

# Package ‘idiogramFISH’

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**Title** Idiograms with Marks and Karyotype Indices

**Version** 1.12.1

**Date** 2020-01-09

**Description** Plot idiograms of several karyotypes having a set of data.frames for chromosome data and optionally mark data. Supports micrometers and Mb. Marks can have square or dot form, its legend (label) can be drawn inline or to the right of karyotypes. 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 (>= 3.0)

**Imports** crayon, plyr, dplyr

**License** GPL (>= 2)

**Encoding** UTF-8

**LazyData** true

**Suggests** ggpubr, ggtree, phytools, ggplot2, treeio, knitr, kableExtra, prettydoc, rvcheck, badger, rmarkdown, RCurl

**VignetteBuilder** knitr, kableExtra, prettydoc, rmarkdown, RCurl, rvcheck, badger

**SystemRequirements** pandoc (>= 2.0)

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

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

**RoxygenNote** 7.0.2

**NeedsCompilation** no

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armRatioCI	<i>FUNCTION to calculate Arm Ratio and C.I. and morphological categories</i>
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### Description

This function reads a data.frame and produces AR (r), CI, Guerra and Levan classifications

### Usage

```
armRatioCI(dfOfChrSize)
```

### Arguments

dfOfChrSize      name of data.frame with columns: shortArmSize, longArmSize

### Value

data.frame

### 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)
```

asymmetry

*FUNCTION to calculate karyotype asymmetry A and A2***Description**

This function reads 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)

related to:

$$CV_{CL} = A_2 * 100$$

(CV = coeff. var.)

**Usage**

```
asymmetry(dfChrSize)
```

**Arguments**

dfChrSize      name of data.frame

**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

**See Also**

[chrbasicdatamono](#)

**Examples**

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

---

asymmetryA2

*FUNCTION to calculate karyotype asymmetry*

---

**Description**

This function reads a data.frame with columns: shortArmSize and longArmSize and optionally OTU and returns a list with the A2 values for the OTUs

If several species present, use column "OTU".

$$A_2 = \frac{sCL}{xCL}$$

(s = std dev, CL = chr. length, x = mean)

related to:

$$CV_{CL} = A_2 * 100$$

(CV = coeff. var.)

**Usage**

```
asymmetryA2(dfChrSize)
```

**Arguments**

dfChrSize      name of data.frame

**Value**

list

**References**

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

**See Also**

[chrbasicdatamono](#)

[chrbasicdataHolo](#)

## Examples

```
asymmetryA2(dfOfChrSize)
as.data.frame(asymmetryA2(bigdfOfChrSize))
asymmetryA2(dfChrSizeHolo)
as.data.frame(asymmetryA2(bigdfChrSizeHolo))
```

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chrbasicdataHolo	<i>Chr. basic data Holo.</i>
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## 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

## See Also

[asymmetryA2](#)

[plotIdiograms](#)

[markdataholo](#)

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chrbasicdatamono      *Chr. basic data Monocen.*

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### Description

dfOfChrSize: Example data for monocentrics

bigdfOfChrSize: Example data for monocentrics for several species, OTU

humChr: Example data for human karyotype (Adler 1994)

allChrSizeSample: Example data for monocentrics for several species, OTU

parentalAndHybChrSize: Example data for monocentrics for GISH

### Usage

dfOfChrSize

bigdfOfChrSize

humChr

allChrSizeSample

parentalAndHybChrSize

### 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

### Source

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

### References

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

**See Also**

[plotIdiograms](#)  
[armRatioCI](#)  
[asymmetry](#)  
[markposDFs](#)

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dfMarkStyle

*Mark characteristics*

---

**Description**

style column does not apply to cen. marks, only color.  
dfMarkColor: Example General data for marks NOT position  
humMarkColor: human mark characteristics  
mydfMaColor: mark characteristics used in vignette of phylogeny

**Usage**

dfMarkColor  
  
humMarkColor  
  
mydfMaColor

**Format**

dfMarkColor a data.frame with columns:  
**markName** name of mark  
**markColor** use R colors  
**style** character, use square or dots, optional

**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](#)

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markdataholo

*Mark Positional data - Holocen.*

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## 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

## See Also

[markposDFs](#)

[plotIdiograms](#)

[chrbasicdataHolo](#)



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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 marks' position

allMarksSample: Example data for marks' position

dfAlloParentMarks: Example data for mark position of GISH of monocen.

## Usage

bigdfOfMarks

dfOfMarks

dfOfMarks2

humMarkPos

allMarksSample

dfAlloParentMarks

## 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)

## Source

Washington U

## References

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

## See Also

[markdataholo](#)  
[plotIdiograms](#)  
[chrbasicdatamono](#)  
[dfMarkColor](#)

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plotIdiograms	<i>FUNCTION to plot idiograms of karyotypes with and without centromere</i>
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## 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,
  Mb,
  MbThresholds = c(10000, 1000),
  addOTUName = TRUE,
  OTUTextSize = 1,
  OTUasNote = FALSE,
  revOTUs = FALSE,
  karHeight = 2,
  karHeiSpace = 2.5,
  karSepar = TRUE,
  amoSepar = 9,
  addMissingOTUafter = NA,
  missOTUspacings = 0,
  n = 50,
  notes,
  notesTextSize = 0.4,
  notesPos = 0.5,
  propWidth = FALSE,
  orderBySize = TRUE,
```

```
chrId = "original",
indexIdTextSize = 1,
distTextChr = 1,
groupUp = FALSE,
chrWidth = 0.5,
chrSpacing = 0.5,
chrColor = "gray",
centromereSize = 1,
cenColor = "gray",
fixCenBorder = TRUE,
roundness = 4,
lwd.chr = 2,
dfMarkPos,
dfCenMarks,
MarkDistanceType,
markDistType = "beg",
origin = "b",
dfMarkColor,
mycolors,
pattern = "",
dotRoundCorr,
useXYfactor = FALSE,
legend = "aside",
legendWidth = 1.7,
legendHeight = NA,
markLabelSize = 1,
markLabelSpacer = 1,
chrIndex = "both",
morpho = "both",
nameChrIndexPos = 2,
karIndex = TRUE,
karIndexPos = 0.5,
ruler = TRUE,
rulerPos = -0.5,
rulerPosMod = 0,
ruler.tck = -0.02,
rulerNumberPos = 0.5,
rulerNumberSize = 1,
ylabline = 0,
xlimLeftMod = 1,
xlimRightMod = 2,
ylimBotMod = 0.2,
ylimTopMod = 0.2,
...
)
```

**Arguments**

dfChrSize	mandatory data.frame, with columns: OTU (optional), chrName (mandatory), shortArmSize, longArmSize for monocen. or chrSize for holocen.
Mb,	deprecated, use MbThresholds
MbThresholds,	numeric vector of length 2. <code>c(10000, 1000)</code> . If <code>chrSize &gt; 10000</code> will be considered Mb. If <code>markSize &gt; 1000</code> will be considered Mb.
addOTUName	boolean, if TRUE adds OTU (species) name to karyotype
OTU textSize	numeric, font size of OTU name (species). Defaults to 1. When <code>OTUasNote</code> is TRUE, use <code>notesTextSize</code> instead
OTUasNote	boolean, if TRUE adds OTU (species) name to the right, see notes
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 <code>karHeiSpace</code> . Defaults to 2
karHeiSpace	numeric, vertical size of karyotypes including spacing. Proportional to <code>karHeight</code> , if overlap, increase
karSepar	boolean, reduce distance among karyotypes FALSE = equally sized karyotypes or TRUE = equally spaced karyotypes. Incompatible with <code>addMissingOTUAfter</code>
amoSepar	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>
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. <code>c("species one", "species five")</code>
missOTU spacings	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
n,	numeric vertices number for round corners
notes,	data.frame, optional, with columns OTU and note for adding notes to each OTU, they appear to the right of chromosomes
notesTextSize	numeric, font size of notes, see notes
notesPos	numeric, move notes to the right
propWidth,	boolean, defaults to FALSE. Diminishes chr. width with increasing number of OTUs
orderBySize	logical value, when TRUE, sorts chromosomes by total length from the largest to the smallest
chrId	character, print name of chromosome, "original" uses the original name in OTU column of <code>dfChrSize</code> , "simple" (just 1 to ...) or "" (none).
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 TRUE
chrWidth	numeric, relative chromosome width. Defaults to 0.5
chrSpacing	numeric, horizontal spacing among chromosomes, see also chrWidth. Defaults to 0.5
chrColor	character, main color for chromosomes
centromereSize	numeric, this establishes the apparent size of cen in the plot in $\mu\text{m}$
cenColor	character, color for centromeres, if GISH use NULL
fixCenBorder	boolean, use chr. color as centromere border color, see cenColor
roundness	numeric, shape of vertices of chromosomes and square marks, higher values more squared
lwd.chr	thick of border of chr. and marks.
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
MarkDistanceType,	deprecated, use 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,	For non-monocentric chr. (for holocentrics only) Use "b" 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.
dfMarkColor	data.frame, optional, specifying colors and style for marks (sites); columns: markName, markColor, style. style accepts: square or dots. (if style missing all are plotted as square)
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(c(dfMarkPos\$markName, dfCenMarks\$markName))
pattern	REGEX pattern to remove from names of marks
dotRoundCorr	numeric, to be deprecated, requires useXYfactor=TRUE corrects roundness of dots and vertices of chromosomes. When style of sites = dots, an increase in this, makes the horizontal radius of the dot smaller. Use asp=1 instead
useXYfactor	boolean, for backwards compatibility, for using dotRoundCorr. Defaults to FALSE

legend	character, "" for no legend; "inline" prints labels near chromosomes; "aside" prints legend to the right of karyotypes (default). See markLabelSpacer
legendWidth	factor to increase width of squares and of legend
legendHeight	factor to increase height of squares and dots of legend
markLabelSize	numeric, only if legend != (not) "", size of the text of labels of marks (legend). Defaults to 1
markLabelSpacer	numeric, only if legend="aside", space from the rightmost chr. to legend. Defaults to 1
chrIndex	character, add arm ratio with "AR" and centromeric index with "CI", or "both" (Default), or "" for none
morpho	character, if "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
ruler	boolean, display ruler to the left of karyotype, when FALSE no ruler
rulerPos	numeric, absolute position of ruler, corresponds to pos argument of axis R plot
rulerPosMod	numeric, modify position of ruler, corresponds to line 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
ylabline,	numeric, modify position of y axis title (Mb). See MbThresholds
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
...	accepts other arguments for the plot, such as, asp

**Value**

plot

**See Also**

[asymmetry](#)  
[armRatioCI](#)  
[chrbasicdatamono](#)  
[chrbasicdataHolo](#)  
[markposDFs](#)  
[markdataholo](#)  
[dfMarkColor](#)

**Examples**

```

data(dfOfChrSize)
plotIdiograms(dfOfChrSize, ylimBotMod = .75)
plotIdiograms(dfChrSizeHolo)

```

---

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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