

Package ‘rbacon’

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Description

Bacon is an approach to age-depth modelling that uses Bayesian statistics to reconstruct accumulation histories for deposits, through combining radiocarbon and other dates with prior information. See Blaauw & Christen (2011) <doi:10.1214/11-BA618>.

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License GPL (>= 2)

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accrate.age	<i>Obtain estimated accumulation rates for any age of a core.</i>
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Description

Obtain accumulation rates (in years per cm, so actually sedimentation times) as estimated by the MCMC iterations for any age of a core.

Usage

```
accrate.age(age, set = get("info"), cmyr = FALSE, BCAD = set$BCAD)
```

Arguments

age	The age for which the accumulation rates need to be returned.
set	Detailed information of the current run, stored within this session's memory as variable info.
cmyr	Accumulation rates can be calculated in cm/year or year/cm. By default cmyr=FALSE and accumulation rates are calculated in year per cm.
BCAD	The calendar scale of graphs and age output-files is in cal BP by default, but can be changed to BC/AD using BCAD=TRUE.

Details

Considering accumulation rates is crucial for age-depth modelling, and even more so if they are subsequently used for calculating proxy influx values, or interpreted as proxy for environmental change such as carbon accumulation. See also `accrate.age.ghost`, `accrate.depth` and `accrate.depth.ghost`. Bacon deals explicitly with accumulation rate and its variability through defining prior distributions. This function obtains accumulation rates (in years per cm, so actually sedimentation times) as estimated by the MCMC iterations for any age of a core. Deals with only 1 age at a time. See also `accrate.depth`.

Value

all MCMC estimates of accumulation rate of the chosen age.

Author(s)

Maarten Blaauw, J. Andres Christen

References

Blaauw, M. and Christen, J.A., Flexible paleoclimate age-depth models using an autoregressive gamma process. *Bayesian Anal.* 6 (2011), no. 3, 457–474. <https://projecteuclid.org/euclid.ba/1339616472>

See Also

http://www.chrono.qub.ac.uk/blaauw/manualBacon_2.3.pdf

Examples

```
Bacon(run=FALSE, coredir=tempfile())
agedepth(yr.res=50, d.res=50, d.by=10)
accrate.a5000 = accrate.age(5000)
plot(accrate.a5000, pch='.')
hist(accrate.a5000)
```

`accrate.age.ghost`

Plot a core's accumulation rates against calendar time.

Description

Plot a grey-scale representation of a core's estimated accumulation rates against time.

Usage

```
accrate.age.ghost(set = get("info"), age.lim = c(), yr.lim = age.lim,
  age.lab = c(), yr.lab = age.lab, age.res = 200, yr.res = age.res,
  grey.res = 50, prob = 0.95, plot.range = TRUE,
  range.col = grey(0.5), range.lty = 2, plot.mean = TRUE,
  mean.col = "red", mean.lty = 2, acc.lim = c(), acc.lab = c(),
  upper = 0.99, dark = 50, BCAD = set$BCAD, cmyr = FALSE,
  rotate.axes = FALSE, rev.age = FALSE, rev.yr = rev.age,
  rev.acc = FALSE, xaxs = "i", yaxs = "i", bty = "l")
```

Arguments

set	Detailed information of the current run, stored within this session's memory as variable info.
age.lim	Minimum and maximum calendar age ranges, calculated automatically by default (age.lim=c()).
yr.lim	Deprecated - use age.lim instead
age.lab	The labels for the calendar axis (default age.lab="cal BP" or "BC/AD" if BCAD=TRUE).
yr.lab	Deprecated - use age.lab instead
age.res	Resolution or amount of greyscale pixels to cover the age scale of the age-model plot. Default age.res=200.
yr.res	Deprecated - use age.res instead
grey.res	Resolution of greyscales. Default grey.res=50, which does not aim to poke fun at a famous novel.
prob	Probability ranges. Defaults to prob=0.95.
plot.range	If plot.range=TRUE, the confidence ranges (two-tailed; half of the probability at each side) are plotted.
range.col	Colour of the confidence ranges.
range.lty	Line type of the confidence ranges.
plot.mean	If plot.mean=TRUE, the means are plotted.
mean.col	Colour of the mean accumulation rates.
mean.lty	Type of the mean lines.
acc.lim	Axis limits for the accumulation rates.
acc.lab	Axis label for the accumulation rate.
upper	Maximum accumulation rates to plot. Defaults to the upper 99%; upper=0.99.
dark	The darkest grey value is dark=1 by default; lower values will result in lighter grey but values >1 are not advised.
BCAD	The calendar scale of graphs and age output-files is in cal BP by default, but can be changed to BC/AD using BCAD=TRUE.

<code>cmyr</code>	Accumulation rates can be calculated in cm/year or year/cm. By default <code>cmyr=FALSE</code> and accumulation rates are calculated in year per cm. Axis limits are difficult to calculate when <code>cmyr=TRUE</code> , so a manual adaptation of <code>acc.lim</code> might be a good idea.
<code>rotate.axes</code>	The default is to plot the calendar age horizontally and accumulation rates vertically. Change to <code>rotate.axes=TRUE</code> value to rotate axes.
<code>rev.age</code>	The direction of the age axis, which can be reversed using <code>rev.age=TRUE</code> .
<code>rev.yr</code>	Deprecated - use <code>rev.age</code> instead
<code>rev.acc</code>	The direction of the accumulation rate axis, which can be reversed (<code>rev.acc=TRUE</code>).
<code>xaxs</code>	Extension of the x-axis. White space can be added to the vertical axis using <code>xaxs="r"</code> .
<code>yaxs</code>	Extension of the y-axis. White space can be added to the vertical axis using <code>yaxs="r"</code> .
<code>bty</code>	Type of box to be drawn around the plot (" <code>n</code> " for none, and " <code>l</code> " (default), " <code>7</code> ", " <code>c</code> ", " <code>u</code> ", or " <code>o</code> " for correspondingly shaped boxes).

Details

Calculating accumulation rates against calendar age will take some time to calculate, and might show unexpected rates around the core's maximum ages (only a few of all age-model iterations will reach such ages and they will tend to have modelled accumulation rates for the lower depths much lower than the other iterations). Axis limits for accumulation rates are estimated automatically, however upper limits can be very variable (and thus hard to predict) if calculated in cm/yr. Therefore you might want to manually adapt the axis limits after plotting with default settings (e.g., `acc.lim=c(0,1)`). See also `accrate.depth.ghost`, `accrate.depth` and `accrate.age`. The grey-scale reconstruction around the oldest ages of any reconstruction often indicates very low accumulation rates. This is due to only some MCMC iterations reaching those old ages, and these iterations will have modelled very slow accumulation rates. Currently does not deal well with hiatuses, so do not interpret accumulation rates close to depths with inferred hiatuses.

Value

A greyscale plot of accumulation rate against calendar age.

Author(s)

Maarten Blaauw, J. Andres Christen

References

Blaauw, M. and Christen, J.A., Flexible paleoclimate age-depth models using an autoregressive gamma process. *Bayesian Anal.* 6 (2011), no. 3, 457–474. <https://projecteuclid.org/euclid.ba/1339616472>

See Also

http://www.chrono.qub.ac.uk/blaauw/manualBacon_2.3.pdf

Examples

```
Bacon(run=FALSE, coredir=tempfile())
agedepth(yr.res=50, d.res=50, d.by=10)
layout(1)
accrate.age.ghost()
```

accrate.depth

Obtain estimated accumulation rates as for any depth of a core.

Description

Obtain accumulation rates (in years per cm, so actually sedimentation times) as estimated by the MCMC iterations for any depth of a core.

Usage

```
accrate.depth(d, set = get("info"), cmyr = FALSE)
```

Arguments

d	The depth for which accumulation rates need to be returned.
set	Detailed information of the current run, stored within this session's memory as variable info.
cmyr	Accumulation rates can be calculated in cm/year or year/cm. By default cmyr=FALSE and accumulation rates are calculated in year per cm.

Details

should take into account hiatuses

Considering accumulation rates is crucial for age-depth modelling, and even more so if they are subsequently used for calculating proxy influx values, or interpreted as proxy for environmental change such as carbon accumulation. Bacon deals explicitly with accumulation rate and its variability through defining prior distributions. This function obtains accumulation rates (in years per cm, so actually sedimentation times) as estimated by the MCMC iterations for any depth of a core. Deals with only 1 depth at a time. See also `accrate.age`.

Value

all MCMC estimates of accumulation rate of the chosen depth.

Author(s)

Maarten Blaauw, J. Andres Christen

References

Blaauw, M. and Christen, J.A., Flexible paleoclimate age-depth models using an autoregressive gamma process. *Bayesian Anal.* 6 (2011), no. 3, 457–474. <https://projecteuclid.org/euclid.ba/1339616472>

See Also

http://www.chrono.qub.ac.uk/blaauw/manualBacon_2.3.pdf

Examples

```
Bacon(run=FALSE, coredir=tempfile())
agedepth(yr.res=50, d.res=50, d.by=10)
d20 <- accrate.depth(20)
hist(d20)
d20 <- accrate.depth(20, cmyr=TRUE) # to calculate accumulation rates in cm/yr
mean(d20)
```

accrate.depth.ghost *Plot modelled accumulation rates against the depths of a core.*

Description

Plot grey-scale representation of modelled accumulation rates over a core's depth. Each section of the core (see Bacon's option "thick") will have modelled accumulation rates.

Usage

```
accrate.depth.ghost(set = get("info"), d = set$elbows, d.lim = c(),
  acc.lim = c(), d.lab = c(), cmyr = FALSE, acc.lab = c(),
  dark = 1, grey.res = 100, prob = 0.95, plot.range = TRUE,
  range.col = grey(0.5), range.lty = 2, plot.mean = TRUE,
  mean.col = "red", mean.lty = 2, rotate.axes = FALSE,
  rev.d = FALSE, rev.acc = FALSE)
```

Arguments

set	Detailed information of the current run, stored within this session's memory as variable info.
d	The depths for which the accumulation rates are to be calculated. Default to the entire core.
d.lim	Axis limits for the depths.
acc.lim	Axis limits for the accumulation rates.
d.lab	Label for the depth axis.

<code>cmyr</code>	Accumulation rates can be calculated in cm/year or year/cm. By default <code>cmyr=FALSE</code> and accumulation rates are calculated in year per cm. Axis limits are difficult to calculate when <code>cmyr=TRUE</code> , so a manual adaptation of <code>acc.lim</code> might be a good idea.
<code>acc.lab</code>	Axis label for the accumulation rate.
<code>dark</code>	The darkest grey value is <code>dark=1</code> by default; lower values will result in lighter grey but values >1 are not advised.
<code>grey.res</code>	Grey-scale resolution. Default <code>grey.res=100</code> .
<code>prob</code>	Probability ranges. Defaults to <code>prob=0.95</code> .
<code>plot.range</code>	If <code>plot.range=TRUE</code> , the confidence ranges (two-tailed; half of the probability at each side) are plotted.
<code>range.col</code>	Colour of the confidence ranges.
<code>range.lty</code>	Line type of the confidence ranges.
<code>plot.mean</code>	If <code>plot.mean=TRUE</code> , the means are plotted.
<code>mean.col</code>	Colour of the mean accumulation rates.
<code>mean.lty</code>	Type of the mean lines.
<code>rotate.axes</code>	The default is to plot the accumulation rates horizontally and the depth vertically (<code>rotate.axes=FALSE</code>). Change <code>rotate.axes</code> value to rotate axes.
<code>rev.d</code>	The direction of the depth axis can be reversed from the default (<code>rev.d=TRUE</code>).
<code>rev.acc</code>	The direction of the accumulation rate axis can be reversed from the default (<code>rev.acc=TRUE</code>).

Details

This plot shows the modelled accumulation rates in grey-scales, where darker grey indicates more likely accumulation rates. Axis limits for accumulation rates are estimated automatically, however upper limits can be very variable (and thus hard to predict) if calculated in cm/yr; therefore you might want to manually adapt the axis limits after plotting with default settings (e.g., `acc.lim=c(0,1)`). See also `accrate.age.ghost`, `accrate.depth` and `accrate.age`.

Value

A grey-scale plot of accumulation rate against core depth.

Author(s)

Maarten Blaauw, J. Andres Christen

References

Blaauw, M. and Christen, J.A., Flexible paleoclimate age-depth models using an autoregressive gamma process. *Bayesian Anal.* 6 (2011), no. 3, 457–474. <https://projecteuclid.org/euclid.ba/1339616472>

See Also

http://www.chrono.qub.ac.uk/blaauw/manualBacon_2.3.pdf

Examples

```
Bacon(run=FALSE, coredir=tempfile())
agedepth(yr.res=50, d.res=50, d.by=10)
layout(1)
accrate.depth.ghost()
```

add.dates

Add dates to age-depth plots

Description

Add dated depths to plots, e.g. to show dates that weren't used in the age-depth model

Usage

```
add.dates(mn, sdev, depth, cc = 1, above = 1e-06, ex = 10,
  normal = TRUE, normalise = TRUE, t.a = 3, t.b = 4,
  age.res = 100, times = 20, col = rgb(1, 0, 0, 0.5),
  border = rgb(1, 0, 0, 0.5), rotate.axes = FALSE, mirror = TRUE,
  up = TRUE, BCAD = FALSE, pch = 4)
```

Arguments

mn	Reported mean of the date. Can be multiple dates.
sdev	Reported error of the date. Can be multiple dates.
depth	Depth of the date.
cc	The calibration curve to use: cc=1 for IntCal13 (northern hemisphere terrestrial), cc=2 for Marine13 (marine), cc=0 for none (dates that are already on the cal BP scale).
above	Threshold for plotting of probability values. Defaults to above=1e-3.
ex	Exaggeration of probability distribution plots. Defaults to ex=50.
normal	By default, Bacon uses the student's t-distribution to treat the dates. Use normal=TRUE to use the normal/Gaussian distribution. This will generally give higher weight to the dates.
normalise	By default, the date is normalised to an area of 1 (normalise=TRUE).
t.a	The dates are treated using the student's t distribution by default (normal=FALSE). The student's t-distribution has two parameters, t.a and t.b, set at 3 and 4 by default (see Christen and Perez, 2010). If you want to assign narrower error distributions (more closely resembling the normal distribution), set t.a and t.b at for example 33 and 34 respectively (e.g., for specific dates in your .csv file). For symmetry reasons, t.a must always be equal to t.b-1.

t.b	The dates are treated using the student's t distribution by default (normal=FALSE). The student's t-distribution has two parameters, t.a and t.b, set at 3 and 4 by default (see Christen and Perez, 2010). If you want to assign narrower error distributions (more closely resembling the normal distribution), set t.a and t.b at for example 33 and 34 respectively (e.g., for specific dates in your .csv file). For symmetry reasons, t.a must always be equal to t.b-1.
age.res	Resolution of the date's distribution. Defaults to date.res=100.
times	The extent of the range to be calculated for each date. Defaults to times=20.
col	The colour of the ranges of the date. Default is semi-transparent red: col=rgb(1,0,0,.5).
border	The colours of the borders of the date. Default is semi-transparent red: border=rgb(1,0,0,0.5).
rotate.axes	The default of plotting age on the horizontal axis and event probability on the vertical one can be changed with rotate.axes=TRUE.
mirror	Plot the dates as 'blobs'. Set to mirror=FALSE to plot simple distributions.
up	Directions of distributions if they are plotted non-mirrored. Default up=TRUE.
BCAD	The calendar scale of graphs is in cal BP by default, but can be changed to BC/AD using BCAD=TRUE.
pch	The shape of any marker to be added to the date. Defaults to a cross, pch=4. To leave empty, use pch=NA.

Details

Sometimes it is useful to add additional dating information to age-depth plots, e.g., to show outliers or how dates calibrate with different estimated offsets.

Value

A date's distribution, added to an age-depth plot.

Author(s)

Maarten Blaauw, J. Andres Christen

References

Blaauw, M. and Christen, J.A., Flexible paleoclimate age-depth models using an autoregressive gamma process. *Bayesian Anal.* 6 (2011), no. 3, 457–474. <https://projecteuclid.org/euclid.ba/1339616472>

See Also

http://www.chrono.qub.ac.uk/blaauw/manualBacon_2.3.pdf

Examples

```
Bacon(run=FALSE, coredir=tempfile())
agedepth()
add.dates(5000, 100, 60)
```

`age.pMC`*Calculate pMC values from C14 ages*

Description

Calculate pMC values from radiocarbon ages

Usage

```
age.pMC(mn, sdev, ratio = 100, decimals = 3)
```

Arguments

<code>mn</code>	Reported mean of the 14C age.
<code>sdev</code>	Reported error of the 14C age.
<code>ratio</code>	Most modern-date values are reported against 100. If it is against 1 instead, use 1 here.
<code>decimals</code>	Amount of decimals required for the pMC value.

Details

Post-bomb dates are often reported as pMC or percent modern carbon. Since Bacon expects radiocarbon ages, this function can be used to calculate pMC values from radiocarbon ages. The reverse function of [pMC.age](#).

Value

pMC values from C14 ages.

Author(s)

Maarten Blaauw, J. Andres Christen

References

Blaauw, M. and Christen, J.A., Flexible paleoclimate age-depth models using an autoregressive gamma process. *Bayesian Anal.* 6 (2011), no. 3, 457–474. <https://projecteuclid.org/euclid.ba/1339616472>

See Also

http://www.chrono.qub.ac.uk/blaauw/manualBacon_2.3.pdf

Examples

```
age.pMC(-2000, 20)
age.pMC(-2000, 20, 1)
```

agedepth

*Plot an age-depth model***Description**

Plot the age-depth model of a core.

Usage

```
agedepth(set = get("info"), BCAD = set$BCAD, depth.unit = "cm",
  age.unit = "yr", unit = depth.unit, d.lab = c(), age.lab = c(),
  yr.lab = age.lab, kcal = FALSE, acc.lab = c(), d.min = c(),
  d.max = c(), d.by = c(), depths = set$depths,
  depths.file = FALSE, age.min = c(), yr.min = age.min,
  age.max = c(), yr.max = age.max, hiatus.option = 1, dark = c(),
  prob = set$prob, rounded = 0, d.res = 400, age.res = 400,
  yr.res = age.res, date.res = 100, grey.res = 100,
  rotate.axes = FALSE, rev.age = FALSE, rev.yr = rev.age,
  rev.d = FALSE, maxcalc = 500, height = 15, calheight = 1,
  mirror = TRUE, up = TRUE, cutoff = 0.001, plot.range = TRUE,
  panels = layout(1), range.col = grey(0.5), range.lty = "12",
  mn.col = "red", mn.lty = "12", med.col = NA, med.lty = "12",
  C14.col = rgb(0, 0, 1, 0.35), C14.border = rgb(0, 0, 1, 0.5),
  cal.col = rgb(0, 0.5, 0.5, 0.35), cal.border = rgb(0, 0.5, 0.5, 0.5),
  dates.col = c(), hiatus.col = grey(0.5), hiatus.lty = "12",
  greyscale = grey(seq(1, 0, length = grey.res)),
  slump.col = grey(0.8), normalise.dists = TRUE,
  same.heights = FALSE, cc = set$cc, title = set$core,
  title.location = "topleft", after = set$after, bty = "l",
  mar = c(3, 3, 1, 1), mgp = c(1.5, 0.7, 0), xaxs = "r",
  yaxs = "i", xaxt = "s", yaxt = "s", plot.pdf = FALSE,
  dates.only = FALSE, model.only = FALSE, talk = FALSE)
```

Arguments

set	Detailed information of the current run, stored within this session's memory as variable info.
BCAD	The calendar scale of graphs and age output-files is in cal BP by default, but can be changed to BC/AD using BCAD=TRUE.
depth.unit	Units of the depths. Defaults to depth.unit="cm".
age.unit	Units of the ages. Defaults to age.unit="yr".
unit	Deprecated and replaced by depth.unit.
d.lab	The labels for the depth axis. Default d.lab="Depth (cm)". See also depth.unit.
age.lab	The labels for the calendar axis (default age.lab="cal BP" or "BC/AD" if BCAD=TRUE).

<code>yr.lab</code>	Deprecated - use <code>age.lab</code> instead
<code>kcal</code>	Use kcal BP. Default is <code>kcal=FALSE</code> .
<code>acc.lab</code>	The labels for the accumulation rate plot (top middle). Default <code>d.lab="Acc. rate (yr/cm)"</code> (or whatever units you're using).
<code>d.min</code>	Minimum depth of age-depth model (use this to extrapolate to depths higher than the top dated depth).
<code>d.max</code>	Maximum depth of age-depth model (use this to extrapolate to depths below the bottom dated depth).
<code>d.by</code>	Depth intervals at which ages are calculated. Default 1. Alternative depth intervals can be provided using, e.g., <code>d.by=0.5</code> .
<code>depths</code>	By default, Bacon will calculate the ages for the depths <code>d.min</code> to <code>d.max</code> in steps of <code>d.by</code> . Alternative depths can be provided as, e.g., <code>depths=seq(0, 100, length=500)</code> or as a file, e.g., <code>depths=read.table("CoreDepths.txt")</code> . See also <code>depths.file</code> .
<code>depths.file</code>	By default, Bacon will calculate the ages for the depths <code>d.min</code> to <code>d.max</code> in steps of <code>d.by</code> . If <code>depths.file=TRUE</code> , Bacon will read a file containing the depths for which you require ages. This file, containing the depths in a single column without a header, should be stored within <code>coredir</code> , and its name should start with the core's name and end with <code>'_depths.txt'</code> . Then specify <code>depths.file=TRUE</code> (default <code>FALSE</code>). See also <code>depths</code> .
<code>age.min</code>	Minimum age of the age-depth plot.
<code>yr.min</code>	Deprecated - use <code>age.min</code> instead
<code>age.max</code>	Maximum age of the age-depth plot.
<code>yr.max</code>	Deprecated - use <code>age.min</code> instead
<code>hiatus.option</code>	How to calculate accumulation rates and ages for sections with hiatuses. Either extrapolate from surrounding sections (default, <code>hiatus.option=1</code>), use a w-weighted mix between the prior and posterior values for depths below the hiatus and prior information only for above the hiatus (<code>hiatus.option=2</code>), or use the originally calculated slopes (<code>hiatus.option=0</code>).
<code>dark</code>	Darkness of the greyscale age-depth model. By default, the darkest grey value is calculated as 10 times the height of the lowest-precision age estimate <code>dark=c()</code> . Lower values will result in lighter grey but values >1 are not allowed.
<code>prob</code>	Confidence interval to report (between 0 and 1, default 0.95 or 95%).
<code>rounded</code>	Rounding of years. Default is to round to single years.
<code>d.res</code>	Resolution or amount of greyscale pixels to cover the depth scale of the age-model plot. Default <code>d.res=200</code> .
<code>age.res</code>	Resolution or amount of greyscale pixels to cover the age scale of the age-model plot. Default <code>yr.res=200</code> .
<code>yr.res</code>	Deprecated - use <code>age.res</code> instead
<code>date.res</code>	Date distributions are plotted using <code>date.res=100</code> points by default.
<code>grey.res</code>	Grey-scale resolution of the age-depth model. Default <code>grey.res=100</code> .
<code>rotate.axes</code>	By default, the age-depth model is plotted with the depths on the horizontal axis and ages on the vertical axis. This can be changed with <code>rotate.axes=TRUE</code> .

<code>rev.age</code>	The direction of the age axis, which can be reversed using <code>rev.age=TRUE</code> .
<code>rev.yr</code>	Deprecated - use <code>rev.age</code> instead
<code>rev.d</code>	The direction of the depth axis, which can be reversed using <code>rev.d=TRUE</code> .
<code>maxcalc</code>	Number of depths to calculate ages for. If this is more than <code>maxcalc=500</code> , a warning will be shown that calculations will take time.
<code>height</code>	The maximum heights of the distributions of the dates on the plot. See also <code>normalise.dists</code> .
<code>calheight</code>	Multiplier for the heights of the distributions of dates on the calendar scale. Defaults to <code>calheight=1</code> .
<code>mirror</code>	Plot the dates as 'blobs'. Set to <code>mirror=FALSE</code> to plot simple distributions.
<code>up</code>	Directions of distributions if they are plotted non-mirrored. Default <code>up=TRUE</code> .
<code>cutoff</code>	Avoid plotting very low probabilities of date distributions (default <code>cutoff=0.001</code>).
<code>plot.range</code>	Whether or not to plot the curves showing the confidence ranges of the age-model. Defaults to (<code>plot.range=TRUE</code>).
<code>panels</code>	Divide the graph panel. Defaults to 1 graph per panel, <code>panels=layout(1)</code> . To avoid dividing into panels, use <code>panels=c()</code> .
<code>range.col</code>	The colour of the curves showing the confidence ranges of the age-model. Defaults to medium grey (<code>range.col=grey(0.5)</code>).
<code>range.lty</code>	The line type of the curves showing the confidence ranges of the age-model. Defaults to <code>range.lty=12</code> .
<code>mn.col</code>	The colour of the mean age-depth model: default <code>mn.col="red"</code> .
<code>mn.lty</code>	The line type of the mean age-depth model. Default <code>mn.lty=12</code> .
<code>med.col</code>	The colour of the median age-depth model: not drawn by default <code>med.col=NA</code> .
<code>med.lty</code>	The line type of the median age-depth model. Default <code>med.lty=12</code> .
<code>C14.col</code>	The colour of the calibrated ranges of the dates. Default is semi-transparent blue: <code>C14.col=rgb(0,0,1,.35)</code> .
<code>C14.border</code>	The colours of the borders of calibrated 14C dates. Default is semi-transparent dark blue: <code>C14.border=rgb(0, 0, 1, 0.5)</code> .
<code>cal.col</code>	The colour of the non-14C dates. Default is semi-transparent blue-green: <code>cal.col=rgb(0,.5,.5,.35)</code> .
<code>cal.border</code>	The colour of the border of non-14C dates in the age-depth plot: default semi-transparent dark blue-green: <code>cal.border=rgb(0,.5,.5,.5)</code> . Not used by default.
<code>dates.col</code>	As an alternative to colouring dates based on whether they are 14C or not, sets of dates can be coloured as, e.g., <code>dates.col=colours()[2:100]</code> .
<code>hiatus.col</code>	The colour of the depths of any hiatuses. Default <code>hiatus.col=grey(0.5)</code> .
<code>hiatus.lty</code>	The line type of the depths of any hiatuses. Default <code>hiatus.lty=12</code> .
<code>greyscale</code>	The function to produce a coloured representation of all age-models. Defaults to grey-scales: <code>greyscale=function(x) grey(1-x)</code> .
<code>slump.col</code>	Colour of slumps. Defaults to <code>slump.col=grey(0.8)</code> .

<code>normalise.dists</code>	By default, the distributions of more precise dates will cover less time and will thus peak higher than less precise dates. This can be avoided by specifying <code>normalise.dists=FALSE</code> .
<code>same.heights</code>	Plot the distributions of the dates all at the same maximum height (default <code>same.height=FALSE</code>).
<code>cc</code>	Calibration curve for 14C dates: <code>cc=1</code> for IntCal13 (northern hemisphere terrestrial), <code>cc=2</code> for Marine13 (marine), <code>cc=3</code> for SHCal13 (southern hemisphere terrestrial). For dates that are already on the cal BP scale use <code>cc=0</code> .
<code>title</code>	The title of the age-depth model is plotted on the main panel. By default this is the core's name. To leave empty: <code>title=""</code> .
<code>title.location</code>	Location of the title. Default <code>title.location='topleft'</code> .
<code>after</code>	Sets a short section above and below <code>hiatus.depths</code> within which to calculate ages. For internal calculations - do not change.
<code>bty</code>	Type of box to be drawn around plots (" <code>n</code> " for none, and " <code>l</code> " (default), " <code>7</code> ", " <code>c</code> ", " <code>u</code> ", or " <code>o</code> " for correspondingly shaped boxes).
<code>mar</code>	Plot margins (amount of white space along edges of axes 1-4). Default <code>mar=c(3,3,1,1)</code> .
<code>mgp</code>	Axis text margins (where should titles, labels and tick marks be plotted). Defaults to <code>mgp=c(1.5, .7, .0)</code> .
<code>xaxs</code>	Extension of x-axis. By default, add some extra white-space at both extremes (<code>xaxs="r"</code>). See <code>?par</code> for other options.
<code>yaxs</code>	Extension of y-axis. By default, add no extra white-space at both extremes (<code>yaxs="i"</code>). See <code>?par</code> for other options.
<code>xaxt</code>	Whether or not to plot the x-axis. Can be used to adapt axes after a plot. See <code>?par</code> for other options.
<code>yaxt</code>	Whether or not to plot the y-axis. Can be used to adapt axes after a plot. See <code>?par</code> for other options.
<code>plot.pdf</code>	Produce a pdf file of the age-depth plot.
<code>dates.only</code>	By default, the age-depth model is plotted on top of the dates. This can be avoided by supplying <code>dates.only=TRUE</code> .
<code>model.only</code>	By default, panels showing the MCMC iterations and the priors and posteriors for accumulation rate and memory are plotted above the main age-depth model panel. This can be avoided by supplying <code>model.only=TRUE</code> . Note however that this removes relevant information to evaluate the age-depth model, so we do recommend to present age-models together with these upper panels.
<code>talk</code>	Provide a summary of the age ranges after producing the age-depth model graph; default <code>talk=FALSE</code> .

Details

After loading a previous run, or after running either the `scissors` or `thinner` command, plot the age-model again using the command `agedepth()`.

Value

A plot of the age-depth model, and estimated ages incl. confidence ranges for each depth.

Author(s)

Maarten Blaauw, J. Andres Christen

References

Blaauw, M. and Christen, J.A., Flexible paleoclimate age-depth models using an autoregressive gamma process. *Bayesian Anal.* 6 (2011), no. 3, 457–474. <https://projecteuclid.org/euclid.ba/1339616472>

See Also

http://www.chrono.qub.ac.uk/blaauw/manualBacon_2.3.pdf

Examples

```
agedepth(yr.res=50, d.res=50, d.by=10)

Bacon(ask=FALSE, coredir=tempfile())
agedepth()
```

agemodel.it

Extract one age-model iteration

Description

For one MCMC iteration (it), extract the corresponding age-depth model.

Usage

```
agemodel.it(it, set = get("info"), BCAD = set$BCAD)
```

Arguments

it	The MCMC iteration of which the age-model should be calculated.
set	Detailed information of the current run, stored within this session's memory as variable info.
BCAD	The calendar scale of graphs and age output-files is in cal BP by default, but can be changed to BC/AD using BCAD=TRUE.

Value

A variable with two columns - depth and the age-depth model of a single iteration.

Author(s)

Maarten Blaauw, J. Andres Christen

References

Blaauw, M. and Christen, J.A., Flexible paleoclimate age-depth models using an autoregressive gamma process. *Bayesian Anal.* 6 (2011), no. 3, 457–474. <https://projecteuclid.org/euclid.ba/1339616472>

See Also

http://www.chrono.qub.ac.uk/blaauw/manualBacon_2.3.pdf

Examples

```
Bacon(run=FALSE, coredir=tempfile())
agedepth(age.res=50, d.res=50, d.by=10)
lines(agemodel.it(5), col="red")
```

AgesOfEvents

Event probabilities against calendar age

Description

Plot probability curves for events in the core, expressed against calendar age.

Usage

```
AgesOfEvents(window, move, set = get("info"), plot.steps = FALSE,
  BCAD = set$BCAD, age.lab = c(), yr.lab = age.lab, age.lim = c(),
  yr.lim = age.lim, prob.lab = "probability", prob.lim = c(),
  rotate.axes = FALSE, rev.age = TRUE, rev.yr = rev.age,
  yaxs = "i", bty = "l")
```

Arguments

window	Width of the window.
move	Step size with which the window moves.
set	Detailed information of the current run, stored within this session's memory as variable info.
plot.steps	Plot probability values step-wise (defaults to plot.steps=FALSE, which plots smooth curves instead).
BCAD	The calendar scale of graphs and age output-files is in cal BP by default, but can be changed to BC/AD using BCAD=TRUE.
age.lab	The labels for the calendar axis (default age.lab="cal BP" or "BC/AD" if BCAD=TRUE).

<code>yr.lab</code>	Deprecated - use <code>age.lab</code> instead
<code>age.lim</code>	Minimum and maximum calendar age ranges, calculated automatically by default (<code>age.lim=c()</code>).
<code>yr.lim</code>	Deprecated - use <code>age.lim</code> instead
<code>prob.lab</code>	Label of the probability axis (default <code>prob.lab="probability"</code>).
<code>prob.lim</code>	Limits of the probability axis (calculated automatically by default).
<code>rotate.axes</code>	The default of plotting age on the horizontal axis and event probability on the vertical one can be changed with <code>rotate.axes=TRUE</code> .
<code>rev.age</code>	The direction of the age axis, which can be reversed using <code>rev.age=TRUE</code> .
<code>rev.yr</code>	Deprecated - use <code>rev.age</code> instead
<code>yaxs</code>	Extension of the y-axis. Defaults to the exact ranges of the probability values. White space can be added to the vertical axis using <code>yaxs="r"</code> .
<code>bty</code>	Type of box to be drawn around plots. Draw a box around the graph (" <code>n</code> " for none, and " <code>l</code> ", " <code>7</code> ", " <code>c</code> ", " <code>u</code> ", " <code>]</code> " or " <code>o</code> " for correspondingly shaped boxes).

Details

Probabilities of depths with 'events' in an age-modelled core can be plotted against time, taking into account chronological uncertainties (Blaauw et al. 2007). Such events could be for example core depths at which proxies indicate changes toward wetter local conditions. This can be expressed as values between 0 (no event) and 1 (event at 100% probability) for each depth.

Blaauw et al. 2010 propose to estimate probabilities of events by finding specific proxy features such as increasing curves. Probabilities are then estimated through resampling from the proxy values, where low to modest rises of proxy curves result in low event probabilities, and clear proxy rises in high probabilities. A smooth spline can be applied to adapt the balance of short-term vs long-term events. To calculate the event probabilities, produce a file with two columns (depth and corresponding proxy-derived probabilities, separated by white spaces). Do not provide headers at the file's first line, and save the file with extension "`_events.txt`" within the core's Bacon folder. See `Cores/MSB2K/MSB2K_events.txt` (or `Bacon_runs/MSB2K/MSB2K_events.txt`) for an example. Events are calculated as the probability that an event took place within specific time windows - or more specifically, that the Bacon age-depth model puts depths with assigned event probabilities in that time window.

does not yet deal correctly with hiatuses.

Value

The resulting probabilities are plotted and saved within the core's folder (file names ending with the window width and "`_probs.txt`").

Author(s)

Maarten Blaauw, J. Andres Christen

References

Blaauw, M., Christen, J.A., Mauquoy, D., van der Plicht, J., Bennett, K.D. (2007) Testing the timing of radiocarbon-dated events between proxy archives. *The Holocene*, *17*, 283-288. Blaauw, M., Wohlfarth, B., Christen, J.A., Ampel, L., Veres, D., Hughen, K.A., Preusser, F., Svensson, A. (2010) Were last glacial climate events simultaneous between Greenland and France? A quantitative comparison using non-tuned chronologies. *Journal of Quaternary Science* *25*, 387-394. <https://projecteuclid.org/euclid.ba/1339616472>

See Also

http://www.chrono.qub.ac.uk/blaauw/manualBacon_2.3.pdf

Examples

```
Bacon(run=FALSE, coredir=tempfile())
agedepth(yr.res=50)
AgesOfEvents(100, 10)
```

Bacon

Main age-depth modelling function

Description

This is the main age-depth modelling function of the rbacon package.

Usage

```
Bacon(core = "MSB2K", thick = 5, coredir = "", prob = 0.95,
      d.min = NA, d.max = NA, d.by = 1, depths.file = FALSE,
      depths = c(), depth.unit = "cm", age.unit = "yr",
      unit = depth.unit, acc.shape = 1.5, acc.mean = 20,
      mem.strength = 4, mem.mean = 0.7, boundary = NA,
      hiatus.depths = NA, hiatus.max = 10000, add = c(),
      after = 1e-04/thick, cc = 1, cc1 = "IntCal13", cc2 = "Marine13",
      cc3 = "SHCal13", cc4 = "ConstCal", ccdir = "", postbomb = 0,
      delta.R = 0, delta.STD = 0, t.a = 3, t.b = 4, normal = FALSE,
      suggest = TRUE, reswarn = c(10, 200), remember = TRUE,
      ask = TRUE, run = TRUE, defaults = "default_settings.txt",
      sep = ",", dec = ".", runname = "", slump = c(), BCAD = FALSE,
      ssize = 2000, th0 = c(), burnin = min(500, ssize), MinAge = c(),
      MaxAge = c(), MinYr = MinAge, MaxYr = MaxAge, cutoff = 0.001,
      plot.pdf = TRUE, dark = 1, date.res = 100, age.res = 200,
      yr.res = age.res, close.connections = TRUE, ...)
```

Arguments

core	Name of the core, given using quotes. Defaults to one of the cores provided with rbacon, core="MSB2K". An alternative core provided with this package is RLGH3 (Jones et al., 1989). To run your own core, produce a .csv file with the dates as outlined in the manual, add a folder with the core's name to the default directory for cores (see coredir), and save the .csv file there. For example, the file's location and name could be Bacon_runs/MyCore/MyCore.csv. Then run Bacon as follows: Bacon("MyCore")
thick	Bacon will divide the core into sections of equal thickness specified by thick (default thick=5).
coredir	Folder where the core's files core are and/or will be located. This will be a folder with the core's name, within either the folder coredir='Bacon_runs/', or the folder Cores/ if it already exists within R's working directory, or a custom-built folder. For example, use coredir="." to place the core's folder within the current working directory, or coredir="F:" if you want to put the core's folder and files on a USB drive loaded under F:. Thinner (and thus more) sections will result in smoother age-models, but too many sections can cause 'run-away' models.
prob	Confidence interval to report. This should lie between 0 and 1, default 0.95 (95 %).
d.min	Minimum depth of age-depth model (use this to extrapolate to depths higher than the top dated depth).
d.max	Maximum depth of age-depth model (use this to extrapolate to depths below the bottom dated depth).
d.by	Depth intervals at which ages are calculated. Defaults to d.by=1.
depths.file	By default, Bacon will calculate the ages for the depths d.min to d.max in steps of d.by. If depths.file=TRUE, Bacon will read a file containing the depths for which you require ages. This file, containing the depths in a single column without a header, should be stored within coredir, and its name should start with the core's name and end with '_depths.txt'. Then specify depths.file=TRUE (default FALSE). See also depths.
depths	By default, Bacon will calculate the ages for the depths d.min to d.max in steps of d.by. Alternative depths can be provided as, e.g., depths=seq(0, 100, length=500) or as a file, e.g., depths=read.table("CoreDepths.txt". See also depths.file.
depth.unit	Units of the depths. Defaults to depth.unit="cm".
age.unit	Units of the ages. Defaults to age.unit="yr".
unit	Deprecated and replaced by depth.unit.
acc.shape	The prior for the accumulation rate consists of a gamma distribution with two parameters. Its shape is set by acc.shape (default acc.shape=1.5; higher values result in more peaked shapes).
acc.mean	The accumulation rate prior consists of a gamma distribution with two parameters. Its mean is set by acc.mean (default acc.mean=20 yr/cm (or whatever age or depth units are chosen), which can be changed to, e.g., 5, 10 or 50 for different kinds of deposits). Multiple values can be given in case of hiatuses or boundaries, e.g., Bacon(hiatus.depths=23, acc.mean=c(5,20))

<code>mem.strength</code>	The prior for the memory (dependence of accumulation rate between neighbouring depths) is a beta distribution, which looks much like the gamma distribution. but its values are always between 0 (no assumed memory) and 1 (100% memory). Its default settings of <code>mem.strength=4</code> (higher values result in more peaked shapes) allow for a large range of posterior memory values.
<code>mem.mean</code>	The prior for the memory is a beta distribution, which looks much like the gamma distribution but its values are always between 0 (no assumed memory) and 1 (100% memory). Its default settings of <code>mem.mean=0.7</code> allow for a large range of posterior memory values.
<code>boundary</code>	The assumed depths of any boundary, which divides sections of different accumulation rate regimes (e.g., as indicated by major change in the stratigraphy). No hiatus is assumed between these sections, and memory is reset crossing the boundary. Different accumulation priors can be set for the sections above and below the boundary, e.g., <code>acc.mean=c(5, 20)</code> . See also <code>hiatus.depths</code> , <code>mem.mean</code> , <code>acc.mean</code> and <code>acc.shape</code> . Setting many boundaries might not work, and having more than one boundary per model section (see 'thick') might not work either.
<code>hiatus.depths</code>	The assumed depths for any hiatus should be provided as, e.g., <code>hiatus.depths=20</code> for one at 20cm depth, and <code>hiatus.depths=c(20,40)</code> for two hiatuses at 20 and 40 cm depth.
<code>hiatus.max</code>	The prior for the maximum length of the hiatus. Hiatus length is a uniform distribution, with equal probabilities between 0 and <code>hiatus.max yr</code> (or whatever other <code>age.unit</code> is chosen).
<code>add</code>	Add a value to the maximum hiatus length if a boundary is chosen. Defaults to 100 yr (or whatever other age unit is chosen). Can be adapted if Bacon complains that the parameters are out of support.
<code>after</code>	Sets a short section above and below <code>hiatus.depths</code> within which to calculate ages. For internal calculations - do not change.
<code>cc</code>	Calibration curve for C-14 dates: <code>cc=1</code> for IntCal13 (northern hemisphere terrestrial), <code>cc=2</code> for Marine13 (marine), <code>cc=3</code> for SHCal13 (southern hemisphere terrestrial). For dates that are already on the cal BP scale use <code>cc=0</code> .
<code>cc1</code>	For northern hemisphere terrestrial 14C dates (IntCal13).
<code>cc2</code>	For marine 14C dates (Marine13).
<code>cc3</code>	For southern hemisphere 14C dates (SHCal13).
<code>cc4</code>	Use an alternative curve (3 columns: cal BP, 14C age, error, separated by white spaces and saved as a plain-text file). See <code>ccdir</code> .
<code>ccdir</code>	Directory where the calibration curves for C14 dates <code>cc</code> are located. By default <code>ccdir=""</code> since they are loaded into R's memory. For example, use <code>ccdir="."</code> to choose current working directory, or <code>ccdir="Curves/"</code> to choose sub-folder Curves/. Note that all calibration curves should reside in the same directory. If you want to add a custom-built curve, put it in the directory where the default calibration curves are (probably <code>list.files(paste0(.libPaths(), "/rbacon/extdata/Curves/"))</code>). Alternatively produce a new folder, and add your curve as well as the default calibration curves there (<code>cc1</code> , <code>cc2</code> and <code>cc3</code> ; e.g., <code>write.table(copyCalibrationCurve(1), ".3Col_intc</code>
<code>postbomb</code>	Use a postbomb curve for negative (i.e. postbomb) 14C ages. 0 = none, 1 = NH1, 2 = NH2, 3 = NH3, 4

<code>delta.R</code>	Mean of core-wide age offsets (e.g., regional marine offsets).
<code>delta.STD</code>	Error of core-wide age offsets (e.g., regional marine offsets).
<code>t.a</code>	The dates are treated using the student's t distribution by default (<code>normal=FALSE</code>). The student's t-distribution has two parameters, <code>t.a</code> and <code>t.b</code> , set at 3 and 4 by default (see Christen and Perez, 2010). If you want to assign narrower error distributions (more closely resembling the normal distribution), set <code>t.a</code> and <code>t.b</code> at for example 33 and 34 respectively (e.g., for specific dates in your .csv file). For symmetry reasons, <code>t.a</code> must always be equal to <code>t.b-1</code> .
<code>t.b</code>	The dates are treated using the student's t distribution by default (<code>normal=FALSE</code>). The student's t-distribution has two parameters, <code>t.a</code> and <code>t.b</code> , set at 3 and 4 by default (see Christen and Perez, 2010). If you want to assign narrower error distributions (more closely resembling the normal distribution), set <code>t.a</code> and <code>t.b</code> at for example 33 and 34 respectively (e.g., for specific dates in your .csv file). For symmetry reasons, <code>t.a</code> must always be equal to <code>t.b-1</code> .
<code>normal</code>	By default, Bacon uses the student's t-distribution to treat the dates. Use <code>normal=TRUE</code> to use the normal/Gaussian distribution. This will generally give higher weight to the dates.
<code>suggest</code>	If initial analysis of the data indicates abnormally slow or fast accumulation rates, Bacon will suggest to change the prior. Also, if the length of the core would cause too few or too many sections with the default settings, Bacon will suggest an alternative section thickness <code>thick</code> . Accept these suggested alternative settings by typing "y" (or "yes please" if you prefer to be polite), or leave as is by typing "n" (or anything else, really). To get rid of these suggestions, use <code>suggest=FALSE</code> .
<code>reswarn</code>	Bacon will warn you if the number of sections lies outside the safe range (default between 10 and 200 sections; <code>reswarn=c(10,200)</code>). Too few sections could lead to an 'elbowy' model while with too many sections the modelling process can get lost, resulting in age-models far away from the dated depths.
<code>remember</code>	Bacon will try to remember which settings you have applied to your cores (default <code>remember=TRUE</code>). If you run into inconsistencies or other problems, try running your core again with <code>remember=FALSE</code> , or, start cleanly by typing <code>Bacon.cleanup()</code> .
<code>ask</code>	By default Bacon will ask you to confirm that you want to run the core with the provided settings. Disable this using <code>ask=FALSE</code> (e.g., for batch runs).
<code>run</code>	In order to load an existing Bacon run instead of producing a new one, you can use <code>run=FALSE</code> .
<code>defaults</code>	Name of the file containing settings for the core. For internal use only - do not change.
<code>sep</code>	Separator between the fields of the plain text file containing the dating information. Default <code>sep=" , "</code> .
<code>dec</code>	Character for decimal points. Default to <code>dec=" . "</code> .
<code>runname</code>	Text to add to the corename for specific runs, e.g., <code>runname="MyCore_Test1"</code> .
<code>slump</code>	Upper and lower depths of any sections of assumed abrupt accumulation, that require excising before age-modelling (and adding after age-modelling). Requires pairs of depths, e.g., <code>slump=c(10,15,60,67)</code> for slumps at 67-60 and 15-10 cm core depth.

BCAD	The calendar scale of graphs and age output-files is in cal BP (calendar or calibrated years before the present, where the present is AD 1950) by default, but can be changed to BC/AD using BCAD=TRUE.
ssize	The approximate amount of iterations to store at the end of the MCMC run. Default 2000; decrease for faster (but less reliable) runs or increase for cores where the MCMC mixing (panel at upper-left corner of age-model graph) appears problematic.
th0	Starting years for the MCMC iterations.
burnin	Amount of initial, likely sub-optimal MCMC iterations that will be removed.
MinAge	Minimum age limit for Bacon runs, default at current year in cal BP. To set plot limits, use <code>yr.min</code> instead.
MaxAge	Maximum age limit for Bacon runs, default at 1,000,000 cal BP. To set plot limits, use <code>yr.max</code> instead.
MinYr	Deprecated - use MinAge instead.
MaxYr	Deprecated - use MaxAge instead.
cutoff	Avoid plotting very low probabilities of date distributions (default <code>cutoff=0.001</code>).
plot.pdf	Produce a pdf file of the age-depth plot. Defaults to <code>plot.pdf=TRUE</code> after a Bacon run.
dark	Darkness of the greyscale age-depth model. The darkest grey value is <code>dark=1</code> by default. Lower values will result in lighter grey but values >1 are not allowed.
date.res	Date distributions are plotted using <code>date.res=100</code> segments by default.
age.res	Resolution or amount of greyscale pixels to cover the age scale of the age-model plot. Default <code>yr.res=200</code> .
yr.res	Deprecated - use <code>age.res</code> instead
close.connections	Internal option to close connections after a run. Default <code>close.connections=TRUE</code> .
...	options for the age-depth graph. See agedepth and calib.plot

Details

Bacon is an approach to age-depth modelling that uses Bayesian statistics in order to reconstruct Bayesian accumulation histories for deposits, through combining radiocarbon and other dates with prior information ('Blaauw' and 'Christen', 2011).

Bacon divides a core into many thin vertical sections (by default of `thick=5` cm thickness), and through millions of Markov Chain Monte Carlo (MCMC) iterations estimates the accumulation rate (in years/cm; so more correctly, sedimentation times) for each of these sections. Combined with an estimated starting date for the first section, these accumulation rates then form the age-depth model. The accumulation rates are constrained by prior information on the accumulation rate (`acc.mean`, `acc.shape`) and its variability between neighbouring depths, or "memory" (`mem.mean`, `mem.strength`). Hiatuses can be introduced as well, also constrained by prior information (`hiatus.max`).

Although Bacon works with any kind of absolute dates (e.g., OSL, tephra or other dates on a calendar scale), it is often used to age-model ¹⁴C-dated sequences. Radiocarbon dates should be calibrated using either IntCal13 (for terrestrial northern hemisphere material; Reimer et al., 2013),

Marine13 (for marine dates; Reimer et al., 2013), SHCal13 (for southern hemisphere dates; Hogg et al., 2013) or any other calibration curve (see below), while modern ¹⁴C dates are calibrated using one of the post-bomb calibration curves (NH1, NH2 or NH3 for the northern hemisphere, SH1-2 or SH3 for the southern hemisphere; Hua et al., 2013). See <http://calib.org/CALIBomb> if you are unsure which postbomb curve you need. If Bacon finds postbomb dates (negative ¹⁴C ages) and you haven't specified a postbomb curve, you will be prompted. Provide postbomb curves as, e.g., postbomb=1 for the NH1 postbomb curve (2 for NH2, 3 for NH3, 4 for SH1-2, 5 for SH3).

For calendar dates, i.e. dates that are already on the calendar scale and thus should not be calibrated, setcc=0.

Value

An age-depth model graph, its age estimates, and a summary.

Author(s)

Maarten Blaauw, J. Andres Christen

References

- Blaauw, M. and Christen, J.A., Flexible paleoclimate age-depth models using an autoregressive gamma process. *Bayesian Anal.* 6 (2011), no. 3, 457–474. <https://projecteuclid.org/euclid.ba/1339616472>
- Christen, J.A., Perez E., S., 2010. A new robust statistical model for radiocarbon data. *Radiocarbon* 51, 1047-1059.
- Reimer, P.J., Bard, E., Bayliss, A., Beck, J.W., Blackwell, P.G., Bronk Ramsey, C., Buck, C.E., Edwards, R.L., Friedrich, M., Grootes, P.M., Guilderson, T.P., Haflidason, H., Hajdas, I., Hatte, C., Heaton, T.J., Hoffmann, D.L., Hogg, A.G., Hughen, K.A., Kaiser, K.F., Kromer, B., Manning, S.W., Niu, M., Reimer, R.W., Richards, D.A., Scott, M.E., Southon, J.R., Turney, C.S.M., van der Plicht, J., 2013. IntCal13 and Marine13 radiocarbon age calibration curves 0-50,000 yr cal BP. *Radiocarbon* 55(4), 1869-1887
- Hogg, A.G., Hua, Q., Blackwell, P.G., Buck, C.E., Guilderson, T.P., Heaton, T.J., Niu, M., Palmer, J., Reimer, P.J., Reimer, R., Turney, C.S.M., Zimmerman, S.R.H., 2013. ShCal13 Southern Hemisphere calibration, 0-50,000 cal yr BP. *Radiocarbon* 55(4), <doi:10.2458/azu_js_rc.55.16783>.
- Hua, Q., Barbetti, M., Rakowski, A.Z., 2013. Atmospheric radiocarbon for the period 1950-2010. *Radiocarbon* 55(4), <doi:10.2458/azu_js_rc.v55i2.16177>.
- Jones, V.J., Stevenson, A.C., Battarbee, R.W., 1989. Acidification of lakes in Galloway, south west Scotland - a diatom and pollen study of the post-glacial history of the Round Loch of Glenhead. *Journal of Ecology* 77: 1-23.

See Also

http://www.chrono.qub.ac.uk/blaauw/manualBacon_2.3.pdf

Examples

```
Bacon(ask=FALSE, coredir=tempfile())
Bacon(cc=2, delta.R=80, delta.STD=40, coredir=tempfile())
```

Bacon.Age.d	<i>Output all ages for a single depth.</i>
-------------	--

Description

Output all MCMC-derived age estimates for a given depth.

Usage

```
Bacon.Age.d(d, set = get("info"), its = set$output, BCAD = set$BCAD,
  remove = FALSE)
```

Arguments

d	The depth of which Bacon age estimates are to be returned. Has to be a single depth.
set	Detailed information of the current run, stored within this session's memory as variable info.
its	The set of MCMC iterations to be used. Defaults to the entire MCMC output, its=set\$output.
BCAD	The calendar scale of graphs and age output-files is in cal BP by default, but can be changed to BC/AD using BCAD=TRUE.
remove	Whether or not to remove NA values (ages within slumps)

Details

Obtaining an age-depth model is often only a step towards a goal, e.g., plotting a core's fossil series ('proxies') against calendar time. Bacon.Age.d can be used to list all MCMC-derived age estimates for a given (single) depth, for example to calculate mean ages for a depth.

Value

Outputs all MCMC-derived ages for a given depth.

Author(s)

Maarten Blaauw, J. Andres Christen

References

Blaauw, M. and Christen, J.A., Flexible paleoclimate age-depth models using an autoregressive gamma process. *Bayesian Anal.* 6 (2011), no. 3, 457–474. <https://projecteuclid.org/euclid.ba/1339616472>

See Also

http://www.chrono.qub.ac.uk/blaauw/manualBacon_2.3.pdf

Examples

```
Bacon(run=FALSE, coredir=tempfile())
agedepth(age.res=50, d.res=50, d.by=10)
ages.d20 = Bacon.Age.d(20)
mean(ages.d20)
```

Bacon.cleanup

Remove files made to produce the current core's age-depth model.

Description

Remove files .bacon, .out, .pdf, _ages.txt, and _settings.txt of current core.

Usage

```
Bacon.cleanup(set = get("info"))
```

Arguments

set Detailed information of the current run, stored within this session's memory as variable info.

Details

If cores behave badly, you can try cleaning up previous runs and settings, by removing files .bacon, .out, .pdf, _ages.txt, and _settings.txt of current core.

Value

A message stating that the files and settings of this run have been deleted.

Author(s)

Maarten Blaauw, J. Andres Christen

See Also

http://www.chrono.qub.ac.uk/blaauw/manualBacon_2.3.pdf

Examples

```
Bacon(run=FALSE, coredir=tempfile())
Bacon.cleanup()
```

Bacon.hist	<i>Calculate age distributions of depths.</i>
------------	---

Description

Calculate the distribution of age estimates of single or multiple depths.

Usage

```
Bacon.hist(d, set = get("info"), BCAD = set$BCAD, age.lab = c(),
  age.lim = c(), hist.lab = "Frequency", calc.range = TRUE,
  hist.lim = c(), draw = TRUE, prob = set$prob,
  hist.col = grey(0.5), hist.border = grey(0.2), range.col = "blue",
  med.col = "green", mean.col = "red")
```

Arguments

d	The depth or depths for which a histogram and age ranges should be provided. If multiple depths are given, then just the age ranges, median and means (no graphs) are provided for each depth.
set	Detailed information of the current run, stored within this session's memory as variable info.
BCAD	The calendar scale of graphs and age output-files is in cal BP by default, but can be changed to BC/AD using BCAD=TRUE.
age.lab	The labels for the calendar axis (default age.lab="cal BP" or "BC/AD" if BCAD=TRUE).
age.lim	Minimum and maximum calendar age ranges, calculated automatically by default (age.lim=c()).
hist.lab	The y-axis is labelled ylab="Frequency" by default.
calc.range	Calculate ranges? Takes time so can be left out
hist.lim	Limits of the y-axis.
draw	Draw a plot or not. Defaults to draw=TRUE, however no plots are made if more than one depth d is provided. If draw=FALSE, then the age ranges, median and mean are given for each depth (as four columns).
prob	Age ranges are given as quantiles, e.g., 2.5% and 97.5% for the default of 95% confidence limits (prob=0.95).
hist.col	Colour of the histogram. Default grey, hist.col=grey(0.5).
hist.border	Colour of the histogram's outline. Default dark grey, hist.border=grey(0.2).
range.col	Colour of confidence ranges. Defaults to range.col="blue".
med.col	Colour of the median. Defaults to med.col="green".
mean.col	Colour of the mean. Defaults to mn.col="red".

Details

Age estimates of specific depths can also be plotted.

Value

A plot with the histogram and the age ranges, median and mean, or just the age ranges, medians and means if more than one depth *d* is given.

Author(s)

Maarten Blaauw, J. Andres Christen

References

Blaauw, M. and Christen, J.A., Flexible paleoclimate age-depth models using an autoregressive gamma process. *Bayesian Anal.* 6 (2011), no. 3, 457–474. <https://projecteuclid.org/euclid.ba/1339616472>

See Also

http://www.chrono.qub.ac.uk/blaauw/manualBacon_2.3.pdf

Examples

```
Bacon(run=FALSE, coredir=tempfile())
agedepth(age.res=50, d.res=50, d.by=10)
Bacon.hist(20)
Bacon.hist(20:30)
```

bacon2clam

Translate Bacon .csv files to clam .csv files.

Description

Reads a Bacon .csv file containing the dates, and transforms it into a clam .csv file.

Usage

```
bacon2clam(core, bacondir = "Bacon_runs", clamdir = "clam_runs",
  sep = ",")
```

Arguments

core	The name of the core for which a Bacon .csv file needs to be translated into a clam .csv file
bacondir	The directory where the Bacon runs reside. Defaults to coredir="Bacon_runs".
clamdir	The directory where the clam runs reside. Defaults to coredir="clam_runs".
sep	The separator for the .csv files. Defaults to sep=",".

Details

Assumes that Bacon .csv files with 4 columns indicate 14C dates. Please make sure this is correct.

Value

A clam .csv file

Author(s)

Maarten Blaauw, J. Andres Christen

See Also

http://www.chrono.qub.ac.uk/blaauw/manualBacon_2.3.pdf

Examples

```
{
  tmpfl <- tempfile()
  Bacon(run=FALSE, ask=FALSE, coredir=tmpfl)
  bacon2clam("MSB2K", bacondir=tmpfl, clmdir=tmpfl)
}
```

Baconvergence	<i>Test to identify poorly mixed MCMC runs.</i>
---------------	---

Description

Test how well-mixed and converged the MCMC runs are with the chosen core and settings, by running the core several times and comparing the different runs using the Gelman and Rubin Reduction factor (Brooks and Gelman, 1998).

Usage

```
Baconvergence(core = "MSB2K", runs = 5, suggest = FALSE, ...)
```

Arguments

core	Name of the core, given using quotes. Defaults to one of the cores provided with rbacon, core="MSB2K".
runs	Amount of runs to test for mixing. Default runs=5.
suggest	If initial analysis of the data indicates abnormally slow or fast accumulation rates, Bacon will suggest to change the prior.
...	additional options that can be given to the Bacon function.

Details

Generally Bacon will perform millions of MCMC iterations for each age-model run, although only a fraction of these will be stored. In most cases the remaining MCMC iterations will be well mixed (the upper left panel of the fit of the iterations shows no strange features such as sudden systematic drops or rises). However if the iterations seem not well mixed, or if too few remain (say less than a few hundred), then you could check the Gelman and Rubin Reduction Factor. Too high differences (high Factors) between runs indicate poor MCMC mixing. Robust MCMC mixing is indicated by a Gelman and Rubin Reduction factor (Brooks and Gelman, 1998) below the 1.05 safety threshold.

Value

NA

Author(s)

Maarten Blaauw, J. Andres Christen

References

Blaauw, M. and Christen, J.A., Flexible paleoclimate age-depth models using an autoregressive gamma process. *Bayesian Anal.* 6 (2011), no. 3, 457–474. <https://projecteuclid.org/euclid.ba/1339616472> Brooks, SP. and Gelman, A. (1998) General methods for monitoring convergence of iterative simulations. *Journal of Computational and Graphical Statistics*, *7*, 434–455.

See Also

http://www.chrono.qub.ac.uk/blaauw/manualBacon_2.3.pdf

Examples

```
Baconvergence(runs=2, ssize=100, coredir=tempfile()) # a quick-and-dirty toy example
```

Bacon_runs

List the folders present in the current core directory.

Description

Lists all folders located within the core's directory.

Usage

```
Bacon_runs(coredir = get("info")$coredir)
```

Arguments

coredir The directory where the Bacon runs reside. Defaults to coredir="Bacon_runs".

Details

The directory is either "Bacon_runs", "Cores" or a custom-named one.

Value

A list of folders

Author(s)

Maarten Blaauw, J. Andres Christen

See Also

http://www.chrono.qub.ac.uk/blaauw/manualBacon_2.3.pdf

Examples

```
Bacon(run=FALSE, coredir=tempfile())
Bacon_runs()
```

calib.plot

Plot the dates

Description

Produce a plot of the dated depths and their dates

Usage

```
calib.plot(set = get("info"), BCAD = set$BCAD, cc = set$cc,
  rotate.axes = FALSE, rev.d = FALSE, rev.age = FALSE,
  rev.yr = rev.age, age.lim = c(), yr.lim = age.lim,
  date.res = 100, d.lab = c(), age.lab = c(), yr.lab = age.lab,
  height = 15, calheight = 1, mirror = TRUE, up = TRUE,
  cutoff = 0.001, C14.col = rgb(0, 0, 1, 0.5), C14.border = rgb(0, 0,
  1, 0.75), cal.col = rgb(0, 0.5, 0.5, 0.5), cal.border = rgb(0, 0.5,
  0.5, 0.75), dates.col = c(), slump.col = grey(0.8),
  new.plot = TRUE, plot.dists = TRUE, same.heights = FALSE,
  normalise.dists = TRUE)
```

Arguments

set	Detailed information of the current run, stored within this session's memory as variable info.
BCAD	The calendar scale of graphs is in cal BP by default, but can be changed to BC/AD using BCAD=TRUE.
cc	Calibration curve to be used (defaults to info\$cc)
rotate.axes	The default of plotting age on the horizontal axis and event probability on the vertical one can be changed with rotate.axes=TRUE.
rev.d	The direction of the depth axis can be reversed from the default (rev.d=TRUE).
rev.age	The direction of the calendar age axis can be reversed from the default (rev.age=TRUE)
rev.yr	Deprecated - use rev.age instead
age.lim	Minimum and maximum calendar age ranges, calculated automatically by default (age.lim=c()).
yr.lim	Deprecated - use age.lim instead
date.res	Date distributions are plotted using date.res=100 points by default.
d.lab	The labels for the depth axis. Default d.lab="Depth (cm)".
age.lab	The labels for the calendar axis (default yr.lab="cal BP" or "BC/AD" if BCAD=TRUE).
yr.lab	Deprecated - use age.lab instead
height	The heights of the distributions of the dates. See also normalise.dists.
calheight	Multiplier for the heights of the distributions of dates on the calendar scale. Defaults to calheight=1.
mirror	Plot the dates as 'blobs'. Set to mirror=FALSE to plot simple distributions.
up	Directions of distributions if they are plotted non-mirrored. Default up=TRUE.
cutoff	Avoid plotting very low probabilities of date distributions (default cutoff=0.001).
C14.col	Colour of the calibrated distributions of the dates. Default is semi-transparent blue: rgb(0,0,1,.35).
C14.border	Colours of the borders of calibrated 14C dates. Default is transparent dark blue: cal.col
cal.col	Colour of the non-14C dates in the age-depth plot: default semi-transparent blue-green: rgb(0,.5,.5,.35).
cal.border	Colour of the of the border of non-14C dates in the age-depth plot: default semi-transparent dark blue-green: rgb(0,.5,.5,.5).
dates.col	As an alternative to colouring dates based on whether they are 14C or not, sets of dates can be coloured as, e.g., dates.col=colours()[2:100].
slump.col	Colour of slumps. Defaults to slump.col=grey(0.8).
new.plot	Start a new plot (new.plot=TRUE) or plot over an existing plot (new.plot=FALSE).
plot.dists	Plot the distributions of the dates (default plot.dists=TRUE).
same.heights	Plot the distributions of the dates all at the same maximum height (default same.height=FALSE).
normalise.dists	By default, the distributions of more precise dates will cover less time and will thus peak higher than less precise dates. This can be avoided by specifying normalise.dists=FALSE.

Details

This function is generally called internally to produce the age-depth graph. It can be used to produce custom-built graphs.

Value

NA

Author(s)

Maarten Blaauw, J. Andres Christen

References

Blaauw, M. and Christen, J.A., Flexible paleoclimate age-depth models using an autoregressive gamma process. *Bayesian Anal.* 6 (2011), no. 3, 457–474. <https://projecteuclid.org/euclid.ba/1339616472>

See Also

http://www.chrono.qub.ac.uk/blaauw/manualBacon_2.3.pdf

Examples

```
Bacon(run=FALSE, coredir=tempfile())
calib.plot()
```

clam2bacon

Translate clam .csv files to Bacon .csv files.

Description

Reads a clam .csv file containing the dates, and transforms it into a Bacon .csv file.

Usage

```
clam2bacon(core, clamdir = "clam_runs", bacondir = "Bacon_runs",
  sep = ",", cc = 1)
```

Arguments

core	The name of the core for which a clam .csv file needs to be translated into a Bacon .csv file
clamdir	The directory where the clam runs reside. Defaults to coredir="clam_runs".
bacondir	The directory where the Bacon runs reside. Defaults to coredir="Bacon_runs".
sep	The separator for the .csv files. Defaults to sep=",".
cc	Calibration curve for C-14 dates: cc=1 for IntCal13 (northern hemisphere terrestrial), cc=2 for Marine13 (marine),

Details

Please ensure that if the clam file has offset (d.R) estimates, that errors (d.STD) are provided manually, since these values cannot be determined automatically from the clam .csv file.

Value

A Bacon .csv file

Author(s)

Maarten Blaauw, J. Andres Christen

See Also

http://www.chrono.qub.ac.uk/blaauw/manualBacon_2.3.pdf

copyCalibrationCurve *Copy a calibration curve.*

Description

Copy one of the the calibration curves into memory.

Usage

```
copyCalibrationCurve(cc = 1, postbomb = FALSE)
```

Arguments

cc	Calibration curve for 14C dates: cc=1 for IntCal13 (northern hemisphere terrestrial), cc=2 for Marine13 (marine), cc=3 for SHCal13 (southern hemisphere terrestrial).
postbomb	Use postbomb=TRUE to get a postbomb calibration curve (default postbbomb=FALSE).

Details

Copy the radiocarbon calibration curve defined by cc into memory.

Value

The calibration curve (invisible).

Author(s)

Maarten Blaauw, J. Andres Christen

See Also

http://www.chrono.qub.ac.uk/blaauw/manualBacon_2.3.pdf

Examples

```
intcal13 <- copyCalibrationCurve(1)
```

flux.age.ghost	<i>Plot flux rates for proxies.</i>
----------------	-------------------------------------

Description

Plot grey-scale representation of estimated flux rates for proxies against calendar age.

Usage

```
flux.age.ghost(proxy = 1, age.lim = c(), yr.lim = age.lim,
  age.res = 200, yr.res = age.res, set = get("info"), flux = c(),
  plot.range = TRUE, prob = 0.8, range.col = grey(0.5),
  range.lty = 2, plot.mean = TRUE, mean.col = "red", mean.lty = 2,
  flux.lim = c(), flux.lab = "flux", upper = 0.95, dark = set$dark,
  BCAD = set$BCAD, age.lab = c(), yr.lab = age.lab,
  rotate.axes = FALSE, rev.flux = FALSE, rev.age = FALSE,
  rev.yr = rev.age)
```

Arguments

proxy	Which proxy to use (counting from the column number in the .csv file after the depths column).
age.lim	Minimum and maximum calendar age ranges, calculated automatically by default (age.lim=c()).
yr.lim	Deprecated - use age.lim instead
age.res	Resolution or amount of greyscale pixels to cover the age scale of the plot. Default age.res=200.
yr.res	Deprecated - use age.res instead
set	Detailed information of the current run, stored within this session's memory as variable info.
flux	Define a flux variable within the R session (consisting of depths and their proxy concentrations in two columns) and provide the name of this variable, e.g.: flux.age.ghost(flux=flux1). If left empty (flux=c()), a flux file is expected (see proxy).
plot.range	Plot curves that indicate a probability range, at resolution of yr.res.
prob	Probability range, defaults to prob=0.8 (10 % at each side).
range.col	Red seems nice.

range.lty	Line type of the confidence ranges.
plot.mean	Plot the mean fluxes.
mean.col	Red seems nice.
mean.lty	Line type of the means.
flux.lim	Limits of the flux axes.
flux.lab	Axis labels. Defaults to flux.lab="flux".
upper	Maximum flux rates to plot. Defaults to the upper 99%; upper=0.99.
dark	The darkest grey value is dark=1 by default; lower values will result in lighter grey but values >1 are not allowed.
BCAD	The calendar scale of graphs and age output-files is in cal BP by default, but can be changed to BC/AD using BCAD=TRUE.
age.lab	The labels for the calendar axis (default age.lab="cal BP" or "BC/AD" if BCAD=TRUE).
yr.lab	Deprecated - use age.lab instead
rotate.axes	The default of plotting calendar year on the horizontal axis and fluxes on the vertical one can be changed with rotate.axes=TRUE.
rev.flux	The flux axis can be reversed with rev.flux=TRUE.
rev.age	The direction of the age axis can be reversed using rev.age=TRUE.
rev.yr	Deprecated - use rev.age instead

Details

To plot flux rates (e.g. pollen grains/cm²/yr) as greyscales, provide a plain text file with headers and the data in columns separated by commas, ending in '_flux.csv' and saved in your core's folder. The first column should contain the depths, and the next columns should contain the proxy concentration values (leaving missing values empty). Then type for example flux.age.ghost(1) to plot the flux values for the first proxy in the .csv file. Instead of using a _flux.csv file, a flux variable can also be defined within the R session (consisting of depths and their proxy concentrations in two columns). Then provide the name of this variable, e.g.: flux.age.ghost(flux=flux1). See Bacon_runs/MSB2K/MSB2K_flux.csv for an example.

Value

A plot of flux rates.

Author(s)

Maarten Blaauw, J. Andres Christen

References

Blaauw, M. and Christen, J.A., Flexible paleoclimate age-depth models using an autoregressive gamma process. Bayesian Anal. 6 (2011), no. 3, 457–474. <https://projecteuclid.org/euclid.ba/1339616472>

See Also

http://www.chrono.qub.ac.uk/blaauw/manualBacon_2.3.pdf

Examples

```
Bacon(run=FALSE, coredir=tempfile())
agedepth(yr.res=50)
flux.age.ghost(1)
```

mix.curves

Build a custom-made, mixed calibration curve.

Description

If two curves need to be ‘mixed’ to calibrate, e.g. for dates of mixed terrestrial and marine carbon sources, then this function can be used.

Usage

```
mix.curves(proportion = 0.5, cc1 = "3Col_intcal13.14C",
           cc2 = "3Col_marine13.14C", name = "mixed.14C", dirname = ".",
           offset = c(0, 0), sep = "\t")
```

Arguments

proportion	Proportion of the first calibration curve required. e.g., change to proportion=0.7 if cc1 should contribute 70% (and cc2 30%) to the mixed curve.
cc1	The first calibration curve to be mixed. Defaults to the northern hemisphere terrestrial curve IntCal13.
cc2	The second calibration curve to be mixed. Defaults to the marine curve IntCal13.
name	Name of the new calibration curve.
dirname	Directory where the file will be written. If using the default dirname=".", the new curve will be saved in current working directory.
offset	Any offset and error to be applied to cc2 (default 0 +- 0).
sep	Separator between fields (tab by default, "\t")

Details

The proportional contribution of each of both calibration curves has to be set.

Value

A file containing the custom-made calibration curve, based on calibration curves cc1 and cc2.

Author(s)

Maarten Blaauw, J. Andres Christen

References

Blaauw, M. and Christen, J.A., Flexible paleoclimate age-depth models using an autoregressive gamma process. *Bayesian Anal.* 6 (2011), no. 3, 457–474. <https://projecteuclid.org/euclid.ba/1339616472>

See Also

http://www.chrono.qub.ac.uk/blaauw/manualBacon_2.3.pdf

Examples

```
mix.curves(, dirname=tempdir())
```

pMC.age

Calculate C14 ages from pMC values.

Description

Calculate C14 ages from pMC values of radiocarbon dates.

Usage

```
pMC.age(mn, sdev, ratio = 100, decimals = 0)
```

Arguments

mn	Reported mean of the pMC.
sdev	Reported error of the pMC.
ratio	Most modern-date values are reported against 100. If it is against 1 instead, use 1 here.
decimals	Amount of decimals required for the radiocarbon age.

Details

Post-bomb dates are often reported as pMC or percent modern carbon. Since Bacon expects radiocarbon ages, this function can be used to calculate radiocarbon ages from pMC values. The reverse function is [age.pMC](#).

Value

Radiocarbon ages from pMC values. If pMC values are above 100%, the resulting radiocarbon ages will be negative.

Author(s)

Maarten Blaauw, J. Andres Christen

References

Blaauw, M. and Christen, J.A., Flexible paleoclimate age-depth models using an autoregressive gamma process. *Bayesian Anal.* 6 (2011), no. 3, 457–474. <https://projecteuclid.org/euclid.ba/1339616472>

See Also

http://www.chrono.qub.ac.uk/blaauw/manualBacon_2.3.pdf

Examples

```
pmc.age(110, 0.5) # a postbomb date, so with a negative 14C age
pmc.age(80, 0.5) # prebomb dates can also be calculated
pmc.age(.8, 0.005, 1) # pmc expressed against 1 (not against 100\%)
```

proxy.ghost

Proxies analysed along the depths of a core can be plotted as 'proxy-ghost' graphs against calendar time while taking into account chronological uncertainties. Here darker grey indicates more likely calendar ages for specific proxy values.

Description

Proxies analysed along the depths of a core can be plotted as 'proxy-ghost' graphs against calendar time while taking into account chronological uncertainties. Here darker grey indicates more likely calendar ages for specific proxy value.

Usage

```
proxy.ghost(proxy = 1, proxy.lab = c(), proxy.res = 250,
  age.res = 200, yr.res = age.res, grey.res = 100,
  set = get("info"), dark = 1, darkest = 1, rotate.axes = FALSE,
  proxy.rev = FALSE, age.rev = FALSE, yr.rev = age.rev,
  plot.mean = FALSE, mean.col = "red", age.lim = c(),
  yr.lim = age.lim, proxy.lim = c(), sep = ",", xaxs = "i",
  yaxs = "i", xaxt = "s", yaxt = "s", bty = "l", BCAD = set$BCAD,
  age.lab = ifelse(BCAD, "BC/AD", "cal yr BP"), yr.lab = age.lab)
```

Arguments

proxy	Which proxy to use (counting from the column number in the .csv file after the depths column).
proxy.lab	Label of the proxy axis. Default names are taken from the csv file.
proxy.res	Greyscale pixels are calculated for proxy.res=250 proxy values by default, as a compromise between image quality and calculation speed. If the output looks very pixel-like (e.g., when choosing to plot only part of the record using proxy.lim), set this option to higher values.
age.res	Resolution or amount of greyscale pixels to cover the age scale of the age-model plot. Default age.res=250 as a compromise between image quality and calculation speed. If the output looks very pixel-like (e.g., when choosing to plot only part of the record using age.lim), set this option to higher values.
yr.res	Deprecated - use age.res instead
grey.res	Grey-scale resolution of the proxy graph. Default grey.res=100.
set	Detailed information of the current run, stored within this session's memory as variable info.
dark	By default, the darkest grey value is assigned to the most likely value within the entire core (normalised to 1; dark=1). By setting dark to, e.g., dark=.8, all values of and above 0.8 will be darkest (and values below that threshold will be lighter grey the lower their probabilities).
darkest	Darkness of the most likely value. Is black by default (darkest=1); lower values will result in lighter grey.
rotate.axes	The default is to plot the calendar horizontally, however the plot can be rotated (rotate.axes=TRUE).
proxy.rev	The proxy axis can be reversed if proxy.rev=TRUE.
age.rev	The calendar axis can be reversed using yr.rev=TRUE.
yr.rev	Deprecated - use age.rev instead
plot.mean	The mean ages of the proxy values can be added using plot.mean=TRUE.
mean.col	Colour of the weighted mean ages of the proxy values.
age.lim	Minimum and maximum calendar age ranges, calculated automatically by default (yr.lim=c()).
yr.lim	Deprecated - use age.lim instead
proxy.lim	Ranges of the proxy axis, calculated automatically by default (proxy.lim=c()).
sep	Separator between the fields of the plain text file containing the depth and proxy data.
xaxs	Extension of x-axis. By default, no white-space will be added at the axis extremes (xaxs="i"). See ?par for other options.
yaxs	Extension of y-axis. By default, no white-space will be added at the axis extremes (xaxs="i"). See ?par for other options.
xaxt	The x-axis is plotted by default, but this can be switched off using xaxt="n".
yaxt	The y-axis is plotted by default, but this can be switched off using yaxt="n".

bty	Type of box to be drawn around the plot ("n" for none, and "1" (default), "7", "c", "u", or "o" for correspondingly shaped boxes).
BCAD	The calendar scale of graphs and age output-files is in cal BP by default, but can be changed to BC/AD using BCAD=TRUE.
age.lab	The labels for the calendar axis (default age.lab="cal BP" or "BC/AD" if BCAD=TRUE).
yr.lab	Deprecated - use age.lab instead

Details

Place a csv file with the values of proxies against depth within your core's folder. The values should be in columns separated by commas (default sep=", "), the first column containing the depths and the first line (header) containing the proxy names. The file name should start with the core's name and end with "_proxies.csv". For an example see "Bacon_coredir/MSB2K/MSB2K_proxies.csv" or "Cores/MSB2K/MSB2K_proxies.csv".

Value

A grey-scale graph of the proxy against calendar age.

Author(s)

Maarten Blaauw, J. Andres Christen

References

Blaauw, M. and Christen, J.A., Flexible paleoclimate age-depth models using an autoregressive gamma process. *Bayesian Anal.* 6 (2011), no. 3, 457–474. <https://projecteuclid.org/euclid.ba/1339616472>

See Also

http://www.chrono.qub.ac.uk/blaauw/manualBacon_2.3.pdf

Examples

```
Bacon(ask=FALSE, coredir=tempfile())  
layout(1)  
proxy.ghost()
```

rbacon	<i>rbacon</i>
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Description

Bacon produces Bayesian age-depth models from dated deposits, reconstructing Bayesian accumulation histories through combining radiocarbon and other dates with prior information (Blaauw and Christen, 2011).

Author(s)

Maarten Blaauw <maarten.blaauw@qub.ac.uk> J. Andres Christen <jac@cimat.mx>

scissors	<i>Remove the first n iterations.</i>
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Description

Removes iterations of the MCMC time series, and then updates the output file.

Usage

```
scissors(burnin, set = get("info"))
```

Arguments

burnin	Number of iterations to remove of the iterative time series. If this value is higher than the amount of remaining iterations, a warning is given and the iterations are not removed. If the provided number is negative, the iterations will be removed from the end of the run, not from the start. If a range is given, this range of iterations is removed.
set	Detailed information of the current run, stored within this session's memory as variable info.

Details

Bacon will perform millions of MCMC iterations for each age-model run by default, although only a fraction of these will be stored. In most cases the remaining MCMC iterations will be well mixed (the upper left panel of the fit of the iterations shows no undesirable features such as trends or sudden systematic drops or rises). If the run has a visible remaining burn-in, scissors can be used to remove them. To remove, e.g., the first 300 iterations, type `scissors(300)`. To remove the last 300 iterations, type `scissors(-300)`. To remove iterations 300 to 600, type `scissors(300:600)`.

Value

NA

Author(s)

Maarten Blaauw, J. Andres Christen

References

Blaauw, M. and Christen, J.A., Flexible paleoclimate age-depth models using an autoregressive gamma process. *Bayesian Anal.* 6 (2011), no. 3, 457–474. <https://projecteuclid.org/euclid.ba/1339616472>

See Also

http://www.chrono.qub.ac.uk/blaauw/manualBacon_2.3.pdf

Examples

```
Bacon(ask=FALSE, coredir=tempfile())
scissors(100)
agedepth()
```

thinner

Thin iterations.

Description

Randomly thin iterations by a given proportion, for example if autocorrelation is visible within the MCMC series.

Usage

```
thinner(proportion = 0.1, set = get("info"))
```

Arguments

proportion	Proportion of iterations to remove. Should be between 0 and 1. Default proportion=0.1.
set	Detailed information of the current run, stored within this session's memory as variable info.

Details

From all iterations, a proportion is removed with to-be-removed iterations sampled randomly among all iterations.

Value

NA

Author(s)

Maarten Blaauw, J. Andres Christen

References

Blaauw, M. and Christen, J.A., Flexible paleoclimate age-depth models using an autoregressive gamma process. *Bayesian Anal.* 6 (2011), no. 3, 457–474. <https://projecteuclid.org/euclid.ba/1339616472>

See Also

http://www.chrono.qub.ac.uk/blaauw/manualBacon_2.3.pdf

Examples

```
Bacon(ask=FALSE, coredir=tempfile())  
thinner(.2)  
agedepth()
```

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