Package 'geoChronR'

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Type Package

Title Tools to analyze and visualize time-uncertain geoscientific data

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Description Time uncertain analysis, including correlation, regression, spectral, and PCA for paleo-geoscientific data.

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LazyData TRUE

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Imports Bchron,
inline,
lomb,
data.table,
devtools,
matrixStats,
mapproj,
maps,
gridExtra,
Hmisc,
ggplot2,
ggmap,
Formula,
survival,
lattice,
plyr,
BBmisc,
jsonlite,
RJSONIO,
Kmisc,
scales,
RgoogleMaps,
geosphere,
jpeg,
proto,
reshape2,

rjson,
MASS,
neotoma,
pbapply

R **topics documented:**

alignTimeseriesBin   *Align and bin two timeseries into comparable bins*

Description

Use this to put two timeseries on different timesteps onto equivalent bins

Usage

```
alignTimeseriesBin(timeX, valuesX, timeY, valuesY, binvec = NA,
  binstep = NA, binfun = mean, max.ens = NA, minObs = 10)
```

Arguments

timeX	matrix of age/time ensembles, or single column
valuesX	matrix of values ensembles, or single column
timeY	matrix of age/time ensembles, or single column
valuesY	matrix of values ensembles, or single column
binvec	vector of bin edges for binning step
binstep	spacing of bins, used to build bin step
binfun	function to use during binning (mean, sd, and sum all work)
max.ens	maximum number of ensemble members to regress
minObs	minimum number of points required to calculate regression

Value

list of binned data output:

- binX: binned values from X
- binY: binned values from Y
- binstep: interval of the binning
- yearBins: bins along time

Author(s)

Nick McKay

---

ar1   *Estimate Auto-Regressive coefficient at 1-timesetep*

Description

estimates ar1 using the arima() function

Usage

```
ar1(X)
```

Arguments

X   a 1-column matrix or numeric dataset

Value

ar coefficient estimate of ar1

Author(s)

Julien Emile-Geay

---

assignColors   *Assign colors for map color scale*

Description

Quick look up for color scale pairs for mapping

Usage

```
assignColors(colors = "temp")
```

Arguments

colors   string to define color scale. Options are "temp", "precip" and "drought"

Value

a pair of high/low colors

Author(s)

Nick McKay

See Also

Other mapping: baseMap, mapLipds, mapLipd

---

axisLabel   *Label axes*

Description

Create an axis label string from a LiPD column vector

Usage

```
axisLabel(varList)
```

Arguments

varList   LiPD "variable list"

Value

axis label as a string

Author(s)

Nick McKay

See Also

Other plot: geoChronRPlotTheme, plotChron, plotCorrEns, plotHistEns, plotLine, plotModelDistributions, plotPcaEns, plotPvalsEnsFdr, plotRegressEns, plotScatterEns, plotSpectraEns, plotSummary, plotTimeseriesEnsLines, plotTimeseriesEnsRibbons, plotTrendLinesEns

---

bamCorrect   *Corrects a Banded Age Model (BAM)*

Description

Generate an ensemble of possible age corrected data:See www.clim-past-discuss.net/9/6077/2013/ for a detailed description of the model. The time series in X are automatically flipped to range from most recent to oldest measurements when the intput t is given in increasing order.

Usage

```
bamCorrect(X, t, model = NULL)
```

Arguments

X   data (vector or matrix n*p)

t   chronology for data X (n*1)

model   a list that describes the model to use in BAM

- model$ns: number of samples
- model$name: 'poisson' or 'bernoulli'
- model$param: probability of growth band being perturbed (default: prob of missing band = prob of doubly-counted band = 0.05)
  - if model$param is a single argument, then the perturbations are symmetric (prob of missing band = prob of doubly-counted band)
  - if model$param = [a1 a2] and a1 neq a2 the model is asymmetric
    * a1 = prob(missing layer) - undercounted
    * a2 = prob(layer counted multiple times) - overcounted
  - if model$param: 2xp matrix, then different miscounting prob. are defined for each time series.
- model$resize: do not resize: 0 (default), resize to shortest sample: -1, resize to longest sample: 1
- model$tm: if a time model is provided, the code returns the corresponding perturbed data

Value

res a list with

- res$Xc: realizations of age-perturbed data matrix of size tn*p*ns (could be 2 or 3d)
- res$tc: new chronology tn*1
- res$tmc: corresponding ensemble of time-correction matrices (tn*p*ns) to map realizations in Xp back to the original data X (2=insert nan, 0=remove double band) (2 or 3d) where tn is the chronology length = n (default), shortest sample or longest sample depending on the chosen resizing option.

Author(s)

Maud Comboul

See Also

Other BAM: runBam, simulateBam

Examples

```
res <- bamCorrect(X,t)
#will generate an ensemble of 1000 age models randomly following
#a Poisson process with rate parameter theta=0.05 used to perturb data X
res <- bamCorrect(X,t,model)
#will correct data X  with the model specified in
#the model structure
```

---

baseMap   *Make a base map*

Description

Create a google or line map of the location of a list of LiPD objects

Usage

```
baseMap(lon, lat, map.type = "google", f = 0.3, restrict.map.range = TRUE,
  projection = "mercator", boundcirc = FALSE, global = FALSE,
  extend.range = 10)
```

Arguments

lon	longitude(s) range to map
lat	latitude(s) range to map
map.type	"google" or "line"
f	buffer for the map range
restrict.map.range	
	TRUE or FALSE. Trim the size of the map to the points, for "line" map type
projection	Map project. All options on: ?mapproject
boundcirc	Draw a boundary circle around a polar projection. TRUE or FALSE(default).
global	Should the scope of the map be global? TRUE or FALSE(default).
extend.range	increase the span of the map by this much (lat/long degrees)

Value

ggmap base map

Author(s)

Nick McKay

See Also

Other mapping: assignColors, mapLipds, mapLipd

---

bin *Bin Data*

Description

function that puts data into appropriate bins, based on the time and the binning vector the bin vector describes the edges of the bins

Usage

```
bin(time, values, binvec, binfun = mean)
```

Arguments

time	vector of time
values	vector of values to bin
binvec	vector of bin edges for describing where to bin
binfun	function to use during binning (mean, sd, and sum all work)

Value

A data.frame of (x) binned time, and (y) binned values

Author(s)

Nick McKay

---

bin2d *Two dimensional binning*

Description

Calculate the density of samples along a 2-dimensional grid

Usage

```
bin2d(x, y, nbins = 100, x.bin = NA, y.bin = NA, filterFrac = NA,
  interpolate = TRUE)
```

Arguments

x	n by m matrix where n is the number of observations and m is >= 1
y	n by j matrix where n is the number of observations and j is >= 1
nbins	number bins over which to calculate intervals. Used to calculate x.bin if not provided.
x.bin	vector of bin edges over which to bin.
y.bin	vector of bin edges over which to bin.
filterFrac	Used to beef up sampling for poorly sampled intervals. Interpolates intervals with less than filterFrac coverage.
interpolate	use interpolation? T/F

Value

A list with a matrix of density, x.bin and y.bin

See Also

Other gridding: `kde_2d`, `quantile2d`

---

binEns   *Bin ensemble data*

Description

takes ensembles in time and/or values and creates a matrix of data for future analysis

Usage

```
binEns(time, values, binvec, binfun = mean, max.ens = NA)
```

Arguments

time	single column vector of time
values	single column vector of values to bin
binvec	vector of bin edges for binning step
binfun	function to use during binning (mean, sd, and sum all work)
max.ens	maximum number of ensemble members to regress
binstep	spacing of bins, used to build bin step

Value

list that includes matrix of binned data and binned time

---

binTs   *Bin every entry in a Timeseries object*

Description

Aggregate data from a timeseries object into the same timeline through binning.

Usage

```
binTs(TS, timeVar = "ageEnsemble", binvec, binfun = mean, max.ens = 1000,
  na.col.rm = TRUE)
```

Arguments

TS	LiPD timeseries object See http://nickmckay.github.io/LiPD-utilities/r/index.html#what-is-a-time-series
binvec	vector of bin edges for describing where to bin
binfun	function to use during binning (mean, sd, and sum all work)
max.ens	Maximum number of ensemble members.
na.col.rm	Remove columns that are all NAs? (TRUE or FALSE)

Value

A list of binned years and values.

Author(s)

Nick McKay

---

clearAll	*Clear all variables and functions from global environment*

Description

Removes all variables and functions from global environment. Use at your own risk.

Usage

```
clearAll()
```

---

convertBP2AD	*Convert years BP to Calendar year (AD/BC or CE)*

Description

Converts a LiPD variable list, or vector from BP to AD/BC/CE/BCE. Also deals with the lack of a year 0.

Usage

```
convertBP2AD(X)
```

Arguments

X	A LiPD variable list or a vector of years BP

Value

X A LiPD variable list or a vector of Calendar years AD

---

corEns   *Ensemble correlation*

Description

Primary function for calculating correlation ensembles

Usage

```
corEns(time1, values1, time2, values2, binvec = NA, binstep = NA,
  binfun = mean, max.ens = NA, percentiles = c(0.025, 0.25, 0.5, 0.75,
  0.975), minObs = 10)
```

Arguments

time1	matrix of age/time ensembles, or single column
values1	matrix of values ensembles, or single column
time2	matrix of age/time ensembles, or single column
values2	matrix of values ensembles, or single column
binvec	vector of bin edges for binning step
binstep	spacing of bins, used to build bin step
binfun	function to use during binning (mean, sd, and sum all work)
max.ens	maximum number of ensemble members to correlate
percentiles	quantiles to calculate for regression parameters
minObs	minimum number of points required to calculate regression

Value

list of ensemble output and percentile information

Author(s)

Nick McKay

---

corMatrix   *Matrix correlation*

Description

Calculates correlations and associated p-values for two ensemble matrices (or vectors)

Usage

```
corMatrix(M1, M2)
```

Arguments

| M1 | matrix of age-uncertain columns to correlate and calculate p-values |
| M2 | matrix of age-uncertain columns to correlate and calculate p-values |

Value

out list of correlation coefficients (r) p-values (p) and autocorrelation corrected p-values (pAdj)

Author(s)

Nick McKay

Julien Emile-Geay

---

createSyntheticTimeseries

Create a synthetic timeseries that emulates the characteristics of a variable

---

Description

create synthetic timeseries based on a timeseries. Useful for null hypothesis testing

Usage

```
createSyntheticTimeseries(time, values, nens = 1)
```

Arguments

time	LiPD "variable list" or vector of year/age values
values	LiPD "variable list" or vector of values
nens	Number of ensemble members to simulate

Value

a vector or matrix of synthetic values

See Also

Other spectra: plotSpectraEns, powerSpectrumEns

Other pca: pcaEns, plotPcaEns

---

detachAll   *Detach all packages*

Description

Detachs all packages

Usage

```
detachAll()
```

effectiveN	*Estimate effective sample size accounting for autocorrelation*

Description

Bretherton et al., 1999 estimate of effective sample size.

Usage

```
effectiveN(X, Y)
```

Arguments

X	a 1-column matrix or numeric dataset
Y	a 1-column matrix or numeric dataset of the same length as X

Value

estimate of the effective sample size

Author(s)

Nick McKay

estimateUncertaintyFromRange	
	Estimate uncertainty estimates from high/low range

Description

Estimate uncertainty (plus/minus values) from a range of values

Usage

```
estimateUncertaintyFromRange(MT, range1 = "age.young", range2 = "age.old")
```

Arguments

MT	LiPD "measurementTable"
range1	name of one of the range variables
range2	name of the other range variable

Value

MT: a LiPD measurementTable with a new unc.estimate variable

See Also

Other LiPD manipulation: `flipCoords`, `getVariableIndex`, `mapAgeEnsembleToPaleoData`, `selectData`

---

fdr	*False Discovery Testing of p-values from multiple testing*

Description

iThis is the main function designed for general usage for determining significance based on the FDR approach, following the Ventura et al. reference below.

Usage

```
fdr(pvals, qlevel = 0.05, method = "original", adjustment.method = NULL,
  adjustment.args = NULL)
```

Arguments

pvals   a vector of pvals on which to conduct the multiple testing

qlevel   the proportion of false positives desired

method   method for performing the testing. 'original' follows Benjamini & Hochberg (1995); 'general' is much more conservative, requiring no assumptions on the p-values (see Benjamini & Yekutieli (2001)). We recommend using 'original', and if desired, using 'adjustment.method="mean" ' to increase power

adjustment.method

method for increasing the power of the procedure by estimating the proportion of alternative p-values, one of "mean", the modified Storey estimator that we suggest in Ventura et al. (2004), "storey", the method of Storey (2002), or "two-stage", the iterative approach of Benjamini et al. (2001)

adjustment.args

arguments to adjustment.method; see propAlt() for description, but note that for "two-stage", qlevel and fdr.method are taken from the qlevel and method arguments to fdr()

Author(s)

Chris Paciorek

References

References: Ventura, V., C.J. Paciorek, and J.S. Risbey. 2004. Controlling the proportion of falsely-rejected hypotheses when conducting multiple tests with climatological data. Journal of Climate, in press. Also Carnegie Mellon University, Department of Statistics technical report 775 (<www.stat.cmu.edu/tr/tr775/tr775.html>). Benjamini, Y, and Y. Hochberg. 1995. Controlling the false discovery rate: a practical and powerful approach to multiple testing. JRSSB 57:289-300. Benjamini, Y. and D. Yekutieli. 2001. The control of the false discovery rate in multiple testing under dependency. Annals of Statistics 29:1165-1188. Benjamini, Y., A. Krieger, and D. Yekutieli. 2001. Two staged linear step up FDR controlling procedure. Technical Report, Department of Statistics and Operations Research, Tel Aviv University. URL: <http://www.math.tau.ac.il/~ybenja/Papers.html> Storey, J. 2002. A direct approach to false discovery rates. JRSSB 64: 479–498. @return NULL if no significant tests, or a vector of the indices of the significant tests @examples signif <- fdr(pvals,method="original",adjustment.method="mean")

See Also

Other FDR: `fdr.master`, `fdrBasic`, `propAlt`, `storey`

---

fdr.master	*FDR Master*

Description

This is an internal function that performs various versions of the FDR procedure, but without the modification described in section 4 of our J of Climate paper.

Usage

```
fdr.master(pvals, qlevel = 0.05, method = "original")
```

Arguments

pvals	(required): a vector of pvals on which to conduct the multiple testing
qlevel	the proportion of false positives desired
method	one of 'original', the original method of Benjamini & Hochberg (1995), or 'general', the method of Benjamini & Yekutieli (2001), which requires no assumptions about the p-values, but which is much more conservative. We recommend 'original' for climatological data, and suspect it works well generally for spatial data.

Value

NULL if no significant tests, or a vector of the indices of the significant tests

Author(s)

Chris Paciorek

See Also

Other FDR: `fdrBasic`, `fdr`, `propAlt`, `storey`

---

fdrBasic	*FDR Basic*

Description

This is an internal function that performs the basic FDR of Benjamini & Hochberg (1995).

Usage

```
fdrBasic(pvals, qlevel = 0.05)
```

Arguments

pvals	(required): a vector of pvals on which to conduct the multiple testing
qlevel	the proportion of false positives desired

Value

NULL if no significant tests, or a vector of the indices of the significant tests

Author(s)

Chris Paciorek

See Also

Other FDR: `fdr.master`, `fdr`, `propAlt`, `storey`

---

flipCoords	*Flip Coordinates*

Description

Swap latitude and longitude in a LiPD object

Usage

```
flipCoords(L)
```

Arguments

L	a LiPD object

See Also

Other LiPD manipulation: `estimateUncertaintyFromRange`, `getVariableIndex`, `mapAgeEnsembleToPaleoData`, `selectData`

---

geoChronRPlotTheme	*Define a plot theme for GeoChronR*

Description

Use this to define a theme across geoChronR

Usage

```
geoChronRPlotTheme(base_size = 11, base_family = "")
```

See Also

Other plot: `axisLabel`, `plotChron`, `plotCorrEns`, `plotHistEns`, `plotLine`, `plotModelDistributions`, `plotPcaEns`, `plotPvalsEnsFdr`, `plotRegressEns`, `plotScatterEns`, `plotSpectraEns`, `plotSummary`, `plotTimeseriesEnsLines`, `plotTimeseriesEnsRibbons`, `plotTrendLinesEns`

---

getOs *What OS is this?*

Description

Returns the OS

Usage

```
getOs()
```

Value

A string ("osx","linux",or "windows")

---

getVariableIndex *Get the index of variable list*

Description

Gets the index for a LiPD "variable list"

Usage

```
getVariableIndex(table, varName = NA, altNames = varName, ignore = NA,
  always.choose = FALSE, strictSearch = FALSE)
```

Arguments

table	a LiPD measurement, ensemble or summary Table
varName	string name of the variable to extract
altNames	A vector of strings for alternative names to search for
ignore	A vector of strings of variableNames to ignore
always.choose	Force selection of the variable from a list
strictSearch	Use a strictSearch to look for the ageEnsemble and depth variables. TRUE(default) or FALSE.

Value

An integer index

See Also

Other LiPD manipulation: estimateUncertaintyFromRange, flipCoords, mapAgeEnsembleToPaleoData, selectData

---

kde_2d   *Two dimensional kernel density estimation*

Description

Use a kernel density estimator to model the density of samples along a 2-dimensional grid

Usage

```
kde_2d(x, y, nbins = 100, x.bin = NA, y.bin = NA)
```

Arguments

x	n by m matrix where n is the number of observations and m is >= 1
y	n by j matrix where n is the number of observations and j is >= 1
nbins	number bins over which to calculate intervals. Used to calculate x.bin if not provided.
x.bin	vector of bin edges over which to bin.
y.bin	vector of bin edges over which to bin.

Value

A list with a matrix of density, x.bin and y.bin

See Also

Other gridding: bin2d, quantile2d

---

loadBaconOutput   *Load the ensemble, summary and distribution data from a Bacon simulation*

Description

Loads the ensemble, summary and distribution data from a Bacon simulation and stores them in the LiPD structure. Will be run in interactive mode if necessary parameters aren't specified. Most users will want to use runBacon for their bacon needs.

Usage

```
loadBaconOutput(L, site.name = L$dataSetName, which.chron = NA,
  baconDir = NA, modelNum = NA, makeNew = NA, maxEns = 1000)
```

Arguments

L	a single LiPD object
site.name	the name used for the bacon model (and directories)
which.chron	the number of the chronData object that you'll be working in
baconDir	the directory where Bacon is installed on this computer.
modelNum	which chronModel do you want to use?
makeNew	do you want to create a new model in chronData? (TRUE, FALSE, NA). NA will try be smart, or ask you for advice.

Value

L the input LiPD file with methods and data added to the chronModel.

Author(s)

Nick McKay

See Also

Other Bacon: `runBacon`, `sampleBaconAges`, `writeBacon`

Examples

```
loadBaconOutput(L)
#Run in interactive mode
```

---

mapAgeEnsembleToPaleoData

> *Map an ageEnsemble variable from a chron model to a paleoMeasurement Table*

Description

Copies an ageEnsemble from chronData (model) to paleoData (measurementTable), by matching depth and interpolating (extrapolating) as necessary.

Usage

```
mapAgeEnsembleToPaleoData(L, which.paleo = NA, which.pmt = NA,
  which.chron = NA, which.model = NA, which.ens = NA,
  max.ensemble.members = NA, strictSearch = FALSE)
```

Arguments

L	a lipd object
which.paleo	an integer that corresponds to which paleoData object (L$paleoData[[?]]) has the measurementTable you want to modify
which.pmt	an integer that corresponds to which paleo measurementTable you want to add the ensemble to?

which.chron	an integer that corresponds to which chronData object (L$crhonData[[?]]) has the model you want to get the ensemble from
which.model	an integer that corresponds to which chron model you want to get the ensemble from?
which.ens	an integer that corresponds to which chron model ensembleTable you want to get the ensemble from?
max.ensemble.members	
	Maximum number of ensemble members to map
strictSearch	Use a strictSearch to look for the ageEnsemble and depth variables. TRUE(default) or FALSE.

Value

L a lipd object

See Also

Other LiPD manipulation: [estimateUncertaintyFromRange](), [flipCoords](), [getVariableIndex](), [selectData]()

---

mapLipd   *Map a LiPD object*

Description

Create a google or line map of the location of the LiPD object

Usage

```
mapLipd(L, color = "red", size = 8, shape = 16, map.type = "google",
  extend.range = 10)
```

Arguments

L	Single LiPD object
color	Color of the location marker
size	Size of the location marker
shape	Shape of the location marker
map.type	"google" or "line"
extend.range	increase the span of the map by this much (lat/long degrees)

Value

ggmap object

Author(s)

Nick McKay

See Also

Other mapping: [assignColors](), [baseMap](), [mapLipds]()

---

mapLipds	*Map a list of LiPD objects*

Description

Create a google or line map of the location of a list of LiPD objects

Usage

```
mapLipds(D, shape = 21, size = 8, color = sapply(D, "[[", "archiveType"),
  map.type = "google", f = 0.3, restrict.map.range = TRUE,
  boundcirc = FALSE, global = FALSE, projection = "mercator")
```

Arguments

D	A list of LiPD objects
shape	Shape of the location marker
size	Size of the location marker
color	Color of the location marker
map.type	"google" or "line"
f	buffer for the map range
restrict.map.range	
	TRUE or FALSE. Trim the size of the map to the points, for "line" map type
boundcirc	Draw a boundary circle around a polar projection. TRUE or FALSE(default).
global	Should the scope of the map be global? TRUE or FALSE(default).
projection	Map project. All options on: ?mapproject
shape.by.archive	
	TRUE or FALSE. Use archiveType to assign shapes.

Value

ggmap object

Author(s)

Nick McKay

See Also

Other mapping: assignColors, baseMap, mapLipd

---

meltDistributionTable   *Melt distribution*

Description

Takes a LiPD model distribution and melt it into a single data.frame

Usage

```
meltDistributionTable(this.dist, dist.plot = 1:length(this.dist))
```

Arguments

this.dist	LiPD "distributionTable" object
dist.plot	vector of distribution tables to plot

Value

data.frame of melted distribution objects.

Author(s)

Nick McKay

---

neotoma2Lipd   *Create a LiPD object from Neotoma*

Description

Uses the Neotoma API to create a LiPD file?

Usage

```
neotoma2Lipd(site)
```

Arguments

site	the site object from the R Neotoma package, output of neotoma::get_site()

Details

Super alpha version 0.00001. Expect updates! get site fist site = get_site("Potato Lake")

Value

A LiPD object

---

pcaEns *Perform principle components analysis (PCA) across an ensemble*

Description

Ensemble PCA, or Monte Carlo Empirical Orthogonal Functions as described in Anchukaitis and Tierney 2012.

Usage

```
pcaEns(bin.list, method = "ppca", weights = NA, PCAtype = "corr",
  nPCs = 4, nEns = 1000)
```

Arguments

bin.list	A list of binned data, the output of binTs()
method	What method to use for PCA? pcaMethods::listPcaMethods() for options. "ppca" is default. Other options may not work in GeoChronR.
weights	Vector of weights to apply to timeseries in the bin.list
PCAtype	Correlation ("corr" - default) or Covariance ("cov"), matrix
nPCs	number of PCs/EOFs to calculate
nens	how many ensemble members?

See Also

Other pca: createSyntheticTimeseries, plotPcaEns

---

plotChron *Plot chronologies*

Description

Plot creates an age model plot with all the bells and whistles, including a spread of ensemble members, probability distributions, and a few example ensemble members.

Usage

```
plotChron(L, chron.number = NA, model.num = NA, probs = c(0.025, 0.25,
  0.5, 0.75, 0.975), x.bin = NA, y.bin = NA, nbins = 100,
  bandColorLow = "white", bandColorHigh = "grey70", bandAlp = 1,
  lineColor = "Black", lineWidth = 1, add.to.plot = ggplot2::ggplot(),
  nEnsLines = 5, ensLineColor = "red", ensLineAlp = 0.7, distAlp = 0.3,
  distType = "violin", distColor = "purple", distThick = 0.1,
  distScale = 0.02, truncateDist = NA)
```

Arguments

L	A LiPD object
probs	quantiles to calculate and plot
x.bin	vector of bin edges over which to bin.
y.bin	vector of bin edges over which to bin.
nbins	number bins over which to calculate intervals. Used to calculate x.bin if not provided.
bandColorLow	Band color of the outer most band.
bandColorHigh	Band color of the inner most band.
lineColor	Line color (following ggplot rules)
lineWidth	Width of the line
add.to.plot	A ggplot object to add this plot to. Default is ggplot() .
nEnsLines	Number of ensemble members to plot
ensLineColor	color of the ensemble lines
ensLineAlp	transparency of the lines
distType	"violin" (default), "up" for one-sided distributions pointed up, "down" for one-sided distributions pointed down
distColor	distribution color (following ggplot rules)
distThick	thickness of the line around the distribution
distScale	controls the vertical span of the probability distribution. Approximately the vertical fraction of the plot that the distribution will cover.
truncateDist	truncate probability density values below this number. NA (default) means no truncation
dist.var	Name of the distribution variable, will be plotted along the x-axis. Use coord_flip() after running the function if you want vertical distributions. "age" by default.
y.var	Name of the y-axis variable. "depth" by default.
bandAlpha	Transparency of the band plot

Value

A ggplot object

Author(s)

Nick McKay

See Also

Other plot: axisLabel, geoChronRPlotTheme, plotCorrEns, plotHistEns, plotLine, plotModelDistributions, plotPcaEns, plotPvalsEnsFdr, plotRegressEns, plotScatterEns, plotSpectraEns, plotSummary, plotTimeseriesEnsLines, plotTimeseriesEnsRibbons, plotTrendLinesEns

Other chron: plotModelDistributions

---

plotCorrEns   *Plot the results of an ensemble correlation*

Description

Plots the output of an ensemble correlation analysis.

Usage

```
plotCorrEns(cor.df, corStats, bins = 40, lineLabels = rownames(corStats),
  add.to.plot = ggplot())
```

Arguments

cor.df	A data.frame correlation r and p-values. Output from corEns()
corStats	A data.frame of correlation quantiles. Output from corEns()
bins	Number of bins in the histogram
lineLabels	Labels for the quantiles lines
add.to.plot	A ggplot object to add these lines to. Default is ggplot() .

Value

A ggplot object

Author(s)

Julien Emile-Geay

Nick McKay

See Also

Other plot: [axisLabel](#), [geoChronRPlotTheme](#), [plotChron](#), [plotHistEns](#), [plotLine](#), [plotModelDistributions](#), [plotPcaEns](#), [plotPvalsEnsFdr](#), [plotRegressEns](#), [plotScatterEns](#), [plotSpectraEns](#), [plotSummary](#), [plotTimeseriesEnsLines](#), [plotTimeseriesEnsRibbons](#), [plotTrendLinesEns](#)

---

plotHistEns   *Plot an ensemble dataset as a histogram*

Description

Plots ensemble data as a histogram

Usage

```
plotHistEns(ensData, quantiles = c(0.025, 0.25, 0.5, 0.75, 0.975),
  bins = 50, lineLabels = rownames(ensStats), add.to.plot = ggplot(),
  alp = 1, fill = "grey50")
```

Arguments

`ensData`	A data.frame of values to plot as a histogram
`bins`	Number of bins in the histogram
`lineLabels`	Labels for the quantiles lines
`add.to.plot`	A ggplot object to add these lines to. Default is ggplot()
`fill`	fill color of the histogram, following ggplot rules
`probs`	quantiles to calculate and plot

Value

A ggplot object

Author(s)

Nick McKay

See Also

Other plot: `axisLabel`, `geoChronRPlotTheme`, `plotChron`, `plotCorrEns`, `plotLine`, `plotModelDistributions`, `plotPcaEns`, `plotPvalsEnsFdr`, `plotRegressEns`, `plotScatterEns`, `plotSpectraEns`, `plotSummary`, `plotTimeseriesEnsLines`, `plotTimeseriesEnsRibbons`, `plotTrendLinesEns`

---

plotLine	*Plot or add a line to plot*

Description

Plots or adds a line to aplot

Usage

```
plotLine(X, Y, color = "black", alp = 1, add.to.plot = ggplot())
```

Arguments

`X`	A LiPD variable list to plot, including values, units, names, and more
`Y`	A LiPD variable list to plot, including values, units, names, and more
`color`	Line color (following ggplot rules)
`alp`	Line transparency
`add.to.plot`	A ggplot object to add these lines to. Default is ggplot() .

Value

A ggplot object

Author(s)

Nick McKay

See Also

Other plot: axisLabel, geoChronRPlotTheme, plotChron, plotCorrEns, plotHistEns, plotModelDistributions, plotPcaEns, plotPvalsEnsFdr, plotRegressEns, plotScatterEns, plotSpectraEns, plotSummary, plotTimeseriesEnsLines, plotTimeseriesEnsRibbons, plotTrendLinesEns

---

plotModelDistributions

Plot probability distributions

Description

Plot or add probability distributions from a paleo or chron model to a plot.

Usage

```
plotModelDistributions(L, dist.var = "age", y.var = "depth",
  mode = "chron", which.data = 1, model.num = 1, add.to.plot = ggplot(),
  alp = 0.5, color = "purple", scaleFrac = 0.02, dist.plot = NA,
  distType = "violin", thick = 0.1, truncateDist = NA)
```

Arguments

L	A LiPD object
dist.var	Name of the distribution variable, will be plotted along the x-axis. Use coord_flip() after running the function if you want vertical distributions. "age" by default.
y.var	Name of the y-axis variable. "depth" by default.
mode	chron or paleo
which.data	number of the chron or paleo Data object
model.num	number of the model object
add.to.plot	A ggplot object to add this plot to. Default is ggplot() .
color	distribution color (following ggplot rules)
scaleFrac	controls the vertical span of the probability distribution. Approximately the vertical fraction of the plot that the distribution will cover.
dist.plot	vector of distribution tables to plot
distType	"violin" (default), "up" for one-sided distributions pointed up, "down" for one-sided distributions pointed down
thick	thickness of the line around the distribution
truncateDist	truncate probability density values below this number. NA (default) means no truncation

Value

A ggplot object

Author(s)

Nick McKay

See Also

Other plot: axisLabel, geoChronRPlotTheme, plotChron, plotCorrEns, plotHistEns, plotLine, plotPcaEns, plotPvalsEnsFdr, plotRegressEns, plotScatterEns, plotSpectraEns, plotSummary, plotTimeseriesEnsLines, plotTimeseriesEnsRibbons, plotTrendLinesEns

Other chron: plotChron

---

plotPcaEns   *Map ensemble pca loadings and plot PC timeseries*

Description

Map ensemble pca loadings and plot PC timeseries

Usage

```
plotPcaEns(ens.PC.out, TS, map.type = "line", which.PCs = c(1, 2),
  f = 0.2, color = "temp", dotsize = 5, restrict.map.range = TRUE,
  shape.by.archive = TRUE, projection = "mollweide", boundcirc = TRUE,
  probs = c(0.025, 0.25, 0.5, 0.75, 0.975))
```

Arguments

ens.PC.out	results of pcaEns()
TS	Timeseries object http://nickmckay.github.io/LiPD-utilities/r/index.html#what-is-a-time-series used in the pcaEns() analysis
map.type	"google" or "line"
which.PCs	vector of PCs to plot. Choose two. c(1,2) is default.
f	zoom buffer for plotting
color	color scale option. See assignColors()
dotsize	How big are the dots on the map
restrict.map.range	
	TRUE or FALSE. Trim the size of the map to the points, for "line" map type
shape.by.archive	
	TRUE or FALSE. Use archiveType to assign shapes.
projection	Map project. All options on: ?mapproject
boundcirc	For polar projects, draw a boundary circle? TRUE or FALSE
probs	quantiles to calculate and plot in the PC timeseries
lineLabels	Labels for the quantiles lines

Value

A gridExtra ggplot object

Author(s)

Nick McKay

See Also

Other plot: axisLabel, geoChronRPlotTheme, plotChron, plotCorrEns, plotHistEns, plotLine, plotModelDistributions, plotPvalsEnsFdr, plotRegressEns, plotScatterEns, plotSpectraEns, plotSummary, plotTimeseriesEnsLines, plotTimeseriesEnsRibbons, plotTrendLinesEns

Other pca: createSyntheticTimeseries, pcaEns

---

plotPvalsEnsFdr	*Plot the the p-values of an ensemble correlation analysis in a rank-pvalue plot*

Description

Plots the output of an ensemble correlation analysis as a rank-pvalue plot

Usage

```
plotPvalsEnsFdr(cor.df, alpha = 0.05)
```

Arguments

cor.df	A data.frame correlation r and p-values. Output from corEns()
alpha	probability threshold

Value

A ggplot object

Author(s)

Julien Emile-Geay

See Also

Other plot: axisLabel, geoChronRPlotTheme, plotChron, plotCorrEns, plotHistEns, plotLine, plotModelDistributions, plotPcaEns, plotRegressEns, plotScatterEns, plotSpectraEns, plotSummary, plotTimeseriesEnsLines, plotTimeseriesEnsRibbons, plotTrendLinesEns

---

plotRegressEns	*Plot ensemble regression results*

Description

Creates a suite of plots to characterize the results of an ensemble regression.

Usage

```
plotRegressEns(regEnsList, alp = 0.2, quantiles = c(0.025, 0.5, 0.975))
```

Arguments

regEnsList	output of regressEns()
alp	Transparency of the scatter plot.
quantiles	quantiles to calculate and plot

Value

A list of ggplot objects

- YPlot - ribbon plot of the prectictand timeseries over the interval of overlap
- XPlot - ribbon plot of the predictor timeseries over the interval of overlap
- scatterplot - ensemble scatter plot of the predictor and predictand timeseries over the interval of overlap
- mHist - distribution of ensemble regression slopes
- bHist - distribution of ensemble regression intercepts
- modeledYPlot - ribbon plot of values modeled by the ensemble regression, incorporating age uncertainty in both the regression and the predictor timeseries
- summaryPlot - grid.arrange object of all the regression plots

Author(s)

Nick McKay

See Also

Other plot: axisLabel, geoChronRPlotTheme, plotChron, plotCorrEns, plotHistEns, plotLine, plotModelDistributions, plotPcaEns, plotPvalsEnsFdr, plotScatterEns, plotSpectraEns, plotSummary, plotTimeseriesEnsLines, plotTimeseriesEnsRibbons, plotTrendLinesEns

Other regress: plotScatterEns, plotTrendLinesEns, regressEns

---

plotScatterEns	*Plot an ensemble of data as a scatterplot*

Description

Plot an ensemble timeseries as a scatter plot. Useful in showing the general impact of uncertainty on a bivariate relationship.

Usage

```
plotScatterEns(X, Y, alp = 0.2, maxPlotN = 1000, add.to.plot = ggplot())
```

Arguments

X	A LiPD variable list to plot, including values, units, names, and more
Y	A LiPD variable list to plot, including values, units, names, and more
alp	Line transparency
maxPlotN	Whats the maximum number of lines to plot?
add.to.plot	A ggplot object to add this plot to. Default is ggplot() .

Value

A ggplot object

Author(s)

Nick McKay

See Also

Other plot: axisLabel, geoChronRPlotTheme, plotChron, plotCorrEns, plotHistEns, plotLine,
plotModelDistributions, plotPcaEns, plotPvalsEnsFdr, plotRegressEns, plotSpectraEns,
plotSummary, plotTimeseriesEnsLines, plotTimeseriesEnsRibbons, plotTrendLinesEns

Other regress: plotRegressEns, plotTrendLinesEns, regressEns

---

plotSpectraEns   *Plot ensemble spectra output*

Description

Plot the output of powerSpectrumEns() as a ribbon plot of distributions, plus confidence levels

Usage

```
plotSpectraEns(spec.ens)
```

Arguments

spec.ens   Output from powerSpectrumEns()

Value

ggplot object of spectrum plot

See Also

Other plot: axisLabel, geoChronRPlotTheme, plotChron, plotCorrEns, plotHistEns, plotLine,
plotModelDistributions, plotPcaEns, plotPvalsEnsFdr, plotRegressEns, plotScatterEns,
plotSummary, plotTimeseriesEnsLines, plotTimeseriesEnsRibbons, plotTrendLinesEns

Other spectra: createSyntheticTimeseries, powerSpectrumEns

---

plotSummary   *Plot a summary figure*

Description

shows a map, timeseries, and age model diagram, and basic simple metadata

Usage

```
plotSummary(L)
```

Arguments

L   A LiPD Object

Value

A gridArrange of ggplot grobs

Author(s)

Nick McKay

See Also

Other plot: axisLabel, geoChronRPlotTheme, plotChron, plotCorrEns, plotHistEns, plotLine, plotModelDistributions, plotPcaEns, plotPvalsEnsFdr, plotRegressEns, plotScatterEns, plotSpectraEns, plotTimeseriesEnsLines, plotTimeseriesEnsRibbons, plotTrendLinesEns

Examples

```
myPlot = summaryPlot(L)
```

---

plotTimeseriesEnsLines
                    Plot an ensemble timeseries as a set of lines

---

Description

Plot an ensemble timeseries as a set of lines. Useful for displaying a handful of ensemble members to characterize individual paths.

Usage

```
plotTimeseriesEnsLines(X, Y, alp = 0.2, color = "blue", maxPlotN = 1000,
  add.to.plot = ggplot())
```

Arguments

X	A LiPD variable list to plot, including values, units, names, and more
Y	A LiPD variable list to plot, including values, units, names, and more
alp	Line transparency
color	Line color (following ggplot rules)
maxPlotN	Whats the maximum number of lines to plot?
add.to.plot	A ggplot object to add these lines to. Default is ggplot() .

Value

A ggplot object

Author(s)

Nick McKay

See Also

Other plot: axisLabel, geoChronRPlotTheme, plotChron, plotCorrEns, plotHistEns, plotLine, plotModelDistributions, plotPcaEns, plotPvalsEnsFdr, plotRegressEns, plotScatterEns, plotSpectraEns, plotSummary, plotTimeseriesEnsRibbons, plotTrendLinesEns

---

plotTimeseriesEnsRibbons

Plot an ensemble timeseries as ribbons of probabilities

Description

Plot an ensemble timeseries as a set of bands of probability. Useful for displaying the full range of probability across ensemble members.

Usage

```
plotTimeseriesEnsRibbons(X, Y, alp = 1, probs = c(0.025, 0.25, 0.5, 0.75,
  0.975), x.bin = NA, y.bin = NA, nbins = 200, colorLow = "white",
  colorHigh = "grey70", lineColor = "Black", lineWidth = 1,
  add.to.plot = ggplot())
```

Arguments

X	A LiPD variable list to plot, including values, units, names, and more
Y	A LiPD variable list to plot, including values, units, names, and more
alp	Line transparency
probs	a vector of probabilities to plot as ribbons. It will create bands as ribbons of quantiles moving inward. If there's an odd number, it plots the middle quantile as a line.
x.bin	vector of bin edges over which to bin.
y.bin	vector of bin edges over which to bin.

nbins	number bins over which to calculate intervals. Used to calculate x.bin if not provided.
colorLow	Band color of the outer most band.
colorHigh	Band color of the inner most band.
lineColor	Line color (following ggplot rules)
lineWidth	Width of the line
add.to.plot	A ggplot object to add this plot to. Default is ggplot() .

Value

A ggplot object

Author(s)

Nick McKay

See Also

Other plot: axisLabel, geoChronRPlotTheme, plotChron, plotCorrEns, plotHistEns, plotLine, plotModelDistributions, plotPcaEns, plotPvalsEnsFdr, plotRegressEns, plotScatterEns, plotSpectraEns, plotSummary, plotTimeseriesEnsLines, plotTrendLinesEns

---

plotTrendLinesEns   *Plot an ensemble of trendlines*

Description

Plot an ensemble of trendlines based on slope and intercept.

Usage

```
plotTrendLinesEns(mb.df, xrange, pXY = 1:nrow(mb.df), alp = 0.2,
  color = "red", add.to.plot = ggplot())
```

Arguments

mb.df	A data.frame of slopes (column 1) and intercepts (column 2)
xrange	range of x values (min and max)
pXY	index of which observations to use
alp	Line transparency
add.to.plot	A ggplot object to add these lines to. Default is ggplot() .

Value

A ggplot object

Author(s)

Nick McKay

See Also

Other plot: axisLabel, geoChronRPlotTheme, plotChron, plotCorrEns, plotHistEns, plotLine, plotModelDistributions, plotPcaEns, plotPvalsEnsFdr, plotRegressEns, plotScatterEns, plotSpectraEns, plotSummary, plotTimeseriesEnsLines, plotTimeseriesEnsRibbons

Other regress: plotRegressEns, plotScatterEns, regressEns

---

powerSpectrumEns   *Calculate ensemble power spectra*

Description

Calculate ensemble power spectra using lomb-scargle

Usage

```
powerSpectrumEns(time, values, max.ens = NA, ofac = 1)
```

Arguments

time	LiPD "variable list" or vector of year/age values
values	LiPD "variable list" or vector of values
max.ens	Maximum number of ensemble members to analyze
ofac	oversampling factor for lomb::lsp

Value

a list of ensemble spectra results

- freqs: vector of frequencies
- power: vector of spectral powers
- powerSyn: matrix of synthetic spectral power results

See Also

Other spectra: createSyntheticTimeseries, plotSpectraEns

---

propAlt *Proportion of alternate hypotheses*

Description

This is an internal function that calculates an estimate of a, the proportion of alternative hypotheses, using one of several methods.

Usage

```
propAlt(pvals, adjustment.method = "mean", adjustment.args = list(edf.lower
  = 0.8, num.steps = 20))
```

Arguments

pvals   a vector of pvals on which to conduct the multiple testing

adjustment.method

                method for increasing the power of the procedure by estimating the proportion of alternative p-values, one of "mean", the modified Storey estimator that we suggest in Ventura et al. (2004), "storey", the method of Storey (2002), or "two-stage", the iterative approach of Benjamini et al. (2001)

adjustment.args

                arguments to adjustment.method; see propAlt() for description, but note that for "two-stage", qlevel and fdr.method are taken from the qlevel and method arguments to fdr()

qlevel   the proportion of false positives desired

Value

estimate of a, the number of alternative hypotheses

Author(s)

Chris Paciorek

See Also

Other FDR: fdr.master, fdrBasic, fdr, storey

Examples

```
a <- propAlt(pvals,adjustment.method="mean")
```

---

pvalPearsonSerialCorrected

Calculate correlation p-value given sample size.

Description

Calculate Pearson p-values accounting for effective sample size

Usage

```
pvalPearsonSerialCorrected(r, n)
```

Arguments

r	correlation coefficient
n	sample size

Value

p-value based on two-tailed t-test

Author(s)

Nick McKay

---

quantile2d

Find quantiles across an ensemble

Description

Determine quantiles across ensembles of x and/or y, as a function of x, using interpolation

Usage

```
quantile2d(x, y, nbins = 500, x.bin = NA, probs = c(0.025, 0.25, 0.5,
  0.75, 0.975), nens = max(c(ncol(x), ncol(y))))
```

Arguments

x	n by m matrix where n is the number of observations and m is >= 1
y	n by j matrix where n is the number of observations and j is >= 1
nbins	number bins over which to calculate intervals. Used to calculate x.bin if not provided.
x.bin	vector of bin edges over which to bin.
probs	quantiles to calculate
nens	number of ensemble members to derive quantiles for

Value

list of quantiles and x.bin

Author(s)

Nick McKay

See Also

Other gridding: `bin2d`, `kde_2d`

---

regress   *Simple ordinary least squeares regression*

Description

Simple regression function. Faster than lm()

Usage

```
regress(X, Y)
```

Arguments

X	a matrix of predictor data
Y	a vector of predictand data

Value

model coefficients

Author(s)

Nick McKay

---

regressEns   *Ensemble regression*

Description

This is the primary function for ensemble regression. It will take ensemble values in time and/or values in the predictor (X), and regress them on ensemble values in time and/or values in Y (the predictand). The function will then apply the ensemble linear model to the full length of X to create a modeled Y. Will also optionally create plots.

Usage

```
regressEns(timeX, valuesX, timeY, valuesY, binvec = NA, binstep = NA,
  binfun = mean, max.ens = NA, percentiles = c(0.025, 0.25, 0.5, 0.75,
  0.975), recon.binvec = NA, minObs = 10)
```

Arguments

`timeX`	matrix of age/time ensembles, or single column
`valuesX`	matrix of values ensembles, or single column
`timeY`	matrix of age/time ensembles, or single column
`valuesY`	matrix of values ensembles, or single column
`binvec`	vector of bin edges for binning step
`binstep`	spacing of bins, used to build bin step
`binfun`	function to use during binning (mean, sd, and sum all work)
`max.ens`	maximum number of ensemble members to regress
`percentiles`	quantiles to calculate for regression parameters
`recon.binvec`	bin vector to use for the modeled regression.
`minObs`	minimum number of points required to calculate regression

Value

list of ensemble output

Author(s)

Nick McKay

See Also

Other regress: `plotRegressEns`, `plotScatterEns`, `plotTrendLinesEns`

---

runBacon	*Generate a Bayesian Reconstruction Age Model (Bacon) and add it into a LiPD object*

Description

This is a high-level function that uses Bacon to simulate an age model, and stores this as an age-ensemble in a model in chronData. If needed input variables are not entered, and cannot be deduced, it will run in interactive mode. See Blaauw and Christen (2011) doi:10.1214/11-BA618 for details.

Usage

```
runBacon(L, which.chron = NA, which.mt = NA, baconDir = NA,
  site.name = L$dataSetName, modelNum = NA, remove.rejected = TRUE,
  overwrite = TRUE, cc = NA, maxEns = 1000)
```

Arguments

`L`	a single LiPD object
`which.chron`	the number of the chronData object that you'll be working in
`which.mt`	the number of the measurementTable you'll be working in
`baconDir`	the directory where Bacon is installed on this computer.
`site.name`	the name used for the bacon model (and directories)
`modelNum`	which chronModel do you want to use?
`remove.rejected`	don't write out dates that are marked as rejected
`overwrite`	overwrite files and directories
`cc`	An integer, or vector of integers corresponding to age that describes the calibration curve. You can specify here (see below) or if it's NA the code will guess based on archiveType

 • cc=1 IntCal13
 • cc=2 MarineCal
 • cc=3 SHCal13

`maxEns`	the maximum number of ensembles to load in (default = 1000)

Value

L The single LiPD object that was entered, with methods, ensembleTable, summaryTable and distributionTable added to the chronData model.

Author(s)

Nick McKay

Maarten Blaauw (Bacon)

See Also

Other Bacon: `loadBaconOutput`, `sampleBaconAges`, `writeBacon`

Examples

```
Run in interactive mode:
L = runBacon(L)

Run in noninteractive mode, describing everything:
L = runBacon(L,which.chron = 1, which.mt = 1, modelNum = 3, baconDir = "~/Bacon/",site.name = "MSB2K", cc = 1)
```

runBam *Generate a Banded Age Model (BAM) and add it into a LiPD object*

Description

This is a high-level function that uses BAM to simulate age uncertainty in layer counted records, and stores this as an age-ensemble in a paleoData measurementTable, and in a model in chronData. If needed input variables are not entered, and cannot be deduced, it will run in interactive mode. BAM produces reasonable results for non-layer counted data, and can generate ensembles for unevenly spaced data, and thus is useful for generating ensembles for tie-point chronologies that are missing the necessary data to calculate ensembles properly. See Comboul et al. (2015) doi:10.5194/cp-10-825-2014 for details.

Usage

```
runBam(L, which.paleo = NA, which.pmt = NA, which.chron = 1,
  which.model = NA, makeNew = FALSE, nens = 1000, model = NA)
```

Arguments

L	a single LiPD object
which.paleo	the number of the paleoData object that you'll be working in
which.pmt	the number of the measurementTable you'll be working in
which.model	the number of the chronData model where you want to store the model information
makeNew	Forces the creation of a new model (TRUE or FALSEdefault)
nens	The number of members in the ensemble
model	a list that describes the model to use in BAM

- model$ns: number of samples
- model$name: 'poisson' or 'bernoulli'
- model$param: probability of growth band being perturbed (default: prob of missing band = prob of doubly-counted band = 0.05)
  - if model$param is a single argument, then the perturbations are symmetric (prob of missing band = prob of doubly-counted band)
  - if model$param = [a1 a2] and a1 neq a2 the model is asymmetric
    * a1 = prob(missing layer) - undercounted
    * a2 = prob(layer counted multiple times) - overcounted
  - if model$param: 2xp matrix, then different miscounting prob. are defined for each time series.
- model$resize: do not resize: 0 (default), resize to shortest sample: -1, resize to longest sample: 1
- model$tm: if a time model is provided, the code returns the corresponding perturbed data

Value

L The single LiPD object that was entered, with ageEnsemble and chronData model added.

Author(s)

Nick McKay

Maud Comboul (BAM)

See Also

Other BAM: bamCorrect, simulateBam

Examples

```
Run in interactive mode:
L = runBam(L)

Run in noninteractive mode, describing everything:
L = runBam(L,which.paleo = 1, which.pmt = 1, which.model = 3, makeNew = TRUE,
nEns = 100, model = list(name = "poisson",param = 0.05, resize = 0, ns = nEns))
```

---

runBchron	*Generate a Bayesian Reconstruction Age Model (Bacon) and add it into a LiPD object*

Description

This is a high-level function that uses Bchron to simulate an age model, and stores this as an age-ensemble in a model in chronData. If needed input variables are not entered, and cannot be deduced, it will run in interactive mode. See Haslett and Parnell (2008) doi:10.1111/j.1467-9876.2008.00623.x for details.

Usage

```
runBchron(L, which.chron = NA, site.name = L$dataSetName, modelNum = NA,
  calCurves = NA)
```

Arguments

L	a single LiPD object
which.chron	the number of the chronData object that you'll be working in
site.name	the name of the site
modelNum	which chronModel do you want to use?
calCurves	The calibration curves to be used. Enter either "marine13", intcal13", "shcal13" or "normal". Will prompt if not provided.

Value

L. The single LiPD object that was entered, with methods, ensembleTable, summaryTable and distributionTable added to the chronData model.

Author(s)

Deborah Khider

Andrew Parnell

Examples

```
Run in interactive mode:
L = runBchron(L)

Run in noninteractive mode:
L = runBchron(L,which.chron = 1, site.name = "MyWonderfulSite", modelNum = 3, calCurves = "marine13")
```

---

runClam   *Run a clam model*

Description

Not functional yet

Usage

```
runClam(L, which.chron = 1, clamDir = NA, remove.reverse = TRUE,
  overwrite = TRUE, cc = NA, site.name = L$dataSetName, modelNum = NA)
```

---

sampleBaconAges   *Sample ensemble ages from Bacon*

Description

Pulls ensemble members from Bacon output. Will be run in interactive mode if necessary parameters aren't specified. Most users will want to use runBacon for their bacon needs.

Usage

```
sampleBaconAges(corename, K = NA, baconDir = NA, maxEns = NA)
```

Arguments

corename	the name used for the bacon model (and directories)
K	the number of intervals over which the model is run, this is appended onto all the Bacon files after the underscore. If NA, will attempt to deduce from the directory.
baconDir	the directory where Bacon is installed on this computer. Willimport if bossible.
maxEns	the maximum number of ensemble members to import

Value

An ensemble table in the LiPD structure

Author(s)

Simon Goring

Nick McKay

See Also

Other Bacon: loadBaconOutput, runBacon, writeBacon

Examples

```
ensTable = sampleBaconAges("MSB2K",maxEns = 1000)
```

---

selectData   *Select a LiPD "variable list"*

Description

Selects and extracts a LiPD "variable list"

Usage

```
selectData(L, varName = NA, where = "paleoData", which.data = NA,
  tableType = "measurement", which.mt = NA, always.choose = FALSE,
  altNames = NA, model.num = 1, which.ens = 1, which.sum = 1,
  strictSearch = FALSE)
```

Arguments

L	a lipd object
varName	string name of the variable to extract
where	"paleoData" or "chronData"
which.data	an integer that corresponds to which paleo or chron Data object (L$<where>Data[[?]]) has the variable you want?
tableType	What type of table do you want to select data from? ("measurement", "summary" or "ensemble")
which.mt	an integer that corresponds to which paleo measurementTable has the variable you want?
always.choose	Force selection of the variable from a list
altNames	A vector of strings for alternative names to search for
model.num	an integer that corresponds to which model that has the variable you want
which.ens	an integer that corresponds to which ensembleTable you want to get the variable from?
which.sum	an integer that corresponds to which summaryTable you want to get the variable from?
strictSearch	Use a strictSearch to look for the ageEnsemble and depth variables. TRUE(default) or FALSE.

Value

A LiPD "variable list" object

See Also

Other LiPD manipulation: estimateUncertaintyFromRange, flipCoords, getVariableIndex, mapAgeEnsembleToPaleoData

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setupGeoChronR *Setup GeoChronR for first time use*

Description

installs special packages. Should have to be run once.

Usage

```
setupGeoChronR()
```

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simulateBam *Simulate a Banded Age Model (BAM)*

Description

Generate an ensemble of possible age corrected data:See www.clim-past-discuss.net/9/6077/2013/ for a detailed description of the model. The time series in X are automatically flipped to range from most recent to oldest measurements when the input t is given in increasing order.

Usage

```
simulateBam(X, t, model = NULL, ageEnsOut = FALSE)
```

Arguments

X	data (vector or matrix n*p)
t	chronology for data X (n*1)
model	a list that describes the model to use in BAM

- model$ns: number of samples
- model$name: 'poisson' or 'bernoulli'
- model$param: probability of growth band being perturbed (default: prob of missing band = prob of doubly-counted band = 0.05)
  - if model$param is a single argument, then the perturbations are symmetric (prob of missing band = prob of doubly-counted band)
  - if model$param = [a1 a2] and a1 neq a2 the model is asymmetric
    * a1 = prob(missing layer) - undercounted
    * a2 = prob(layer counted multiple times) - overcounted
  - if model$param: 2xp matrix, then different miscounting prob. are defined for each time series.
- model$resize: do not resize: 0 (default), resize to shortest sample: -1, resize to longest sample: 1
- model$tm: if a time model is provided, the code returns the corresponding perturbed data

ageEnsOut	TRUE or FALSE - return the ageEnsemble

Value

res a list with

- res$Xc: realizations of age-perturbed data matrix of size tn*p*ns (could be 2 or 3d)

- res$tc: new chronology tn*1

- res$tmc: corresponding ensemble of time-correction matrices (tn*p*ns) to map realizations in Xp back to the original data X (2=insert nan, 0=remove double band) (2 or 3d) where tn is the chronology length = n (default), shortest sample or longest sample depending on the chosen resizing option.

- res$ageEnsemble (optional): Returnd the full age ensemble if desired.

Author(s)

Maud Comboul

See Also

Other BAM: bamCorrect, runBam

Examples

```
res <- simulateBam(X,t)
#will generate an ensemble of 1000 age models randomly following
#a Poisson process with rate parameter theta=0.05 used to perturb data X

res <- simulateBam(X,t,model)
#will perturb data X  with the model specified in
#the model structure
```

---

storey   *Storey estimator*

Description

This is an internal function that calculates the basic Storey (2002) estimator of a, the proportion of alternative hypotheses.

Usage

```
storey(edf.quantile, pvals)
```

Arguments

edf.quantile   (required): the quantile of the empirical distribution function at which to esti-
                 mate a

pvals   (required): a vector of pvals on which to conduct the multiple testing

Value

estimate of a, the number of alternative hypotheses

Author(s)

Chris Paciorek

See Also

Other FDR: `fdr.master`, `fdrBasic`, `fdr`, `propAlt`

| writeBacon | *Create the input file for a Bacon model from a LiPD object* |

Description

This generates the csv file that is used for input to Bacon. Will be run in interactive mode if necessary parameters aren't specified. Most users will want to use runBacon for their bacon needs.

Usage

```
writeBacon(L, which.chron = NA, which.mt = NA, baconDir = NA,
  remove.rejected = TRUE, overwrite = TRUE, cc = NA,
  site.name = L$dataSetName, modelNum = NA)
```

Arguments

`L`	a single LiPD object
`which.chron`	the number of the chronData object that you'll be working in
`which.mt`	the number of the measurementTable you'll be working in
`baconDir`	the directory where Bacon is installed on this computer.
`remove.rejected`	
	don't write out dates that are marked as rejected
`overwrite`	overwrite files and directories
`cc`	An integer, or vector of integers corresponding to age that describes the calibration curve. You can specify here (see below) or if it's NA the code will guess based on archiveType
	• cc=1 IntCal13
	• cc=2 MarineCal
	• cc=3 SHCal13
`site.name`	the name used for the bacon model (and directories)
`modelNum`	which chronModel do you want to use?

Value

L the input LiPD file with methods added to the chronModel.

Author(s)

Nick McKay

See Also

Other Bacon: [loadBaconOutput](), [runBacon](), [sampleBaconAges]()

Examples

```
writeBacon(L)
#Run in interactive mode

writeBacon(L,which.chron=1,which.mt = 1,baconDir="~/Bacon/",remove.rejected=TRUE,overwrite=TRUE,cc=NA,site.
```

| writeClam | *write files for running a clam model* |

Description

Not functional yet

Usage

```
writeClam(L, which.chron = 1, clamDir = NA, remove.reverse = TRUE,
  overwrite = TRUE, cc = NA, site.name = L$dataSetName, modelNum = NA)
```

Index