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, 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 7.2.3

NeedsCompilation no

Author Fernando Roa [aut, cre],
    Mariana PC Telles [ctb]

Maintainer Fernando Roa <froao@unal.edu.co>

Repository CRAN

Date/Publication 2023-08-22 16:50:02 UTC

R topics documented:

---

armRatioCI   *FUNCTIONS armRatioCI and swapChrRegionDfSizeAndMarks.*

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 Rhoeo 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 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)
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   *FUNCTION 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   *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' characterisitcs

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   *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

---

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 - 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

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*π)
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 != 0 (diff.), corrects alignment of labels. Defaults to 0

Value

data.frame

---

perMark   *FUNCTION perMark*

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   *Plot idiograms of karyotypes/genomes with and without centromere*

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,
OTUTextSize = 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, excHoloFrArrToSide = 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, 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,
    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. Defautl 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,	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 *Citrus* chr. types names. Creates subindex pos. for FL. Defaults to TRUE. Incompatible with parseStr2lang
parseStr2lang,	
	bolean, 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 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`

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","centStyle", "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", "centStyle", "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

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`
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, 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 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

Index