

# Package ‘idiogramFISH’

September 30, 2021

**Title** Shiny App. Idiograms with Marks and Karyotype Indices

**Version** 2.0.6

**Date** 2021-09-27

**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 (when not circular). Supports micrometers, cM and Mb or any unit. Three styles of centromeres are available: triangular, 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](https://doi.org/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

**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** 7.1.2

**NeedsCompilation** no

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armRatioCI	<i>FUNCTIONS armRatioCI and swapChrRegionDfSizeAndMarks.</i>
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## 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

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*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 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

### Usage

dfMarkColor

humMarkColor

mydfMaColor

dfMarkColor5S25S

### 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.

**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 genBankReadIF</i>
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**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>
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---

**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>
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---

**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

### Usage

```
bigdfMarkPosHolo
```

```
dfMarkPosHolo
```

```
dfAlloParentMarksHolo
```

```
bigdfOfMarks3Mb
```

### 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.

### 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 15 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 != 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	<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, 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, 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, dfCenMarks,
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,
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

<code>karHeight</code>	numeric, vertical size of karyotypes. See also <code>karHeiSpace</code> . Defaults to 2
<code>karHeiSpace</code>	numeric, vertical size of karyotypes including spacing. Use with <code>karSepar=FALSE</code> . Proportional to <code>karHeight</code> , if overlap, increase. Default value 2.5
<code>karSepar</code>	boolean, reduce distance among karyotypes FALSE = equally sized karyotypes or TRUE = equally spaced karyotypes. Incompatible with <code>addMissingOTUAfter</code>
<code>amoSepar</code>	numeric, depends on <code>karSepar=TRUE</code> , if zero your karyotypes will have no distance among them, if overlap, increase this and <code>karHeiSpace</code>
<code>addMissingOTUAfter</code>	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. <code>c("species one", "species five")</code>
<code>addMissingOTUBefore</code>	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. <code>c("species one", "species five")</code>
<code>missOTUspacings</code>	numeric, when you use <code>addMissingOTUAfter</code> this numeric vector should have the same length and corresponds to the number of free spaces (ghost OTUs) to add after each OTU respectively
<code>moveKarHor</code>	character, OTUs' names of karyotypes that should be moved horizontally. See <code>mkhValue</code>
<code>moveAllKarValueHor</code>	numeric, similar to <code>mkhValue</code> , but affects all karyotypes.
<code>moveAllKarValueY</code>	numeric, similar to <code>moveAllKarValueHor</code> , but affects y axis.
<code>karAnchorLeft</code>	character, OTUs' add anchor to the left of this OTU names of karyotypes. For <code>verticalPlot=FALSE</code>
<code>karAnchorRight</code>	character, OTUs' add anchor to the right of this OTU names of karyotypes. For <code>verticalPlot=FALSE</code>
<code>anchor</code>	boolean, when TRUE, plots a parent progeny structure in karyotypes in <code>moveKarHor</code> . Or a horizontal anchor to the left/right of <code>karAnchorLeft</code> , <code>karAnchorRight</code> when <code>verticalPlot=FALSE</code>
<code>anchorLineLty</code>	numeric, type of line in anchor, corresponds to <code>lty</code> . Defaults to 1
<code>anchorText</code>	character, text to add to anchor structure near symbol. See <code>anchor</code> . Defaults to ""
<code>anchorTextMParental</code>	character, designed to fill with a character object the space left of a missing parental in the anchor structure.
<code>anchorTextMoveX</code>	numeric, for vertical plots with <code>anchorText</code> move text in X axis. Defaults to 0.5
<code>anchorTextMoveY</code>	numeric, for horizontal plots with <code>anchorText</code> 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
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, (to the right), with columns OTU and note for adding notes to each OTU, they appear to the right of chromosomes
leftNotes,	data.frame, (to the left), with columns OTU and note for adding notes to each OTU, they appear to the left of chromosomes
leftNotesUp,	data.frame, (to the left), 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 $\mu m$ (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 $\mu m$
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
chrId	character, print name of chromosome, "original" uses the original name in OTU column of dfChrSize, "simple" (just 1 to ...) or "none" 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. A value of TRUE modifies excHoloFrArrToSide to TRUE always.
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 $\mu\text{m}$ . 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
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
dfCenMarks	data.frame, specific for centromeric marks. columns: chrName and markName. See also dfMarkPos for another option to pass cen. marks
defaultStyleMark	character, default style of mark, only used when style column of dfMarkColor data.frame is missing or in absence of this data.frame. Use "square" (default), "squareLeft", "dots", "cM", "cMLeft", "cenStyle", "upArrow", "downArrow".
markDistType	character, if "cen" = the distance you provided in data.frame (dfMarkPos) column markDistCen or markPos is to the center of the mark, if "beg" = the distance you provided is to the beginning of the mark (Default)
protruding	numeric, when style of mark is "cM", fraction of chrWidth to stretch marker. Defaults to 0.2. Introduced in 1.13
startPos	numeric, factor to increase separation of exProtein marks to chromosome. Defaults to 0
pMarkFac	numeric, fraction of chr. size for exProtein style marks. Defaults to 0.25
origin,	For non-monocentric chr. (for holocentrics only) Use "b" (default) if distance to mark in ("markPos" column in "dfMarkPos") data.frame measured from bottom of chromosome, use "t" for distance to mark from top of chr.
efZero,	numeric, numbers below this one will be considered as zero, for comparison purposes. Defaults to 1e-5



<code>cMBeginCenter</code> ,	boolean, start position of <code>cM</code> and <code>cMLeft</code> marks. If TRUE, starts in the center (width) of chr. Defaults to FALSE
<code>arrowhead</code>	numeric, proportion of head of arrow (mark styles: <code>upArrow</code> , <code>downArrow</code> ). Defaults to 0.3
<code>shrinkArrow</code>	numeric, proportion, shrinks body of arrow. Defaults to 0.3333
<code>arrowheadWidthShrink</code>	numeric, proportion, shrinks head of arrow. Defaults to 0.1
<code>arrowsToSide</code>	boolean, when FALSE use a centered arrow, instead of an arrow next to chr. margins (TRUE, default). See <code>arrowsBothChr</code>
<code>useOneDot</code>	boolean, use one dot instead of two in style of marks dots. Defaults to FALSE. Not useful for <code>chromatids=TRUE</code>
<code>dotsAsOval</code>	boolean, use oval instead of two dots in style of marks dots. Defaults to FALSE. See <code>useOneDot</code> . Not useful for <code>chromatids=TRUE</code> or <code>circularPlot=TRUE</code>
<code>dfMarkColor</code>	data.frame, optional, specifying colors and style for marks (sites); columns: <code>markName</code> , <code>markColor</code> , <code>style</code> . <code>style</code> accepts: <code>square</code> , <code>squareLeft</code> , <code>dots</code> , <code>cM</code> , <code>cMLeft</code> , <code>cenStyle</code> , <code>upArrow</code> , <code>downArrow</code> , <code>exProtein</code> . (if column <code>style</code> missing all (except 5S) are plotted as in param. <code>defaultStyleMark</code> ).
<code>mycolors</code>	character vector, optional, i.e. <code>c("blue", "red", "green")</code> for specifying color of marks in order of appearance. if diverges with number of marks will be recycled if <code>dfMarkColor</code> present, <code>mycolors</code> will be ignored. To know the order of your marks use something like: <code>unique(c(dfMarkPos\$markName, dfCenMarks\$markName) )</code>
<code>borderOfWhiteMarks</code>	boolean, if TRUE (Default) uses black border for white marks. See <code>dfMarkColor</code> . Does not apply to marks with style <code>cenStyle</code>
<code>colorBorderMark</code>	character, without default, pass a name of a color to use as border of marks. See <code>borderOfWhiteMarks</code>
<code>lwd.mimicCen</code>	thickness of lines of <code>cenStyle</code> marks; affects only lateral borders. Defaults to <code>lwd.chr</code>
<code>defCenStyleCol</code>	character, color of outer part of <code>cenStyle</code> marks. Defaults to white
<code>pattern</code>	REGEX pattern to remove from names of marks
<code>legend</code>	character, "" for no legend; "inline" prints labels near chromosomes; "aside" prints legend to the right of karyotypes (default). See <code>markLabelSpacer</code>
<code>remSimiMarkLeg</code>	boolean, when <code>legend="aside"</code> , if you use <code>pattern</code> , 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.
<code>bannedMarkName</code>	character, character string or vector with mark names to be removed from plot. Not the marks but the labels. Except when <code>bMarkNameAside</code> is used.
<code>bMarkNameAside</code>	boolean, when TRUE and <code>legend="inline"</code> , shows marks in <code>bannedMarkName</code> as <code>legend="aside"</code> .

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 "" for none
morpho	character, when "both" (default) prints the Guerra and Levan classif of cen. position, use also "Guerra" or "Levan" or "" 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
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. ( $-0.5 * \pi$ )
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
OTUlabelSpacex	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)
```

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posCalc	<i>FUNCTION posCalc and fillMarkInfo</i>
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## 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")
```

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runBoard	<i>FUNCTION runBoard</i>
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**Description**

runBoard: run shinyApp

**Usage**

```
runBoard(installAll = FALSE)
```

**Arguments**

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

shiny

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