Package ‘rplum’

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Type Package

Title Bayesian Age-Depth Modelling of Cores Dated by Pb-210

Version 0.5.2

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Description An approach to age-depth modelling that uses Bayesian statistics to reconstruct accumulation histories for 210Pb-dated deposits using prior information. It can combine 210Pb, radiocarbon, and other dates in the chronologies. See Aquino et al. (2018) <doi:10.1007/s13253-018-0328-7>. Note that parts of the code underlying 'rplum' are derived from the 'rbacon' package by the same authors, and there remains a degree of overlap between the two packages.

Encoding UTF-8

License GPL (>= 2)

NeedsCompilation no

Imports grDevices, graphics, stats, utils, rintcal (>= 1.1.3), rice (>= 1.1.1), rbacon (>= 3.4.1)

RoxygenNote 7.3.2

Suggests knitr, rmarkdown, utf8

VignetteBuilder knitr

Language en-GB

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Repository CRAN

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Contents

`agedepth` *Plot an age-depth model*

Description

Plot the age-depth model of a core.

Usage

```
agedepth(
  set = get("info"),
  BCAD = set$BCAD,
  depth.unit = set$depth.unit,
  age.unit = "yr",
  unit = depth.unit,
  d.lab = c(),
  age.lab = c(),
  yr.lab = age.lab,
  kcal = FALSE,
  acc.lab = c(),
  mem.lab = c(),
  d.min = c(),
  d.max = c(),
  d.by = c(),
  depths = set$depths,
  depths.file = FALSE,
  accordion = c(),
  plotatthesedepths = c(),
  age.min = c(),
  yr.min = age.min,
  age.max = c(),
  yr.max = age.max,
  hiatus.option = 1,
  dark = c(),
  prob = set$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,
ex = 1,
mirror = TRUE,
up = TRUE,
cutoff = 0.1,
plot.range = TRUE,
range.col = grey(0.5),
range.lty = "12",
range.lwd = 1,
mn.col = "red",
mn.lty = "12",
mn.lwd = 1,
med.col = NA,
med.lty = "12",
med.lwd = 1,
C14.col = rgb(0, 0, 1, 0.35),
C14.border = rgb(0, 0, 1, 0.5),
cal.col = rgb(0, 0.5, 0.5, 0.35),
cal.border = rgb(0, 0.5, 0.5, 0.5),
dates.col = c(),
pb.background = 0.5,
pbmodelled.col = function(x) rgb(0, 0, 1, 0.5 * x),
pbmeasured.col = "blue",
pb.lim = c(),
supp.col = rgb(0.5, 0, 0.5, 0.5),
remove.tail = TRUE,
MCMC.resample = TRUE,
hiatus.col = grey(0.5),
hiatus.lty = "12",
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$after,
  bty = "l",
  mar.left = c(3, 3, 1, 0.5),
  mar.middle = c(3, 0, 1, 0.5),
  mar.right = c(3, 0, 1, 0.5),
  mar.main = c(3, 3, 1, 1),
  righthand = 3,
  mgp = c(1.7, 0.7, 0),
  xaxs = "r",
  yaxs = "i",
  MCMC.col = grey(0.4),
  post.col = grey(0.8),
  post.border = grey(0.4),
  prior.col = 3,
  prior.lwd = 2,
  prior.fontcol = 2,
  prior.ticks = "n",
  prior.fontsize = 0.9,
  toppanel.fontsize = 0.9,
  mainpanel.tickfontsize = 1,
  mainpanel.labelfontsize = 1,
  acc.xlim = c(),
  acc.ylim = c(),
  mem.xlim = c(),
  mem.ylim = c(),
  hiatus.xlim = c(),
  hiatus.ylim = c(),
  phi.xlim = c(),
  phi.ylim = c(),
  supp.xlim = c(),
  supp.ylim = c(),
  xaxt = "s",
  yaxt = "s",
  plot.pb = TRUE,
  pb.lty = 1,
  plot.pdf = FALSE,
  dates.only = FALSE,
  model.only = FALSE,
  verbose = TRUE,
  roundby = 2,
  save.info = set$save.info
)
```

Arguments

`set`	Detailed information of the current run, stored within this session's memory as variable `info`.
`BCAD`	The calendar scale of graphs and age output-files is in `cal BP` by default, but can be changed to BC/AD using `BCAD=TRUE`.
`depth.unit`	Units of the depths. Defaults to the one provided in the Bacon() command, `depth.unit=set$depth.unit`.
`age.unit`	Units of the ages. Defaults to `age.unit="yr"`.
`unit`	Deprecated and replaced by `depth.unit`.
`d.lab`	The labels for the depth axis. Default `d.lab="Depth (cm)"`. See also `depth.unit`.
`age.lab`	The labels for the calendar axis (default `age.lab="cal BP"` or `"BC/AD"` if `BCAD=TRUE`).
`yr.lab`	Deprecated - use age.lab instead
`kcal`	Use kcal BP. Default is `kcal=FALSE`.
`acc.lab`	The labels for the accumulation rate plot (top middle). Default `d.lab="Acc. rate (yr/cm)"` (or whatever units you're using).
`mem.lab`	The labels for the memory plot (top right). Default `d.lab="Memory"`.
`d.min`	Minimum depth of age-depth model (use this to extrapolate to depths higher than the top dated depth).
`d.max`	Maximum depth of age-depth model (use this to extrapolate to depths below the bottom dated depth).
`d.by`	Depth intervals at which ages are calculated. Default 1. Alternative depth intervals can be provided using, e.g., d.`d.by=0.5`.
`depths`	By default, Bacon will calculate the ages for the depths `d.min` to `d.max` in steps of `d.by`. Alternative depths can be provided as, e.g., `depths=seq(0, 100, length=500)` or as a file, e.g., `depths=read.table("CoreDepths.txt"`. See also `depths.file`.
`depths.file`	By default, Bacon will calculate the ages for the depths `d.min` to `d.max` in steps of `d.by`. If `depths.file=TRUE`, Bacon will read a file containing the depths for which you require ages. This file, containing the depths in a single column without a header, should be stored within `coredir`, and its name should start with the core's name and end with '_depths.txt'. Then specify `depths.file=TRUE` (default `FALSE`). See also `depths`.
`accordion`	An experimental option to squeeze and stretch depths below a boundary. Needs 2 parameters: boundary depth and compression ratio, e.g., `accordion=c(25,20)`. Defaults to inactive, `accordion=c()`.
`plotatthesedepths`	An option to plot ages at different depths (e.g., if a core has been compressed during a run). Use with extreme caution!
`age.min`	Minimum age of the age-depth plot.
`yr.min`	Deprecated - use age.min instead.
`age.max`	Maximum age of the age-depth plot.
`yr.max`	Deprecated - use age.min instead.

`hiatus.option`	How to calculate accumulation rates and ages for sections with hiatuses. Either extrapolate from surrounding sections (default, `hiatus.option=1`), use a w-weighted mix between the prior and posterior values for depths below the hiatus and prior information only for above the hiatus (`hiatus.option=2`), or use the originally calculated slopes (`hiatus.option=0`).
`dark`	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`.
`ex`	As an alternative to ’height’ and ’calheight’, the distribution heights can be set as either a single value (e.g., `ex=1`) or for each date (for example, `myex=rep(1, nrow(info$dets)); myex[1:5] <- 10; agedepth(ex=myex)`).
`mirror`	Plot the dates as ’blobs’. Set to `mirror=FALSE` to plot simple distributions.
`up`	Directions of distributions if they are plotted non-mirrored. Default `up=TRUE`.
`cutoff`	Avoid plotting very low probabilities of date distributions (default `cutoff=0.1`).
`plot.range`	Whether or not to plot the curves showing the confidence ranges of the age-model. Defaults to (`plot.range=TRUE`).
`range.col`	The colour of the curves showing the confidence ranges of the age-model. Defaults to medium grey (`range.col=grey(0.5)`).
`range.lty`	The line type of the curves showing the confidence ranges of the age-model. Defaults to `range.lty=12`.
`range.lwd`	Widths of the lines of the ranges of the age-depth model. Default `range.lwd=1`.
`mn.col`	The colour of the mean age-depth model: default `mn.col="red"`.

`mn.lty`	The line type of the mean age-depth model. Default `mn.lty=12`.
`mn.lwd`	Width of the line of the mean age-depth model. Default `mn.lwd=1`.
`med.col`	The colour of the median age-depth model: not drawn by default `med.col=NA`.
`med.lty`	The line type of the median age-depth model. Default `med.lty=12`.
`med.lwd`	Width of the line of the median age-depth model. Default `med.lwd=1`.
`C14.col`	The colour of the calibrated ranges of the dates. Default is semi-transparent blue: `C14.col=rgb(0,0,1,.35)`.
`C14.border`	The colours of the borders of calibrated 14C dates. Default is semi-transparent dark blue: `C14.border=rgb(0, 0, 1, 0.5)`.
`cal.col`	The colour of the non-14C dates. Default is semi-transparent blue-green: `cal.col=rgb(0,.5,.5,.35)`.
`cal.border`	The colour of the border of non-14C dates in the age-depth plot: default semi-transparent dark blue-green: `cal.border=rgb(0,.5,.5,.5)`. Not used by default.
`dates.col`	As an alternative to colouring dates based on whether they are 14C or not, sets of dates can be coloured as, e.g., `dates.col=colours()[2:100]`.
`pb.background`	Probability at which total Pb values are considered to have reached background values, or in other words, that their modelled values are at or below supported + detection limit (Al)). Setting this at 0.5 means that any depth with a Pb measurement, where at least half of the iterations model Pb values reaching background values, is flagged as having reached background. The age-model is not extended to any Pb measurements that have reached background.
`pbmodelled.col`	Colour of the modelled 210Pb values. Defaults to shades of blue: `pbmodelled.col=function(x) rgb(0,0,1,x)`.
`pbmeasured.col`	Colour of the measured 210Pb values (default `pbmeasured.col="blue"`). Draws rectangles of the upper and lower depths as well as the Pb values with 95 percent error ranges.
`pb.lim`	Axis limits for the Pb-210 data. Calculated automatically by default (`pblim=c()`).
`supp.col`	Colour of supported Pb-210. Defaults to semi-transparent purple, because why not.
`remove.tail`	Whether or not to remove the tail measurements when plotting. Sometimes automated removal might go wrong, so then this option can be used to avoid removing the tail measurements.
`MCMC.resample`	After the MCMC run, if there are more MCMC iterations than requested, only the last 'ssize' iterations will be retained. Defaults to TRUE.
`hiatus.col`	The colour of the depths of any hiatuses. Default `hiatus.col=grey(0.5)`.
`hiatus.lty`	The line type of the depths of any hiatuses. Default `hiatus.lty=12`.
`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 `"l"` (default), `"7"`, `"c"`, `"u"`, or `"o"` for correspondingly shaped boxes).
`mar.left`	Plot margins for the topleft panel (amount of white space along edges of axes 1-4). 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, 0.7, 0.0)`.

`xaxs`	Extension of x-axis. By default, add some extra white-space at both extremes (`xaxs="r"`). See ?par for other options.
`yaxs`	Extension of y-axis. By default, add no extra white-space at both extremes (`yaxs="i"`). See ?par for other options.
`MCMC.col`	Colour of the MCMC output. Defaults to `post.col=grey(0.4))`.
`post.col`	Colour of the posterior histogram. Defaults to `post.col=grey(0.8))`.
`post.border`	Colour of the posterior border. Defaults to `post.border=grey(0.4))`.
`prior.col`	Colour of the prior curve. Defaults to light green, `prior.col=3)`.
`prior.lwd`	Line width of the prior curve. Defaults to `prior.lwd=2)`.
`prior.fontcol`	Colour of the font accompanying the posterior histograms. Defaults to red, `prior.fontcol=2)`.
`prior.ticks`	Plot tickmarks and values on the vertical axes for the prior and posterior distributions. Defaults to no tick marks (`prior.ticks="n"`). Set to `prior.ticks="s"` to plot the tick marks. Note that these values are of little practical use, as they correspond poorly to, e.g., the mean and strength values. All that matters is that the areas of both the prior and the posterior distributions sum to 1; wider distributions tend to give lower peaks, and narrower distributions higher peaks.
`prior.fontsize`	Font size of the prior, relative to R's standard size. Defaults to `prior.fontsize=0.9`.
`toppanel.fontsize`	Font size of the top panels, relative to R's standard size. Defaults to `prior.fontsize=0.9`.
`mainpanel.tickfontsize`	Font size of values at the tick marks in the main panel, relative to R's standard size. Defaults to `mainpanel.tickfontsize=1`.
`mainpanel.labelfontsize`	Font size of axis labels in the main panel, relative to R's standard size. Defaults to `mainpanel.labelsize=1`.
`acc.xlim`	Horizontal axis limits of the accumulation rate panel. Calculated automatically by default.
`acc.ylim`	Vertical axis limits of the accumulation rate panel. Calculated automatically by default.
`mem.xlim`	Horizontal axis limits of the memory panel. Calculated automatically by default.
`mem.ylim`	Vertical axis limits of the memory panel. Calculated automatically by default.
`hiatus.xlim`	Horizontal axis limits of the hiatus size panel. Calculated automatically by default.
`hiatus.ylim`	Vertical axis limits of the hiatus size panel. Calculated automatically by default.
`phi.xlim`	Horizontal axis limits of the phi panel. Calculated automatically by default.
`phi.ylim`	Vertical axis limits of the phi panel. Calculated automatically by default.
`supp.xlim`	Horizontal axis limits of the supported-Pb panel. Calculated automatically by default.
`supp.ylim`	Vertical axis limits of the supported-Pb panel. Calculated automatically by default.

`xaxt`	Whether or not to plot the x-axis. Can be used to adapt axes after a plot. See ?par for other options.
`yaxt`	Whether or not to plot the y-axis. Can be used to adapt axes after a plot. See ?par for other options.
`plot.pb`	Plot the 210Pb data (if present). Defaults to `plot.pb=TRUE`.
`pb.lty`	Line type of measured Pb-210 data.
`plot.pdf`	Produce a pdf file of the age-depth plot.
`dates.only`	By default, the age-depth model is plotted on top of the dates. This can be avoided by supplying `dates.only=TRUE`.
`model.only`	By default, panels showing the MCMC iterations and the priors and posteriors for accumulation rate and memory are plotted above the main age-depth model panel. This can be avoided by supplying `model.only=TRUE`. Note however that this removes relevant information to evaluate the age-depth model, so we do recommend to present age-models together with these upper panels.
`verbose`	Provide a summary of the age ranges after producing the age-depth model graph; default `verbose=FALSE`.
`roundby`	Rounding of the values reported at the end of the function. Defaults to 2 decimals.
`save.info`	By default, a variable called ‘info’ with relevant information about the run (e.g., core name, priors, settings, ages, output) is saved into the working directory. Note that this will overwrite any existing variable with the same name - as an alternative, one could run, e.g., `myvar <- Bacon()`, followed by supplying the variable `myvar` in any subsequent commands.

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

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

`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). Defaults 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

`Plum` *Main 210Pb age-depth modelling function*

Description

This is the main age-depth modelling function of the rplum package for 210Pb age-modelling.

Usage

```
Plum(
  core = "HP1C",
  thick = 1,
  otherdates = NA,
  coredir = "",
  phi.shape = 2,
  phi.mean = 50,
  s.shape = 5,
  s.mean = 10,
  Al = 0.1,
  date.sample = c(),
  n.supp = c(),
  remove.tail = TRUE,
```

```
ra.case = c(),
Bqkg = TRUE,
seed = NA,
prob = 0.95,
d.min = 0,
d.max = NA,
d.by = 1,
depths.file = FALSE,
depths = c(),
depth.unit = "cm",
age.unit = "yr",
unit = depth.unit,
acc.shape = 1.5,
acc.mean = 10,
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 = "",
postbomb = 0,
F14C = c(),
pMC = c(),
delta.R = 0,
delta.STD = 0,
t.a = 3,
t.b = 4,
normal = FALSE,
suggest = TRUE,
reswarn = c(10, 200),
remember = TRUE,
ask = TRUE,
run = TRUE,
defaults = "defaultPlum_settings.txt",
sep = ",",
dec = ".",
runname = "",
slump = c(),
BCAD = FALSE,
ssize = 4000,
th0 = c(),
```

```
  burnin = min(500, ssize),
  MinAge = c(),
  youngest.age = c(),
  MaxAge = c(),
  oldest.age = c(),
  cutoff = 0.001,
  rounded = 1,
  plot.pdf = TRUE,
  dark = 1,
  date.res = 100,
  age.res = 200,
  close.connections = TRUE,
  save.info = 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 rplum, `core="HP1C"` also reported by Aquino-Lopez et al. (2018). Also available is LL14, a core kindly provided by Dr Lysanna Anderson (USGS). LL14 has ra-226 data (so can be run with `ra.case=1` or `ra.case=2`, see below), and also has additional C-14 and cal BP data (these can be added using `otherdates="LL14_14C.csv"`). The original LL14 core has more 14C data than provided here (for reasons of brevity). 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 `Plum_runs/MyCore/MyCore.csv`. Then run Plum as follows: `Plum("MyCore")`. Note that for Pb-210 data, the depth in the .csv should be the bottom of the slice, not the mid-point. (For any non-Pb data, depths are the midpoints of their slices). Also make sure that the thickness and density are given correctly for each Pb-210 data point.
`thick`	Plum will divide the core into sections of equal thickness specified by thick (default `thick=1`).
`otherdates`	Name of (optional) file with radiocarbon dates. This file should have the same format as the one used for rbacon. For example, `Bacon("LL14", otherdates="LL14_14C.csv")`.
`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='Plum_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.

`phi.shape`	Shape parameter of the prior gamma distribution used for the influx of Pb-210 to the sediment, default `phi.shape=2`.
`phi.mean`	Mean parameter of the prior gamma distribution used for the influx of Pb-210 to the sediment, default `phi.mean=50`.
`s.shape`	Shape parameter of the prior gamma distribution used for the supported Pb-210 to the sediment, default `s.shape=5`.
`s.mean`	Mean parameter of the prior gamma distribution used for the supported Pb-210 to the sediment, default `s.mean=10`.
`Al`	Parameter used to limit the chronologies described in Aquino-Lopez et al. (2018) for the minimum distinguishable unsupported activity; default `Al=0.1`.
`date.sample`	Date (in calendar years, e.g., AD 2023) at which the core was measured for Pb-120. This date will be used as a surface date and is assumed to have no uncertainty. If the date is not provided (in the .csv file or as `date.sample`), Plum will ask for it.
`n.supp`	This value will delete n.supp data points from the deepest part of the core, and these points will then be used exclusively to estimate the supported activity. If this option is used, a constant supported Pb-210 will be assumed, `n.supp=-1`.
`remove.tail`	Whether or not to remove the tail measurements when plotting. Sometimes automated removal might go wrong, or additional dates exist further down, so then this option can be used to avoid removing the tail 210Pb measurements. Is set to FALSE if there are non-210Pb data further down the core.
`ra.case`	How to use radium-226 measurements if they are provided in the core's .csv file. 1 = assume constant radium, 2 = assume varying radium and use the radium measurements as individual estimates of supported Pb-210. If no radium measurements are present, use `ra.case=0`.
`Bqkg`	This variable indicates whether total Pb-210 is expressed in Bq/kg (default; `Bqkg=TRUE`) or dpm/g if set to FALSE.
`seed`	Seed used for C++ executions; if it is not assigned then the seed is set by system. Default `seed=NA`.
`prob`	Confidence interval to report. This should lie between 0 and 1, default `prob=0.95` (95 %).
`d.min`	Minimum depth of age-depth model (use this to extrapolate to depths higher than the top dated depth).
`d.max`	Maximum depth of age-depth model (use this to extrapolate to depths below the bottom dated depth).
`d.by`	Depth intervals at which ages are calculated. Defaults to `d.by=1`.
`depths.file`	By default, Plum will calculate the ages for the depths `d.min` to `d.max` in steps of `d.by`. If `depths.file=TRUE`, Plum 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, Plum will calculate the ages for the depths `d.min` to `d.max` in steps of `d.by`. Alternative depths can be provided as, e.g., `depths=seq(0, 100, length=500)` or as a file, e.g., `depths=read.table("CoreDepths.txt"`. See also `depths.file`
`depth.unit`	Units of the depths. Defaults to `depth.unit="cm"`.
`age.unit`	Units of the ages. Defaults to `age.unit="yr"`.
`unit`	Deprecated and replaced by `depth.unit`.
`acc.shape`	The prior for the accumulation rate consists of a gamma distribution with two parameters. Its shape is set by acc.shape (default `acc.shape=1.5`; higher values result in more peaked shapes).
`acc.mean`	The accumulation rate prior consists of a gamma distribution with two parameters. Its mean is set by acc.mean (default `acc.mean=10` 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., Plum(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.
`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.
`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 Plum complains that the parameters are out of support.
`after`	Sets a short section above and below hiatus.depths within which to calculate ages. For internal calculations - do not change.
`cc`	Calibration curve for C-14 dates: `cc=1` for IntCal20 (northern hemisphere terrestrial), `cc=2` for Marine20 (marine), `cc=3` for SHCal20 (southern hemisphere terrestrial). For dates that are already on the cal BP scale use `cc=0`.

`cc1`	For northern hemisphere terrestrial 14C dates (IntCal20).
`cc2`	For marine 14C dates (Marine20).
`cc3`	For southern hemisphere 14C dates (SHCal20).
`cc4`	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`.
`cc.dir`	Directory where the calibration curves for C14 dates `cc` are located. By default `cc.dir=""` since they are loaded into R's memory. For example, use `cc.dir="."` to choose current working directory, or `cc.dir="Curves/"` to choose sub-folder `Curves/`. Note that all calibration curves should reside in the same directory. If you want to add a custom-built curve, put it in the directory where the default calibration curves are (probably `list.files(paste0(.libPaths(), "/IntCal/extdata/"))`). Alternatively produce a new folder, and add your curve as well as the default calibration curves there (cc1, cc2 and cc3; e.g., `write.table(copyCalibrationCurve(1), "./3Col_intcal20.14C", sep="\t")`.)
`postbomb`	Use a postbomb curve for negative (i.e. postbomb) 14C ages. `0 = none, 1 = NH1, 2 = NH2, 3 = NH3, 4 = SH1-2, 5 = SH3`
`F14C`	Radiocarbon ages can be provided as F14C values. If doing so, please indicate here which dates were entered as F14C (e.g., if the first 4 dates are in F14C, write `F14C=1:4`). The F14C values in your .csv file will then be replaced by their corresponding C14 ages.
`pMC`	Radiocarbon ages can be provided as pMC values. If doing so, please indicate here which dates were entered as pMC (e.g., if the first 4 dates are in pMC, write `pMC=1:4`). The pMC values in your .csv file will then be replaced by their corresponding C14 ages.
`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-distribution has two parameters, t.a and t.b, set at 3 and 4 by default (see Christen and Perez, 2009). If you want to assign narrower error distributions (more closely resembling the normal distribution), set t.a and t.b at for example 33 and 34 respectively (e.g., for specific dates in your .csv file). For symmetry reasons, t.a must always be equal to t.b-1.
`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.
`normal`	By default, Plum 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, Plum will suggest to change the prior. Also, if the length of the core would cause too few or too many sections with the default settings, Plum will suggest an alternative section thickness `thick`, and it will suggest approaches

	to estimating supported Pb-120. 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`	Plum 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`	Plum 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 `Plum.cleanup()`.
`ask`	By default Plum 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 Plum run instead of producing a new one, you can use `run=FALSE`.
`defaults`	Name of the file containing settings for the core. For internal use only - do not change.
`sep`	Separator between the fields of the plain text file containing the dating information. Default `sep=","`.
`dec`	Character for decimal points. Default to `dec="."`.
`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.
`BCAD`	The calendar scale of graphs and age output-files is in cal BP (calendar or calibrated years before the present, where the present is AD 1950) by default, but can be changed to BC/AD using `BCAD=TRUE`.
`ssize`	The approximate amount of iterations to store at the end of the MCMC run. Default 2000; decrease for faster (but less reliable) runs or increase for cores where the MCMC mixing (panel at upper-left corner of age-model graph) appears problematic.
`th0`	Starting years for the MCMC iterations.
`burnin`	Amount of initial, likely sub-optimal MCMC iterations that will be removed.
`MinAge`	Deprecated - use youngest.age instead.
`youngest.age`	Minimum age limit for Bacon runs, default at current year in cal BP. To set plot limits, use `age.min` instead.
`MaxAge`	Deprecated - use oldest.age instead.
`oldest.age`	Maximum age limit for Bacon runs, default at 1,000,000 cal BP. To set plot limits, use `age.max` instead.
`cutoff`	Avoid plotting very low probabilities of date distributions (default `cutoff=0.001`).
`rounded`	Rounding of calendar years. Defaults to 1 decimal.
`plot.pdf`	Produce a pdf file of the age-depth plot. Defaults to `plot.pdf=TRUE` after a Plum 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`.
`close.connections`	Internal option to close connections after a run. Default `close.connections=TRUE`.
`save.info`	By default, a variable called ‘info’ with relevant information about the run (e.g., core name, priors, settings, ages, output) is saved into the working directory. Note that this will overwrite any existing variable with the same name - as an alternative, one could run, e.g., `myvar <- Bacon()`, followed by supplying the variable `myvar` in any subsequent commands.
`older.than`	an option to enable dates at the limit of C-14 dating. If there are older.than dates (works only for non-210Pb data), 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 ’otherdates’ .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 (works only for non-210Pb data), 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 ’otherdates’ .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, ending in "_elbowages.txt".
`verbose`	Provide feedback on what is happening (default `verbose=TRUE`).
`...`	options for the age-depth graph. See the agedepth and calib.plot functions.

Details

Plum is an approach to age-depth modelling that uses Bayesian statistics in order to reconstruct accumulation histories for 210Pb-dated deposits by taking into account prior information, and can combine 210Pb, radiocarbon and other dates (Aquino et al. 2018).

Plum handles 210Pb and other dated depths within in a core, by dividing a core into many thin vertical sections (by default of `thick=1` cm thickness), and through millions of Markov Chain Monte Carlo (MCMC) iterations estimates the flux of 210Pb and supported 210Pb, as well as 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 and values for 210Pb then form the age-depth and 210Pb 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`). The 210Pb flux (phi) and supported 210Pb (s) are constrained by priors `phi.mean`, `phi.shape`, `s.mean` and `s.shape`.

Although Plum was developed for 210Pb dates, it can also include absolute dates (e.g., 14C, OSL, tephra or other dates on a calendar scale). Radiocarbon dates should be calibrated using either IntCal20 (for terrestrial northern hemisphere material; Reimer et al., 2020), Marine20 (for marine dates; Hughen et al., 2020), SHCal20 (for southern hemisphere dates; Hogg et al., 2020) or any other calibration curve (see below), while modern 14C dates are calibrated using one of the post-bomb calibration curves (NH1, NH2 or NH3 for the northern hemisphere, SH1-2 or SH3 for the southern hemisphere; Hua et al., 2022). See `http://calib.org/CALIBomb/` if you are unsure which postbomb curve you need. If Plum 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`. Plum also needs the date of sampling, in AD (`date.sample`).

rplum works by calling the rbacon package. 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.

Value

An age-depth model graph, its age estimates, a summary, and the info variable which contains all relevant information.

Author(s)

Maarten Blaauw, J. Andres Christen, Marco A. Aquino L.

References

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Reimer et al., 2020. The IntCal20 Northern Hemisphere radiocarbon age calibration curve (0–55 cal kBP). Radiocarbon 62, 725-757.

Examples

```
Plum(ask=FALSE, ssize=1000, coredir=tempfile(), date.sample=2018.5, ra.case=0, n.supp=3)
```

`Plum.cleanup` *Remove files made to produce the current core's age-depth model.*

Description

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

Usage

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

Arguments

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

Details

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

Value

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

Author(s)

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`Plum_runs` *List the folders present in the current core directory.*

Description

Lists all folders located within the core's directory.

Usage

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

Arguments

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

Details

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

Value

A list of folders

Author(s)

Maarten Blaauw, J. Andres Christen

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