

# Package ‘dplRCon’

February 26, 2015

**Type** Package

**Title** Concordance for Dendroclimatology

**Version** 1.0

**Date** 2015-01-16

**Author** Maryann Pirie

**Maintainer** M R Pirie <maryann.pirie@agresearch.co.nz>

**Description** The concordance method is a non-parametric method based on bootstrapping that is used to test the hypothesis that two subsets of time series are similar in terms of mean, variance or both. This method was developed to address a concern within dendroclimatology that young trees may produce a differing climate response to older more established trees. Details of this method are available in Pirie, M. (2013). The Climate of New Zealand reconstructed from kauri tree rings: Enhancement through the use of novel statistical methodology. PhD. Dissertation, School of Environment and Department of Statistics, University of Auckland, New Zealand. This package also produces a figure with 3 panels, each panel is for a different climate variable. An example of this figure is included in ``On the influence of tree size on the climate - growth relationship of New Zealand kauri (*Agathis australis*): insights from annual, monthly and daily growth patterns. J Wunder, AM Fowler, ER Cook, M Pirie, SPJ McCloskey. *Trees* 27 (4), 937-948''. For further R functions for loading your own dendroclimatology datasets and performing dendrochronology analysis refer to the R package ``dplR: Dendrochronology Program Library in R''. The concordance procedure is intended to add to the standard dendrochronology techniques provided in ``dplR''.

**License** GPL

**LazyLoad** yes

**LazyData** yes

**Depends** R (>= 2.10)

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2015-02-26 01:56:47

## R topics documented:

boot.0.20 . . . . .	2
boot.20.2000 . . . . .	3
climate.anom.dendro.season . . . . .	4
concordance.indices . . . . .	5
correlation.function . . . . .	6
dbh.po.nc . . . . .	7
exact.ci . . . . .	9
Example 1 . . . . .	9
Example 2 . . . . .	11
Figure.correlation.barplot . . . . .	12
figure.function.concordance . . . . .	13
function.id . . . . .	14
function.id.master . . . . .	14
names.stat . . . . .	15
overall.concordance.period . . . . .	15
precipitation . . . . .	17
ring.raw . . . . .	18
ring.stand . . . . .	18
series.bootstrap . . . . .	19
site.chron . . . . .	20
SOI . . . . .	20
stat . . . . .	21
SumNotNa . . . . .	21
temperature . . . . .	22
TruncSeriesPithoffset . . . . .	23

## Index

24

boot.0.20

*Bootstrapped matrix of time series for young material.*

### Description

This is the bootstrapped matrices of mean time series produced from the "series.bootstrap" function.

### Usage

```
data(boot.0.20)
```

### Format

The format is: num [1:515, 1:999] NaN NaN NaN NaN NaN NaN NaN NaN ...

## Examples

```

data(boot.0.20)
## maybe str(boot.0.20) ; plot(boot.0.20) ...
## Not run:
# This dataset was produced by running the following.
data(ring.raw)
data(ring.stand)
data(dbh.po.nc)

#Subset "near-pith" is the material within 0 -20cm from the estimated pith
spline200.sub0.20.n <- TruncSeriesPithoffset( ring.raw, ring.stand, dbh.po.nc, c(1,200))

boot.0.20 <- series.bootstrap( spline200.sub0.20.n$sub.series.stand, stat, 999,
names.stat, aver.by.tree = FALSE)

boot.0.20 <- boot.0.20$boot.series.mean

## End(Not run)

```

boot.20.2000

*Bootstrapped matrix of time series for old material.*

## Description

This is the bootstrapped matrices of mean time series produced from the "series.bootstrap" function.

## Usage

```
data(boot.20.2000)
```

## Format

The format is: num [1:515, 1:999] 1.26 1.045 0.731 0.74 0.705 ...

## Examples

```

data(boot.20.2000)
## maybe str(boot.20.2000) ; plot(boot.20.2000) ...

## Not run:
# This dataset was produced by running the following.
data(ring.raw)
data(ring.stand)
data(dbh.po.nc)

# Subset "far-pith" is the material further than 20cm from the estimated pith
spline200.sub20.2000.n <- TruncSeriesPithoffset( ring.raw, ring.stand, dbh.po.nc, c(200,200000))

boot.20.2000 <- series.bootstrap(spline200.sub20.2000.n$sub.series.stand, stat, 999,

```

```

names.stat, aver.by.tree = FALSE)

boot.20.2000 <- boot.20.2000$boot.series.mean

## End(Not run)

```

**climate.anom.dendro.season**  
*Seasonal Data*

## Description

Changes monthly climate data to seasonal climate data.

## Usage

```
climate.anom.dendro.season(climate.data, year1, year2, year.start, is.anomaly)
```

## Arguments

climate.data	This is a matrix, normally loaded into R in CSV form with the columns: year, jan, feb, mar,..,dec
year1	is the start of the period used to calculate climate anomalies.
year2	is the end of the period used to calculate climate anomalies.
year.start	is the start date of the climate data,
is.anomaly	accepts true or false. True will calculate the anomalies; departures from the mean from the period specified in year1 and year2

## Details

This is required to change the monthly data, such as the data used in this package, to the seasons; Sept-Oct-Nov, Dec-Jan-Feb, Mar-Apr-May, Jun-Jul-Aug.

## Value

Return a matrix of time series with col names season for the seasons including lagged seasons; "SON\_2","DJF\_2","MAM\_2","JJA\_2","SON\_1","DJF\_1","MAM\_1","JJA\_1","SON","DJF","MAM","JJA";

## Author(s)

Maryann Pirie

## Examples

```
data(SOI) # this is the Southern Oscillation Index data loaded with this package.
data(temperature) # this is the temperature data loaded with this package.
data(precipitation) # this is the precipitation data loaded with this package.
SOI.anom.season.data <- climate.anom.dendro.season( SOI, 1933, 1992, 1876,
  is.anomaly="TRUE")
temp.anom.season.data <- climate.anom.dendro.season( temperature, 1933, 1992, 1876,
  is.anomaly="TRUE")
prec.anom.season.data <- climate.anom.dendro.season( precipitation, 1933, 1992, 1876,
  is.anomaly="TRUE")
```

concordance.indices     *Concordance*

## Description

This is an internal function called in the function "Overall Concordance". It is used to calculate the concordance indices for each time, t, using the bootstrapped means.

## Usage

```
concordance.indices(sort.boot.x, sort.boot.y, t, trim.alpha, nx, ny)
```

## Arguments

sort.boot.x	A matrix of the bootstrapped means from subset X
sort.boot.y	A matrix of the bootstrapped means from subset Y
t	The time index
trim.alpha	The level of outside trimming
nx	A vector providing the number of series at each time for subset X
ny	A vector providing the number of series at each time for subset Y

## Details

The procedure for calculating the concordance is provided in "Concordance: A measure of similarity between matrices of time series with applications in dendroclimatology".

## Value

A vector containing the a, b and the concordance

`correlation.function` *Performs correlations functions*

## Description

Uses the imported climate variables and tree ring data to produce seasonal correlation functions. Also, uses the bootstrapped chronologies to produce confidence intervals.

## Usage

```
correlation.function(climate.anom.season.data, site.chron.data, site.boot.data,
                     period.RF, col.names.season, Climate.name, Subset.name)
```

## Arguments

<code>climate.anom.season.data</code>	climate data anomalies for seasons
<code>site.chron.data</code>	site chronologies, matrix: rows=year, col=subset.1, subset.2,fullest
<code>site.boot.data</code>	bootstrapped site chronologies, list: matrices for each subset with: row=year, col=bootstrapped series
<code>period.RF</code>	the period used to calculate response functions, vector: (start,end)
<code>col.names.season</code>	col.names.season<- list("SON_2", "DJF_2", "MAM_2", "JJA_2", "SON_1", "DJF_1", "MAM_1", "JJA_1", "SON", "DJF", "MAM", "JJA")
<code>Climate.name</code>	name of the climate variable for which correlation functions are being calculated
<code>Subset.name</code>	names given to each of the subsets.

## Value

<code>corr.site.1</code>	The correlations between the climate variable and the site chronology for the 1st subset.
<code>corr.site.2</code>	The correlations between the climate variable and the site chronology for the 12st subset.
<code>percentile.ci.1</code>	The percentile confidence intervals for the 1st subset.
<code>percentile.ci.2</code>	The percentile confidence intervals for the 2st subset.

Other summary variables

<code>summary.ci.1</code>	
<code>summary.ci.2</code>	
<code>t.mean</code>	Test for correlation equal zero
<code>t.meanequal</code>	Test for correlations from the two subsets are equal
<code>percentile.ci</code>	

### Note

site.chron.data, and site.boot.data must be in the same order and confidence intervals plotted are for the 1st two subsets.

### Examples

```

## Not run:
period.RF<-c(1900,1990)
col.names.season <- list("SON_2", "DJF_2", "MAM_2", "JJA_2", "SON_1", "DJF_1", "MAM_1","JJA_1",
                         "SON", "DJF", "MAM", "JJA")
## Full dataset
site.full <- site.chron(spline200.sub0.2000.n$sub.series.stand, aver.by.tree=F)
site.chron.data <- cbind(site.full$aver.site, site.full$aver.site)
site.boot.full <- ts(boot.full$boot.series.mean, start=tsp(site.full$aver.site)[1] )
site.boot.data<-list(site.boot.full, site.boot.full)

corr.SOI.full<-correlation.function(SOI.anom.season.data, site.chron.data,site.boot.data,
                                      period.RF, col.names.season,
                                      Climate.name="SOI", Subset.name=c("0-20cm","20-200cm" ) )
corr.prec.full<-correlation.function(prec.anom.season.data, site.chron.data,site.boot.data,
                                       period.RF, col.names.season,
                                       Climate.name="SOI", Subset.name=c("0-20cm","20-200cm" ) )
corr.temp.full<-correlation.function(temp.anom.season.data, site.chron.data,site.boot.data,
                                       period.RF, col.names.season,
                                       Climate.name="SOI", Subset.name=c("0-20cm","20-200cm" ) )

## Near vs Far
site.0.20  <- site.chron(spline200.sub0.20.n$sub.series.stand, aver.by.tree=F)
site.20.200 <- site.chron(spline200.sub20.2000.n$sub.series.stand, aver.by.tree=F)
site.chron.data <- cbind(site.0.20$aver.site, site.20.200$aver.site)

site.boot.0.20 <- ts(boot.0.20$boot.series.mean, start=tsp(site.0.20$aver.site)[1] )
site.boot.20.200 <- ts(boot.20.2000$boot.series.mean, start=tsp(site.20.200$aver.site)[1] )
site.boot.data<-list(site.boot.0.20, site.boot.20.200)

corr.SOI<-correlation.function(SOI.anom.season.data, site.chron.data, site.boot.data,
                                 period.RF, col.names.season,
                                 Climate.name="SOI",Subset.name=c("0-20cm","20-200cm" ) )
corr.prec<-correlation.function(prec.anom.season.data, site.chron.data,           site.boot.data,
                                 period.RF, col.names.season,
                                 Climate.name="SOI", Subset.name=c("0-20cm","20-200cm" ) )
corr.temp<-correlation.function(temp.anom.season.data, site.chron.data, site.boot.data,
                                 period.RF, col.names.season,
                                 Climate.name="SOI", Subset.name=c("0-20cm","20-200cm" ) )

## End(Not run)

```

## Description

Includes: DBH, pithoffset estimation plus the method used in the estimation, the length of the outer non-crossdated distance and the length of the bark.

## Usage

```
data(dbh.po.nc)
```

## Format

A data frame with 135 observations on the following 6 variables.

**Series.ID** a factor with levels HUP004A HUP004B HUP004C HUP004D HUP013A HUP013B HUP036A  
 HUP036B HUP036C HUP036D HUP036E HUP037A HUP037B HUP037C HUP037D HUP040A HUP040B  
 HUP040C HUP040D HUP040E HUP040F HUP050A HUP050B HUP050C HUP050D HUP052A HUP052B  
 HUP052C HUP052D HUP055A HUP055B HUP055C HUP056A HUP056B HUP060A HUP060B HUP062A  
 HUP062B HUP063A HUP063B HUP065A HUP065B HUP065C HUP066A HUP066B HUP066C HUP073A  
 HUP073B HUP074A HUP074B HUP074C HUP079A HUP079B HUP079C HUP098A HUP098B HUP098C  
 HUP100A HUP100B HUP100C HUP113A HUP113B HUP113C HUP125A HUP125B HUP125C HUP137A  
 HUP137B HUP141A HUP141B HUP141C HUP141D HUP142A HUP142B HUP142C HUP142D HUP163A  
 HUP163B HUP163C HUP163D HUP163E HUP189A HUP189B HUP189C HUP189D HUP197A HUP197B  
 HUP197C HUP197D HUP197E HUP197F HUP198A HUP198B HUP198C HUP198D HUP198E HUP199A  
 HUP199B HUP199C HUP199D HUP199E HUP199F HUP199g HUP200A HUP200B HUP200C HUP200D  
 HUP200E HUP200F HUP201A HUP201B HUP201C HUP201D HUP202A HUP202B HUP202C HUP202D  
 HUP202E HUP202F HUP208A HUP208B HUP208C HUP228A HUP228B HUP228C HUP228D HUP228E  
 HUP232A HUP232B HUP232C HUP242A HUP242B HUP242C HUP242D HUP242E HUP247A HUP247B  
 HUP247C HUP247D HUP248A HUP248B HUP248C HUP249A HUP249B HUP251A HUP251B HUP251C  
 HUP251D HUP251E HUP251F HUP251g HUP251h HUP251I HUP257A HUP257B HUP257C HUP257D  
 HUP259A HUP259B HUP259C HUP259D HUP279A HUP279B HUP301A HUP301B HUP301C HUP301D  
 HUP303A HUP303B HUP303C HUP304A HUP304B HUP306A HUP306B HUP306C HUP310A HUP310B  
 HUP310C HUP400A HUP400B

**DCH** a numeric vector

**pithoffset** a numeric vector

**method** a factor with levels BE\_DBH\_1M BE\_length\_min\_tree Duncan partial\_arc pith RADIUS

**Outer.dis.non.crossdated** a numeric vector

**Bark** a numeric vector

## Source

With permission from School of Environment, University of Auckland

## Examples

```
data(dbh.po.nc)
str(dbh.po.nc)
```

---

exact.ci*Exact Confidence Intervals*

---

**Description**

Calculate the exact confidence intervals for proportions, based in Pearson's approach.

**Usage**

```
exact.ci(p.adjust, size.x, size.y, i)
```

**Arguments**

p.adjust	A vector of concordance indices, these are proportions for which you want to calculate the confidence interval.
size.x	A vector of the number of series used to calculate each index in matrix X.
size.y	A vector of the number of series used to calculate each index in matrix Y.
i	A recursive variables (i.e. use this function in Apply.)

**Value**

A vector with 2 elements indicating the lower and upper confidence intervals for the concordance indices.

---

Example 1*Example 1: Producing correlation figure*

---

**Description**

This describes the workflow required to generate the correlation figure published in "On the influence of tree size on the climate - growth relationship of New Zealand kauri (*Agathis australis*): insights from annual, monthly and daily growth patterns. J Wunder, AM Fowler, ER Cook, M Pirie, SPJ McCloskey. Trees 27 (4), 937-948".

**Examples**

```
## Not run:
#library('dplRCon')
#loading data
data(ring.raw)
data(ring.stand)
data(dbh.po.nc)
data(SOI)
data(temperature)
data(precipitation)
```

```

#Subset "near-pith" is the material within 0 -20cm from the estimated pith
spline200.sub0.20.n <- TruncSeriesPithoffset( ring.raw, ring.stand, dbh.po.nc, c(1,200))
# Subset "far-pith" is the material further than 20cm from the estimated pith
spline200.sub20.2000.n <- TruncSeriesPithoffset( ring.raw, ring.stand, dbh.po.nc, c(200,200000))
# Whole dataset, through truncated functions to get in the same format as the above two datasets
spline200.sub0.2000.n <- TruncSeriesPithoffset( ring.raw, ring.stand, dbh.po.nc, c(00,200000))

#series.bootstapped
boot.0.20 <- series.bootstrap( spline200.sub0.20.n$sub.series.stand, stat, 999,
names.stat, aver.by.tree = FALSE)
boot.20.2000 <- series.bootstrap(spline200.sub20.2000.n$sub.series.stand, stat, 999,
names.stat, aver.by.tree = FALSE)
boot.full <- series.bootstrap(spline200.sub0.2000.n$sub.series.stand, stat, 999,
names.stat, aver.by.tree = FALSE)

#calculate seasonal climate
SOI.anom.season.data <- climate.anom.dendro.season( SOI, 1933, 1992, 1876, is.anomaly="TRUE")
temp.anom.season.data <- climate.anom.dendro.season( temperature, 1933, 1992, 1876,
is.anomaly="TRUE")
prec.anom.season.data <- climate.anom.dendro.season( precipitation, 1933, 1992, 1876,
is.anomaly="TRUE")

# Calculate the correlations for each of the climate variables
period.RF<-c(1900,1990)
col.names.season <- list("SON_2", "DJF_2", "MAM_2", "JJA_2", "SON_1", "DJF_1", "MAM_1","JJA_1",
"SON", "DJF", "MAM", "JJA")

## Full dataset
site.full <- site.chron(spline200.sub0.2000.n$sub.series.stand, aver.by.tree=FALSE)
site.chron.data <- cbind(site.full$aver.site, site.full$aver.site)
site.boot.full <- ts(boot.full$boot.series.mean, start=tsp(site.full$aver.site)[1] )
site.boot.data<-list(site.boot.full, site.boot.full)
corr.SOI.full<-correlation.function(SOI.anom.season.data, site.chron.data, site.boot.data,
period.RF,col.names.season, Climate.name="SOI",
Subset.name=c("0-20cm","20-200cm" ) )
corr.prec.full<-correlation.function(prec.anom.season.data, site.chron.data, site.boot.data,
period.RF, col.names.season, Climate.name="SOI",
Subset.name=c("0-20cm","20-200cm" ) )
corr.temp.full<-correlation.function(temp.anom.season.data, site.chron.data, site.boot.data,
period.RF, col.names.season, Climate.name="SOI",
Subset.name=c("0-20cm","20-200cm" ) )

## Near vs Far
site.0.20 <- site.chron(spline200.sub0.20.n$sub.series.stand, aver.by.tree=FALSE)
site.20.200 <- site.chron(spline200.sub20.2000.n$sub.series.stand, aver.by.tree=FALSE)
site.chron.data <- cbind(site.0.20$aver.site, site.20.200$aver.site)

site.boot.0.20 <- ts(boot.0.20$boot.series.mean, start=tsp(site.0.20$aver.site)[1] )
site.boot.20.200 <- ts(boot.20.2000$boot.series.mean, start=tsp(site.20.200$aver.site)[1] )
site.boot.data<-list(site.boot.0.20, site.boot.20.200)

```

```

corr.SOI<-correlation.function(SOI.anom.season.data, site.chron.data,site.boot.data, period.RF,
col.names.season, Climate.name="SOI", Subset.name=c("0-20cm","20-200cm" ) )
corr.prec<-correlation.function(prec.anom.season.data, site.chron.data, site.boot.data, period.RF,
col.names.season, Climate.name="SOI", Subset.name=c("0-20cm","20-200cm" ) )
corr.temp<-correlation.function(temp.anom.season.data, site.chron.data, site.boot.data, period.RF,
col.names.season, Climate.name="SOI",Subset.name=c("0-20cm","20-200cm" ) )

#Plotting
Figure.correlation.barplot(corr.temp, corr.prec, corr.SOI,
corr.temp.full, corr.prec.full, corr.SOI.full,
col.names.season)

## End(Not run)

```

**Example 2***Example 2: Calculate the cordance***Description**

This describes the workflow required to calculate the concordance published in the Application section of the "Concordance: A measure of similarity between matrices of time series with applications in dendroclimatology".

**Examples**

```

#library('dplRCon')
#loading data
data(ring.raw)
data(ring.stand)
data(dbh.po.nc)

#Subset "near-pith" is the material within 0 -20cm from the estimated pith
spline200.sub0.20.n <- TruncSeriesPithoffset( ring.raw, ring.stand, dbh.po.nc, c(1,200))
# Subset "far-pith" is the material further than 20cm from the estimated pith
spline200.sub20.2000.n <- TruncSeriesPithoffset( ring.raw, ring.stand, dbh.po.nc, c(200,200000))
# Whole dataset, through truncated functions to get in the same formate as the above two datasets
spline200.sub0.2000.n <- TruncSeriesPithoffset( ring.raw, ring.stand, dbh.po.nc, c(00,200000))

## Not run:
#series.bootstapped
boot.0.20 <- series.bootstrap( spline200.sub0.20.n$sub.series.stand, stat, 999,
names.stat, aver.by.tree = FALSE)
boot.20.2000 <- series.bootstrap(spline200.sub20.2000.n$sub.series.stand, stat, 999,
names.stat, aver.by.tree = FALSE)

boot.0.20 <- boot.0.20$boot.series.mean
boot.20.2000 <- boot.20.2000$boot.series.mean

## End(Not run)

```

```

data(boot.0.20)
data(boot.20.2000)

overall.precision.HUP <- overall.concordance.period(spline200.sub20.2000.n$sub.series.stand ,
spline200.sub0.20.n$sub.series.stand, boot.20.2000,
boot.0.20 ,1 , concordance.indices,
c(1880,1999), trim.alpha=0.005, concordance.beta=0.5)

figure.function.concordance (overall.precision.HUP, x.lim=c(1880,2000))

```

---

### **Figure.correlation.barplot**

*Produces a Figure of the correlation coefficients.*

---

### **Description**

Produce a figure with 3 panels, each panel is for a different climate variable. An example of this figure is included in "On the influence of tree size on the climate - growth relationship of New Zealand kauri (*Agathis australis*): insights from annual, monthly and daily growth patterns. J Wunder, AM Fowler, ER Cook, M Pirie, SPJ McCloskey. Trees 27 (4), 937-948"

### **Usage**

```
Figure.correlation.barplot(corr.1, corr.2, corr.3, corr.1.full, corr.2.full,
corr.3.full, col.names.season)
```

### **Arguments**

corr.1	the output from using function 'correlation.function' for the 1st climate variable comparing near and far-pith. Depending on the order of the inputs into the function 'correlation.function' will determine the color of the resultant box-plot (1st item is black, and 2nd item is gray)
corr.2	same as corr.1 but for the second climate variable
corr.3	same as corr.1 but for the third climate variable
corr.1.full	the output from using function 'correlation.function' for the full dataset. correlations for the full dataset are shown as a grey dashed line.
corr.2.full	same as corr.1.full but for the second climate variable
corr.3.full	same as corr.1.full but for the third climate variable
col.names.season	col.names.season<- list("SON_2", "DJF_2", "MAM_2", "JJA_2", "SON_1", "DJF_1", "MAM_1", "JJA_1", "SON", "DJF", "MAM", "JJA")

### **Value**

This returns a figure.

## Examples

```
## Not run: Figure.correlation.barplot(corr.temp, corr.prec, corr.SOI,
  corr.temp.full, corr.prec.full, corr.SOI.full, col.names.season)
## End(Not run)
```

figure.function.concordance

*Figure: Plots the Concordances*

## Description

Plots the concordance indices. This is used to generate the Figure in Concordance: A measure of similarity between matrices of time series with applications in dendroclimatology".

## Usage

```
figure.function.concordance(con.indices, x.lim)
```

## Arguments

con.indices	This is the output generated from the function overall.concordance.period.
x.lim	This is a vector with the start and end year for the required plot.

## Value

A figure with the concordance indices and their confidence intervals, a smoother fitted through the indices and the confidence interval for the mean concordance.

## Author(s)

Maryann Pirie

## Examples

```
## Not run:
#Subset "near-pith" is the material within 0 -20cm from the estimated pith
spline200.sub0.20.n <- TruncSeriesPithoffset( ring.raw, ring.stand, dbh.po.nc, c(1,200))
spline200.sub20.2000.n <- TruncSeriesPithoffset( ring.raw, ring.stand, dbh.po.nc, c(200,200000))
boot.0.20 <- series.bootstrap( spline200.sub0.20.n$sub.series.stand, stat, 999,
  names.stat, aver.by.tree = FALSE)
boot.20.2000 <- series.bootstrap(spline200.sub20.2000.n$sub.series.stand, stat, 999,
  names.stat, aver.by.tree = FALSE)

overall.precision.HUP <- overall.concordance.period(spline200.sub20.2000.n$sub.series.stand ,
  spline200.sub0.20.n$sub.series.stand,
  boot.20.2000$boot.series.mean, boot.0.20$boot.series.mean ,1 , concordance.indices,
  c(1880,1999), trim.alpha=0.005, concordance.beta=0.5)

figure.function.concordance (overall.precision.HUP, x.lim=c(1880,2000))
## End(Not run)
```

function.id	<i>Core IDs</i>
-------------	-----------------

### Description

Take the series ID's and convert into a useable format. This produces series ID in a form that can be compared to pith offset file.

### Usage

```
function.id(cores, site.id, tree.id, core.id)
```

### Arguments

cores	A vector containing core Ids.
site.id	A vector specifying the position of start and end for the site ID.
tree.id	A vector specifying the position of start and end for the tree ID.
core.id	A vector specifying the position of start and end for the core ID.

### Value

A vector of core ids, re-formatted.

function.id.master	<i>Master ID</i>
--------------------	------------------

### Description

Produces series ID in a form that can be compared to pith offset file for the master chronology.

### Usage

```
function.id.master(cores, site.id, tree.id, core.id)
```

### Arguments

cores	A vector containing core Ids
site.id	A vector specifying the position of start and end for the site ID.
tree.id	A vector specifying the position of start and end for the tree ID.
core.id	A vector specifying the position of start and end for the core ID.

### Value

A vector of core ids, re-formatted.

---

names.stat	<i>names.stat</i>
------------	-------------------

---

**Description**

names.stat

**Usage**

names.stat

**Format**

chr [1:2] "mean" "median"

---

overall.concordance.period	<i>Overall Concordance period</i>
----------------------------	-----------------------------------

---

**Description**

Produces the concordance indices for each year over the period of interest and the average of these indices. Trimmed and different levels of concordance indices in the overall concordance, size adjusted (mean concordance indices)

**Usage**

```
overall.concordance.period(x, y, x.boot, y.boot, min.series,
                           concordance.indices, period, trim.alpha = 0, concordance.beta = 0.5)
```

**Arguments**

- x A matrix containing the standardized ring width indices for subset X, column heading tree ID, row names is time
- y As x, but for subset Y
- x.boot the bootstrapped replicates for matrix x. with bootstrapped replicate as row names, and time as the column headings
- y.boot the bootstrapped replicates for matrix y.
- min.series is a number indicating the minimum number of series for calculating the concordance statistic, recommend 10.
- concordance.indices The function used for calculating the concordance indices for each t.
- period Time period for which the concordance is to be calculated, vector of form c(start, end)

**trim.alpha** this is the amount of trimming of the extreme concordance indices, default is 0 (no trimming). Recommend that a 0.005 be used.

**concordance.beta**

This is used to calculate the proportion of indices above this cut off. Default is proportion above 0.5.

### Value

**pre.in** Concordance indices.

**min.series** Minimum number of series used to calculate concordance.

**num.series.at.t.x**

Number of series in matrix X for each time, t.

**num.series.at.t.y**

Number of series in matrix Y for each time, t.

**pre.in.greater.ts.period**

Concordance indices, as time series, when minimum number of series was available.

**period** The time period used to calculate the concordance.

**pre.overall.period**

The Concordance Statistic.

### Examples

```
#loading data
## Not run:
data(ring.raw)
data(ring.stand)
data(dbh.po.nc)

#Subset near-pith is the material within 0 -20cm from the estimated pith
spline200.sub0.20.n <- TruncSeriesPithoffset( ring.raw, ring.stand, dbh.po.nc, c(1,200))
# Subset far-pith is the material further than 20cm from the estimated pith
spline200.sub20.2000.n <- TruncSeriesPithoffset( ring.raw, ring.stand, dbh.po.nc, c(200,200000))

# series.bootstrapped
boot.0.20 <- series.bootstrap( spline200.sub0.20.n$sub.series.stand,
                                stat, 999, names.stat, aver.by.tree = FALSE)
boot.20.2000 <- series.bootstrap(spline200.sub20.2000.n$sub.series.stand,
                                   stat, 999, names.stat, aver.by.tree = FALSE)

overall.precision.HUP <- overall.concordance.period(spline200.sub20.2000.n$sub.series.stand ,
                                                      spline200.sub0.20.n$sub.series.stand,
                                                      boot.20.2000$boot.series.mean, boot.0.20$boot.series.mean ,
                                                      1 , concordance.indices, c(1880,1999), trim.alpha=0.005, concordance.beta=0.5)

## End(Not run)
```

---

precipitation	<i>Monthly Precipitation Data</i>
---------------	-----------------------------------

---

## Description

Monthly Precipitation Data

## Usage

```
data(precipitation)
```

## Format

A data frame with 153 observations on the following 13 variables.

YEAR a numeric vector  
Jan a numeric vector  
Feb a numeric vector  
Mar a numeric vector  
Apr a numeric vector  
May a numeric vector  
Jun a numeric vector  
Jul a numeric vector  
Aug a numeric vector  
Sep a numeric vector  
Oct a numeric vector  
Nov a numeric vector  
Dec a numeric vector

## Source

NIWA (The National Institute of Water and Atmosphere Research, New Zealand)

## Examples

```
data(precipitation)
## maybe str(precipitation) ; plot(precipitation) ...
```

**ring.raw***Matrix of time series of raw ring widths.***Description**

Matrix of time series of raw ring widths, each series in aligned in columns, with the column heading matching the series ID.

**Usage**

```
data(ring.raw)
```

**Format**

The format is: mts [1:515, 1:135] NA ... - attr(\*, "dim-names")=List of 2 ..\$ : NULL ..\$ : chr [1:135] "HUP004A" "HUP004B" "HUP004C" "HUP004D" ... - attr(\*, "tsp")= num [1:3] 1483 1997 1 - attr(\*, "class")= chr [1:3] "mts" "ts" "matrix"

**Source**

Sourced from The School of Environment, University of Auckland with permission

**Examples**

```
data(ring.raw)
## maybe str(ring.raw) ; plot(ring.raw) ...
```

**ring.stand***Matrix of time series for the standardised tree ring indices.***Description**

Matrix of time series of standardised ring widths, each series in aligned in columns, with the column heading matching the series ID.

**Usage**

```
data(ring.stand)
```

**Format**

The format is: mts [1:515, 1:135] NA ... - attr(\*, "dim-names")=List of 2 ..\$ : NULL ..\$ : chr [1:135] "HUP004A" "HUP004B" "HUP004C" "HUP004D" ... - attr(\*, "tsp")= num [1:3] 1483 1997 1 - attr(\*, "class")= chr [1:3] "mts" "ts" "matrix"

## Source

Sourced from The School of Environment, University of Auckland with permission

## Examples

```
data(ring.stand)
## maybe str(ring.stand) ; plot(ring.stand) ...
```

series.bootstrap	<i>Series bootstrap</i>
------------------	-------------------------

## Description

This function calculate the bootstrapped replicated series for calculating concordance

## Usage

```
series.bootstrap(data.boot, stat, R, names.stat, aver.by.tree.input)
```

## Arguments

data.boot	Data matrix containing standardized ring width indices from which the bootstrapped replicates are calculated.
stat	A function giving the statistics that are to be calculated
R	The number of bootstrapped replicates
names.stat	the names of the statistics contained in function "stat"
aver.by.tree.input	This is a True/False. If True then averages tree series, then average tree means. If False then average all series

## Value

org.stat	The original input statistics
boot.stat	The statistics of the bootstrapped replicates, c('mean','median')
bias	The bias of the boot.stat
std.error	The standard error of boot.stat
boot.series.mean	The bootstrapped replicates mean series
boot.series.std	The bootstrapped replicates standard deviation series

## Examples

```
## Not run: #Subset "near-pith" is the material within 0 -20cm from the estimated pith
spline200.sub0.20.n <- TruncSeriesPithoffset( ring.raw, ring.stand, dbh.po.nc, c(1,200))
boot.0.20 <- series.bootstrap( spline200.sub0.20.n$sub.series.stand, stat, 999,
                                names.stat, aver.by.tree = FALSE)
## End(Not run)
```

**site.chron***site.chron***Description**

This function calculate the site chronology for the data matrix

**Usage**

```
site.chron(data.m, aver.by.tree.input)
```

**Arguments**

<code>data.m</code>	A data matrix contains standardized ring width indices
<code>aver.by.tree.input</code>	If True then averages tree series, then average tree means. If False then average all series

**Value**

<code>aver.site</code>	The average for the site.
<code>std.site</code>	The standard deviation of the site.
<code>aver.tree</code>	A time series for average of each tree.
<code>number.trees</code>	The total number of trees used to produce the site chronology.
<code>core.per.tree</code>	The number of cores for each tree.

**Examples**

```
## Not run:
site.full <- site.chron(spline200.sub0.2000.n$sub.series.stand, aver.by.tree=FALSE)

## End(Not run)
```

**SOI***SOI data***Description**

Southern Oscillation Index Data

**Usage**

```
data(SOI)
```

**Format**

The format is: chr "SOI"

**Source**

BOM (Australian Bureau of Meteorology)

**Examples**

```
data(SOI)
## maybe str(SOI) ; plot(SOI) ...
```

---

stat                    *Stat*

---

**Description**

To be used internally in series.bootstrapped this is the summary that is calculated during bootstrapping.

**Usage**

```
stat(data)
```

**Arguments**

data	data matrix (produced within series.bootstrapped)
------	---

**Value**

results required output for series.bootstrapped

---

SumNotNa              *Sum non Na's*

---

**Description**

Count the number of non na values. This is an internal function used in an apply function.

**Usage**

```
SumNotNa(x)
```

**Arguments**

x	Vector to be counted containing Na's
---	--------------------------------------

**Value**

The sum of the non na's values.

temperature

*Monthly Temperature Data***Description**

Monthly Temperature Data

**Usage**

```
data(temperature)
```

**Format**

A data frame with 154 observations on the following 13 variables.

YEAR	a numeric vector
Jan	a numeric vector
Feb	a numeric vector
Mar	a numeric vector
Apr	a numeric vector
May	a numeric vector
Jun	a numeric vector
Jul	a numeric vector
Aug	a numeric vector
Sep	a numeric vector
Oct	a numeric vector
Nov	a numeric vector
Dec	a numeric vector

**Source**

NIWA (The National Institute of Water and Atmosphere Research, New Zealand)

**Examples**

```
data(temperature)
## maybe str(temperature) ; plot(temperature) ...
```

---

`TruncSeriesPithoffset` *Truncate series by range pithoffsets*

---

## Description

The following function truncate the data by a given range from the estimated pith.

## Usage

```
TruncSeriesPithoffset(file.raw, file.stand, pithoffset, range)
```

## Arguments

<code>file.raw</code>	data file containing the raw ring widths, in mm
<code>file.stand</code>	data file containing the standardized ring widths
<code>pithoffset</code>	data set containing the pith offsets for each core, in mm.
<code>range</code>	The distance from the pith use for truncation, given in mm from the core. e.g. <code>range &lt;- c(1,200)</code> truncates values outside this range.

## Value

<code>sub.series.raw</code>	A truncated series of raw ring widths (in miromilmeter).
<code>sub.series.stand</code>	A truncated series of standardized ring widths (in miromilmeter).

## Examples

```
## Not run:
data(ring.raw)
data(ring.stand)
data(dbh.po.nc)
#Subset near-pith is the material within 0 -20cm from the estimated pith
spline200.sub0.20.n <- TruncSeriesPithoffset( ring.raw, ring.stand, dbh.po.nc, c(1,200))
# Subset far-pith is the material further than 20cm from the estimated pith
spline200.sub20.2000.n <- TruncSeriesPithoffset( ring.raw, ring.stand, dbh.po.nc, c(200,200000))
# Whole dataset, through truncated functions to get in the same formate as the above two datasets
spline200.sub0.2000.n <- TruncSeriesPithoffset( ring.raw, ring.stand, dbh.po.nc, c(00,200000))
## End(Not run)
```

# Index

\*Topic **datasets**  
boot.0.20, 2  
boot.20.2000, 3  
dbh.po.nc, 7  
names.stat, 15  
precipitation, 17  
ring.raw, 18  
ring.stand, 18  
SOI, 20  
temperature, 22

stat, 21  
SumNotNa, 21

temperature, 22  
TruncSeriesPithoffset, 23

boot.0.20, 2  
boot.20.2000, 3

climate.anom.dendro.season, 4  
concordance.indices, 5  
correlation.function, 6

dbh.po.nc, 7

exact.ci, 9  
Example 1, 9  
Example 2, 11

Figure.correlation.barplot, 12  
figure.function.concordance, 13  
function.id, 14  
function.id.master, 14

names.stat, 15

overall.concordance.period, 15

precipitation, 17

ring.raw, 18  
ring.stand, 18

series.bootstrap, 19  
site.chron, 20  
SOI, 20