = "black", # mark border color
    OTUfont = 3 # italics
  )
)

---

**dfMarkStyle**

**Mark characteristics**

**Description**

style column does not apply to cen. marks, only color.

- dfMarkColor: Example General data for marks NOT position
- humMarkColor: human bands’ characteristics, from Adler (1994)
- mydfMaColor: mark characteristics used in vignette of phylogeny
- dfMarkColor5S25S: mark characteristics used in circular plot vignette
- dfMarkColorIn: mark characteristics

**Usage**

- dfMarkColor
- humMarkColor
- mydfMaColor
- dfMarkColor5S25S
- dfMarkColorIn
**Format**

dfMarkColor a data.frame with columns:

- **markName** name of mark
- **markColor** use R colors
- **style** character, use square or dots, optional
- **protruding** numeric, modifies aspect of cM/cMLeft marks, see parameter protruding in `plotIdiograms`, optional

An object of class data.frame with 395 rows and 3 columns.
An object of class data.frame with 6 rows and 3 columns.
An object of class data.frame with 2 rows and 3 columns.
An object of class data.frame with 5 rows and 3 columns.

**Source**

http://www.pathology.washington.edu/research/cytopages/idiograms/human/

**References**


**See Also**

- `plotIdiograms`
- `markposDFs`
- `markdataholo`

---

**Description**

genBankReadIF: creates a list of data.frames from a genbank format file or a rentrez object
Requires tidyr

**Usage**

genBankReadIF(filename.gb, forbiddenFields = "translation")
make.uniqueIF

FUNCTION make.uniqueIF

Description
make.uniqueIF: produces unique strings from duplicated

Usage
make.uniqueIF(string, sep = "_", letter = FALSE)

Arguments
string name of char. vector
sep separator
letter boolean, use numbers when FALSE

Value
character vector

Examples
make.uniqueIF(c(1, 1, 2, 2))
makedfMarkColorMycolors

*FUNCTION to make a data.frame of Marks' characteristics*

**Description**

This function reads character vector with marks names, a character vector of prohibited colors and a custom list of colors to be associated with the mark names.

It returns a data.frame with color and style for each mark.

**Usage**

```r
makedfMarkColorMycolors(
  markNames,
  mycolors,
  colorstoremove = NULL,
  defaultStyleMark = "square"
)
```

**Arguments**

- `markNames`: names of marks.
- `mycolors`: character vector of names of colors.
- `colorstoremove`: character vector of colors to remove from `mycolors`. Default NULL.
- `defaultStyleMark`: character vector with default style "square". Other options: "squareLeft", "cM" "cMLeft", "dots", "upArrow", "downArrow", "cenStyle".

**Value**

`data.frame`

---

mapGGChr

*FUNCTIONS mapGGChr and mapGGChrMark (for ggplot)*

**Description**

Currently works for holocentrics when only one OTU. See vignette.

mapGGChr: reads a data.frame and produces coordinates for `ggplot` of chr.

mapGGChrMark: reads data.frames and produces data.frames for `ggplot` of chr. and marks.
Usage

mapGGChr(dfChrSize, chrSpacing = 0.5, squareness = 4, n = 50)
mapGGChrMark(dfChrSize, dfMarkPos, chrSpacing = 0.5, squareness = 4, n = 50)

Arguments

dfChrSize character, name of data.frame with columns: chrSize
chrSpacing numeric, 1 - chrSpacing will be the width of chr.
squareness numeric, squareness
n numeric, vertices number for rounded portions
dfMarkPos (mapGGChrMark) name of data.frame of marks

Value

list
list

Description

When several OTUs, some can be monocen. and others holocen. Marks distance for monocen. are measured from cen. and for holocen. from top or bottom depending on param origin. See vignettes.

bigdfMarkPosHolo: Example data for mark position of holocentrics with column OTU
dfMarkPosHolo: Example data for mark position of holocentrics
dfAlloParentMarksHolo: Example data for mark position of GISH
bigdfOfMarks3Mb: Example data for mark position in Mb
bigdfMarkPosHolo2: Example data for mark position

Usage

bigdfMarkPosHolo
dfMarkPosHolo
dfAlloParentMarksHolo
bigdfOfMarks3Mb
bigdfMarkPosHolo2
markposDFs

Format

data.frame with columns:

- **OTU**: OTU, species, optional
- **chrName**: name of chromosome
- **markName**: name of mark
- **markPos**: position from bottom or top (see parameter origin in plotIdiograms)
- **markSize**: size of mark in micrometers or Mb

An object of class `data.frame` with 6 rows and 4 columns.
An object of class `data.frame` with 13 rows and 4 columns.
An object of class `data.frame` with 12 rows and 5 columns.
An object of class `data.frame` with 18 rows and 6 columns.

See Also

- markposDFs
- plotIdiograms
- chrbasicdataHolo

---

| markposDFs | *Mark Positional data - monocentrics* |

Description

When several OTUs, some can be monocen. and others holocen. Marks distance for monocen. are measured from cen. and for holocen. from top or bottom depending on param origin. See vignettes.

- bigdfOfMarks: Example data for mark position with column OTU
- dfOfMarks: Example data for marks’ position
- dfOfMarks2: Marks’ position including cen. marks
- humMarkPos: human karyotype bands’ (marks) positions, measured from Adler (1994)
- allMarksSample: Example data for marks’ position
- dfAlloParentMarks: Example data for mark position of GISH of monocen.
- traspaMarks: T. spathacea (Rhoeo) marks’ positions, from Golczyk et al. (2005)
Usage

bigdfOfMarks
df0fMarks
df0fMarks2
humMarkPos
allMarksSample
dfAlloParentMarks
traspaMarks

Format

bigdfOfMarks a data.frame with columns:

- **OTU**  OTU, species, mandatory if in dfChrSize
- **chrName**  name of chromosome
- **markName**  name of mark
- **chrRegion**  use p for short arm, q for long arm, and cen for centromeric
- **markDistCen**  distance of mark to centromere (not for cen)
- **markSize**  size of mark (not for cen)

An object of class data.frame with 4 rows and 5 columns.
An object of class data.frame with 6 rows and 5 columns.
An object of class data.frame with 395 rows and 5 columns.
An object of class data.frame with 43 rows and 6 columns.
An object of class data.frame with 16 rows and 4 columns.
An object of class data.frame with 18 rows and 7 columns.

Source

Washington U

References


namesToColumns

FUNCTION that modifies marks’ names into columns

See Also
  markdataholo
  plotIdiograms
  chrbasicdatamono
  dfMarkColor

Description

Reads a data.frame with marks’ of styles downArrow, upArrow, cM, cMLeft positions. It separates names in columns, avoiding overlap when multiple close names

Exceptionally this function requires the column style in the data.frame of marks’ positions.

Returns a data.frame

Usage

namesToColumns( marksDf, dfChrSize, markType = c("downArrow", "upArrow", "cMLeft", "cM"), amountofSpaces = 13, colNumber = 2, protruding = 0.2, protrudingInt = 0.5, circularPlot = TRUE, rotation = 0.5, defaultStyleMark = "square", orderChr = "size", halfModDown = NA, halfModUp = NA, rotatMod = 0 )

Arguments

marksDf data.frame with columns: markName, style, markPos
dfChrSize data.frame, size of chr. Same of plot.
markType character, use c("downArrow", "upArrow", "cM", "cMLeft") or a subset
amountofSpaces numeric, number of spaces for each column
colNumber numeric, number of columns
protruding numeric, same as plot, minimal protruding for arrow marks, equivalent to cM protruding
protrudingInt numeric, spacing of columns in terms of width of chr. percent 1 = 100%. Defaults to 0.5
circularPlot boolean, use TRUE for circular plots. Use FALSE otherwise
rotation numeric, same as plot, anti-clockwise rotation, defaults to 0.5 which rotates chr. from top to -90 degrees. (-0.5*π)
defaultStyleMark character, if some data in column style missing fill with this one. Defaults to "square"
**perMark**

**Description**

Calculates fraction (%) of chromosome for each mark.

**Usage**

```r
perMark(dfMarkPos, listOfdfChromSize, result = "list", bToRemove = "")
```

**Arguments**

- `dfMarkPos`: data.frame, of marks' position
- `listOfdfChromSize`: list of data.frames or data.frame of chr. sizes.
- `result`: character, type of return, "data.frame" or "list"
- `bToRemove`: character vector, bands to ignore

**Value**

list

**Examples**

```r
load(system.file("shinyApps", "iBoard/www/rda/monoholoCS.rda", package = "idiogramFISH"))
load(system.file("shinyApps", "iBoard/www/rda/monoholoMarks.rda", package = "idiogramFISH"))
monoholoMarks2 <- fillMarkInfo(monoholoMarks, monoholoCS)
perMark(monoholoMarks2, monoholoCS, result = "data.frame")
```
Description

This function reads a data.frame passed to dfChrSize with columns: chrName (mono/holo) and shortArmSize and longArmSize for monocentrics or a column chrSize for holocentrics and produces a plot of idiograms. If more than one species, a column named OTU is needed.

Optionally, it reads another data.frame passed to dfMarkPos with the position of marks (sites). Examples: markposDFs. Another data.frame for mark characteristics can be used dfMarkColor or a character vector passed to mycolors

Usage

```
plotIdiograms( dfChrSize, defaultFontFamily, revOTUs = FALSE, 
karHeight = 2, karHeiSpace = 2.5, karSepar = TRUE, amoSepar = 10, 
addMissingOTUAfter = NA, addMissingOTUBefore = NA, missOTUSpacings = 0, 
moveKarHor = "", moveAllKarValueHor = 0, moveAllKarValueY = 0, 
karAnchorLeft = "", karAnchorRight = "", anchor = FALSE, anchorLineLty = 1, 
anchorText = "", anchorTextMParental, anchorTextMoveX = 0.5, 
anchorTextMoveY = 1, anchorTextMoveParenX = 0, anchorTextMoveParenY = 0, 
anchorVsSizeF = 0.5, anchorHsizeF = 1, pchAnchor = 23, moveAnchorY = 0, 
moveAnchorH = 0, mkhValue = 0.5, n = 50, markN = 25, notes, leftNotes, 
leftNotesUp, notesTextSize = 1, leftNotesTextSize = 1, leftNotesUpTextSize = 1, 
notesLeft, notesPosX = 0.5, notesPosY = 0, leftNotesPosX = 0.5, 
leftNotesPosY = 0, leftNotesUpPosX = 0.5, leftNotesUpPosY = 0, noteFont = 1, 
leftNoteFont = 1, leftNoteFontUp = 1, parseTypes = TRUE, parseStr2lang = FALSE, 
propWidth = FALSE, MbThreshold = 10000, threshold = 35, MbUnit = "Mb", 
yTitle = "\u00b5m", specialyTitle = "cM", specialOTUNames = "", addOTUName = TRUE, 
OUTextSize = 1, OUTFont, OUTFamily = "", OUTasNote = FALSE, 
OUTasLeftNote = FALSE, orderChr = "size", chrId = "original", 
classMbName = "Pm.", classMName = "L.G.", classChrName = "Chr.", 
classChrNameUp = "Type", classGroupName = "", chrNameUp = FALSE, 
chrIdPatternRem, indexIdTextSize = 1, distTextChr = 1, groupUP = FALSE, 
groupName = TRUE, groupSepar = 0.5, chromatids = TRUE, arrowsBothChrt = TRUE, 
holocenNotAsChromatids = FALSE, excHoloFrArrToSide = FALSE, xModifier = 12, 
xModMonoHoloHoloRate = 1, chrWidth = 0.5, chrSpacing = 0.5, specialChrWidth = 0.3, 
specialChrSpacing = 0.7, chrColor = "gray", chrBorderColor, centromereSize = 0, 
autoCenSize = TRUE, cenColor, fixCenBorder = NULL, gishCenBorder = FALSE, 
hideCenLines = 1.75, roundedCen, cenFormat = "rounded", cenFactor = 1, 
squareness = 4, lwd.chr = 0.5, lwd.cm, lwd.marks = 99, dfMarkPos, 
defaultStyleMark = "square", markDistType = "beg", protruding = 0.2, 
startPos = 0, pMarkFac = 0.25, origin = "b", efZero = 1e-05, 
cMBeginCenter = FALSE, origin = "b", eZero = 1e-05, 
arrowhead = 0.3, shrinkArrow = 0.3333, 
arrowsToSide = TRUE, useOneDot = FALSE, 
dotsAsOval = FALSE, dfMarkColor, mycolors, alpha_val = 1, 
```

borderOfWhiteMarks = TRUE, colorBorderMark = "", lwd.mimicCen, defCenStyleCol, pattern = "", legend = "aside", remSimiMarkLeg = TRUE, bannedMarkName, bMarkNameAside = FALSE, forbiddenMark, legendWidth = 1.7, legendHeight = NA, markLabelSize = 1, markLabelSpacer = 1, legendYcoord = 0, markNewLine = NA, mylheight = 0.7, chrSize = FALSE, nsmall = 1, chrSizeMbp = FALSE, markPer = "", showMarkPos = FALSE, bToRemove = "", perAsFraction = FALSE, chrIndex = "both", morpho = "both", nameChrIndexPos = 2, karIndex = TRUE, karIndexPos = 0.5, rrule = TRUE, useMinorTicks = FALSE, miniTickFactor = 10, rulerPos = 0, ruler.tck = -0.02, rulerNumberPos = 0.5, rulerNumberSize = 1, collapseCen = TRUE, rulerInterval = 0, rulerIntervalcM = 0, yPosRulerTitle = 0, rulerTitleSize = 1, callPlot = TRUE, asp = 1, circularPlot = FALSE, verticalPlot = TRUE, karSpaceHor = 0, shrinkFactor = 0.9, separatFactor = 1.5, labelSpacing = 0.7, labelOutwards = FALSE, chrLabelSpacing = 0.5, radius = 0.5, rotation = 0.5, circleCenter = 1, circleCenterY = 1, OTUlabelSpacing = 0.3, OTUsrt = 0, OTUplacing = "first", OTULabelSpacerx = 0, OTULabelSpacery = 0, OTUcentered = TRUE, OTUjustif = 0, OTUlegendHeight = NA, roundness, ...

Arguments

dfChrSize mandatory data.frame, with columns: OTU (optional), chrName (mandatory), shortArmSize, longArmSize for monocen. or chrSize for holocen.
defaultFontFamily character. use this as the font family. No default value.
revOTUs boolean, The order of species is the one in the main data.frame, use TRUE to reverse
karHeight numeric, vertical size of karyotypes. See also karHeiSpace. Defaults to 2
karHeiSpace numeric, vertical size of karyotypes including spacing. Use with karSepar=FALSE. Proportional to karHeight, if overlap, increase. Default value 2.5
karSepar boolean, reduce distance among karyotypes FALSE = equally sized karyotypes or TRUE = equally spaced karyotypes. Incompatible with addMissingOTUAfter
amoSepar numeric, depends on karSepar=TRUE, if zero your karyotypes will have no distance among them, if overlap, increase this and karHeiSpace
addMissingOTUAfter character, when you want to add space (ghost OTUs) after one or several OTUs, pass the names of OTUs preceding the desired space in a character vector i.e. c("species one", "species five")
addMissingOTUBefore character, when you want to add space (ghost OTUs) before one or several OTUs, pass the names of OTUs after the desired space in a character vector i.e. c("species one", "species five")
missOTUspacings numeric, when you use addMissingOTUAfter this numeric vector should have the same length and corresponds to the number of free spaces (ghost OTUs) to add after each OTU respectively
moveKarHor character, OTUs’ names of karyotypes that should be moved horizontally. See mkhValue
moveAllKarValueHor numeric, similar to mkhValue, but affects all karyotypes.
moveAllKarValueY numeric, similar to moveAllKarValueHor, but affects y axis.
karAnchorLeft character, OTUs’ add anchor to the left of this OTU names of karyotypes. For verticalPlot=FALSE
karAnchorRight character, OTUs’ add anchor to the right of this OTU names of karyotypes. For verticalPlot=FALSE
anchor boolean, when TRUE, plots a parent progeny structure in karyotypes in moveKarHor. Or a horizontal anchor to the left/right of karAnchorLeft, karAnchorRight when verticalPlot=FALSE
anchorLineLty numeric, type of line in anchor, corresponds to lty. Defaults to 1
anchorText character, text to add to anchor structure near symbol. See anchor. Defaults to ""
anchorTextMParental character, designed to fill with a character object the space left of a missing parental in the anchor structure.
anchorTextMoveX numeric, for vertical plots with anchorText move text in X axis. Defaults to 0.5
anchorTextMoveY numeric, for horizontal plots with anchorText move text in Y axis. Defaults to 1
anchorTextMoveParenX numeric, for plots with anchorTextMParental move text in X axis. Defaults to 0
anchorTextMoveParenY numeric, for plots with anchorTextMParental move text in Y axis. Defaults to 0
anchorVsizeF numeric, factor to modify vertical size of anchor 0.5 (default). Size itself is equal to karHeiSpace
anchorHsizeF numeric, factor to modify horizontal size of anchor 1 (default).
pchAnchor numeric, symbol for anchor, see ?points and anchor
moveAnchorV numeric, displace anchor vertical portion to right or left. See anchor
moveAnchorH numeric, displace anchor horizontal portion to right or left. See anchor
mkhValue numeric, value to move kar. hor. See moveKarHor
n, numeric vertices number for round corners
markN, numeric vertices number for round corners of marks
notes, data.frame, or csv file name in quotes, (shown to the right of kar.), with columns OTU and note for adding notes to each OTU, they appear to the right of chromosomes
leftNotes, leftNotesUp, data.frame, or csv file name in quotes (shown to the left), with columns OTU and note for adding notes to each OTU, they appear to the left of chromosomes. 

notesTextSize, numeric, font size of notes, see notes
leftNotesTextSize, numeric, font size of notes, see leftNotes
leftNotesUpTextSize, numeric, font size of notes, see leftNotesUp

notesLeft, numeric, font size of notes, see leftNotes
notesPosX, numeric, move right notes to the right or left (x axis)
notesPosY, numeric, move right notes down or up (y axis)
leftNotesPosX, numeric, move left notes to the right or left (x axis)
leftNotesPosY, numeric, move left notes (leftNotes) down or up (y axis)
leftNotesUpPosX, numeric, move up left notes to the right or left (x axis)
leftNotesUpPosY, numeric, move up left notes (leftNotesUp) down or up (y axis)

noteFont, numeric 1 for normal, 2 for bold, 3 for italics, 4 for bold-italics. See notes
leftNoteFont, numeric 1 for normal, 2 for bold, 3 for italics, 4 for bold-italics. See leftNotes
leftNoteFontUp, numeric 1 for normal, 2 for bold, 3 for italics, 4 for bold-italics. See leftNotesUp

parseTypes, boolean, parse in notes the Citrus chr. types names. Creates subindex pos. for FL. Defaults to TRUE. Incompatible with parseStr2lang
parseStr2lang, boolean, parse string in notes with function str2lang(paste0("paste("note,"")") for ex: "italic("C. sinensis"), 'Author'"). See notes, leftNotes, leftNotesUp

propWidth, boolean, defaults to FALSE. Diminishes chr. width with increasing number of OTUs

MbThreshold, numeric, if greater than this number (defaults to 10000), MbUnit will apply and specialyTitle will not.

threshold, this is the max. value allowed for the main two significative digits, otherwise scale will shrink. For example, after 35 µm (Default), apparent size will be 3.5 and scale interval will change. See also ceilingFactor, you may have to use ~1. Introduced in 1.13

MbUnit, character, text of units of title when MbThreshold met and OTU not in specialOTUNames. See specialyTitle Defaults to "Mb", but anything can be used. Introduced in 1.13. See specialyTitle

yTitle, character, units for common title. Defaults to µm
specialyTitle, character, title of ruler if OTU is in specialOTUNames. Will not apply if MbThreshold met. In that case use MbUnit
specialOTUNames
character vector, normally title of ruler is micrometer or Mb (big numbers). Use this param. to be able to put a different unit in ruler title. See "specialyTitle"

addOTUName
boolean, when TRUE adds OTU (species) name to karyotype

OTUTextSize
numeric, font size of OTU name (species). Defaults to 1. When OTUasNote is TRUE, use notesTextSize instead

OTUfont
numeric, 1 for normal, 2 for bold, 3 for italics, 4 for bold-italics

OTUfamily
character, font family for OTU name.

OTUasNote
boolean, when TRUE adds OTU (species) name to the right, see notes

OTUasLeftNote
boolean, when TRUE adds OTU (species) name to the left-up, see leftNotesUp

orderChr
character, when "size", sorts chromosomes by total length from the largest to the smallest. "original": preserves d.f. order. "name": sorts alphabetically; "group": sorts by group name; "chrNameUp": sorts according to column chrNameUp. See chrNameUp

chrId
character, print name of chromosome, "original" uses the original name in OTU column of dfChrSize, "simple" (just 1 to ...) or "none".

classMbName
character, name of "chromosome" when in Mb. Defaults to "Pm". See MbUnit

classcMName
character, name of "chromosome" when OTU in specialOTUNames. Defaults to "L.G."

classChrName
character, name of "chromosome" when in micrometers (apparently). Defaults to "Chr.". See specialOTUNames, classMbName, classcMName

classChrNameUp
character, name of "chromosome" for col. "chrNameUp". Defaults to "Type"

classGroupName
character, name of groups. Defaults to ""

chrNameUp
boolean, when TRUE adds secondary chromosome name from col. chrNameUp over chrs. Defaults to FALSE

chrIdPatternRem
character, regex pattern to remove from chr. names

indexIdTextSize
numeric, font size of chr. and kar. indices and chromosome name. Defaults to 1

distTextChr
numeric, distance from name of chromosome to chromosome, also affects vertical separation of indices. Defaults to 1

groupUp
boolean, when TRUE when groups present, they appear over the chr. name. Defaults to FALSE

groupName
boolean, when TRUE (default), shows group names. When FALSE only line

groupSepar
numeric, factor for affecting chr. spacing chrSpacing among groups. Defaults to 0.5

chromatids
boolean, when TRUE shows separated chromatids. Defaults to TRUE

arrowsBothChrt
boolean, when TRUE (default) (for chromatids=TRUE) shows upArrow, downArrow styles of marks in both chromatids when arrowsToSide=TRUE.

holocenNotAsChromatids
boolean, when TRUE and chromatids=TRUE does not plot holocen kar. with chromatids. Defaults to FALSE.
excHoloFrArrToSide  
boolean, when arrowsToSide=TRUE, excludes holocen. from this behaviour, plotting a centered arrow only.

xModifier  
numeric, for chromatids=TRUE, separation among chromatids. Quotient for chrWidth. Defaults to 12 : chrWidth/12

xModMonoHoloRate  
numeric, factor to shrink chromatid separ. for holocen. 5 means 5 times smaller (quotient).

chrWidth  
numeric, relative chromosome width. Defaults to 0.5

chrSpacing  
numeric, horizontal spacing among chromosomes, see also chrWidth. Defaults to 0.5

specialChrWidth  
numeric, relative chromosome width. Defaults to 0.5 for OTUs in specialOTUNames

specialChrSpacing  
numeric, horizontal spacing among chromosomes for OTUs in specialOTUNames, see also chrWidth. Defaults to 0.5

chrColor  
character, main color for chromosomes. Defaults to "gray"

chrBorderColor  
character, color for border of chromosomes, defaults to chrColor

centromereSize  
numeric, optional, this establishes the apparent size of cen. in the plot in µm. See autoCenSize=TRUE. Default: 0. Use with autoCenSize=FALSE

autoCenSize  
boolean, when TRUE ignores centromereSize

cenColor  
character, color for centromeres, if GISH use NULL or NA. Defaults to chrColor

fixCenBorder  
boolean, when TRUE uses chrColor as centromere (and cen. mark) border color. See also cenColor, chrColor, colorBorderMark, borderOfWhiteMarks. No default value. When chrColor is "white" this turns into "black".

gishCenBorder  
boolean, when TRUE, cen. mark border color is the same as mark color, ignoring colorBorderMark. No default.

hideCenLines  
numeric, factor to multiply line width (lwd) used for covering cen. border, when chrColor is white or when gishCenBorder=TRUE

roundedCen  
deprecated, see cenFormat

cenFormat  
boolean, when "triangle", cen. has triangular aspect. When "rounded", it has rounded aspect (Default). "inProtein" for using the mark with style of same name.

cenFactor  
numeric, modifies any cen. mark and cen. size. Defaults to 1

squareness  
numeric, shape of vertices of chromosomes and square marks, higher values more squared. Defaults to 4

lwd.chr  
thickness of border of chr., some marks and ruler. Thick of cM marks when lwd.cM absent and other marks when lwd.marks absent. Defaults to 0.5

lwd.cM  
thickness of cM marks. Defaults to lwd.chr

lwd.marks  
thickness of most marks. Except cM marks and centr. related marks. See lwd.chr, lwd.cM. Defaults to lwd.chr value when 99
dfMarkPos: data frame of marks (sites); columns: OTU (opt), chrName, markName (name of site), chrRegion (for monocen. and opt for whole arm (w) in holocen.), markDistCen (for monocen.), markPos (for holocen.), markSize; column chrRegion: use p for short arm, q for long arm, cen for centromeric mark and w for whole chr. mark; column markDistCen: use distance from centromere to mark, not necessary for cen. marks (cen), w, p, q (when whole arm). See also param. markDistType

defaultStyleMark
character, default style of mark, only used when style column of dfMarkColor data.frame is missing or in absence of this data.frame. Use "square" (default), "squareLeft", "dots", "cM", "cMLeft","cenStyle", "upArrow", "downArrow".

markDistType
character, if "cen" = the distance you provided in data.frame (dfMarkPos) column markDistCen or markPos is to the center of the mark, if "beg" = the distance you provided is to the beginning of the mark (Default)

protruding
numeric, when style of mark is "cM", fraction of chrWidth to stretch marker. Defaults to 0.2. Introduced in 1.13

startPos
numeric, factor to increase separation of exProtein marks to chromosome. Defaults to 0

pMarkFac
numeric, fraction of chr. size for exProtein style marks. Defaults to 0.25

origin,
For non-monocentric chr. (for holocentrics only) Use "b" (default) if distance to mark in ("markPos" column in "dfMarkPos") data.frame measured from bottom of chromosome, use "t" for distance to mark from top of chr.

efZero,
numeric, numbers below this one will be considered as zero, for comparison purposes. Defaults to 1e-5

cMBeginCenter,
boolean, start position of cM and cMLeft marks. If TRUE, starts in the center (width) of chr. Defaults to FALSE

arrowhead
numeric, proportion of head of arrow (mark styles: upArrow, downArrow). Defaults to 0.3

shrinkArrow
numeric, proportion, shrinks body of arrow. Defaults to 0.3333

arrowheadWidthShrink
numeric, proportion, shrinks head of arrow. Defaults to 0.1

arrowsToSide
boolean, when FALSE use a centered arrow, instead of an arrow next to chr. margins (TRUE, default). See arrowsBothChrt

useOneDot
boolean, use one dot instead of two in style of marks dots. Defaults to FALSE. Not useful for chromatids=TRUE

dotsAsOval
boolean, use oval instead of two dots in style of marks dots. Defaults to FALSE. See useOneDot. Not useful for chromatids=TRUE or circularPlot=TRUE

dfMarkColor
data.frame, optional, specifying colors and style for marks (sites); columns: markName, markColor, style. style accepts: square, squareLeft, dots, cM, "cMLeft", "cenStyle", "upArrow", "downArrow", "exProtein". (if column style missing all (except 5S) are plotted as in param. defaultStyleMark).

mycolors
character vector, optional, i.e. c("blue", "red", "green") for specifying color of marks in order of appearance. if diverges with number of marks will be
recycled if dfMarkColor present, mycolors will be ignored. To know the order of your marks use something like: unique(dfMarkPos$markName)

alpha_val numeric vector, make marks transparent, accepts values from 0 to 1, @see scales::alpha

borderOfWhiteMarks boolean, if TRUE (Default) uses black border for white marks. See dfMarkColor. Does not apply to marks with style cenStyle

colorBorderMark character, without default, pass a name of a color to use as border of marks. See borderOfWhiteMarks

lwd.mimicCen thickness of lines of cenStyle marks; affects only lateral borders. Defaults to lwd.chr

defCenStyleCol character, color of outer part of cenStyle marks. Defaults to white

pattern REGEX pattern to remove from names of marks

legend character, "none" for no legend: "inline" prints labels near chromosomes; "aside" prints legend to the right of karyotypes (default). See markLabelSpacer

remSimiMarkLeg boolean, when legend="aside", if you use pattern, you can have several marks with same name. When TRUE this remove this pseudoduplicates from legend. Be sure that this pseudoduplicates have the same color, otherwise you should use FALSE.

bannedMarkName character, character string or vector with mark names to be removed from plot. Not the marks but the labels. Except when bMarkNameAside is used.

bMarkNameAside boolean, when TRUE and legend="inline", shows marks in bannedMarkName as legend="aside".

forbiddenMark, character, character string or vector with mark names to be removed from plot. Not the marks but the labels.

legendWidth numeric, factor to increase width of squares and of legend. Defaults to 1.7

legendHeight numeric, factor to increase height of squares and dots of legend. Automatic.

markLabelSize numeric, only if legend != (not) "", size of the font of labels of marks (legend). Defaults to 1

markLabelSpacer numeric, only if legend="aside", space from the rightmost chr. to legend. Defaults to 1

legendYcoord numeric, modify Y position of legend when legend="aside"

markNewLine, character, character to split mark Names into different lines. Applies to square marks. Defaults to NA

mylheight, numeric, for markNewLine!=NA: is equivalent to lheight of par: "The line height multiplier. The height of a line of text (used to vertically space multi-line text) is found by multiplying the character height both by the current character expansion and by the line height multiplier." Defaults to 0.7.

chrSize boolean, when TRUE adds total chr size under each chr. Defaults to FALSE

nsmall numeric, rounding decimals for chrSize parameter. Defaults to 1
<table>
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<tr>
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<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>chrSizeMbp</code></td>
<td>boolean, when TRUE adds total Mbp chr. size to each chr. provided, there is a Mbp column in <code>dfChrSize</code> data.frame. Defaults to FALSE. If data in columns <code>shortArmSize</code>, or col. <code>chrSize</code> is in millions (&quot;Mbp&quot;). Use <code>chrSize=TRUE</code> not this one (not column Mbp, you don't need this).</td>
</tr>
<tr>
<td><code>markPer</code></td>
<td>character vector, name of mark(s) to calculate % of mark in chr. and add it to plot. See <code>perAsFraction</code></td>
</tr>
<tr>
<td><code>showMarkPos</code></td>
<td>boolean, adds position of marks under karyotype (fraction 0-1) when TRUE. Defaults to FALSE</td>
</tr>
<tr>
<td><code>bToRemove</code></td>
<td>character vector, bands to remove from calc. of pos., when <code>showMarkPos = TRUE</code></td>
</tr>
<tr>
<td><code>perAsFraction</code></td>
<td>boolean, when TRUE % is shown as fraction. Defaults to FALSE. See <code>markPer</code></td>
</tr>
<tr>
<td><code>chrIndex</code></td>
<td>character, add arm ratio with &quot;AR&quot; and centromeric index with &quot;CI&quot;, or &quot;both&quot; (Default), or &quot;none&quot; for none</td>
</tr>
<tr>
<td><code>morpho</code></td>
<td>character, when &quot;both&quot; (default) prints the Guerra and Levan classif of cen. position, use also &quot;Guerra&quot; or &quot;Levan&quot; or &quot;none&quot; for none. See also <code>?armRatioCI</code>.</td>
</tr>
<tr>
<td><code>nameChrIndexPos</code></td>
<td>numeric, modify position of name of chr. indices</td>
</tr>
<tr>
<td><code>karIndex</code></td>
<td>logical, add karyotype indices A (intrachromosomal - centromere pos.) and A2 (interchromosomal asymmetry, variation among chromosome sizes)</td>
</tr>
<tr>
<td><code>karIndexPos</code></td>
<td>numeric, move karyotype index. Defaults to 0.5</td>
</tr>
<tr>
<td><code>ruler</code></td>
<td>boolean, display ruler to the left of karyotype, when FALSE no ruler</td>
</tr>
<tr>
<td><code>useMinorTicks</code></td>
<td>boolean, display minor ticks between labeled ticks in ruler. See <code>miniTickFactor</code>. Defaults to FALSE. (ticks without label)</td>
</tr>
<tr>
<td><code>miniTickFactor</code></td>
<td>numeric, number of minor ticks for each labeled tick. See <code>useMinorTicks</code>. Defaults to 1</td>
</tr>
<tr>
<td><code>rulerPos</code></td>
<td>numeric, absolute position of ruler, corresponds to <code>pos</code> argument of <code>axis</code> R plot</td>
</tr>
<tr>
<td><code>ruler.tck</code></td>
<td>numeric, tick size of ruler, corresponds to <code>tck</code> argument of <code>axis</code> R plot. Defaults to -0.02</td>
</tr>
<tr>
<td><code>rulerNumberPos</code></td>
<td>numeric, modify position of numbers of ruler. Defaults to 0.5</td>
</tr>
<tr>
<td><code>rulerNumberSize</code></td>
<td>numeric, size of number's font in ruler. Defaults to 1</td>
</tr>
<tr>
<td><code>collapseCen</code></td>
<td>boolean, avoid spacing in ruler between short arm and long arm.</td>
</tr>
<tr>
<td><code>rulerInterval</code></td>
<td>numeric, intervals in ruler. No default, automatic.</td>
</tr>
<tr>
<td><code>rulerIntervalM</code></td>
<td>numeric, intervals in ruler of OTU in <code>specialOTUNames</code>. No default. Introduced in 1.13</td>
</tr>
<tr>
<td><code>rulerIntervalMb</code></td>
<td>numeric, intervals in ruler of OTU with data in Mb (&gt;MbThreshold) and absent from <code>specialOTUNames</code>. No default. Use data in millions</td>
</tr>
<tr>
<td><code>ceilingFactor</code></td>
<td>numeric, affects number of decimals for ceiling. Affects max. value of ruler. Defaults to 0. When threshold is greater than 35 this may have to be negative. Introduced in 1.13</td>
</tr>
</tbody>
</table>
xPosRulerTitle,
numeric, modify position of ruler title. See yTitle, specialyTitle, MbUnit. Defaults to 2.6. A value of 2.6 means 2.6 times the value of chrSpacing to the left, from the first chr.

yPosRulerTitle,
numeric, affects vertical position of ruler title. Defaults to 0

rulerTitleSize,
numeric font size of units of ruler. See also xPosRulerTitle

xlimLeftMod numeric, modifies xlim left argument of plot

xlimRightMod numeric, xlim right side modification by adding space to the right of idiograms. Defaults to 2

ylimBotMod numeric, modify ylim bottom argument of plot

ylimTopMod numeric, modify ylim top argument of plot

callPlot boolean, create new plot in your device. Defaults to TRUE

asp numeric, y x aspect of plot. Defaults to 1

circularPlot boolean, if TRUE chromosomes/karyotypes are plotted in concentric circles. Defaults to FALSE

verticalPlot boolean, when TRUE karyotypes are plotted vertically, otherwise, horizontally Defaults to TRUE

karSpaceHor numeric, separation among horizontal karyotypes. When verticalPlot=FALSE. Defaults to 0

shrinkFactor numeric, for circularPlot=TRUE percentage of usage of circle. Defaults to 0.9

separFactor numeric, for circularPlot=TRUE modify separation of concentric karyotypes. Defaults to 1.5

labelSpacing numeric, for circularPlot=TRUE. Spacing of mark labels. Defaults to 0.7

labelOutwards boolean, inline labels projected outwards

chrLabelSpacing numeric, for circularPlot=TRUE. Spacing of chr. labels. Defaults to 0.5

radius numeric, for circularPlot=TRUE. Affects radius of karyotypes. Defaults to 0.5

rotation numeric, anti-clockwise rotation, defaults to 0.5 which rotates chr. from top to -90 degrees. (-0.5*π)

circleCenter numeric, for circularPlot=TRUE. Coordinate X of center of circles. Affects legend="aside" position. Defaults to 1

circleCenterY numeric, for circularPlot=TRUE. Coordinate Y of center of circles. Affects legend="aside" position. Defaults to 1

OTUlabelSpacing numeric, for circularPlot=TRUE. Spacing for OTU names. Defaults to 0.3

OTUsrt numeric, for circularPlot=TRUE. Angle to use for OTU names. Defaults to θ

OTUplacing character, for circularPlot=TRUE. location of OTU name. Defaults to “first” plots name near first chr. “number” places number near 1st chr. and index and name to the right or center. “simple” place name to the right or center without numbering. See also OTUcentered
plotIdiograms

OTULabelSpacerX
numeric, for circularPlot=TRUE and OTUplacing="number" or "simple". Modifies x names position

OTULabelSpacery
numeric, for circularPlot=TRUE and OTUplacing="number" or "simple". Modifies y names position

OTUcentered
boolean, for circularPlot=TRUE and OTUplacing="number" or "simple". OTU name in center of circle when TRUE, otherwise, to the right.

OTUjustif
numeric, for circularPlot=TRUE and OTUplacing="number" or "simple". Justification of OTU name. 0 = left (Default); use 0.5 for centered. See ?text -> adj

OTUlegendHeight
numeric, for circularPlot=TRUE and OTUplacing="number" or "simple". Modifies y names separation

roundness
deprecated, use squareness

... accepts other arguments for the plot, see, ?plot

Value

plot

See Also

asymmetry
armRatioCI
chrbasicdatamono
chrbasicdataHolo
markposDFs
markdataholo
dfMarkColor

Examples

data(dfOfChrSize)
plotIdiograms(dfOfChrSize, ylimBotMod = .75, rulerPos = -.5)
plotIdiograms(dfOfChrSize, circularPlot = TRUE, chrLabelSpacing = 1)
plotIdiograms(dfChrSizeHolo, rulerPos = -.5)
posCalc

**FUNCTION posCalc and fillMarkInfo**

**Description**

calculates position of marks in fraction of (%) chromosome units (0-1)

**Usage**

```r
posCalc(
  dfMarkPos,
  listOfdfChromSize,
  bToRemove = "",
  markDistType = "beg",
  origin = "b",
  showBandList = FALSE,
  result = "tibble"
)
```

```r
fillMarkInfo2(dfMarkPos, dfChrSize)
```

```r
fillMarkInfo(dfMarkPos, dfChrSize, markDistType = "beg", origin = "b")
```

**Arguments**

- `dfMarkPos` data.frame of marks' position
- `listOfdfChromSize` list (for posCalc) or data.frames of chr. sizes.
- `bToRemove`, character, bands to remove from calc. of pos.
- `markDistType` markDistType character, if "cen" = the distance you provided in data.frame (dfMarkPos) column markDistCen or markPos is to the center of the mark, if "beg" = the distance you provided is to the beginning of the mark (Default)
- `origin`, character, For non-monocentric chr. (for holocentrics only) Use "b" (default) if distance to mark in ("markPos" column in "dfMarkPos") data.frame measured from bottom of chromosome, use "t" for distance to mark from top of chr.
- `showBandList`, boolean, show row of all bands in tibble, see "result"
- `result` character, use "tibble" to get results in tibble, "data.frame", or other string results in a list
- `dfChrSize` data.frame of chr. sizes

**Value**

- list, tibble
data.frame of marks
data.frame of marks
Examples

load(system.file("shinyApps", "iBoard/www/rda/monoholoCS.rda", package = "idiogramFISH"))
load(system.file("shinyApps", "iBoard/www/rda/monoholoMarks.rda", package = "idiogramFISH"))
monoholoMarks2 <- fillMarkInfo(monoholoMarks, monoholoCS)
posCalc(monoholoMarks2, monoholoCS, result = "data.frame")

robert

FUNCTION to produce a Robertsonian translocation

Description

This function reads a data.frame with chr. sizes chrbasicdatamono and another with marks’ positions, markposDFS and gets as arguments two chr. names and two arms, respectively.

It returns a list with two data.frames. One with the chr. size of the resulting translocation and another with the marks’ positions for the derivative chr.

Usage

robert(dfChrSize, dfMarkPos, chr1, chr2, arm1, arm2)

Arguments

dfChrSize name of data.frame of chr. sizes

dfMarkPos name of data.frame of chr marks’ positions

chr1 name of chr.

chr2 name of chr.

arm1 arm of chr1 to be included

arm2 arm of chr2 to be included

Value

list

References


Examples

data(humChr)
data(humMarkPos)
chrt13q14q <- robert(humChr, humMarkPos, 13, 14, "q", "q")
runBoard

FUNCTION runBoard

Description

runBoard: run shinyApp

Usage

runBoard(installAll = FALSE)

Arguments

installAll boolean, when TRUE dependences are installed without asking. Defaults to FALSE

Value

shiny
Index

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