Package 'rbacon'

October 22, 2026

Type Package

Title Age-Depth Modelling using Bayesian Statistics

Version 4.0.2

Description 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 on accumulation rates and their variability. See Blaauw & Christen (2011).

Encoding UTF-8

URL https://github.com/Maarten14C/rbacon,
https://CRAN.R-project.org/package=rbacon

Repository CRAN

License GPL (>= 2)

Language en-GB

NeedsCompilation yes

ByteCompile true

Imports coda (>= 0.19-4.1), graphics, grDevices, Rcpp (>= 1.1.1), stats, utils, data.table, rintcal (>= 1.4.2), rice (>= 2.3.0)

Depends R (>= 3.5.0)

LinkingTo Rcpp

Suggests knitr, rmarkdown, utf8

VignetteBuilder knitr

Maintainer Maarten Blaauw <maarten.blaauw@qub.ac.uk>

Config/roxygen2/version 8.1.1

Author Maarten Blaauw [aut, cre] (ORCID: <https://orcid.org/0000-0002-5680-1515>), J. Andres Christen [aut, ctb, cph] (ORCID: <https://orcid.org/0000-0002-5795-4345>), Marco A. Aquino Lopez [aut] (ORCID: <https://orcid.org/0000-0002-5076-7205>), Judith Esquivel Vazquez [ctb], Oscar M. Gonzalez V. [ctb],

Ted Belding [cph],
James Theiler [cph],
Brian Gough [cph],
Charles Karney [cph]

Date/Publication 2026-10-22 13:50:02 UTC

Contents

A.modelled . . . 3
accrate.age . . . 4
accrate.age.ghost . . . 5
accrate.age.summary . . . 8
accrate.depth . . . 10
accrate.depth.ghost . . . 11
accrate.depth.summary . . . 14
accrates.core . . . 15
add.dates . . . 17
agedepth . . . 19
agemodel.it . . . 30
ageranges . . . 31
AgesOfEvents . . . 33
background . . . 35
Bacon . . . 35
Bacon.Age.d . . . 44
Bacon.cleanup . . . 45
Bacon.d.Age . . . 46
Bacon.hist . . . 47
bacon2clam . . . 49
Baconvergence . . . 50
Bacon_runs . . . 51
calib.plot . . . 52
clam2bacon . . . 54
draw.pbmeasured . . . 55
draw.pbmodelled . . . 56
flux.age.ghost . . . 58
MCMC.diagnostics . . . 61
proxy.ghost . . . 62
scissors . . . 65
set.initvals . . . 66
squeeze . . . 67
stretch . . . 67
thinner . . . 68
tofu . . . 69

Index **71**

`A.modelled` *calculate modelled 210Pb*

Description

Calculate modelled 210Pb values of a sample slice, based on the parameters of the age-model (i.e., time passed since deposition of the bottom and top of the slice), supported and influx

Usage

```
A.modelled(
  d.top,
  d.bottom,
  dens,
  set = get("info"),
  phi = set$phi,
  sup = set$ps
)
```

Arguments

`d.top`	top depth of the slice
`d.bottom`	bottom depth of the slice
`dens`	Density of the slice (in g/cm3)
`set`	Detailed information of the current run, stored within this session's memory as variable `info`.
`phi`	The modelled values of the 210Pb influx
`sup`	The modelled values of the supported 210Pb

Value

a list of modelled values of A

Author(s)

Maarten Blaauw

`accrate.age` *obtain estimated accumulation rates for any age of a core*

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,
  ages = c(),
  BCAD = set$BCAD,
  silent = TRUE,
  na.rm = FALSE
)
```

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.
`ages`	The ages of the age-depth model. Not provided by default, but can be provided to speed things up if the function is called repeatedly
`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`.
`silent`	Warn when ages are outside the core's range. Default `silent=TRUE`.
`na.rm`	Remove NA entries. These are NOT removed by default, ensuring that always the same amount of iterations is returned.

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

Examples

```
## Not run:
  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)

## End(Not run)
```

---

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(),
  age.lab = c(),
  na.rm = TRUE,
  kcal = FALSE,
  age.res = 400,
  acc.res = 200,
  cutoff = 0.001,
  zero.col = "white",
  max.col = "black",
  dark = 1,
  darkest = 1,
  rgb.scale = c(0, 0, 0),
  rgb.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,
  plot.median = TRUE,
  median.col = "blue",
  median.lty = 2,
  acc.lim = c(),
  acc.lab = c(),
  BCAD = set$BCAD,
  cmyr = FALSE,
  rotate.axes = FALSE,
  rev.age = FALSE,
  rev.acc = FALSE,
  use.raster = FALSE,
  flip.acc = FALSE,
  flip.age = 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()).
age.lab	The labels for the calendar axis (default age.lab="cal BP" or "BC/AD" if BCAD=TRUE).
na.rm	Remove NA entries. These are NOT removed by default, ensuring that always the same amount of iterations is returned.
kcal	Use kcal BP. Default is kcal=FALSE.
age.res	Resolution or amount of greyscale pixels to cover the age scale of the plot. Default age.res=400.
acc.res	Resolution or amount of greyscale pixels to cover the accumulation rate scale plot. Default age.res=400.
cutoff	Point below which colours will no longer be printed. Default cutoff=0.001.
zero.col	The colour where the ghost is 0. Defaults to zero.col="white", which together with max.col="black" results in a greyscale. More creative colour gradients can be implemented by checking the 600+ colours in colours().
max.col	The colour where the ghost is at its maximum. Defaults to max.col="black", which together with zero.col="white" results in a greyscale. More creative colour gradients can be implemented by checking the 600+ colours in colours().
dark	The value beyond which any higher values will be clipped. Set to 1 by default. This can be set to lower values if for example only a very small area in the plot obtains the darkest values - then lowering the 'dark' value will darker a larger area.

darkest	The darkest grey value is darkest=1 by default; lower values will result in lighter maximum colours; values >1 are not advised.
rgb.scale	The function to produce a coloured representation of all age-models. Needs 3 values for the intensity of red, green and blue. Defaults to grey-scales: rgb.scale=c(0,0,0), but could also be, say, scales of red (rgb.scale=c(1,0,0)).
rgb.res	Resolution of the colour spectrum depicting the age-depth model. Default rgb.res=100.
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.
plot.median	If plot.mean=TRUE, the medians are plotted.
median.col	Colour of the median accumulation rates.
median.lty	Type of the median lines.
acc.lim	Axis limits for the accumulation rates.
acc.lab	Axis label for the accumulation rate.
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.
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. Axis limits are difficult to calculate when cmyr=TRUE, so a manual adaptation of acc.lim might be a good idea.
rotate.axes	The default is to plot the calendar age horizontally and accumulation rates vertically. Change to rotate.axes=TRUE value to rotate axes.
rev.age	The direction of the age axis, which can be reversed using rev.age=TRUE.
rev.acc	The direction of the accumulation rate axis, which can be reversed (rev.acc=TRUE.
use.raster	Rasters can be aligned or not in the underlying image function. Setting use.raster=FALSE takes a bit longer to draw and sometimes causes strange lines owing to anti-aliasing. Therefore, use.raster=TRUE is the default, however on some devices (e.g., Mac OS quartz) this causes greyscales to 'flip'. If this is the case, use 'flip.acc=TRUE'.
flip.acc	When using use.raster=TRUE, sometimes greyscales are flipped. If this is the case, see if setting flip.acc=TRUE solves this.
flip.age	When using use.raster=TRUE, sometimes greyscales are flipped. If this is the case, see if setting flip.age=TRUE solves this.
xaxs	Extension of the x-axis. White space can be added to the vertical axis using xaxs="r".
yaxs	Extension of the y-axis. White space can be added to the vertical axis using yaxs="r".
bty	Type of box to be drawn around the plot ("n" for none, and "l" (default), "7", "c", "u", or "o" 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 greyscale 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. If warning messages such as "In min(x) : no non-missing arguments to min; returning Inf" appear, Bacon likely became confused about whether or not to use BC/AD. Best run your core again with the desired setting for BCAD.

Value

A greyscale plot of accumulation rate against calendar age, and (invisibly) the list of ages and their accumulation rates (ranges, medians, means).

Author(s)

Maarten Blaauw, J. Andres Christen

Examples

```
## Not run:
  Bacon(run=FALSE, coredir=tempfile())
  agedepth(age.res=20, d.res=20, d.by=10)
  layout(1)
  tmp <- accrate.age.ghost(age.res=200, acc.res=100)
  head(tmp)

## End(Not run)
```

`accrate.age.summary` *provide a summary of the estimated accumulation rates for any age of a core*

Description

Obtain a summary (95% range, 68% range, median, mean) of the 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.summary(
  age,
  set = get("info"),
  cmyr = FALSE,
  na.rm = TRUE,
  probs = c(0.025, 0.16, 0.84, 0.975, 0.5)
)
```

Arguments

age	The age 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.
na.rm	Remove NA entries. These are NOT removed by default, so that always the same amount of iterations is returned.
probs	The probability ranges to be returned. Defaults to the minima and maxima of the 95% and 68% ranges, as well as the median: probs=c(.025, .16, .84, .975, .5).

Value

A summary of the estimated accumulation rate of the chosen depth: minimum of the 95% interval, minimum of the 68% interval, maximum of the 68% interval, maximum of the 95% interval, median (i.e., 50%) and mean.

Author(s)

Maarten Blaauw

Examples

```
## Not run:
  Bacon(run=FALSE, coredir=tempfile())
  agedepth(yr.res=50, d.res=50, d.by=10)
  accrate.age.summary(5000)

## End(Not run)
```

`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,
  remove.hiatuses = TRUE,
  na.rm = FALSE,
  inversion.threshold = 1e-06
)
```

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.
`remove.hiatuses`	Any hiatuses will affect apparent accumulation rates within sections. Therefore, by default the hiatus jumps will be removed from the accumulation rates within sections containing hiatuses.
`na.rm`	Remove NA entries. These are NOT removed by default, ensuring that always the same amount of iterations is returned.
`inversion.threshold`	Very small accumulation rate values will become very large when their inverse is calculated. By default, any accumulation rate smaller than 1e-6 is set to 1e-6.

Details

should take into account hiatuses and slumps (I think it does though)

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

Examples

```
## Not run:
  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)

## End(Not run)
```

`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,
  darkest = 0.8,
  cutoff = 0.001,
  zero.col = "white",
  max.col = "black",
  rgb.scale = c(0, 0, 0),
  rgb.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,
  plot.median = TRUE,
  median.col = "blue",
  median.lty = 2,
  rotate.axes = FALSE,
  rev.d = FALSE,
  rev.acc = FALSE,
  xaxs = "r",
  yaxs = "r",
  bty = "l",
  remove.laststep = TRUE,
  use.raster = FALSE,
  flip.acc = FALSE,
  remove.hiatuses = TRUE
)
```

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.
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. Axis limits are difficult to calculate when cmyr=TRUE, so a manual adaptation of acc.lim might be a good idea.
acc.lab	Axis label for the accumulation rate.
dark	The value beyond which any higher values will be clipped. Set to 1 by default. This can be set to lower values if for example only a very small area in the plot obtains the darkest values - then lowering the 'dark' value will darker a larger area.
darkest	The darkest grey value is darkest=1 by default; lower values will result in lighter maximum colours; values >1 are not advised.
cutoff	Point below which colours will no longer be printed. Default cutoff=0.001.
zero.col	The colour where the ghost is 0. Defaults to zero.col="white", which together with max.col="black" results in a greyscale. More creative colour gradients can be implemented by checking the 600+ colours in colours().
max.col	The colour where the ghost is at its maximum. Defaults to max.col="black", which together with zero.col="white" results in a greyscale. More creative colour gradients can be implemented by checking the 600+ colours in colours().

rgb.scale	The function to produce a coloured representation of all age-models. Needs 3 values for the intensity of red, green and blue. Defaults to grey-scales: rgb.scale=c(0,0,0), but could also be, say, scales of red (rgb.scale=c(1,0,0)).
rgb.res	Resolution of the colour spectrum depicting the age-depth model. Default rgb.res=100.
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.
plot.median	If plot.mean=TRUE, the medians are plotted.
median.col	Colour of the median accumulation rates.
median.lty	Type of the median lines.
rotate.axes	The default is to plot the accumulation rates horizontally and the depth vertically (rotate.axes=FALSE). Change rotate.axes value to rotate axes.
rev.d	The direction of the depth axis can be reversed from the default (rev.d=TRUE.
rev.acc	The direction of the accumulation rate axis can be reversed from the default (rev.acc=TRUE).
xaxs	Extension of x-axis. By default, add some extra white-space at both extremes (xaxs="r"). See ?par for other options.
yaxs	Extension of y-axis. By default, add no extra white-space at both extremes (yaxs="i"). See ?par for other options.
bty	Type of box to be drawn around the plot ("n" for none, and "l" (default), "7", "c", "u", or "o" for correspondingly shaped boxes).
remove.laststep	Add a white line to remove spurious lines at the extreme of the graph. Defaults to TRUE.
use.raster	Rasters can be aligned or not in the underlying image function. Setting use.raster=FALSE, default takes a bit longer to draw and sometimes causes strange lines owing to anti-aliasing. However, the alternative of use.raster=TRUE causes greyscales on some devices (e.g., Mac OS quartz) to 'flip'. If this is the case, use 'flip.acc=TRUE'.
flip.acc	When using use.raster=TRUE, sometimes greyscales are flipped. If this is the case, see if setting flip.acc=TRUE solves this.
remove.hiatuses	Any hiatuses will affect apparent accumulation rates within sections. Therefore, by default the hiatus jumps will be removed from the accumulation rates within sections containing hiatuses.

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, and (invisibly) the list of depths and their accumulation rates (ranges, medians, means).

Author(s)

Maarten Blaauw, J. Andres Christen

Examples

```
## Not run:
  Bacon(run=FALSE, coredir=tempfile())
  agedepth(yr.res=50, d.res=50, d.by=10)
  layout(1)
  tmp <- accrate.depth.ghost()
  head(tmp)

## End(Not run)
```

---

accrate.depth.summary *provide a summary of the estimated accumulation rates for any depth of a core*

Description

Obtain a summary (95% range, 68% range, 50%=median, mean) of the 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.summary(
  d,
  set = get("info"),
  cmyr = FALSE,
  remove.hiatuses = TRUE,
  na.rm = FALSE,
  probs = c(0.025, 0.16, 0.84, 0.975, 0.5)
)
```

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.
remove.hiatuses	Hiatuses will affect apparent accumulation rates within sections. Therefore, by default the hiatus jumps will be removed from the accumulation rates within sections containing hiatuses.
na.rm	Remove NA entries. These are NOT removed by default, so that always the same amount of iterations is returned. NAs will however be removed if a core has slumps.
probs	The probability ranges to be returned. Defaults to the minima and maxima of the 95% and 68% ranges, as well as the median: probs=c(.025, .16, .84, .975, .5).

Value

A summary of the estimated accumulation rate of the chosen depth: minimum of the 95% interval, minimum of the 68% interval, maximum of the 68% interval, maximum of the 95% interval, median (i.e., 50%) and mean.

Author(s)

Maarten Blaauw

Examples

```
## Not run:
  Bacon(run=FALSE, coredir=tempfile())
  agedepth(yr.res=50, d.res=50, d.by=10)
  accrate.depth.summary(20)

## End(Not run)
```

---

accrates.core *provide a summary of the estimated accumulation rates for a range of core depths*

Description

Obtain a summary (95% range, 68% range, median, mean) of the accumulation rates (in years per cm, so actually sedimentation times) as estimated by the MCMC iterations for a range of depths of a core, and optionally write this as a file to the core directory (ending in '_accrates.txt').

Usage

```
accrates.core(
  dseq = c(),
  set = get("info"),
  cmyr = FALSE,
  remove.hiatuses = TRUE,
  na.rm = TRUE,
  probs = c(0.025, 0.16, 0.84, 0.975, 0.5),
  round = 2,
  write = TRUE,
  sep = "\t"
)
```

Arguments

dseq	The sequence of depths for which accumulation rates need to be returned. Defaults to whatever info$dseq is, which most often is a sequence from the top to the bottom of the core at 1 cm increments.
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.
remove.hiatuses	Any hiatuses will affect apparent accumulation rates within sections. Therefore, by default the hiatus jumps will be removed from the accumulation rates within sections containing hiatuses.
na.rm	Remove NA entries. These are NOT removed by default, so that always the same amount of iterations is returned.
probs	The probability ranges to be returned. Defaults to the minima and maxima of the 95% and 68% ranges, as well as the median: `probs=c(.025, .16, .84, .975, .5)`.
round	The number of decimals to report. Defaults to `round=2`.
write	Whether or not to write the summary to a file, in the core's directory and ending in '_accrates.txt'.
sep	Character to separate the entries within the file. Defaults to a tab, `sep="\t"`.

Value

A summary of the estimated accumulation rate for all selected depths: minimum of the 95% interval, minimum of the 68% interval, maximum of the 68% interval, maximum of the 95% interval, median (i.e., 50%) and mean. This is optionally written to a file in the core directory.

Author(s)

Maarten Blaauw

Examples

```
## Not run:
  Bacon(run=FALSE, coredir=tempfile())
  agedepth(yr.res=50, d.res=50, d.by=10)
  myaccrates <- accrates.core()

## End(Not run)
```

`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,
  BCAD = FALSE,
  above = 1e-06,
  postbomb = 0,
  normal = TRUE,
  is.F = FALSE,
  is.pMC = FALSE,
  delta.R = 0,
  delta.STD = 0,
  t.a = 3,
  t.b = 4,
  date.res = 100,
  height = 1,
  calheight = 1,
  agesteps = 1,
  cutoff = 0.005,
  col = rgb(1, 0, 0, 0.5),
  border = rgb(1, 0, 0, 0.5),
  rotate.axes = FALSE,
  mirror = TRUE,
  up = TRUE,
  pch = 4,
  cc.dir = c()
)
```

Arguments

mn	Reported mean of the date. Can be multiple dates. Negative numbers indicate postbomb dates (if cc > 0).
sdev	Reported error of the date. Can be multiple dates.
depth	Depth of the date.
cc	The calibration curve to use: cc=1 for IntCal20 (northern hemisphere terrestrial), cc=2 for Marine20 (marine), cc=0 for none (dates that are already on the cal BP scale).
BCAD	The calendar scale is in cal BP by default, but can be changed to BC/AD using BCAD=TRUE.
above	Threshold for plotting of probability values. Defaults to above=1e-3.
postbomb	Use a postbomb curve for negative (i.e. postbomb) 14C ages. 0 = none, 1 = NH1, 2 = NH2, 3 = NH3, 4 = SH1-2, 5 = SH3
normal	By default, Bacon uses the t-distribution (Christen and Perez 2009) to treat the dates. Use normal=TRUE to use the normal/Gaussian distribution. This will generally give higher weight to the dates.
is.F	Dates can be provided as F14C values. Defaults to is.F=FALSE.
is.pMC	Dates can be provided as pMC values. Defaults to is.pMC=FALSE.
delta.R	Mean of core-wide age offsets (e.g., regional marine offsets).
delta.STD	Error of core-wide age offsets (e.g., regional marine offsets).
t.a	The dates are treated using the t distribution by default (normal=FALSE). The t model 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 t distribution by default (normal=FALSE). The 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.
date.res	Resolution of the date's distribution. Defaults to date.res=100.
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.
agesteps	Step size for age units of the distribution. Default agesteps=1.
cutoff	Avoid plotting very low probabilities of date distributions (default cutoff=0.005).
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.
pch	The shape of any marker to be added to the date. Defaults to a cross, pch=4. To leave empty, use pch=NA.
cc.dir	Directory where the calibration curves for C14 dates cc are located. By default cc.dir=c().

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. Calls rice's draw.dates function.

Value

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

Author(s)

Maarten Blaauw, J. Andres Christen

Examples

```
plot(0, type="n", xlim=c(0, 100), ylim=c(0, 8000))
add.dates(5000, 100, 60)
```

---

agedepth *plot an age-depth model*

Description

Plot the age-depth model of a core.

Usage

```
agedepth(
  set = get("info"),
  BCAD = set$BCAD,
  depth.unit = set$depth.unit,
  age.unit = "yr",
  unit = depth.unit,
  d.lab = c(),
  age.lab = c(),
  yr.lab = age.lab,
  kcal = FALSE,
  acc.lab = c(),
  mem.lab = c(),
```

```
d.min = c(),
d.max = c(),
d.by = c(),
depths = set$depths,
depths.file = FALSE,
accordion = c(),
plotatthesedepths = c(),
age.min = c(),
yr.min = age.min,
age.max = c(),
yr.max = age.max,
hiatus.option = 1,
dark = 1,
darkest = 1,
prob = set$prob,
rounded = c(),
d.res = 500,
age.res = 500,
yr.res = age.res,
date.res = 100,
rotate.axes = FALSE,
rev.age = FALSE,
rev.yr = rev.age,
rev.d = FALSE,
use.raster = TRUE,
flip.age = FALSE,
flip.d = FALSE,
maxcalc = 500,
height = 1,
calheight = 1,
ex = 1,
mirror = TRUE,
up = TRUE,
cutoff = 0.1,
plot.range = TRUE,
range.col = grey(0.5),
range.lty = "12",
range.lwd = 1,
mn.col = "red",
mn.lty = "12",
mn.lwd = 1,
med.col = NA,
med.lty = "12",
med.lwd = 1,
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(),
    pb.background = 0.5,
    pbmodelled.col = function(x) rgb(0, 0, 1, 0.5 * x),
    pbmeasured.col = "blue",
    pb.lim = c(),
    supp.col = rgb(0.5, 0, 0.5, 0.5),
    remove.tail = TRUE,
    MCMC.resample = TRUE,
    hiatus.col = grey(0.5),
    hiatus.lty = "12",
    from.col = "white",
    to.col = "black",
    rgb.scale = c(0, 0, 0),
    rgb.res = 100,
    slump.col = grey(0.8),
    olderthan.size = 1,
    olderthan.col = "black",
    youngerthan.size = 1,
    youngerthan.col = "black",
    normalise.dists = TRUE,
    same.heights = FALSE,
    cc = set$cc,
    title = set$core,
    title.location = "topleft",
    title.size = 1.5,
    plot.labels = FALSE,
    labels = c(),
    label.age = 1,
    label.size = 0.8,
    label.col = "black",
    label.offset = c(0, 0),
    label.adj = c(0.5, 0),
    label.rot = 0,
    after = set$after,
    bty = "l",
    mar.left = c(),
    mar.middle = c(),
    mar.right = c(),
    mar.main = c(),
    righthand = 3,
    mgp = c(1.7, 0.7, 0),
    xaxs = "r",
    yaxs = "i",
    MCMC.col = grey(0.4),
    post.col = rgb(0, 0, 0, 0.2),
    post.border = rgb(0, 0, 0, 0.4),
    acc.post.col = c(),
    acc.post.border = c(),
```

```
    mem.post.col = c(),
    mem.post.border = c(),
    hiatus.post.col = c(),
    hiatus.post.border = c(),
    phi.post.col = c(),
    phi.post.border = c(),
    s.post.col = c(),
    s.post.border = c(),
    prior.col = 3,
    prior.lwd = 2,
    prior.fontcol = 2,
    prior.ticks = "n",
    prior.fontsize = 0.9,
    toppanel.fontsize = 0.9,
    mainpanel.tickfontsize = 1,
    mainpanel.labelfontsize = 1,
    acc.xlim = c(),
    acc.ylim = c(),
    mem.xlim = c(),
    mem.ylim = c(),
    hiatus.xlim = c(),
    hiatus.ylim = c(),
    phi.xlim = c(),
    phi.ylim = c(),
    supp.xlim = c(),
    supp.ylim = c(),
    xaxt = "s",
    yaxt = "s",
    plot.pb = TRUE,
    pb.lty = 1,
    plot.pdf = FALSE,
    quartz = FALSE,
    cairo = FALSE,
    dates.only = FALSE,
    model.only = FALSE,
    verbose = TRUE,
    roundby = 2,
    save.info = set$save.info,
    write.summary = TRUE,
    ssize = 4000,
    use.cpp = TRUE,
    version.legend = TRUE,
    version.location = c(),
    version.cex = 0.7,
    version.col = grey(0.5)
  )
```

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 the one provided in the Bacon() command, depth.unit=set$depth.unit.
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).
yr.lab	Deprecated - use age.lab instead
kcal	Use kcal BP. Default is kcal=FALSE.
acc.lab	The labels for the accumulation rate plot (top middle). Default d.lab="Acc. rate (yr/cm)" (or whatever units you're using).
mem.lab	The labels for the memory plot (top right). Default d.lab="Memory".
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. Default 1. Alternative depth intervals can be provided using, e.g., d.d.by=0.5.
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.
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.
accordion	An experimental option to squeeze and stretch depths below a boundary. Needs 2 parameters: boundary depth and compression ratio, e.g., accordion=c(25,20). Defaults to inactive, accordion=c().
plotatthesedepths	An option to plot ages at different depths (e.g., if a core has been compressed during a run). Use with extreme caution!
age.min	Minimum age of the age-depth plot.
yr.min	Deprecated - use age.min instead.
age.max	Maximum age of the age-depth plot.
yr.max	Deprecated - use age.min instead.

hiatus.option	How to calculate accumulation rates and ages for sections with hiatuses. Either extrapolate from surrounding sections (default, hiatus.option=1), use a w-weighted mix between the prior and posterior values for depths below the hiatus and prior information only for above the hiatus (hiatus.option=2), or use the originally calculated slopes (hiatus.option=0).
dark	The value beyond which any higher values will be clipped. Set to 1 by default. This can be set to lower values if for example only a very small area in the plot obtains the darkest values - then lowering the 'dark' value will darker a larger area.
darkest	The darkest grey value is darkest=1 by default; lower values will result in lighter maximum colours; values >1 are not advised.
prob	Confidence interval to report (between 0 and 1, default 0.95 or 95%).
rounded	Rounding of years. Default is to round to single years (1 digit for plum models).
d.res	Resolution or amount of greyscale pixels to cover the depth scale of the age-model plot. Default d.res=200.
age.res	Resolution or amount of greyscale pixels to cover the age scale of the age-model plot. Default yr.res=200.
yr.res	Deprecated - use age.res instead.
date.res	Date distributions are plotted using date.res=100 points by default.
rotate.axes	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 rotate.axes=TRUE.
rev.age	The direction of the age axis, which can be reversed using rev.age=TRUE.
rev.yr	Deprecated - use rev.age instead.
rev.d	The direction of the depth axis, which can be reversed using rev.d=TRUE.
use.raster	Raster output (use.raster=TRUE, default) is often faster and can avoid anti-aliasing artefacts (such as faint lines between cells) seen with vector rendering. However, some graphics devices may render greyscales incorrectly or invert colour scales. If this occurs, set use.raster=FALSE or try flip.acc=TRUE. Defaults to use.raster=FALSE. Playing around with this option could be useful if pdf copies of the graph cause large file sizes.
flip.age	When using use.raster=TRUE, sometimes greyscales are flipped. If this is the case, see if setting flip.age=TRUE can flip the ages back again.
flip.d	When using use.raster=TRUE, sometimes greyscales are flipped. If this is the case, see if setting flip.d=TRUE can flip the depths back again.
maxcalc	Number of depths to calculate ages for. If this is more than maxcalc=500, a warning will be shown that calculations will take time.
height	The maximum heights of the distributions of the dates on the plot. See also normalise.dists.
calheight	Multiplier for the heights of the distributions of dates on the calendar scale. Defaults to calheight=1.
ex	As an alternative to 'height' and 'calheight', the distribution heights can be set as either a single value (e.g., ex=1) or for each date (for example, myex=rep(1, nrow(info$dets)); myex[1:5] <- 10; agedepth(ex=myex)).

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=0.1).
plot.range	Whether or not to plot the curves showing the confidence ranges of the age-model. Defaults to (plot.range=TRUE).
range.col	The colour of the curves showing the confidence ranges of the age-model. Defaults to medium grey (range.col=grey(0.5)).
range.lty	The line type of the curves showing the confidence ranges of the age-model. Defaults to range.lty=12.
range.lwd	Widths of the lines of the ranges of the age-depth model. Default range.lwd=1.
mn.col	The colour of the mean age-depth model: default mn.col="red".
mn.lty	The line type of the mean age-depth model. Default mn.lty=12.
mn.lwd	Width of the line of the mean age-depth model. Default mn.lwd=1.
med.col	The colour of the median age-depth model: not drawn by default med.col=NA.
med.lty	The line type of the median age-depth model. Default med.lty=12.
med.lwd	Width of the line of the median age-depth model. Default med.lwd=1.
C14.col	The colour of the calibrated ranges of the dates. Default is semi-transparent blue: C14.col=rgb(0,0,1,.35).
C14.border	The colours of the borders of calibrated 14C dates. Default is semi-transparent dark blue: C14.border=rgb(0, 0, 1, 0.5).
cal.col	The colour of the non-14C dates. Default is semi-transparent blue-green: cal.col=rgb(0,.5,.5,.35).
cal.border	The colour of the border of non-14C dates in the age-depth plot: default semi-transparent dark blue-green: cal.border=rgb(0,.5,.5,.5). Not used by default.
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].
pb.background	Probability at which total Pb values are considered to have reached background values, or in other words, that their modelled values are at or below supported + detection limit (Al)). Setting this at 0.5 means that any depth with a Pb measurement, where at least half of the iterations model Pb values reaching background values, is flagged as having reached background. The age-model is not extended to any Pb measurements that have reached background.
pbmodelled.col	Colour of the modelled 210Pb values. Defaults to shades of blue: pbmodelled.col=function(x) rgb(0,0,1,x).
pbmeasured.col	Colour of the measured 210Pb values (default pbmeasured.col="blue"). Draws rectangles of the upper and lower depths as well as the Pb values with 95 percent error ranges.
pb.lim	Axis limits for the Pb-210 data. Calculated automatically by default (pblim=c()).
supp.col	Colour of supported Pb-210. Defaults to semi-transparent purple, because why not.

`remove.tail` Whether or not to remove the tail measurements when plotting. Sometimes automated removal might go wrong, so then this option can be used to avoid removing the tail measurements.

`MCMC.resample` After the MCMC run, if there are more MCMC iterations than requested, only the last 'ssize' iterations will be retained. Defaults to TRUE.

`hiatus.col` The colour of the depths of any hiatuses. Default `hiatus.col=grey(0.5)`.

`hiatus.lty` The line type of the depths of any hiatuses. Default `hiatus.lty=12`.

`from.col` Starting colour of the gradient for the ghost plot of the age-depth model. Defaults to `from.col="white"`.

`to.col` Colour of the gradient for the ghost plot of the age-depth model. Defaults to a greyscale, `to.col="black"`.

`rgb.scale` As alternative to 'from.col' and 'to.col', rgb.scale can be used to produce a coloured representation of all age-models. Needs 3 values for the intensity of red, green and blue. Defaults to grey-scales: `rgb.scale=c(0,0,0)`, but could also be, say, scales of red (`rgb.scale=c(1,0,0)`).

`rgb.res` Resolution of the colour spectrum depicting the age-depth model, if using 'rgb.scale'. Default `rgb.res=100`.

`slump.col` Colour of slumps. Defaults to `slump.col=grey(0.8)`.

`olderthan.size` size of the upward arrow to indicate 'olderthan' dates (where the model goes to ages older than said date). Defaults to size 1.

`olderthan.col` colour of the upward arrow to indicate 'olderthan' dates (where the model goes to ages older than said date). Defaults to black.

`youngerthan.size` size of the downward arrow to indicate 'youngerthan' dates (where the model goes to ages younger than said date). Defaults to size 1.

`youngerthan.col` colour of the downward arrow to indicate 'youngerthan' dates (where the model goes to ages younger than said date). Defaults to black.

`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`.

`same.heights` Plot the distributions of the dates all at the same maximum height (default `same.height=FALSE`).

`cc` Calibration curve for 14C dates: `cc=1` for IntCal20 (northern hemisphere terrestrial), `cc=2` for Marine20 (marine), `cc=3` for SHCal20 (southern hemisphere terrestrial). For dates that are already on the cal BP scale use `cc=0`.

`title` The title of the age-depth model is plotted on the main panel. By default this is the core's name. To leave empty: `title=""`.

`title.location` Location of the title. Default `title.location='topleft'`.

`title.size` Size of the title font. Defaults to `title.size=1.5`.

`plot.labels` Whether or not to plot labels next to the dated depths. Defaults to `FALSE`.

labels	Add labels to the dates (as given by the first column of the .csv file). FALSE by default.
label.age	Position on the age axis of the date labels. By default draws them before the youngest age (1), but can also draw them after the oldest age (2), or above its mean (3).
label.size	Size of labels.
label.col	Colour of the labels. Defaults to the colour given to the borders of the dates.
label.offset	Offsets of the positions of the labels, giving the x and y offsets. Defaults to c(0,0).
label.adj	Justification of the labels. Follows R's adj option: A value of '0' produces left-justified text, '0.5' (the default) centered text and '1' right-justified text.
label.rot	Rotation of the label. 0 by default (horizontal).
after	Sets a short section above and below hiatus.depths within which to calculate ages. For internal calculations - do not change.
bty	Type of box to be drawn around plots ("n" for none, and "l" (default), "7", "c", "u", or "o" for correspondingly shaped boxes).
mar.left	Plot margins for the topleft panel (amount of white space along edges of axes 1-4). If left empty, it is set to mar.left=c(3,3,1,1).
mar.middle	Plot margins for the middle panel(s) at the top (amount of white space along edges of axes 1-4). If left empty, it is set to mar.middle=c(3,3,1,1).
mar.right	Plot margins for the topright panel (amount of white space along edges of axes 1-4). If left empty, it is set to mar.right=c(3,3,1,1).
mar.main	Plot margins for the main panel (amount of white space along edges of axes 1-4). If left empty, it is set to mar.main=c(3,3,1,1).
righthand	Adapt the righthand margins by a certain amount (default 2) to allow a righthand axis to be plotted (for plum)
mgp	Axis text margins (where should titles, labels and tick marks be plotted). Defaults to mgp=c(1.7, 0.7, 0.0).
xaxs	Extension of x-axis. By default, add some extra white-space at both extremes (xaxs="r"). See ?par for other options.
yaxs	Extension of y-axis. By default, add no extra white-space at both extremes (yaxs="i"). See ?par for other options.
MCMC.col	Colour of the MCMC output. Defaults to post.col=grey(0.4)).
post.col	Colour of the posterior histogram. Defaults to post.col=grey(0.8)). In case of hiatuses/boundaries, you can provide colours for the individual sections, e.g., post.col=c(2,3,4).
post.border	Colour of the posterior border. Defaults to post.border=grey(0.4)). In case of hiatuses/boundaries, you can provide colours for the individual sections, e.g., post.col=c(2,3,4).
acc.post.col	Colour of the posterior of the accumulation rate (yr/cm). Defaults to post.col=grey(0.8)). Multiple colours can be provided. See post.col.

`acc.post.border`
: Colour of the posterior border of the accumulation rate (yr/cm). Defaults to `post.border=grey(0.4)`). Multiple colours can be provided. See post.border.

`mem.post.col`
: Colour of the posterior of the memory. Defaults to `post.col=grey(0.8)`). See post.col.

`mem.post.border`
: Colour of the posterior of the memory. Defaults to `post.border=grey(0.4)`). See post.border.

`hiatus.post.col`
: Colour of the posterior of the hiatus length. Defaults to `post.col=grey(0.8)`). Multiple colours can be provided. See post.col.

`hiatus.post.border`
: Colour of the border of the hiatus length. Defaults to `post.border=grey(0.4)`). Multiple colours can be provided. See post.border.

`phi.post.col`
: Colour of the posterior of the 210Pb influx phi. Defaults to `post.col=grey(0.8)`). See post.col.

`phi.post.border`
: Colour of the posterior border of the 210Pb influx phi. Defaults to `post.border=grey(0.4)`). See post.border.

`s.post.col`
: Colour of the posterior of the supported 210Pb. Defaults to `post.col=grey(0.8)`). See post.col.

`s.post.border`
: Colour of the border of the posterior supported 210Pb. Defaults to `post.border=grey(0.4)`). See post.border.

`prior.col`
: Colour of the prior curves. Defaults to light green, `prior.col=3`).

`prior.lwd`
: Line width of the prior curves. Defaults to `prior.lwd=2`).

`prior.fontcol`
: Colour of the font accompanying the posterior histograms. Defaults to red, `prior.fontcol=2`).

`prior.ticks`
: Plot tickmarks and values on the vertical axes for the prior and posterior distributions. Defaults to no tick marks (`prior.ticks="n"`). Set to `prior.ticks="s"` to plot the tick marks. Note that these values are of little practical use, as they correspond poorly to, e.g., the mean and strength values. All that matters is that the areas of both the prior and the posterior distributions sum to 1; wider distributions tend to give lower peaks, and narrower distributions higher peaks.

`prior.fontsize`
: Font size of the prior, relative to R's standard size. Defaults to `prior.fontsize=0.9`.

`toppanel.fontsize`
: Font size of the top panels, relative to R's standard size. Defaults to `prior.fontsize=0.9`.

`mainpanel.tickfontsize`
: Font size of values at the tick marks in the main panel, relative to R's standard size. Defaults to `mainpanel.tickfontsize=1`.

`mainpanel.labelfontsize`
: Font size of axis labels in the main panel, relative to R's standard size. Defaults to `mainpanel.labelsize=1`.

`acc.xlim`
: Horizontal axis limits of the accumulation rate panel. Calculated automatically by default.

acc.ylim	Vertical axis limits of the accumulation rate panel. Calculated automatically by default.
mem.xlim	Horizontal axis limits of the memory panel. Calculated automatically by default.
mem.ylim	Vertical axis limits of the memory panel. Calculated automatically by default.
hiatus.xlim	Horizontal axis limits of the hiatus size panel. Calculated automatically by default.
hiatus.ylim	Vertical axis limits of the hiatus size panel. Calculated automatically by default.
phi.xlim	Horizontal axis limits of the phi panel. Calculated automatically by default.
phi.ylim	Vertical axis limits of the phi panel. Calculated automatically by default.
supp.xlim	Horizontal axis limits of the supported-Pb panel. Calculated automatically by default.
supp.ylim	Vertical axis limits of the supported-Pb panel. Calculated automatically by default.
xaxt	Whether or not to plot the x-axis. Can be used to adapt axes after a plot. See ?par for other options.
yaxt	Whether or not to plot the y-axis. Can be used to adapt axes after a plot. See ?par for other options.
plot.pb	Plot the 210Pb data (if present). Defaults to `plot.pb=TRUE`.
pb.lty	Line type of measured Pb-210 data.
plot.pdf	Produce a pdf file of the age-depth plot.
quartz	Use quartz-based pdf plots if available (on Mac OS). Defaults to FALSE.
cairo	Use cairo-based pdf plots if available (on Mac OS). Defaults to FALSE.
dates.only	By default, the age-depth model is plotted on top of the dates. This can be avoided by supplying `dates.only=TRUE`.
model.only	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 `model.only=TRUE`. 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.
verbose	Provide a summary of the age ranges after producing the age-depth model graph; default `verbose=FALSE`.
roundby	Rounding of the values reported at the end of the function. Defaults to 2 decimals.
save.info	By default, a variable called 'info' with relevant information about the run (e.g., core name, priors, settings, ages, output) is saved into the working directory. Note that this will overwrite any existing variable with the same name - as an alternative, one could run, e.g., `myvar <- Bacon()`, followed by supplying the variable `myvar` in any subsequent commands.
write.summary	Whether or not to write a file to the core's folder, which summarizes the run (MCMC, model fit, priors, posteriors, learning).
ssize	Number of MCMC iterations to use.

use.cpp	Whether or not to use a cpp function to calculate the ages. Defaults to TRUE, but can be set to FALSE (much slower but less experimental)
version.legend	Whether to print version information (including calibration curves used) inside the main panel
version.location	Location of the version information. Defaults to bottom right for rbacon, top right for rplum.
version.cex	Size of the version legend. Defaults to small, cex=0.7.
version.col	Colour of the version legend. Defaults to light grey.

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

Examples

```
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,
  depths = c(),
  set = get("info"),
  BCAD = set$BCAD,
  save.info = set$save.info
)
```

Arguments

it	The MCMC iteration of which the age-model should be calculated.
depths	The depths for which the age estimates are to be returned.
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.
save.info	If TRUE, a variable called 'info' with relevant information about the run (e.g., core name, priors, settings, ages, output) is saved into the working directory. Note that this will overwrite any existing variable with the same name.

Value

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

Author(s)

Maarten Blaauw, J. Andres Christen

Examples

```
## Not run:
  Bacon(run=FALSE, coredir=tempfile())
  agedepth(age.res=50, d.res=50, d.by=10)
  lines(agemodel.it(5), col="red")

## End(Not run)
```

---

ageranges *save age ranges of depth(s)*

Description

Calculates an age summary (min/max probability range, median and mean) of a depth or a series of depths. The depths are returned and can be saved to a file.

Usage

```
ageranges(
  d = c(),
  file = c(),
  sep = "\t",
  set = get("info"),
  BCAD = set$BCAD,
  na.rm = TRUE,
  prob = 0.95,
```

```
  d.by = 1,
  roundby = 1,
  show.progress = TRUE,
  verbose = TRUE,
  use.cpp = TRUE,
  age.bins = 1
)
```

Arguments

d	Depth or depths for which age summaries are to be calculated. If left empty, a sequence of depths is calculated from the top to the bottom of the core, see 'd.by'.
file	The name of the file where the age summary has to be stored. If empty (default), the ages are returned.
sep	Separator for the fields, if saving to a file (defaults to a tab, "\t").
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 (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.
na.rm	Whether or not NAs are to be removed. Defaults to na.rm=TRUE. NAs will still be returned for depths outside of the core's depth range.
prob	Probability range. Half of the range is taken away from both sides of the distribution (e.g., 2.5% for the default of prob=0.95).
d.by	Steps for calculation of depths, if 'd' is left empty. Defaults to steps of 1.
roundby	Rounding for the age estimates. Defaults to 1 decimal.
show.progress	Show a progress bar. Defaults to TRUE.
verbose	Inform the user of what is happening. Defaults to TRUE.
use.cpp	Whether or not to use a cpp function to calculate the ages. Defaults to TRUE, but can be set to FALSE (much slower but less experimental)
age.bins	Size of the age bins (in years) if use.cpp=TRUE. Defaults to every 1 year.

Value

The minimum and maximum of the probability range (default 2.5

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).
yr.lab	Deprecated - use age.lab instead
age.lim	Minimum and maximum calendar age ranges, calculated automatically by default (age.lim=c()).
yr.lim	Deprecated - use age.lim instead
prob.lab	Label of the probability axis (default prob.lab="probability").

prob.lim	Limits of the probability axis (calculated automatically by default).
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.age	The direction of the age axis, which can be reversed using rev.age=TRUE.
rev.yr	Deprecated - use rev.age instead
yaxs	Extension of the y-axis. Defaults to the exact ranges of the probability values. White space can be added to the vertical axis using yaxs="r".
bty	Type of box to be drawn around plots. Draw a box around the graph ("n" for none, and "l", "7", "c", "u", "]" or "o" 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.

Examples

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

`background` *calculate probabilities that Pb-210 data have reached background levels*

Description

Checks which of the Pb-210 data most likely have reached background levels and thus are below the detection limit Al (probabilities between 0 and 1)

Usage

```
background(set = get("info"), Al = set$Al)
```

Arguments

`set`	Detailed information of the current run, stored within this session's memory as variable `info`.
`Al`	The detection limit. Default `Al=0.1`.

Value

a list of probabilities for each Pb-210 data point

Author(s)

Maarten Blaauw

`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,
  add.bottom = TRUE,
  d.by = 1,
  seed = NA,
  depths.file = FALSE,
  depths = c(),
  depth.unit = "cm",
  age.unit = "yr",
  unit = depth.unit,
  acc.shape = 1.5,
  acc.mean = 20,
  mem.strength = 10,
  mem.mean = 0.5,
  boundary = NA,
  hiatus.depths = NA,
  hiatus.mean = 1000,
  hiatus.shape = 0.5,
  hiatus.max = 10000,
  add = c(),
  after = 1e-04/thick,
  cc = 1,
  cc1 = "IntCal20",
  cc2 = "Marine20",
  cc3 = "SHCal20",
  cc4 = "ConstCal",
  cc.dir = c(),
  postbomb = 0,
  F14C = c(),
  pMC = c(),
  hot.stop = TRUE,
  delta.R = 0,
  delta.STD = 0,
  t.a = 3,
  t.b = 4,
  normal = FALSE,
  suggest = TRUE,
  accept.suggestions = FALSE,
  adjust.dby = TRUE,
  reswarn = c(10, 200),
  remember = TRUE,
  ask = TRUE,
```

```
  run = TRUE,
  defaults = "defaultBacon_settings.txt",
  sep = ",",
  dec = ".",
  fast = TRUE,
  runname = "",
  slump = c(),
  remove = FALSE,
  BCAD = FALSE,
  ssize = 4000,
  th0 = c(),
  burnin = min(500, ssize),
  youngest.age = c(),
  oldest.age = c(),
  MinAge = c(),
  MaxAge = c(),
  cutoff = 0.01,
  plot.pdf = TRUE,
  quartz = FALSE,
  cairo = FALSE,
  dark = 1,
  date.res = 100,
  age.res = 200,
  yr.res = age.res,
  close.connections = TRUE,
  save.info = TRUE,
  older.than = c(),
  younger.than = c(),
  save.elbowages = FALSE,
  verbose = TRUE,
  use.cpp = 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).

`add.bottom` Add a model section at the bottom of the core, in order to ensure the bottommost date is taken into account. Default `add.bottom=TRUE`. This is a new option and can cause age-models to differ from previous version. Please re-run the model if in doubt.

`d.by` Depth intervals at which ages are calculated. Defaults to `d.by=1`. Please ensure that the value of d.by is smaller than that of 'thick', otherwise plots might turn out wrong.

`seed` Seed used for C++ executions. If it is not assigned (`seed=NA`; default) then the seed is set by system.

`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))

`mem.strength` 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 `mem.strength=10` (higher values result in more

peaked shapes) allow for a large range of posterior memory values. Please note that the default memory prior has been updated from rbacon version 2.5.1 on, to repair a bug.

`mem.mean` 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 `mem.mean=0.5` allow for a large range of posterior memory values. Please note that the default memory prior has been updated from rbacon version 2.5.1. on, to repair a bug.

`boundary` 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., `acc.mean=c(5, 20)`. See also `hiatus.depths`, `mem.mean`, `acc.mean` and `acc.shape`. Setting many boundaries might not work, and the maximum numbers of boundaries per model section (see `'thick'`) is 1.

`hiatus.depths` The assumed depths for any hiatus should be provided as, e.g., `hiatus.depths=20` for one at 20 cm depth, and `hiatus.depths=c(20,40)` for two hiatuses at 20 and 40 cm depth.

`hiatus.mean` The prior for the mean of the hiatus gamma prior. Defaults to 1000 and should be >0.

`hiatus.shape` The prior for the shape of the hiatus gamma prior. Set to 0.5 (default) to favour short time gaps but enable larger ones. Set to 1 for an exponential prior distribution, and to >1 for a distribution that peaks around hiatus.mean. The influence of hiatus.mean on the posterior chronology depends on hiatus.shape. Larger values of hiatus.shape produce a more informative prior and thus constrain posterior hiatus estimates more strongly around hiatus.mean, whereas smaller values allow the dating evidence to dominate.

`hiatus.max` The hiatus prior used to be a uniform distribution with hiatus.max as its limits. Please use hiatus.mean and hiatus.shape instead. Will be deprecated.

`add` 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.

`after` Sets a short section above and below hiatus.depths within which to calculate ages. For internal calculations - do not change.

`cc` Calibration curve for C-14 dates: `cc=1` for IntCal20 (northern hemisphere terrestrial), `cc=2` for Marine20 (marine), `cc=3` for SHCal20 (southern hemisphere terrestrial). For dates that are already on the cal BP scale use `cc=0`.

`cc1` For northern hemisphere terrestrial 14C dates (IntCal20).

`cc2` For marine 14C dates (Marine20).

`cc3` For southern hemisphere 14C dates (SHCal20).

`cc4` Provide the name of an alternative curve (3 columns: cal BP, 14C age, error, separated by white spaces and saved as a plain-text file). It is important here to first produce a tailor-made folder for your and the default calibration curves to live in. See `cc.dir`. Defaults to `cc4="mixed.14C"`.

`cc.dir` Directory where the calibration curves for C14 dates `cc` are located. By default uses the location of the rintcal package which provides the calibration curves. If you want to use custom-made calibration curves, first set up a new folder using the function new.ccdir() in the rintcal package, e.g., `new.ccdir="MyCurves"`, then place the custom curve in that folder using `rintcal::mix.ccurves(, cc.dir="MyCurves", save=TRUE)`.

`postbomb` Use a postbomb curve for negative (i.e. postbomb) 14C ages. `0 = none, 1 = NH1, 2 = NH2, 3 = NH3, 4 = SH1-2, 5 = SH3`

`F14C` Radiocarbon ages can be provided as F14C values. If doing so (for example if some of your dates are modern/postbomb), please indicate here which dates were entered as F14C (e.g., if the first 4 dates are in F14C, write `F14C=1:4`). The F14C values in your core's .csv file will then be replaced by their corresponding C14 ages.

`pMC` Radiocarbon ages can be provided as pMC values. If doing so, please indicate here which dates were entered as pMC (e.g., if the first 4 dates are in pMC, write `pMC=1:4`). The pMC values in your core's .csv file will then be replaced by their corresponding C14 ages.

`hot.stop` Stop with a warning if provided F14C or pMC values (see above) are negative or above 3 resp. 300. Defaults to `hot.stop=TRUE`.

`delta.R` Mean of core-wide age offsets (e.g., regional marine offsets).

`delta.STD` Error of core-wide age offsets (e.g., regional marine offsets).

`t.a` The dates are treated using the t distribution (Christen and Perez 2009) by default (`normal=FALSE`). This 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 t distribution by default (`normal=FALSE`). The t-distribution has two parameters, t.a and t.b, set at 3 and 4 by default (see Christen and Perez, 2009). 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.

`normal` By default, Bacon uses the t-distribution to treat the dates. Use `normal=TRUE` to use the normal/Gaussian distribution. This will generally give higher weight to the dates.

`suggest` If initial analysis of the data indicates abnormally slow or fast accumulation rates, Bacon will suggest to change the prior.

`accept.suggestions` Automatically accept the suggested values. Use with care. Default `accept.suggestions=FALSE`.

`adjust.dby` Automatically adjust d.by to a value smaller than thick. Defaults to `adjust.dby=TRUE`. 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 `thick`. 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 `suggest=FALSE`.

reswarn	Bacon will warn you if the number of sections lies outside the safe range (default between 10 and 200 sections; reswarn=c(10,200)). 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.
remember	Bacon will try to remember which settings you have applied to your cores (default remember=TRUE). If you run into inconsistencies or other problems, try running your core again with remember=FALSE, or, start cleanly by typing Bacon.cleanup().
ask	By default Bacon will ask you to confirm that you want to run the core with the provided settings. Disable this using ask=FALSE (e.g., for batch runs).
run	In order to load an existing Bacon run instead of producing a new one, you can use run=FALSE.
defaults	Name of the file containing settings for the core. For internal use only - do not change.
sep	Separator between the fields of the plain text file containing the dating information. Default sep=",".
dec	Character for decimal points. Default to dec=".".
fast	Whether or not to use the fread function to read files quickly. Set to FALSE if there are problems with your core's .csv file (e.g. unexpected encoding).
runname	Text to add to the corename for specific runs, e.g., runname="MyCore_Test1".
slump	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., slump=c(10,15,60,67) for slumps at 67-60 and 15-10 cm core depth.
remove	Whether or not to remove depths within slumps. Defaults to remove=FALSE.
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 amount of iterations to store at the end of the MCMC run. Default 4000; 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. These are randomly chosen by default.
burnin	Amount of initial, likely sub-optimal MCMC iterations that will be removed.
youngest.age	Minimum age limit for Bacon runs, default at current year in cal BP. To set plot limits, use age.min instead.
oldest.age	Maximum age limit for Bacon runs, default at 1,000,000 cal BP. To set plot limits, use age.max instead.
MinAge	Deprecated - use youngest.age instead.
MaxAge	Deprecated - use oldest.age instead.
cutoff	Avoid plotting very low probabilities of date distributions (default cutoff=0.001).
plot.pdf	Produce a pdf file of the age-depth plot. Defaults to plot.pdf=TRUE after a Bacon run.

quartz	Use quartz-based pdf plots if available (on Mac OS). Defaults to FALSE.
cairo	Use cairo-based pdf plots if available (on Mac OS). Defaults to FALSE.
dark	Darkness of the greyscale age-depth model. The darkest grey value is dark=1 by default. Lower values will result in lighter grey but values >1 are not allowed.
date.res	Date distributions are plotted using date.res=100 segments by default.
age.res	Resolution or amount of greyscale pixels to cover the age scale of the age-model plot. Default yr.res=200.
yr.res	Deprecated - use age.res instead
close.connections	Internal option to close connections after a run. Default close.connections=TRUE.
save.info	By default, a variable called 'info' with relevant information about the run (e.g., core name, priors, settings, ages, output) is saved into the working directory. Note that this will overwrite any existing variable with the same name - as an alternative, one could run, e.g., myvar <- Bacon(), followed by supplying the variable myvar in any subsequent commands.
older.than	an option to enable dates at the limit of C-14 dating. If there are older.than dates, they tell us that the core should be older than a certain age at that depth. For example, if the 7th and 8th dates in the core's .csv file are older-than dates, use as older.than=c(7,8). The MCMC run could be problematic if the older-than ages do not fit with the other information. If so, then use the 'set.initvals()' function to manually provide initial ballpark values for the age-depth model, at the older end.
younger.than	an option to provide younger-than ages, for example a historical pollen marker. If there are younger-than dates, they tell us that the core should be younger than a certain age at that depth. For example, if the 7th and 8th dates in the core's .csv file are younger.than dates, use as younger.than=c(7,8). The MCMC run could be problematic if the younger.than ages do not fit with the other information. If so, then use the 'set.initvals()' function to manually provide initial ballpark values for the age-depth model, at the younger end.
save.elbowages	If you want to have a file with the MCMC-derived ages for all the age-depth model's elbows, set save.elbowages=TRUE and a file with the ages will be saved in the core's folder, starting with the core name, followed by its number of sections, d.min, and section thickness, and ending in "_elbowages.txt".
verbose	Provide feedback on what is happening (default verbose=TRUE).
use.cpp	Whether or not to use a cpp function to calculate the ages. Defaults to TRUE, but can be set to FALSE (much slower but less experimental)
...	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.mean, hiatus.shape`).

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 IntCal20 (for terrestrial northern hemisphere material; Reimer et al., 2020), Marine20 (for marine dates; Hughen et al., 2020), SHCal20 (for southern hemisphere dates; Hogg et al., 2020) 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., 2022). 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, set`cc=0`.

Since version 3.1.0, rbacon can also handle younger-than and older-than ages, with the model aiming to either go 'above' or 'below' such dates as requested. If the resulting combination of parameters becomes problematic (e.g., no initial combination of parameters can be found that obeys the priors or is in chronological order), then the output will often be wrong. If so, using the function set.initvals could help.

By default, the initial MCMC values of the Bacon age-depth model (upper ages and accumulation rate for each model section) are estimated randomly. Since version 3.1.0, these starting values can also be provided in a file with extension _bacon.init, placed within the core's folder. This file will need to have two rows, each for one of the two initial sets of parameters required (the t-walk requires two starting estimates for all MCMC parameters). If such a file is found (and correctly formatted), Bacon will use the values within this file as starting points for the MCMC run. See function set.initvals for more information.

From version 2.5.1 on (i.e., since February 2021), the default memory prior has changed to `mem.mean=0.5` and `mem.strength=10`. Previously used c++ code contained a bug which caused the prior information for the memory not to be taken into account correctly. Now that this bug has been repaired, the default memory prior has been updated such that it should work for most types of cores, and should result in similar output to previous versions of Bacon. There is no need to re-do previous runs. However, it is considered good practice to test the impact of different settings on a site's age-depth model (e.g., thick, acc.mean, acc.shape, mem.mean, acc.strength).

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., 2011. Flexible paleoclimate age-depth models using an autoregressive gamma process. Bayesian Anal. 6(3): 457-474.

Christen, J.A., Perez E., S., 2010. A new robust statistical model for radiocarbon data. Radiocarbon 51: 1047-1059.

Reimer et al., 2020. The IntCal20 Northern Hemisphere radiocarbon age calibration curve (0–55 cal kBP). Radiocarbon 62(4): 725-757. doi:10.1017/RDC.2020.41

Hogg et al. 2020 SHCal20 Southern Hemisphere calibration, 0-55,000 years cal BP. Radiocarbon 62(4): 759-778. doi:10.1017/RDC.2020.59

Hughen et al. 2020 Marine20-the marine radiocarbon age calibration curve (0-55,000 cal BP). Radiocarbon 62(4): 779-820. doi:10.1017/RDC.2020.68

Hua et al. 2022 Atmospheric radiocarbon for the period 1950-2019. Radiocarbon 64(4), 723-745, doi:10.1017/RDC.2021.95

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.

Examples

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

`Bacon.Age.d` *output all ages for a single depth*

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,
  na.rm = 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.
na.rm	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. See also Bacon.d.Age which calculates the depths of a single age estimate.

Value

Outputs all MCMC-derived ages for a given depth.

Author(s)

Maarten Blaauw, J. Andres Christen

Examples

```
## Not run:
  Bacon(run=FALSE, coredir=tempfile())
  agedepth(age.res=50, d.res=50, d.by=10)
  ages.d20 = Bacon.Age.d(20)
  mean(ages.d20)

## End(Not run)
```

Bacon.cleanup *remove files made to produce the current core's age-depth model*

Description

Remove files ending in .bacon, .plum (if it exists), .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, *.plum, *.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

Examples

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

Bacon.d.Age *output all depths for a single age*

Description

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

Usage

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

Arguments

age	The age estimate for which depths are to be returned. Has to be a single age.
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.
its	The set of MCMC iterations to be used. Defaults to the entire MCMC output, its=set$output.
na.rm	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.d.Age can be used to list all MCMC-derived depths belonging to a given (single) age, for example to calculate mean depths belonging to a modelled depth. This function was kindly written and provided by Timon Netzel (Bonn University). See also Bacon.Age.d, which calculates the ages for a single depth.

Value

Outputs all MCMC-derived depths for a given age.

Author(s)

Maarten Blaauw, J. Andres Christen

Examples

```
## Not run:
  Bacon(run=FALSE, coredir=tempfile())
  agedepth(age.res=50, d.res=50, d.by=10)
  ages.d20 = Bacon.Age.d(20)
  mean(ages.d20)

## End(Not run)
```

Bacon.hist *calculate age distributions of depths*

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",
  verbose = TRUE,
  progress = TRUE,
  save.info = set$save.info
)
```

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".
verbose	Provide feedback on what is happening (default verbose=TRUE).
progress	Show a progress bar (default progress=TRUE).
save.info	A variable called 'info' with relevant information about the run (e.g., core name, priors, settings, ages, output) can be saved into the working directory. Note that this will overwrite any existing variable with the same name - as an alternative, one could run, e.g., myvar <- Bacon(), followed by supplying the variable myvar in any subsequent commands.

Details

Age estimates of specific depths can also be plotted.

Value

A variable called 'hists', and 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

Examples

```
## Not run:
  Bacon(run=FALSE, coredir=tempfile())
  agedepth(age.res=50, d.res=50, d.by=10)
  Bacon.hist(20)
  Bacon.hist(20:30)

## End(Not run)
```

---

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

Examples

```
{

 tmpfl <- tempfile()
  Bacon(run=FALSE, ask=FALSE, coredir=tmpfl)
  bacon2clam("MSB2K", bacondir=tmpfl, clamdir=tmpfl)

}
```

`Baconvergence` *test to identify poorly mixed MCMC runs*

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, verbose = TRUE, ...)
```

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.
`verbose`	Provide feedback on what is happening (default `verbose=TRUE`).
`...`	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

Brooks, SP. and Gelman, A. (1998) General methods for monitoring convergence of iterative simulations. _Journal of Computational and Graphical Statistics_, *7*, 434-455.

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(set = get("info"), coredir = set$coredir)
```

Arguments

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

`calib.plot` *Plot the dates*

Description

Produce a plot of the dated depths and their dates

Usage

```
calib.plot(
  set = get("info"),
  dets = set$dets,
  accordion = c(),
  BCAD = set$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 = 1,
  calheight = 1,
  ex = 1,
  mirror = TRUE,
  up = TRUE,
  cutoff = 0.1,
  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
)
```

Arguments

`set`	Detailed information of the current run, stored within this session's memory as variable `info`.
`dets`	The set of determinations to be plotted.

accordion	If depths have to be squeezed/stretched, the parameters can be set here. Defaults to being empty, but requires 2 parameters if active, e.g., accordion=c(10,20).
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$cc)
rotate.axes	The default of plotting age on the horizontal axis and event probability on the vertical one can be changed with rotate.axes=TRUE.
rev.d	The direction of the depth axis can be reversed from the default (rev.d=TRUE).
rev.age	The direction of the calendar age axis can be reversed from the default (rev.age=TRUE)
rev.yr	Deprecated - use rev.age instead
age.lim	Minimum and maximum calendar age ranges, calculated automatically by default (age.lim=c()).
yr.lim	Deprecated - use age.lim instead
date.res	Date distributions are plotted using date.res=100 points by default.
d.lab	The labels for the depth axis. Default d.lab="Depth (cm)".
age.lab	The labels for the calendar axis (default yr.lab="cal BP" or "BC/AD" if BCAD=TRUE).
yr.lab	Deprecated - use age.lab instead
height	The heights of the distributions of the dates. See also normalise.dists.
calheight	Multiplier for the heights of the distributions of dates on the calendar scale. Defaults to calheight=1.
ex	Alternative for providing heights of the dates' distributions. Defaults to 1 for all dates, but could also provide individual ex values for each date, e.g., ex=rep(1, nrow(set$dets)); ex[1:4] <- 2
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=0.1).
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), which instead normalises the distributions (all have an area of 1).

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

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 IntCal20 (northern hemisphere terrestrial), `cc=2` for Marine20 (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

---

draw.pbmeasured *plot the 210Pb data*

Description

Produce a plot of the 210Pb data and their depths

Usage

```
draw.pbmeasured(
  set = get("info"),
  rotate.axes = FALSE,
  rev.d = FALSE,
  rev.age = FALSE,
  BCAD = set$BCAD,
  pb.lim = c(),
  age.lim = c(),
  d.lim = c(),
  d.lab = c(),
  pb.lab = c(),
  pbmeasured.col = "blue",
  pbmeasured.lty = 2,
  pb.log = FALSE,
  supp.col = "purple",
  newplot = TRUE,
  on.agescale = FALSE
)
```

Arguments

set	Detailed information of the current run, stored within this session's memory as variable info.
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)
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.
pb.lim	Minimum and maximum of the 210Pb axis ranges, calculated automatically by default (pb.lim=c()).
age.lim	Minimum and maximum of the age ranges to be used to plot 210Pb values. Calculated automatically by default (age.lim=c()).
d.lim	Minimum and maximum depths to plot; calculated automatically by default (d.lim=c()).
d.lab	The labels for the depth axis. Default d.lab="Depth (cm)".
pb.lab	The label for the 210Pb axis (default pb.lab="210Pb (Bq/kg)" or "210Pb (dpm/g)").
pbmeasured.col	The label for the measured 210Pb data. pbmeasured.col="blue".
pbmeasured.lty	Line type of the measured 210Pb data. Defaults to continuous lines.
pb.log	Use a log scale for the 210Pb-axis (default pb.log=FALSE).
supp.col	Colour of the supported 210Pb data. Defaults to red: supp.col="red".
newplot	make new plot (default TRUE)
on.agescale	Plot the Pb-210 on the cal BP scale. Defaults to FALSE.

Details

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

Value

A plot of the measured 210Pb values

Author(s)

Maarten Blaauw, J. Andres Christen, Marco Aquino-Lopez

---

draw.pbmodelled *plot the 210Pb data*

Description

Produce a plot of the 210Pb data and their depths

Usage

```
draw.pbmodelled(
  set = get("info"),
  BCAD = set$BCAD,
  rotate.axes = FALSE,
  rev.d = FALSE,
  rev.age = FALSE,
  pb.lim = c(),
  d.lim = c(),
  d.lab = c(),
  pb.lab = c(),
  pbmodelled.col = function(x) rgb(0, 0, 1, x),
  pbmeasured.col = "blue",
  supp.col = "purple",
  plot.measured = TRUE,
  age.lim = c(),
  mgp = mgp,
  pb.lty = 1,
  save.info = 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.
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)
pb.lim	Minimum and maximum of the 210Pb axis ranges, calculated automatically by default (pb.lim=c()).
d.lim	Minimum and maximum depths to plot; calculated automatically by default (d.lim=c()).
d.lab	The labels for the depth axis. Default d.lab="Depth (cm)".
pb.lab	The label for the 210Pb axis (default pb.lab="210Pb (Bq/kg)" or "210Pb (dpm/g)").
pbmodelled.col	Colour of the modelled 210Pb values. Defaults to scales of blue: pbmodelled.col=function(x) rgb(0,0,1,x).
pbmeasured.col	Colour of the measured 210Pb values. Defaults to blue.
supp.col	Colour of the supported 210Pb data. Defaults to red: supp.col="red".
plot.measured	Plot the measured 210Pb values (default plot.measured=TRUE).
age.lim	values of the age axis. Used to calculate where to plot the pb values on the secondary axis

mgp	Axis text margins (where should titles, labels and tick marks be plotted). Defaults to mgp=c(1.7, .7, .0).
pb.lty	Line type of measured Pb-210 data.
save.info	By default, a variable called 'info' with relevant information about the run (e.g., core name, priors, settings, ages, output) is saved into the working directory. Note that this will overwrite any existing variable with the same name.

Details

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

Value

A plot of the modelled (and optionally the measured) 210Pb values

Author(s)

Maarten Blaauw, J. Andres Christen, Marco Aquino-Lopez

---

flux.age.ghost *plot flux rates for proxies*

Description

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

Usage

```
flux.age.ghost(
  column = 1,
  flux = c(),
  set = get("info"),
  coredir = set$coredir,
  remove.hiatuses = TRUE,
  age.lab = c(),
  age.lim = c(),
  age.rev = FALSE,
  age.res = 500,
  age.compress = -0.01,
  flux.lim = c(),
  flux.rev = FALSE,
  flux.lab = "flux (proxy/yr)",
  flux.res = 500,
  BCAD = set$BCAD,
  prob = 0.95,
  clip.prob = 0.99,
```

```
  plot.range = TRUE,
  range.col = grey(0.5),
  range.lty = 2,
  plot.mean = TRUE,
  mean.col = "red",
  mean.lty = 2,
  plot.median = TRUE,
  median.col = "blue",
  median.lty = 2,
  flux.cols = col.scales(256, "white", "black", darkest = darkest),
  dark = 0.9,
  darkest = 1,
  rotate.axes = FALSE,
  use.raster = FALSE,
  xaxs = "i",
  yaxs = "i",
  bty = "l"
)
```

Arguments

column	Which proxy to use (counting from the column number in the .csv file after the depths column).
flux	Instead of using a file, the data can also be provided as a variable. The first column should be the depths, and the variable 'column' should indicate which column (after the depth column) contains the proxy of interest. For example, if using Plum we could produce a greyscale of the mass accumulation rate: myflux <- info$detsPlum[,c(4,6)];
set	Detailed information of the current run, stored within this session's memory as variable info.
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:.
remove.hiatuses	Hiatuses will affect apparent accumulation rates within sections. Therefore, by default the hiatus jumps will be removed from the accumulation rates within sections containing hiatuses.
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()).
age.rev	The direction of the age axis can be reversed using age.rev=TRUE.
age.res	Resolution or amount of greyscale pixels to cover the age scale of the plot. Default age.res=500.

age.compress	Since the bottom and top edges of age-models often show weird flux behaviour, the top and bottom half are shaved off by default (1%, age.compress=-0.01).
flux.lim	Limits of the flux axes.
flux.rev	The flux axis can be reversed with flux.rev=TRUE.
flux.lab	Axis labels. Defaults to flux.lab="flux".
flux.res	Resolution or amount of greyscale pixels to cover the flux scale of the plot. Default flux.res=500.
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.
prob	Probability for the flux ranges; defaults to prob=0.95.
clip.prob	Since some iterations show very high flux values, it is useful to clip the top values. Defaults to clip.prob=0.975.
plot.range	Plot curves that indicate a probability range.
range.col	Grey seems nice (default range.col=grey(0.5)).
range.lty	Line type of the flux ranges. Defaults to dashed, range.lty=2.
plot.mean	Plot the mean fluxes. Default TRUE.
mean.col	Red seems nice.
mean.lty	Line type of the means. Defaults to dashed, range.lty=2.
plot.median	Plot the median fluxes. Default TRUE
median.col	Blue seems nice.
median.lty	Line type of the medians. Defaults to dashed, range.lty=2.
flux.cols	Colour of the flux ghost graph. Defaults to greyscales, flux.cols=gray.colors(256, start=darkest, end=0).
dark	Any (normalised) flux value above this threshold is set to the threshold; default is dark=0.9.
darkest	The darkest value. Set to 1 for the darkest colour to be black if using a greyscale.
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.
use.raster	Rasters can be aligned or not in the underlying image function. By default, we use use.raster=FALSE. This takes a bit longer to draw and sometimes causes strange lines owing to anti-aliasing.
xaxs	Limits of the horizontal axis. By default does not extend, xaxs="i".
yaxs	Limits of the vertical axis. By default does not extend, yaxs="i".
bty	Type of box to plot around the graph. Defaults to L-shaped, bty="l".

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, and the underlying greyscales, means, medians and ranges (invisibly).

Author(s)

Maarten Blaauw, J. Andres Christen

Examples

```
## Not run:
  Bacon(run=FALSE, coredir=tempfile())
  agedepth(yr.res=50)
  flux.age.ghost(1)

## End(Not run)
```

MCMC.diagnostics *test mixing and stationarity of the MCMC run*

Description

Test how well-mixed and stationary the MCMC run is. A good value for the effective sample size ('ess', number of effective independent samples from the MCMC iterations) is >200 (>1000 indicates an excelling mixing). Besides the mixing, stationarity 'z' is also measured (the start of the run is compared with the end). A 'z' below 1.96 (1 standard deviation) indicates no drift, and if it is >2.58 (2 standard deviations) then the MCMC chain is likely drifting.

Usage

```
MCMC.diagnostics(set = get("info"), ssize = nrow(set$output), talk = TRUE)
```

Arguments

set	Detailed information of the current run, stored within this session's memory as variable info.
ssize	Number of MCMC iterations.
talk	Whether or not to provide feedback. Defaults to TRUE.

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 (ess, and also visually check that the upper left panel of the fit of the iterations shows no strange features such as sudden systematic drops or rises).

Value

The 'ess' and 'z' scores, together with an evaluation of the values.

Examples

```
Bacon(ssize=100, coredir=tempfile()) # check the reported warnings
```

---

proxy.ghost *greyscale plot of a proxy against time*

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 = NULL,
  proxy.res = 200,
  age.res = 500,
  yr.res = age.res,
  zero.col = "white",
  max.col = "black",
  rgb.scale = c(0, 0, 0),
  rgb.res = 100,
  set = get("info"),
  cutoff = 0.001,
  dark = 1,
  darkest = 1,
  rotate.axes = FALSE,
  rev.proxy = FALSE,
  rev.age = FALSE,
  yr.rev = rev.age,
  plot.mean = FALSE,
  mean.col = "red",
  plot.median = FALSE,
  median.col = "blue",
  age.lim = NULL,
  yr.lim = age.lim,
  proxy.lim = NULL,
  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,
  verbose = TRUE,
  add = FALSE,
  use.cpp = TRUE
)
```

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
zero.col	The colour where the ghost is 0. Defaults to zero.col="white", which together with max.col="black" results in a greyscale. More creative colour gradients can be implemented by checking the 600+ colours in colours().
max.col	The colour where the ghost is at its maximum. Defaults to max.col="black", which together with zero.col="white" results in a greyscale. More creative colour gradients can be implemented by checking the 600+ colours in colours().
rgb.scale	The function to produce a coloured representation of all age-models. Needs 3 values for the intensity of red, green and blue. Defaults to grey-scales: rgb.scale=c(0,0,0), but could also be, say, scales of red (rgb.scale=c(1,0,0)).
rgb.res	Resolution of the colour spectrum depicting the age-depth model. Default rgb.res=100.
set	Detailed information of the current run, stored within this session's memory as variable info.
cutoff	Point below which colours will no longer be printed. Default cutoff=0.001.
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).
rev.proxy	The proxy axis can be reversed if rev.proxy=TRUE.
rev.age	The calendar axis can be reversed using rev.age=TRUE.

yr.rev	Deprecated - use rev.age 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. Defaults to red.
plot.median	The median ages of the proxy values can be added using plot.median=TRUE.
median.col	Colour of the weighted mean ages of the proxy values. Defaults to blue.
age.lim	Minimum and maximum calendar age ranges, calculated automatically by default (yr.lim=NULL).
yr.lim	Deprecated - use age.lim instead
proxy.lim	Ranges of the proxy axis, calculated automatically by default (proxy.lim=NULL).
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 "l" (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
verbose	Provide feedback on what is happening (default verbose=TRUE).
add	Add to an existing graph (default add=FALSE).
use.cpp	To speed things up, optionally a c++ function can be used to calculate the histograms behind the ghostplot. Defaults to use.cpp=TRUE.

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

Examples

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

`scissors` *remove the first n iterations*

Description

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

Usage

```
scissors(burnin, set = get("info"), write = TRUE, save.info = set$save.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`.
`write`	Whether or not to write the changes to the output file. Defaults to TRUE.
`save.info`	By default, a variable called 'info' with relevant information about the run (e.g., core name, priors, settings, ages, output) is saved into the working directory. Note that this will overwrite any existing variable with the same name - as an alternative, one could run, e.g., `myvar <- Bacon()`, followed by supplying the variable `myvar` in any subsequent commands.

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

Examples

```
Bacon(ask=FALSE, coredir=tempfile())
nrow(info$output)
scissors(100)
nrow(info$output)
```

---

set.initvals *set initial values for the Bacon MCMC run*

Description

Select initial values th0 and th1 for a Bacon MCMC run and write them into a file that can be read by Bacon.

Usage

```
set.initvals(set = get("info"), core = set$core, values = c(), click = 1)
```

Arguments

set	Detailed information of the current run, stored within this session's memory as variable info.
core	The name of the core for which a bacon.init file needs to be made
values	use this if you wish to provide the values (2 rows with starting age, accumulation rates for each model section, and memory parameter w).
click	use this if you wish to use the cursor to manually select age-depth points from the current graphic device. This is the default option. Right click once you have selected all datapoints, or provide the number of expected datapoints as a value (e.g., click=5).

Details

By default, the initial MCMC values th0 and th1 of the Bacon age-depth model (upper ages and accumulation rate for each model section) are estimated randomly. Since version 3.1.0, these starting values can also be provided in a file with extension _bacon.init, placed within the core's folder. This file will need to have two rows, each for one of the two initial sets of parameters required (the t-walk requires two starting estimates for all MCMC parameters). If such a file is found (and correctly formatted), Bacon will use the values within this file as starting points for the MCMC run.

Value

A .bacon.init file

Author(s)

Maarten Blaauw, J. Andres Christen

`squeeze` *squeeze some depths of a core*

Description

Squeeze or compress depths below a boundary by a certain amount. Accompanies the stretch function; see the stretch function for code on running the accordion

Usage

```
squeeze(d, boundary, times)
```

Arguments

`d`	The depth(s) to be squeezed
`boundary`	The depth below which depths should be squeezed
`times`	The factor by which the depths should be squeezed

Value

The squeezed depth(s)

Author(s)

Maarten Blaauw

Examples

```
squeeze(40,25,20)
```

`stretch` *stretch some depths of a core*

Description

Stretch squeezed depths e.g., calculate the original depths of depths that were squeezed. Accompanies the squeeze function.

Usage

```
stretch(d, boundary, times)
```

Arguments

d	The depth(s) to be stretched
boundary	The depth below which depths should be stretched
times	The factor by which the depths should be stretched

Value

The stretched depth(s)

Author(s)

Maarten Blaauw

Examples

```
  stretch(25.75,25,20)
## Not run:
  # To play the accordion, first squeeze an existing core.
  # Let's squeeze the depths below 10 cm core depth 20 times:
  Bacon("accordion", 1)
  dets <- info$dets
  dets[,4] <- squeeze(dets[,4], 10, 20)

  # make a new directory for the squeezed core, and place the dets file there:
  dir.create("Bacon_runs/squeezed")
  write.table(dets, "Bacon_runs/squeezed/squeezed.csv", row.names=FALSE, sep=",")

 # now run that squeezed core, adding a boundary (10cm) and adapting the acc.mean prior (20x):
  Bacon("squeezed", 1, boundary=10, acc.mean=c(5, 20*5))
  # finally, plot while stretching the depths onto the original scale:
  agedepth(accordion=c(10,20))

## End(Not run)
```

---

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"),
  write = TRUE,
  save.info = set$save.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`.
`write`	Whether or not to write the changes to the output file. Defaults to TRUE.
`save.info`	By default, a variable called 'info' with relevant information about the run (e.g., core name, priors, settings, ages, output) is saved into the working directory. Note that this will overwrite any existing variable with the same name - as an alternative, one could run, e.g., `myvar <- Bacon()`, followed by supplying the variable `myvar` in any subsequent commands.

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

Examples

```
Bacon(ask=FALSE, coredir=tempfile())
nrow(info$output)
thinner(.2)
nrow(info$output)
```

`tofu` *Bacon for vegans*

Description

Bacon for vegans

Usage

```
tofu(...)
```

Arguments

`...`	options for the Bacon command. See Bacon

Details

A vegan wrapper for Bacon - does everything Bacon does, but without the meat.

Value

A tofu age-model

Index

A.modelled, 3
accrate.age, 4
accrate.age.ghost, 5
accrate.age.summary, 8
accrate.depth, 10
accrate.depth.ghost, 11
accrate.depth.summary, 14
accrates.core, 15
add.dates, 17
agedepth, 19, *42*
agemodel.it, 30
ageranges, 31
AgesOfEvents, 33

background, 35
Bacon, 35, *69*
Bacon.Age.d, 44
Bacon.cleanup, 45
Bacon.d.Age, 46
Bacon.hist, 47
bacon2clam, 49
Bacon_runs, 51
Baconvergence, 50

calib.plot, *42*, 52
clam2bacon, 54

draw.pbmeasured, 55
draw.pbmodelled, 56

flux.age.ghost, 58

MCMC.diagnostics, 61

proxy.ghost, 62

scissors, *30*, 65
set.initvals, *43*, 66
squeeze, 67
stretch, 67

thinner, *30*, 68
tofu, 69