

Package ‘idiogramFISH’

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Title Shiny App. Idiograms with Marks and Karyotype Indices

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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) <<https://onlinelibrary.wiley.com/doi/abs/10.1111/j.1601-5223.1964.tb01953.x>>, karyotype indices of Watanabe et al. (1999) <[doi:10.1007/PL00013869](https://doi.org/10.1007/PL00013869)> and Romero-Zarco (1986) <[doi:10.2307/1221906](https://doi.org/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

License GPL (>= 2)

Encoding UTF-8

LazyData true

Suggests rentrez, ggplot2, ggpubr, ggtree, phytools, treeio, rmdformats, knitr, kableExtra, rvcheck, badger, rmarkdown, RCurl, shiny, shinydashboard, rhandsontable, gtools, rclipboard, clipr, shinyjs

VignetteBuilder rmdformats, knitr, kableExtra, rmarkdown, RCurl, rvcheck, badger, rentrez

SystemRequirements pandoc (>= 2.0)

URL <https://ferroao.gitlab.io/manualidiogramfish/>,
<https://ferroao.gitlab.io/idiogramfishhelppages>

BugReports <https://gitlab.com/ferroao/idiogramFISH/-/issues>

RoxygenNote 7.2.1

NeedsCompilation no

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| | |
|------------|--|
| armRatioCI | <i>FUNCTIONS armRatioCI and swapChrRegionDfSizeAndMarks.</i> |
|------------|--|

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)
```

Arguments

dfChrSize name of data.frame with columns: shortArmSize, longArmSize
 rnumeric 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.

Guerra. 1986. Reviewing the chromosome nomenclature of Levan et al. Braz. Jour. Gen. Vol IX, 4, 741-743

See Also

[chrbasicdatamono](#)

Examples

```
armRatioCI(dfOfChrSize)
armRatioCI(bigdfOfChrSize)

swapChrRegionDfSizeAndMarks(dfOfChrSize,dfOfMarks,"1")
```

 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

$$A = \frac{\sum_{i=1}^n \frac{longArm_i - shortArm_i}{CL_i}}{n}$$

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

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

```
asymmetryA2(dfChrSize)
```

Arguments

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

Value

list

References

Watanabe K, Yahara T, Denda T, Kosuge K. 1999. Chromosomal evolution in the genus *Brachyscome* (Asteraceae, Astereae): Statistical tests regarding correlation between changes in karyotype and habit using phylogenetic information. *Journal of Plant Research* 112: 145-161. 10.1007/PL00013869

A2: Romero-Zarco. 1986. A New Method for Estimating Karyotype Asymmetry. *Taxon* Vol. 35, No. 3 pp. 526-530

Paszko B. 2006. A critical review and a new proposal of karyotype asymmetry indices. *Plant Syst Evol* 258:39-48.

See Also

[chrbasicdatamono](#)

[chrbasicdatamono](#)

[chrbasicdataHolo](#)

Examples

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

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:

OTU OTU, species, optional if only one OTU (species)

chrName name of chromosome

shortArmSize size of short arm, micrometers

longArmSize size of long arm, micrometers

group chr group, optional

chrNameUp optional name over kar.

Mbp optional name to show size in Mbp, use only when shortArmSize is not in Mbp

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.

Source

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

References

Adler 1994. Idiogram Album. <http://www.pathology.washington.edu/research/cytopages/idiograms/human/>

Golczyk H, Hasterok R, Joachimiak AJ (2005) FISH-aimed karyotyping and characterization of Renner complexes in permanent heterozygote Rhoeco spathacea. Genome 48:145–153.

See Also

[plotIdiograms](#)

[armRatioCI](#)

[asymmetry](#)

[markposDFs](#)

`citrusSize`

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 FLO, this conversion is automatic. So, in plot you will never see FLO_1, FLO_2, for example.

Usage

```
citrusSize( A = 0, B = 0, C = 0, D = 0, E = 0, F = 0, FL = 0, FLO = 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) |
| FL0 | number of FL0 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

Carvalho, R., Soares Filho, W. S., Brasileiro-Vidal, A. C., & Guerra, M. (2005). The relationships among lemons, limes and citron: A chromosomal comparison. *Cytogenetic and Genome Research*, 109(1–3), 276–282. <https://doi.org/10.1159/000082410>

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<-markOverCMA(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

Adler 1994. Idiogram Album. URL: <http://www.pathology.washington.edu/research/cytopages/idiograms/human/>

See Also

[plotIdiograms](#)

[markposDFs](#)

[markdataholo](#)

| | |
|---------------|-------------------------------|
| genBankReadIF | <i>FUNCTION</i> genBankReadIF |
|---------------|-------------------------------|

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")
```

Arguments

filename.gb name of file to read, downloaded from genBank, or, object from `rentrez::entrez_fetch(db="nuccore", id="theID", rettype="gbwithparts", retmode = "text")`

forbiddenFields names of field of feature (CDS, gene) to ignore, separated by |. Defaults to "translation"

Value

list

| | |
|---------------|-------------------------------|
| make.uniqueIF | <i>FUNCTION make.uniqueIF</i> |
|---------------|-------------------------------|

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 | <i>FUNCTION to make a data.frame of Marks' characteristics</i> |
|-------------------------|--|

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

```
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 | <i>FUNCTIONS mapGGChr and mapGGChrMark (for ggplot)</i> |
|----------|---|

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

 markdataholo

Mark Positional data - Holocen.

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

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 - monocentric*

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``dfOfMarks``dfOfMarks2``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

Adler 1994. Idiogram Album. URL: [Washington U](#).

Golczyk H, Hasterok R, Joachimiak AJ (2005) FISH-aimed karyotyping and characterization of Renner complexes in permanent heterozygote Rhoeo spathacea. Genome 48:145–153.

See Also

[markdataholo](#)

[plotIdiograms](#)

[chrbasicdatamono](#)

[dfMarkColor](#)

namesToColumns

FUNCTION that modifies marks' names into columns

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. ($-0.5 * \pi$) |
| defaultStyleMark | character, if some data in column style missing fill with this one. Defaults to "square" |
| orderChr | character, replaces orderBySize - deprecated 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 |
| halfModDown | numeric, for circ. plots, when plotting several chromosomes in a circular plot, using a small value 0.05 corrects for alignment problems of downArrows, cmLeft labels. Defaults to NA |
| halfModUp | numeric, for circ. plots, when plotting several chromosomes in a circular plot, using a small value 0.05 corrects for alignment problems of upArrows, cM labels. Defaults to NA |
| rotatMod | numeric, for circ. plots, when rotation $\neq 0$ (diff.), corrects alignment of labels. Defaults to 0 |

Value

data.frame

| | |
|---------|-------------------------|
| perMark | <i>FUNCTION perMark</i> |
|---------|-------------------------|

Description

calculates fraction (%) of chromosome for each mark

Usage

```
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

```
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")
```

| | |
|---------------|---|
| plotIdiograms | <i>FUNCTION to plot idiograms of karyotypes with and without centromere</i> |
|---------------|---|

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,
anchorVsizeF = 0.5, anchorHsizeF = 1, pchAnchor = 23, moveAnchorV = 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 = "µm", specialyTitle = "cM", specialOTUNames = "", addOTUName = TRUE,
OTU textSize = 1, OTUfont, OTUfamily = "", OTUasNote = FALSE,
OTUasLeftNote = FALSE, orderChr = "size", chrId = "original",
classMbName = "Pm.", classcMName = "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, exHoloFrArrToSide = FALSE, xModifier = 12,
xModMonoHoloRate = 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, arrowhead = 0.3, shrinkArrow = 0.3333,
arrowheadWidthShrink = 0.1, arrowsToSide = TRUE, useOneDot = FALSE,
dotsAsOval = FALSE, dfMarkColor, mycolors, 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,
ruler = TRUE, useMinorTicks = FALSE, miniTickFactor = 10, rulerPos = 0,
ruler.tck = -0.02, rulerNumberPos = 0.5, rulerNumberSize = 1,
collapseCen = TRUE, rulerInterval = 0, rulerIntervalcM = 0,
rulerIntervalMb = 0, ceilingFactor = 0, xPosRulerTitle = 2.6,
yPosRulerTitle = 0, rulerTitleSize = 1, xlimLeftMod = 1, xlimRightMod = 2,
ylimBotMod = 0.2, ylimTopMod = 0.2, callPlot = TRUE, asp = 1,
circularPlot = FALSE, verticalPlot = TRUE, karSpaceHor = 0, shrinkFactor = 0.9,
separFactor = 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")

missOTUs spacings 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, | 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 |
| leftNotesUp, | data.frame, or csv file name in quotes, (shown to the left-up), similar to leftNotes, but intended for placement over chr. |
| 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 | deprecated, use a data.frame for 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 <i>Citrus</i> chr. types names. Creates subindex pos. for FL. Defaults to TRUE. Incompatible with parseStr2lang |
| parseStr2lang, | boolean, parse string in notes with function <code>str2lang(paste0("paste(", note, ")"))</code> for ex: <code>"italic('C. sinensis'), ' Author '"</code> . 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 significant 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 |
| OTU textSize | 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 |

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| 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 Mbp. 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 |

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| 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 |

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| 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 arrowsBothChr |
| 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) |
| 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 |
| chrSizeMbp | boolean, when TRUE adds total Mbp chr. size to each chr. provided, there is a Mbp column in dfChrSize data.frame. Defaults to FALSE. If data in columns shortArmSize, or col. chrSize is in millions ("Mbp"). Use chrSize=TRUE not this one (not column Mbp, you don't need this). |
| markPer | character vector, name of mark(s) to calculate % of mark in chr. and add it to plot. See perAsFraction |
| showMarkPos | boolean, adds position of marks under karyotype (fraction 0-1) when TRUE. Defaults to FALSE |
| bToRemove, | character vector, bands to remove from calc. of pos., when showMarkPos = TRUE |
| perAsFraction | boolean, when TRUE % is shown as fraction. Defaults to FALSE. See markPer |
| chrIndex | character, add arm ratio with "AR" and centromeric index with "CI", or "both" (Default), or "none" for none |
| morpho | character, when "both" (default) prints the Guerra and Levan classif of cen. position, use also "Guerra" or "Levan" or "none" for none. See also ?armRatioCI. |
| nameChrIndexPos | numeric, modify position of name of chr. indices |
| karIndex | logical, add karyotype indices A (intrachromosomal - centromere pos.) and A2 (interchromosomal asymmetry, variation among chromosome sizes) |
| karIndexPos | numeric, move karyotype index. Defaults to 0.5 |

| | |
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| ruler | boolean, display ruler to the left of karyotype, when FALSE no ruler |
| useMinorTicks | boolean, display minor ticks between labeled ticks in ruler. See miniTickFactor. Defaults to FALSE. (ticks without label) |
| miniTickFactor | numeric, number of minor ticks for each labeled tick. See useMinorTicks. Defaults to 10 |
| rulerPos | numeric, absolute position of ruler, corresponds to pos argument of axis R plot |
| ruler.tck | numeric, tick size of ruler, corresponds to tck argument of axis R plot. Defaults to -0.02 |
| rulerNumberPos | numeric, modify position of numbers of ruler. Defaults to 0.5 |
| rulerNumberSize | numeric, size of number's font in ruler. Defaults to 1 |
| collapseCen | boolean, avoid spacing in ruler between short arm and long arm. |
| rulerInterval | numeric, intervals in ruler. No default, automatic. |
| rulerIntervalcM | numeric, intervals in ruler of OTU in specialOTUNames. No default. Introduced in 1.13 |
| rulerIntervalMb | numeric, intervals in ruler of OTU with data in Mb (>MbThreshold) and absent from specialOTUNames. No default. Usa data in millions |
| ceilingFactor | 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 |
| xPosRulerTitle, | numeric, modify position of ruler title. See yTitle, specialtyTitle, 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. $(-0.5 * \pi)$ |
| 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 0 |
| 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 |
| 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

```

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

fillMarkInfo2(dfMarkPos, dfChrSize)

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

Robertson, W. R. B. (1916). Chromosome studies. I. Taxonomic relationships shown in the chromosomes of Tettigidae and Acrididae: V-shaped chromosomes and their significance in Acrididae, Locustidae, and Gryllidae: chromosomes and variation. *Journal of Morphology*, 27(2), 179-331.

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

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