Package 'isocir'

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Title Isotonic Inference for Circular Data

Depends R(>= 3.0.1), circular(>= 0.4-8), TSP(>= 1.0-7)

Imports combinat(>= 0.0-8)

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Description A bunch of functions to deal with circular data under order restrictions.

License GPL (>= 3)

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Contents

`isocir-package` *Isotonic Inference with Circular data.*

Description

This is an R package to draw ISOtonic inference for CIRcular data.

Details

Package:	isocir
Version:	2.0
Depends:	combinat, circular
License:	GPL (>=3)

Author(s)

Author(s): Sandra Barragán mainly based on the SAS code written by Miguel A. Fernández. Maintainer: <sandra.barragan@gmail.com>

References

Mardia, K. and Jupp, P. (2000). *Directional Statistics*, Chichester: Wiley.

Barragan, S., Fernandez, M.A., Rueda, C. and Peddada, S.D. (2015). isocir: An R Package for Constrained Inference Using Isotonic Regression for Circular Data, with an Application to Cell Biology. *Journal of Statistical Software*, **54**, n1: pp 1–17. doi: 10.18637/jss.v054.i04.

Rueda, C., Fernandez, M. A. and Peddada, S. D. (2009). Estimation of parameters subject to order restrictions on a circle with application to estimation of phase angles of cell-cycle genes. *Journal of the American Statistical Association*, **104**, n485; pp 338–347. `https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2742472/`

Fernandez, M. A., Rueda, C. and Peddada, S. D. (2012). Identification of a core set of signature cell cycle genes whose relative order of time to peak expression is conserved across species, *Nucl. Acids Res.* **40**, n7: pp 2823–2832. doi:10.1093/nar/gkr1077. `https://academic.oup.com/nar/article/40/7/2823/1183140`

Barragan, S., Rueda, C., Fernandez, M.A. and Peddada, S.D. (2015). Determination of Temporal Order among the Components of an Oscillatory System. *PLOS ONE*. **10**, n7: pp 1–14. doi: 10.1371/journal.pone.0124842. `https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4495067/`

See Also

`CIRE`, `sce`, `cond.test`, `mrl`, `datareplic`, `cirdata`, `cirgenes`.

`ACO` *Aggregation of Circular Orders*

Description

This function computes the aggregation of circular orders.

Usage

```
ACO(data, method=c("Naive", "CB", "CMC", "TSP", "CH"),
control.method, ws=NULL, coef=1)
```

Arguments

`data`	vector or matrix of data to be processed. See details.
`method`	"Naive", "CB", "CMC", "TSP", "CH".
`control.method`	"tau", "MSCE", "pos", "cirmean", "cirmed", "1", "2", "3", "4m", "4c", "bin", "pos", "alpha1", "alpha2", "alpha3", "alpha4","alphainf", "time", "arc", "chord", "bin", "pos", "cos", "cmean", "mrl", "e3", "ave", "qua", "nat", "natp", "natb".
`ws`	the weights.
`coef`	The coeficient for TSP method.

Details

This function computes the aggregation of circular orders.

The possible methods are: `Naive`: the naive method of choosing the order from the data. `CB`: the circular Borda method. `TSP`: the Traveling Salesperson Problem apply to aggregation of circular orders. `CH`: the circular Hodge method.

The `coef` argument is the proportion of maximum presolutions check respect to the number of elements n. It means that when the TSP is solved by heuristics, a maximum of the best coef*n possible solutions are proned to be the final solution, they are checked and the one with the best SCE is chosen.

Value

A list with the elements:

`aggre_order`	the circular aggregated order.
`msce`	the MSCE corresponding to the circular aggregated order.
`mtau`	the circular Kendall tau corresponding to the circular aggregated order.
`mintour`	the order corresponding to the tour of minimum length in case of TSP.
`mt_msce`	in case of TSP, the MSCE corresponding to the tour of minimum length.
`tour_length`	in case of TSP, the length of the tour.
`scores`	in case of TSP, the length of each edge. In case of circular Hodge, the scores.

`out`	in case of circular Hodge, the element where the circle is cut.
`error1`	in case of circular Hodge method, the error1.
`error2`	in case of circular Hodge method, the error2.

Author(s)

Author(s): Sandra Barragán. Maintainer: <sandra.barragan@gmail.com>

References

Rueda, C., Fernandez, M. A. and Peddada, S. D. (2009). Estimation of parameters subject to order restrictions on a circle with application to estimation of phase angles of cell-cycle genes. *Journal of the American Statistical Association*, **104**, n485; pp 338–347. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2742472/

Fernandez, M. A., Rueda, C. and Peddada, S. D. (2012). Identification of a core set of signature cell cycle genes whose relative order of time to peak expression is conserved across species, *Nucl. Acids Res.* **40**, n7: pp 2823–2832. doi:10.1093/nar/gkr1077. https://academic.oup.com/nar/article/40/7/2823/1183140

Barragan, S., Rueda, C., Fernandez, M.A. and Peddada, S.D. (2015). Determination of Temporal Order among the Components of an Oscillatory System. *PLOS ONE*. **10**, n7: pp 1–14. doi: 10.1371/journal.pone.0124842. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4495067/

See Also

`eq.test`, `sce`, `cond.test`, `mrl`, `isocir`, `plot.isocir`.

Examples

```
data(cirgenes)
ACO(cirgenes[,c(1:5)], method="TSP", control.method="alpha3")
#datos<- rbind (c(0, 1/10, 1/9, 1, 11/10, 10/9)*pi,c(0, 1/2, 1/10, 1, 3/2, 11/10)*pi)
#ACO(datos, method="TSP", control.method="alpha3")
```

`cirdata` *Random Circular Data.*

Description

An example data set. The data have been created randomly for the purpose of running some examples of the functions of the package **isocir**.

Usage

```
data(cirdata)
```

Details

Every data of the vector come from the unit circle $[0, 2\pi]$.

References

Mardia, K. and Jupp, P. (2000). *Directional Statistics*, Chichester: Wiley.

See Also

`cirgenes`, `datareplic`.

Examples

```
data(cirdata)

# Put groups of the order in the correct form:
orderGroups <- c(1,1,1,2,2,3,4,4)


# execute CIRE to obtain the CIRE with circular order:
example1CIRE <- CIRE(cirdata, groups = orderGroups, circular = TRUE)
example1CIRE

# if the user wants the graphics:
#plot(example1CIRE)
#plot(example1CIRE, option="cirmeans")
```

`CIRE` *Circular Isotonic Regresssion Estimator*

Description

This function obtains the Circular Isotonic Regression Estimator (CIRE) of a set of data assuming an order among them. See details for a full explanation.

Usage

```
CIRE (data, groups=NULL, circular = TRUE)
```

Arguments

`data`	vector or matrix of data to be processed. See details.
`groups`	a numeric vector representing the assumed order of data.
`circular`	logical, by default `TRUE` is the order wrapped around the circle (circular order). If `FALSE` the order is not closed.

Details

It uses the algorithm developed in Rueda et al (2009). The final solution is found in a computationally efficient way by searching for the feasible solution with the smallest SCE, see `sce`. The order can be chosen by the user and is set using the `groups` argument. The order is defined in `groups` by a numeric vector with the positions in the order of each element. An example of order would be the simple circular order, defined by the set C_{sco}.

$$C_{sco} = \{\phi = (\phi_1, \phi_2, \ldots, \phi_q) \in [0, 2\pi]^q : \phi_1 \leq \phi_2 \leq \ldots \leq \phi_q \leq \phi_1\}$$

This order is wrapped around the circle. However, if the user wants the order not to be wrapped, then `circular = FALSE` and the order would be the simple order, for instance:

$$C_{so} = \{\phi = (\phi_1, \phi_2, \ldots, \phi_q) \in [0, 2\pi]^q : 0 \leq \phi_1 \leq \phi_2 \leq \ldots \leq \phi_q \leq 2\pi\}$$

For further information see the vignette of this package **isocir**.

The argument `data` is a vector with the unrestricted circular means or a matrix whose columns are the replications of the data and the rows are the populations. All the values must belong to the interval $[0, 2\pi]$.

The argument `groups` is a numeric vector with length equal to the number of populations, q. Each value of the argument establishes the level of the order the corresponding population is assigned to. The default value is the sequence corresponding to the simple order (1, 2, ..., q), circular if `closed=TRUE`. Notice that no particular order is assumed among the populations belonging to the same level set.

Value

It returns an S3 object of class `isocir` that is a list with the next elements:

`cirmeans`	A list with the unrestricted circular means in the same form as the order introduced by `groups`.
`SCE`	Sum of Circular Errors of the final CIRE.
`CIRE`	A list with the ordered estimations, the result of the algorithm that obtained the CIRE.

The Circular Isotonic Regression Estimator is returned as a list just to see the groups of the order. In case you would like to use it as a vector just run: `unlist(object$CIRE)`.

Author(s)

Author(s): Sandra Barragán based on the SAS routines written by Miguel A. Fernández. Maintainer: <sandra.barragan@gmail.com>

References

Mardia, K. and Jupp, P. (2000). *Directional Statistics*, Chichester: Wiley.

Rueda, C., Fernandez, M. A. and Peddada, S. D. (2009). Estimation of parameters subject to order restrictions on a circle with application to estimation of phase angles of cell-cycle genes. *Journal of* *the American Statistical Association*, **104**, n485; pp 338–347. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2742472/

Fernandez, M. A., Rueda, C. and Peddada, S. D. (2012). Identification of a core set of signature cell cycle genes whose relative order of time to peak expression is conserved across species, *Nucl. Acids Res.* **40**, n7: pp 2823–2832. doi:10.1093/nar/gkr1077. https://academic.oup.com/nar/article/40/7/2823/1183140

See Also

`sce`, `cond.test`, `mrl`, `isocir`, `plot.isocir`.

Examples

```
# We consider the following data from the package that are random circular data:
data(cirdata)
circular_ordered_estimator <- CIRE(cirdata)
# We can take the vector of the CIRE estimators:
circular_ordered_estimator $CIRE
# And the SCE:
circular_ordered_estimator $SCE

# Random data with a more complex order:
CIRE(cirdata, groups=c(1,1,2,3,5,3,4,6))
```

`cirgenes` *A set of angular measurements from cell-cycle experiments with genes.*

Description

A data set taken from some cell-cycle experiments with the purpose of running some examples of the functions of the package **isocir**. See details.

Usage

```
data(cirgenes)
```

Format

The set has a single element:

`cirgenes` a matrix with the measures of several cell-cycle experiments.

Details

This data are located in the unit circle $[0, 2\pi]$.

That matrix `cirgenes` has in its rows the peak expression points for the genes, see Source. The columns of the matrix are the experiments. There are 16 genes (rows) and 10 experiments (columns). The experiments are not held under the same conditions so that the data cannot be considered as replications.

Source

Initially, the data come from the experiments of Oliva et al. (2005), Peng et al. (2005) and Rustici et al. (2004). They are the observed points of peak expressions of some genes along the cell cycle of the S. Pombe yeast and have been obtained using the Random Periods Model developed in Liu et al. (2004). The source of that data is http://www.cyclebase.org/CyclebaseSearch, Gauthier (2007).

References

Fernandez, M. A., Rueda, C. and Peddada, S. D. (2012). Identification of a core set of signature cell cycle genes whose relative order of time to peak expression is conserved across species, *Nucl. Acids Res.* **40**, n7: pp 2823–2832. doi:10.1093/nar/gkr1077. https://academic.oup.com/nar/article/40/7/2823/1183140

Gauthier, N. (2007). Cyclebase.org - A Comprehensive Multi-Organism Online Database of Cell-Cycle Experiments. *Nucleic Acids Research*. **36**, pp 854–859. http://www.cyclebase.org/CyclebaseSearch.

Liu, D., Umbach, D., Peddada, S., Li, L., Crockett, P., Weinberg, C. (2004). A Random Periods Model for Expression of Cell-Cycle Genes. *The National Academy of Sciences of the USA*. **101**(19), pp 7240–7245.

Oliva, A., Rosebrock, A., Ferrezuelo, F., Pyne, S., Chen, H., Skiena, S., Futcher, B. and Leatherwood, J. (2005). The Cell Cycle-Regulated Genes of Schizosaccharomyces pombe. *Plos biology*. **3**.

Peng, X., Karuturi, R., Miller, L., Lin, K., Jia, Y., Kondu, P., Wang, L., Wong, L., Liu, E., Balasubramanian, M. and Liu, J. (2005). Identification of Cell Cycle-Regulated Genes in Fission Yeast. *The American Society for Cell Biology*. **16**, pp 1026–1042.

Rustici, G., Mata, J., Kivinen, K., Lio, P., Penkett, C., Burns, G., Hayles, J., Brazma, A., Nurse, P., and Bahler, J. (2004). Periodic Gene Expression program of the fission yeast cell cycle. *Nature Genetics*. **36**.

See Also

`datareplic`, `cirdata`.

Examples

```
data(cirgenes)

# These values of kappa estimations were obtained by using the calculations
# explained in Fern?ndez et al (2012).

kappas <- c(2.64773, 3.24742, 2.15936, 4.15314, 4.54357,
               29.07610, 6.51408, 14.19445, 5.66920, 11.12889)

allresults <- list()
resultIsoCIRE <- matrix(ncol = ncol(cirgenes), nrow = nrow(cirgenes))

SCEs <- vector(mode = "numeric", length = nrow(cirgenes))
pvalues <- vector(mode = "numeric", length = nrow(cirgenes))

for (i in 1 : nrow(cirgenes)) {
```

```
    k <- kappas[i]
    genes <- as.numeric(cirgenes[i, ])
    allresults[[i]] <- cond.test(genes, groups=c(1:length(genes)), kappa = k)
  resultIsoCIRE[i, !is.na(cirgenes[i, ])] <- round(unlist(allresults[[i]]$CIRE), digits = 3)
    SCEs[i] <- allresults[[i]]$SCE
    pvalues[i] <- allresults[[i]]$pvalue
 }

# resultIsoCIRE is a matrix with the CIRE for each experiment
# pvalues is a vector with the result of the test
```

`cirKendall` *Circular Kendall's Tau*

Description

This function obtains the circular Kendall's tau between two sets of data.

Usage

```
cirKendall(phi1, phi2, test = FALSE, control.test = c("noteq", "upper", "lower"))
```

Arguments

`phi1`	a numeric vector of data to be processed. See details.
`phi2`	a numeric vector of data.
`test`	logical, by default `FALSE`.
`control.test`	"noteq", "upper" or "lower".

Details

This function obtains the circular Kendall's tau between two data set.

Value

It returns the value of the circular Kendall's tau. If `test=TRUE`, it returns also the pvalue of the test.

Author(s)

Author(s): Sandra Barragán. Maintainer: <sandra.barragan@gmail.com>

References

Fisher,N.I. (1993).*Statistical analysis of circular data.* Cambridge University Press.

See Also

`sce`, `cond.test`, `mrl`, `isocir`, `plot.isocir`.

Examples

```
data(cirgenes)
cirKendall(cirgenes[1,],cirgenes[2,])
# Even with missing values:
cirKendall(cirgenes[1,],cirgenes[8,])
```

`CLM` *Circular Local Minimization*

Description

This function computes the Circular Local Minimization.

Usage

```
CLM(data, order0, ws=NULL, control.method=c("msce","cirktau"))
```

Arguments

`data`	matrix of circular data to be processed.
`order0`	the initial order to be improved.
`ws`	the weights.
`control.method`	by default "msce", maximization of "cirktau".

Details

This function computes the Circular Local Minimization of the MSCE by default. It computes the Circular Local Maximization of the Circular Kendall Tau if `control.method="cirktau"`.

Value

This function returns a list with the next elements:

`order0`	the initial order introduced in the arguments.
`msce0`	the mean sum of circular errors of the initial order with the data.

or itemtau0the mean circular Kendall Tau of the initial order with the data.

`final_order`	the final order after proccess the Circular Local Minimization.
`bestsce`	the msce of the final order with the data.

or

`bestau`	the mean circular Kendall Tau of the final order with the data.

Author(s)

Author(s): Sandra Barragán. Maintainer: <sandra.barragan@gmail.com>

References

DWORK, C., KUMAR, R., NAOR, M. and SIVAKUMAR, D. (2001), Rank Aggregation Methods for the Web, Proceedings of the 10th International World Wide Web Conference, pp. 613–622.

See Also

`sce`, `cond.test`, `mrl`, `isocir`, `plot.isocir`.

Examples

```
data(cirgenes)
aggre_order <- ACO(cirgenes[,c(1:5)], method="TSP", control.method="time")$TSP_order[1,]
CLM(cirgenes[,c(1:5)], order0 = c(1:5))
#datos<- rbind (c(0, 1/10, 1/9, 1, 11/10, 10/9)*pi,c(0, 1/2, 1/10, 1, 3/2, 11/10)*pi)
#CLM(datos, order0 = c(1:6))
```

`cond.test` *Conditional Test for Contrasting Circular Order*

Description

This function calculates the p-value corresponding to the conditional test where the hypotheses are whether the data follow a fixed circular order or not.

Usage

```
cond.test(data, groups=NULL, kappa=NULL, biasCorrect=TRUE)
```

Arguments

`data`	vector or matrix with the data. See details.
`groups`	a numeric vector with the circular order to be contrasted.
`kappa`	numeric and positive, if NULL, it will be estimated.
`biasCorrect`	logical, if `TRUE`, the correction of the bias is done in the estimation of kappa.

Details

This function performs the conditional test to constrast the hypotheses:

H_0 : The circular parameters follow a fixed circular order.

H_1 : H_0 is not true.

This conditional test is a modification of the likelihood ratio test. See Fern?ndez et al. (2011) for full details about the conditional test. For a whole explanation of the use of this function, see the vignette of this package where some examples are shown.

The circular order to be tested is defined in the argument `groups` by a numeric vector with the positions in the order of each element. The result of `cond.test` is the p-value of this test. There are two cases depending on whether κ is known or not.

If κ is known, `data` is usually a vector with the unrestricted circular means. In this case the value of κ has to be introduced in the argument `kappa`. `data` could also be a matrix with replications and the user knows the value of κ, then if it is introduced in the argument `kappa` it will be used by the function to perform the contrast instead of using the estimation.

When κ is unknown, replications are needed in order to calculate the estimation. Then, `data` must be a matrix where each column is a replication while each row is a population. κ is estimated internally using the function `mle.vonmises` developed in the package **circular**. By default, the correction of the bias is done, if the user prefers not correcting the bias, just set the argument `biasCorrect=FALSE`.

For both cases (κ known or unknown), the order to be contrasted is introduced in `groups` in the form of a numeric vector with length equal to the number of populations. Each value of the argument establishes the level of the order the corresponding population is assigned to. The default value is the sequence corresponding to the simple order (1, 2, ..., q). Notice that no particular order is assumed among the populations belonging to the same level set.

Value

The output is an S3 object of class `isocir`, similar to the result in the function `CIRE` but adding the following values:

`pvalue`	numeric, it is the p-value what results of the conditional test.
`kappa`	numeric, it is the value of kappa.

The attribute `estkappa` shows if kappa is estimated or known.

Author(s)

Author(s): Sandra Barragán based on the SAS code written by Miguel A. Fernández. Maintainer:<sandra.barragan@gmail.com>

References

Mardia, K. and Jupp, P. (2000). *Directional Statistics*, Chichester: Wiley.

Rueda, C., Fernandez, M. A. and Peddada, S. D. (2009). Estimation of parameters subject to order restrictions on a circle with application to estimation of phase angles of cell-cycle genes. *Journal of the American Statistical Association*, **104**, n485; pp 338–347. `https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2742472/`

Fernandez, M. A., Rueda, C. and Peddada, S. D. (2012). Identification of a core set of signature cell cycle genes whose relative order of time to peak expression is conserved across species, *Nucl. Acids Res.* **40**, n7: pp 2823–2832. doi:10.1093/nar/gkr1077. `https://academic.oup.com/nar/article/40/7/2823/1183140`

See Also

`CIRE`,`sce`, `mrl`, `isocir`, `plot.isocir`.

Examples

```
data(cirdata)
# Example without replications and a partial circular order:
orderGroups <- c(1,1,1,2,2,3,4,4)
cond.test(cirdata, groups = orderGroups, kappa = 0.2)
# Example with replications and the next circular order:
orderGroups2 <- c(1:8)
data(datareplic)
cond.test(data = datareplic, groups = orderGroups2)
```

`datareplic` *Random Circular Data with Replications.*

Description

An example data set. The data have been created randomly for the purpose of running some examples of the functions of the package **isocir**.

Usage

```
data(datareplic)
```

Details

Every data of the matrix come from the unit circle $[0, 2\pi]$.

The data in the matrix `datareplic` are random angular measurements. Its columns are the 10 replications and its rows are the 8 populations.

References

Mardia, K. and Jupp, P. (2000). *Directional Statistics*, Chichester: Wiley.

See Also

`cirgenes`, `cirdata`.

Examples

```
data(datareplic)

# example testing the next order:
orderGroups2 <- c(1:8)

example2test <- cond.test(datareplic, groups = orderGroups2, bias = TRUE)
example2test


round(unlist(example2test$cirmeans), digits = 3)
```

eq.test *Test of Equality of Circular Orders*

Description

This function calculates the test of equality of circular orders in different populations.

Usage

```
eq.test(data, popu, ws=NULL, method=NULL, control.method=NULL, output=NULL, coef=1, N=500)
```

Arguments

`data`	matrix or data.frame with the data. See details.
`popu`	a numeric vector with population to each experiment belongs.
`ws`	a numeric vector with the values to be used as weight per experiment.
`method`	The method to be used to aggregate circular orders with ACO function.
`control.method`	The argument to control the method in ACO function.
`output`	The path where write the output of the global orders.
`coef`	The coefficient to use in case of method=TSP, by default 1.
`N`	The number of randomization selections, by default 500.

Details

This function performs the test to constrast equality of circular orders:

H_0 : The circular parameters follow the same circular order in all populations.

H_1 : H_0 is not true.

The `data` must have the elements in the columns and the experiments in the rows.

Value

The output is a list with the following values:

`allorders`	matrix, in each row the circular order obtained with all selected experiments and the value for the statistic test in that selection.
`pvalue`	numeric, it is the p-value what results of the test.
`global_order`	numeric vector with the elements ordered as the global circular order estimate.
`CC`	numeric, the confidence coefficient (in percentage) of the global order.
`MFO`	numeric vector with the elements ordered as the Most Frequent global Order in the randomization procedure.
`CCMFO`	numeric, the confidence coefficient (in percentage) of the Most Frequent global Order.

Two additional outputs could be obtained in the form of .csv files written in the path given by the user in the argument `output`:

`globalorders.csv`	all the global orders obtained from the randomization procedure and the value of the statistic in each selection.
`frequencydist.csv`	the frequency distribution of all the global orders.

Author(s)

Author(s): Sandra Barrag?n. Maintainer:<sandra.barragan@gmail.com>

References

Rueda, C., Fernandez, M. A. and Peddada, S. D. (2009). Estimation of parameters subject to order restrictions on a circle with application to estimation of phase angles of cell-cycle genes. *Journal of the American Statistical Association*, **104**, n485; pp 338–347. `https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2742472/`

Fernandez, M. A., Rueda, C. and Peddada, S. D. (2012). Identification of a core set of signature cell cycle genes whose relative order of time to peak expression is conserved across species, *Nucl. Acids Res.* **40**, n7: pp 2823–2832. doi:10.1093/nar/gkr1077. `https://academic.oup.com/nar/article/40/7/2823/1183140`

Barragan, S., Rueda, C., Fernandez, M.A. and Peddada, S.D. (2015). Determination of Temporal Order among the Components of an Oscillatory System. *PLOS ONE*. **10**, n7: pp 1–14. doi: 10.1371/journal.pone.0124842. `https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4495067/`

See Also

`ACO`, `CIRE`,`sce`, `mrl`, `isocir`, `plot.isocir`.

Examples

```
data(cirgenes)
eq.test(cirgenes[-8,c(1:5)], popu=c(rep(1,5),rep(2,4)),
ws=c(1,2,3.5,2,1,8,4.2,1.35,6), method="TSP",control.method="alpha3",N=2)
```

`isocir` *S3 Objects of Class isocir.*

Description

This function creates an S3 object of class `isocir`. There are also some methods described for the class `isocir`.

Usage

```
isocir(cirmeans = NULL, SCE =NULL, CIRE = NULL, pvalue = NULL, kappa = NULL)
is.isocir(x)
## S3 method for class 'isocir'
print(x, decCIRE = 3, decpvalue = 4, deckappa = 2, ...)
```

Arguments

`cirmeans`	NULL by default, the unrestricted circular means
`SCE`	NULL by default, the Sum of Circular Errors.
`CIRE`	NULL by default, the Circular Isotonic Regression Estimator.
`pvalue`	NULL by default, the result of the conditional test
`kappa`	NULL by default.
`x`	an object of class CIRE.
`decCIRE`	the number of decimal places to round the CIRE and the SCE.
`decpvalue`	the number of decimal places to round the pvalue.
`deckappa`	the number of decimal places to round kappa.
`...`	futher parameters passed to `print.default`.

Details

With the function `isocir` a list of class `isocir` is created with the elements: `cirmeans`, `SCE`, `CIRE` even if they are NULL. However, `pvalue` and `kappa` are added just in the case that they have any value.

The argument `x` must be of class `isocir`.

Value

An object of class `isocir`.

Author(s)

Sandra Barragán.

See Also

`CIRE`, `cond.test`.

Examples

```
data(cirdata)
x <- CIRE(cirdata)
print(x)
is.isocir(x)
class(x)

plot(x)
```

```
class(x)

# If you want to use the CIRE in other calculations you can obtain it as a vector:
unlist(x$CIRE)
# But be careful because this unclass and lost attributes!

# To create a new object of class CIRE:
y <- isocir()
```

`mcirktau` *Mean Circular Kendall's Tau.*

Description

This function computes the mean Circular Kendall's tau between a circular order and a data set.

Usage

```
mcirktau(data, posorder, ws=NULL)
```

Arguments

`data`	vector or matrix of data to be processed. See details.
`posorder`	The posicions of the order.
`ws`	the weights.

Details

This function computes the mean Circular Kendall's tau between a circular order and a data set.

Value

A list with the elements:

`mtau`	mean circular Kendall's tau.
`ntaus`	a vector with the circular Kendall's tau of all the experiment.

Author(s)

Author(s): Sandra Barragán. Maintainer: <sandra.barragan@gmail.com>

See Also

`sce`, `cond.test`, `cirKendall`, `isocir`, `plot.isocir`.

Examples

```
data(cirgenes)
mcirktau(cirgenes, posorder = c(1:ncol(cirgenes)))
```

`mrl` *Mean Resultant Length*

Description

This function calculates the mean resultant length as defined in Mardia et al. (2000).

Usage

```
mrl(data)
```

Arguments

`data`	matrix with the data

Details

It is supposed that we have n replications for each population.

$$\overline{R} = \frac{1}{n}\sqrt{S^2 + C^2}$$

$$where \quad S = \sum_{k=1}^{n} \sin\theta_k \quad and \quad C = \sum_{k=1}^{n} \cos\theta_k$$

The argument `data` could be a matrix with n columns and q rows, q is the number of populations. `data` could also be a vector. For both cases the function `rho.circular` from the package **circular** is used in the calculations.

Missing values in the replications are allowed.

Value

`mrl`	numeric vector of dimension q with the mean resultant lengths. The i element is the mean resultant lenght of the i population which is in the row i of the matrix `data`.

Author(s)

Author(s): Sandra Barragán. Maintainer: <sandra.barragan@gmail.com>

References

Mardia, K. and Jupp, P. (2000). *Directional Statistics*, Chichester: Wiley.

Rueda, C., Fernandez, M. A. and Peddada, S. D. (2009). Estimation of parameters subject to order restrictions on a circle with application to estimation of phase angles of cell-cycle genes. *Journal of the American Statistical Association*, **104**, n485; pp 338–347. `https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2742472/`

Fernandez, M. A., Rueda, C. and Peddada, S. D. (2012). Identification of a core set of signature cell cycle genes whose relative order of time to peak expression is conserved across species, *Nucl. Acids Res.* **40**, n7: pp 2823–2832. doi:10.1093/nar/gkr1077. `https://academic.oup.com/nar/article/40/7/2823/1183140`

See Also

`CIRE`, `sce`, `cond.test`.

Examples

```
data(datareplic)
mrl(datareplic)
```

`msce` *Mean Sum of Circular Errors.*

Description

This function computes the MSCE between and order and a set of data.

Usage

```
msce(data, posorder, ws=NULL, ...)
```

Arguments

`data`	vector or matrix of data to be processed. See details.
`posorder`	The posicions of the order.
`...`	arguments to pass to CIRE.
`ws`	the weights.

Details

This function computes the MSCE between and order and a set of data.

Value

A list with the elements:

`msce`	The mean of the mean sum of circular errors.
`msces`	a vector with the mean sum of circular errors for each experiment.

Author(s)

Author(s): Sandra Barragán. Maintainer: <sandra.barragan@gmail.com>

See Also

sce, cond.test, mrl, isocir, plot.isocir.

Examples

```
data(cirgenes)
msce(cirgenes, posorder = c(1:ncol(cirgenes)))
```

---

plot.isocir *S3 Method to Plot S3 Objects of Class isocir*

Description

This is a function to plot an object of class `isocir` that is the result of the function `CIRE` and `cond.test`. It creates a plot of circular data points on the current graphics device. Data points are either plotted as points on the unit circle, or the range of the circle is divided into a specified number of bins, and points are stacked in the bins corresponding to the number of observations in each bin.

Usage

```
## S3 method for class 'isocir'
plot(x, option=c("CIRE", "cirmeans"), cex = 1, stack = TRUE,
  axes = TRUE, sep = 0.025, shrink = 1, bins = 300, ticks = FALSE,
  tcl = 0.025, tcl.text = 0.125, col = NULL, tol = 0.04, uin = NULL,
  xlim = c(-1, 1), ylim = c(-1, 1), digits = 2, units = NULL,
  template = NULL, zero = NULL, rotation = NULL,
  main = NULL, sub=NULL, xlab = "", ylab = "",
  control.circle=circle.control(), ...)
```

Arguments

`x`	an object of class `isocir`.
`option`	The points that are used in the plot: If `CIRE`, the Circular Isotonic Regression Estimator. If `cirmeans`, the unrestricted circular means. Default is `CIRE`.
`cex`	point character size. See help on `par`.
`stack`	logical; if `TRUE`, points are stacked on the perimeter of the circle. Otherwise, all points are plotted on the perimeter of the circle. Default is `TRUE`.
`axes`	logical; if `TRUE` axes are plotted according to properties of `x`.
`sep`	constant used to specify the distance between stacked points, if `stack==TRUE` or in the case of more than one dataset. Default is 0.025; smaller values will create smaller spaces.
`shrink`	parameter that controls the size of the plotted circle. Default is 1. Larger values shrink the circle, while smaller values enlarge the circle.
`bins`	if `stack==TRUE`, bins is the number of arcs to partition the circle with. Default is 300.

`ticks`	logical; if `TRUE` ticks are plotted according to the value of `bins`.
`tcl`	length of the ticks.
`tcl.text`	The position of the axis labels.
`col`	color of the points. The values are recycled if needed.
`tol`	proportion of white space at the margins of plot.
`uin`	desired values for the units per inch parameter. If of length 1, the desired units per inch on the x axis.
`xlim`, `ylim`	the ranges to be encompassed by the x and y axes. Useful for centering the plot.
`digits`	number of digits used to print axis values.
`main`, `sub`, `xlab`, `ylab`	title, subtitle, x label and y label of the plot.
`units`	the units used in the plot.
`template`	the template used in the plot.
`zero`	the zero used in the plot.
`rotation`	the rotation used in the plot.
`control.circle`	parameters passed to `plot.default` in order to draw the circle. The function `circle.control` is used to set the parameters.
`...`	futher parameters passed to `points.default`.

Details

When there are many closely distributed observations, stacking is recommended. When stacking the points, if there are many points in a particular bin, it may be necessary to shrink the plot of the circle so that all points fit. This is controlled with the parameter `shrink`. Generally the parameter `sep` does not need adjustment, however, when shrinking the plot, or for a very large number of observations, it may be helpful.

Value

A list with information on the plot: zero, rotation and next.points.

Note

Some codes from `eqscplot` in MASS is used besides some from `plot.circular` in the circular package.

Author(s)

Sandra Barragán based on the code of Claudio Agostinelli and Ulric Lund from the package **circular**.

See Also

`cond.test`, `CIRE`, `isocir`.

Examples

```
data(cirdata)
result<-CIRE(cirdata)
plot(result)
plot(result,option="cirmeans")
```

`sce` *Sum of Circular Error*

Description

This function calculates the distance between two q dimensional points, or between a point and a set of points, in the circular space.

Usage

```
sce(arg1, arg2, meanrl=1)
```

Arguments

`arg1`	vector with the values for the first point.
`arg2`	vector (or matrix) with the values for the second point (set of points).
`meanrl`	vector with the mean resultant lenght, by default 1.

Details

This function is useful to measure the circular error when an estimator is used to estimate an unknown q-dimensional parameter. It plays a role in the circular space similar to that of the mean squared error in the usual Euclidean space.

When `arg2` is a vector:

$$SCE(arg1, arg2) = \sum_{i=1}^{q} r_i[1 - \cos(arg1_i - arg2_i)]$$

If `arg1` and `arg2` are just to q dimensional points, both arguments must be vectors with the same length and `meanrl` is not needed because r_i=1.

If `arg2` is a mean vector coming from several replications, the corresponding mean resultant lengths (r_i) have to be introduced in the argument `meanrl`.

When `arg2` is a matrix:

$$SCE(arg1, arg2) = \sum_{i=1}^{q}\sum_{k=1}^{n}[1 - \cos(arg1_i - arg2_{ik})]$$

If `arg2` is a matrix with the replications in its columns, `meanrl` is not needed as the mean resultant lengths are calculated internally.

Value

The value of the Sum of Circular Error.

Author(s)

Author(s): Sandra Barragán based on the SAS routine written by Miguel A. Fernández. Maintainer: <sandra.barragan@gmail.com>

References

Mardia, K. and Jupp, P. (2000). *Directional Statistics*, Chichester: Wiley.

Rueda, C., Fernandez, M. A. and Peddada, S. D. (2009). Estimation of parameters subject to order restrictions on a circle with application to estimation of phase angles of cell-cycle genes. *Journal of the American Statistical Association*, **104**, n485; pp 338–347. `https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2742472/`

Fernandez, M. A., Rueda, C. and Peddada, S. D. (2012). Identification of a core set of signature cell cycle genes whose relative order of time to peak expression is conserved across species, *Nucl. Acids Res.* **40**, n7: pp 2823–2832. doi:10.1093/nar/gkr1077. `https://academic.oup.com/nar/article/40/7/2823/1183140`

See Also

`CIRE`, `cond.test`, `mrl`.

Examples

```
data(cirdata)
exampledata1 <- cirdata
exampledata2 <- (cirdata+(pi/4))
sce(exampledata1,exampledata2)
```

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