Package ‘rbacon’

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**Type** Package

**Title** Age-Depth Modelling using Bayesian Statistics

**Version** 3.2.0

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**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

**Repository** CRAN

**License** GPL (>= 2)

**NeedsCompilation** yes

**Imports** coda (>= 0.19-1), graphics, grDevices, Rcpp (>= 0.12.12), stats, utils, data.table

**Depends** rintcal (>= 0.6.4), R (>= 3.5.0)

**LinkingTo** Rcpp

**RoxygenNote** 7.2.3

**Suggests** knitr, rmarkdown, utf8

**VignetteBuilder** knitr

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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, so 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

```r
## 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**

**Description**

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

**Usage**

```r
accrate.age.ghost(
  set = get("info"),
  age.lim = c(),
  age.lab = c(),
  kcal = FALSE,
  age.res = 400,
  acc.res = 200,
  cutoff = 0.001,
  dark = 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,
  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). |
| **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 acc.res=400. |
| **cutoff** | Point below which colours will no longer be printed. Default cutoff=0.001. |
| **dark** | The darkest grey value is dark=1 by default; lower values will result in lighter grey but 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.median=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. |
| **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 "1" (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 grey-scale reconstruction around the oldest ages of any reconstruction often indicates very low accumulation rates. This is due to only some MCMC iterations reaching those old ages, and these iterations will have modelled very slow accumulation rates. Currently does not deal well with hiatuses, so do not interpret accumulation rates close to depths with inferred hiatuses.

Value

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

Author(s)

Maarten Blaauw, J. Andres Christen

Examples

```r
## 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)
```

<table>
<thead>
<tr>
<th>accrate.depth</th>
</tr>
</thead>
<tbody>
<tr>
<td>Obtain estimated accumulation rates as for any depth of a core.</td>
</tr>
</tbody>
</table>

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

```r
accrate.depth(d, set = get("info"), cmyr = FALSE, na.rm = FALSE)
```
Arguments

- **d**
  - The depth for which accumulation rates need to be returned.

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

- **cmyr**
  - Accumulation rates can be calculated in cm/year or year/cm. By default cmyr=FALSE and accumulation rates are calculated in year per cm.

- **na.rm**
  - Remove NA entries. These are NOT removed by default, so that always the same amount of iterations is returned.

Details

should take into account hiatuses

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

Value

all MCMC estimates of accumulation rate of the chosen depth.

Author(s)

Maarten Blaauw, J. Andres Christen

Examples

```r
## 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

```r
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,
  cutoff = 0.001,
  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
)
```

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 darkest grey value is dark=1 by default; lower values will result in lighter
grey but values >1 are not advised.
cutoff
Point below which colours will no longer be printed. Default cutoff=0.001.
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.

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, how-
ever upper limits can be very variable (and thus hard to predict) if calculated in cm/yr; there-
fore 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.
add.dates

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

```r
## 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)
```

Description

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

Usage

```r
add.dates(
  mn,
  sdev,
  depth,
  cc = 1,
  set = get("info"),
  above = 1e-06,
  postbomb = 0,
  normal = TRUE,
  delta.R = set$delta.R,
  delta.STD = set$delta.STD,
  t.a = set$t.a,
  t.b = set$t.b,
  date.res = 100,
  height = 0.1,
  calheight = 1,
  agesteps = 1,
  cutoff = 0.005,
  col = rgb(1, 0, 0, 0.5),
)```

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).

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

**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.

**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,.5).

rotate.axes
The default of plotting age on the horizontal axis and event probability on the vertical one can be changed with rotate.axes=TRUE.

mirror
Plot the dates as 'blobs’. Set to mirror=FALSE to plot simple distributions.

up
Directions of distributions if they are plotted non-mirrored. Default up=TRUE.

BCAD
The calendar scale of graphs is in cal BP by default, but can be changed to BC/AD using BCAD=TRUE.

pch
The shape of any marker to be added to the date. Defaults to a cross, pch=4. To leave empty, use pch=NA.

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 rintcal’s draw.dates function.

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

Author(s)
Maarten Blaauw, J. Andres Christen

Examples

Bacon(run=FALSE, coredir=tempfile())
agedepth()
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(),
    d.min = c(),
    d.max = c(),
    d.by = c(),
    depths = set$depths,
    depths.file = FALSE,
    accordion = c(),
    plotatthesedepths = c(),
    age.min = c(),
    yr.min = age.min,
    age.max = c(),
    yr.max = age.max,
    hiatus.option = 1,
    dark = c(),
    prob = set$prob,
    rounded = c(),
    d.res = 400,
    age.res = 400,
    yr.res = age.res,
    date.res = 100,
    rotate.axes = FALSE,
    rev.age = FALSE,
    rev.yr = rev.age,
    rev.d = FALSE,
    maxcalc = 500,
    height = 1,
    calheight = 1,
    mirror = TRUE,
    up = TRUE,
    cutoff = 0.1,
    plot.range = TRUE,
    range.col = grey(0.5),
    range.lty = "12",
    mn.col = "red",
    mn.lty = "12",
    med.col = NA,
    med.lty = "12",
)
C14.col = rgb(0, 0, 1, 0.35),
C14.border = rgb(0, 0, 1, 0.5),
cal.col = rgb(0, 0.5, 0.5, 0.35),
cal.border = rgb(0, 0.5, 0.5, 0.5),
dates.col = c(),
pb.background = 0.5,
pbmodelled.col = function(x) rgb(0, 0, 1, 0.5 * x),
pbmeasured.col = "blue",
pb.lim = c(),
supp.col = "purple",
plot.tail = TRUE,
remove.tail = TRUE,
MCMC.resample = TRUE,
hiatus.col = grey(0.5),
hiatus.lty = "12",
rgb.scale = c(0, 0, 0),
rgb.res = 100,
slump.col = grey(0.8),
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 = "1",
mar.left = c(3, 3, 1, 0.5),
mar.middle = c(3, 0, 1, 0.5),
mar.right = c(3, 0, 1, 0.5),
mar.main = c(3, 3, 1, 1),
righthand = 3,
mgp = c(1.7, 0.7, 0),
xaxs = "r",
yaxs = "i",
prior.ticks = "n",
prior.fontsize = 0.9,
toppanel.fontsize = 0.9,
mainpanel.tickfontsize = 1,
mainpanel.labelfontsize = 1,
acc.xlim = c(),
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).

**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.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  Darkness of the greyscale age-depth model. By default, the darkest grey value is calculated as 10 times the height of the lowest-precision age estimate dark=c(). Lower values will result in lighter grey but values >1 are not allowed.

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.

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.
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 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.

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.

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.

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 be 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 (pb.lim=c()).

supp.col
Colour of supported Pb-210. Defaults to purple, because why not.

plot.tail
The depth axis can extend to all Pb measurements (plot.tail=TRUE), or leave out the ones where background has been reached.

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. Quite similar to plot.tail.
**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.

**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.

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

**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 "1" (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). Default 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). Default 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). Default 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). Default 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, .7, .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.

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.labelfontsize=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.

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.

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

**Arguments**

- **it**
  - The MCMC iteration of which the age-model should be calculated.

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

- **BCAD**
  - The calendar scale of graphs and age output-files is in cal BP by default, but can be changed to BC/AD using BCAD=TRUE.

**Value**

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

**Author(s)**

Maarten Blaauw, J. Andres Christen

**Examples**

```r
## 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)
```

---

**AgesOfEvents**

*Event probabilities against calendar age*

**Description**

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

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


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**

```r
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**

```r
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.max = 10000,
add = c(),
after = 1e-04/thick,
cc = 1,
cc1 = "IntCal20",
cc2 = "Marine20",
cc3 = "SHCal20",
cc4 = "ConstCal",
cc.dir = c(),
postbomb = 0,
delta.R = 0,
delta.STD = 0,
t.a = 3,
t.b = 4,
normal = FALSE,
suggest = TRUE,
accept.suggestions = FALSE,
reswarn = c(10, 200),
remember = TRUE,
ask = TRUE,
run = TRUE,
defaults = "defaultBacon_settings.txt",
sep = ",",
dec = ".",
runname = "",
slump = c(),
remove = FALSE,
BCAD = FALSE,
ssize = 4000,
theta = c(),
burnin = min(500, ssize),
youngest.age = c(),
oldest.age = c(),
MinAge = c(),
MaxAge = c(),
cutoff = 0.01,
plot.pdf = TRUE,
Bacon

dark = 1,
date.res = 100,
age.res = 200,
yr.res = age.res,
close.connections = TRUE,
older.than = c(),
younger.than = c(),
save.elbowages = FALSE,
verbose = 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 \( d_{\text{min}} \) to \( d_{\text{max}} \) in steps of \( d_{\text{by}} \). 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 \( d_{\text{min}} \) to \( d_{\text{max}} \) in steps of \( d_{\text{by}} \). 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 having more than one boundary per model section (see 'thick') might not work either.

hiatus.depths  The assumed depths for any hiatus should be provided as, e.g., hiatus.depths=20 for one at 20cm depth, and hiatus.depths=c(20,40) for two hiatuses at 20 and 40 cm depth.
hiatus.max  The prior for the maximum length of the hiatus. Hiatus length is a uniform
distribution, with equal probabilities between 0 and hiatus.max yr (or whatever
other age unit is chosen).

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 com-
plains 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.

calibration curve for C-14 dates: cc=1 for IntCal20 (northern hemisphere ter-
residual), 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  Use an alternative curve (3 columns: cal BP, 14C age, error, separated by white
spaces and saved as a plain-text file). See cc.dir.

c.c.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 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

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 Chris-
ten 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. 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=",".

dec
Character for decimal points. Default to dec="."

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.
Bacon

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.
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.
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.
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.
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).
...
Options for the age-depth graph. See agedepth and calib.plot

Details

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

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

Although Bacon works with any kind of absolute dates (e.g., OSL, tephra or other dates on a calendar scale), it is often used to age-model 14C-dated sequences. Radiocarbon dates should be
calibrated using either 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., 2013). See http://calib.org/CALIBomb/ if you are unsure which postbomb curve you need. If Bacon finds postbomb dates (negative 14C ages) and you haven’t specified a postbomb curve, you will be prompted. Provide postbomb curves as, e.g., postbomb=1 for the NH1 postbomb curve (2 for NH2, 3 for NH3, 4 for SH1-2, 5 for SH3). For calendar dates, i.e. dates that are already on the calendar scale and thus should not be calibrated, set cc=0.

Since version 3.1.0, Bacon 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
Bacon.Age.d


Examples

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

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

```r
## 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.
## Bacon.d.Age

**Author(s)**
Maarten Blaauw, J. Andres Christen

**Examples**

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

**Description**

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

**Usage**

```r
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

```r
## 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

```r
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
)
```

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

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.

The labels for the calendar axis (default age.lab="cal BP" or "BC/AD" if BCAD=TRUE).

Minimum and maximum calendar age ranges, calculated automatically by default (age.lim=c()).

The y-axis is labelled ylab="Frequency" by default.

Calculate ranges? Takes time so can be left out

Limits of the y-axis.

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).

Age ranges are given as quantiles, e.g., 2.5% and 97.5% for the default of 95% confidence limits (prob=0.95)).

Colour of the histogram. Default grey, hist.col=grey(0.5).

Colour of the histogram’s outline. Default dark grey, hist.border=grey(0.2).

Colour of confidence ranges. Defaults to range.col="blue".

Colour of the median. Defaults to med.col="green".

Colour of the mean. Defaults to mn.col="red".

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

Age estimates of specific depths can also be plotted.

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.

Maarten Blaauw, J. Andres Christen

## 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)
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

Examples

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

---

**calib.plot**

*Plot the dates*

---

**Description**

Produce a plot of the dated depths and their dates

**Usage**

```r
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,
  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.

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).
clam2bacon

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**

```r
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
)

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). De-faults to mgp=c(1.7,.7,.0).
pb.lty     Line type of measured Pb-210 data.
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(
  proxy = 1,
  age.lim = c(),
  yr.lim = age.lim,
  age.res = 200,
  yr.res = age.res,
  set = get("info"),
  flux = c(),
  plot.range = TRUE,
  prob = 0.8,
  range.col = grey(0.5),
  range.lty = 2,
  plot.mean = TRUE,
  mean.col = "red",
  mean.lty = 2,
  plot.median = TRUE,
  median.col = "blue",
  median.lty = 2,
  flux.lim = c(),
  flux.lab = expression("flux (g cm^{-1} * " yr^{-1} * ")",
  upper = 0.95,
  rgb.scale = c(0, 0, 0),
  rgb.res = 100,
  dark = set$dark,
  cutoff = 0.001,
  BCAD = set$BCAD,
Arguments

proxy Which proxy to use (counting from the column number in the .csv file after the depths column).

age.lim Minimum and maximum calendar age ranges, calculated automatically by default (age.lim=c()).

yr.lim Deprecated - use age.lim instead

age.res Resolution or amount of greyscale pixels to cover the age scale of the plot. Default age.res=200.

yr.res Deprecated - use age.res instead

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

flux Define a flux variable within the R session (consisting of depths and their proxy concentrations in two columns) and provide the name of this variable, e.g.: flux.age.ghost(flux=flux1). If left empty (flux=c()), a flux file is expected (see proxy).

prob Probability range, defaults to prob=0.8 (10% at each side).

range.col Red seems nice.

range.lty Line type of the confidence ranges.

plot.mean Plot the mean fluxes.

mean.col Red seems nice.

mean.lty Line type of the means.

plot.median Plot the median fluxes.

median.col Blue seems nice.

median.lty Line type of the medians.

flux.lim Limits of the flux axes.

flux.lab Axis labels. Defaults to flux.lab="flux".

upper Maximum flux rates to plot. Defaults to the upper 99%; upper=0.99.

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.
dark The darkest grey value is dark=1 by default; lower values will result in lighter grey but values >1 are not allowed.
cutoff Point below which colours will no longer be printed. Default cutoff=0.001.
BCAD The calendar scale of graphs and age output-files is in cal BP by default, but can be changed to BC/AD using BCAD=TRUE.
age.lab The labels for the calendar axis (default age.lab="cal BP" or "BC/AD" if BCAD=TRUE).
yr.lab Deprecated - use age.lab instead
rotate.axes The default of plotting calendar year on the horizontal axis and fluxes on the vertical one can be changed with rotate.axes=TRUE.
rev.flux The flux axis can be reversed with rev.flux=TRUE.
rev.age The direction of the age axis can be reversed using rev.age=TRUE.
rev.yr Deprecated - use rev.age instead

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

Value
A plot of flux rates.

Author(s)
Maarten Blaauw, J. Andres Christen

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

## End(Not run)
```
Proxies analysed along the depths of a core can be plotted as 'proxy-ghost' graphs against calendar time while taking into account chronological uncertainties. Here darker grey indicates more likely calendar ages for specific proxy values.

**Usage**

```r
proxy.ghost(
  proxy = 1,
  proxy.lab = NULL,
  proxy.res = 250,
  age.res = 200,
  yr.res = age.res,
  rgb.scale = c(0, 0, 0),
  rgb.res = 100,
  set = get("info"),
  cutoff = 0.001,
  dark = 1,
  darkest = 1,
  rotate.axes = FALSE,
  proxy.rev = FALSE,
  age.rev = FALSE,
  yr.rev = age.rev,
  plot.mean = FALSE,
  mean.col = "red",
  age.lim = 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
)
```
## Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>proxy</code></td>
<td>Which proxy to use (counting from the column number in the .csv file after the depths column).</td>
</tr>
<tr>
<td><code>proxy.lab</code></td>
<td>Label of the proxy axis. Default names are taken from the csv file.</td>
</tr>
<tr>
<td><code>proxy.res</code></td>
<td>Greyscale pixels are calculated for <code>proxy.res=250</code> 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 <code>proxy.lim</code>), set this option to higher values.</td>
</tr>
<tr>
<td><code>age.res</code></td>
<td>Resolution or amount of greyscale pixels to cover the age scale of the age-model plot. Default <code>age.res=250</code> 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 <code>age.lim</code>), set this option to higher values.</td>
</tr>
<tr>
<td><code>yr.res</code></td>
<td>Deprecated - use <code>age.res</code> instead</td>
</tr>
<tr>
<td><code>rgb.scale</code></td>
<td>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: <code>rgb.scale=c(0,0,0)</code>, but could also be, say, scales of red (<code>rgb.scale=c(1,0,0)</code>).</td>
</tr>
<tr>
<td><code>rgb.res</code></td>
<td>Resolution of the colour spectrum depicting the age-depth model. Default <code>rgb.res=100</code>.</td>
</tr>
<tr>
<td><code>set</code></td>
<td>Detailed information of the current run, stored within this session’s memory as variable info.</td>
</tr>
<tr>
<td><code>cutoff</code></td>
<td>Point below which colours will no longer be printed. Default <code>cutoff=0.001</code>.</td>
</tr>
<tr>
<td><code>dark</code></td>
<td>By default, the darkest grey value is assigned to the most likely value within the entire core (normalised to 1; <code>dark=1</code>). By setting dark to, e.g., <code>dark=.8</code>, all values of and above 0.8 will be darkest (and values below that threshold will be lighter grey the lower their probabilities).</td>
</tr>
<tr>
<td><code>darkest</code></td>
<td>Darkness of the most likely value. Is black by default (<code>darkest=1</code>); lower values will result in lighter grey.</td>
</tr>
<tr>
<td><code>rotate.axes</code></td>
<td>The default is to plot the calendar horizontally, however the plot can be rotated (<code>rotate.axes=TRUE</code>).</td>
</tr>
<tr>
<td><code>proxy.rev</code></td>
<td>The proxy axis can be reversed if <code>proxy.rev=TRUE</code>.</td>
</tr>
<tr>
<td><code>age.rev</code></td>
<td>The calendar axis can be reversed using <code>yr.rev=TRUE</code>.</td>
</tr>
<tr>
<td><code>yr.rev</code></td>
<td>Deprecated - use <code>age.rev</code> instead</td>
</tr>
<tr>
<td><code>plot.mean</code></td>
<td>The mean ages of the proxy values can be added using <code>plot.mean=TRUE</code>.</td>
</tr>
<tr>
<td><code>mean.col</code></td>
<td>Colour of the weighted mean ages of the proxy values.</td>
</tr>
<tr>
<td><code>age.lim</code></td>
<td>Minimum and maximum calendar age ranges, calculated automatically by default (<code>yr.lim=NULL</code>).</td>
</tr>
<tr>
<td><code>yr.lim</code></td>
<td>Deprecated - use <code>age.lim</code> instead</td>
</tr>
<tr>
<td><code>proxy.lim</code></td>
<td>Ranges of the proxy axis, calculated automatically by default (<code>proxy.lim=NULL</code>).</td>
</tr>
<tr>
<td><code>sep</code></td>
<td>Separator between the fields of the plain text file containing the depth and proxy data.</td>
</tr>
<tr>
<td><code>xaxs</code></td>
<td>Extension of x-axis. By default, no white-space will be added at the axis extremes (<code>xaxs=&quot;i&quot;</code>). See <code>?par</code> for other options.</td>
</tr>
</tbody>
</table>
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).

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)
set.initvals

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.

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

squeezesqueeze 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(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:
```r
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**

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

**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.

**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)

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
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