Package 'BayLum'

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Type Package

Title Chronological Bayesian Models Integrating Optically Stimulated
Luminescence and Radiocarbon Age Dating

Description Bayesian analysis of luminescence data and C-14 age estimates. Bayesian mod-
els are based on the following publica-
tions: Combes, B. & Philippe, A. (2017) <doi:10.1016/j.quageo.2017.02.003> and Combes et al (2015) <doi:10.1016/j.q
cludes, amongst others, data import, export, application of age models and palaeodose model.

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Imports stats, graphics, grDevices, methods, hexbin, rjags (>= 4-6),
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R topics documented:

BayLum–package	*Chronological Bayesian Models Integrating Optically Stimulated Luminescence and C-14 Dating*

Description

A collection of various R functions for Bayesian analysis of luminescence data and C-14 age estimates. This includes, amongst others, data import, export, application of age and palaeodose models.

Details

This package is based on the functions: Generate_DataFile and Generate_DataFile_MG to import luminisecence data. These functions create a list containing all informations to compute age of Single-grain OSL measurements for the first function and Multi-grain OSL measurements for the second.

The functions: Age_Computation and AgeS_Computation use Bayesian analysis for OSL age estimation for one or various samples according to differents models (e.g. different dose-response curves and different equivalent dose distributions around the palaeodose).

It is possible to consider various BIN/BINX-files per sample, to compute ages of samples in stratigraphic constraints and to integrate systematic errors.

It is possible to calibrate C-14 age with the function AgeC14_Computation. We can also estimate chronology containing 14C age and OSL samples with the function Age_OSLC14.

Author(s)

Claire Christophe, Anne Philippe, Sebastian Kreutzer, Guillaume Guérin

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AgeC14_Computation   *Bayesian analysis for age estimation of 14C age of various samples*

Description

This function calibrate 14C age of samples to get an age (years). The user can choose one of the following radiocarbon calibration curve: Northern or Sourthen Hemisphere or marine atmospheric. It must be the same curve for all samples.

Usage

```
AgeC14_Computation(Data_C14Cal, Data_SigmaC14Cal, SampleNames, Nb_sample,
  PriorAge = rep(c(10, 50), Nb_sample), SavePdf = FALSE,
  OutputFileName = c("MCMCplot", "HPD_Cal14CCurve", "summary"),
  OutputFilePath = c(""), SaveEstimates = FALSE,
  OutputTableName = c("DATA"), OutputTablePath = c(""),
  StratiConstraints = c(), sepSC = c(","), Model = c("full"),
  CalibrationCurve = c("AtmosphericNorth"), Iter = 50000, t = 5,
  Nb_chaines = 3, quiet = FALSE)
```

Arguments

Data_C14Cal	numeric vector: corresponding to 14C age estimate.
Data_SigmaC14Cal	
	numeric vector: correponding to the error of 14C age estimates.
SampleNames	character vector: names of sample. The length of this vector is equal to Nb_sample.
Nb_sample	integer: number of samples.
PriorAge	numeric vector (with default): lower and upper bounds for age parameter of each sample in years (not in ka). Note that, length(PriorAge)=2*Nb_sample and PriorAge[2i-1,2i] correponds to the lower and upper bounds of sample whose number ID is equal to i.
SavePdf	boolean (with default): if TRUE save graphs in pdf file named OutputFileName in folder OutputFilePath.
OutputFileName	character (with default): name of the pdf file that will be generated by the function if SavePdf=TRUE, length(OutputFileName)=3, see **PLOT OUTPUT** in **Value** section for more informations.
OutputFilePath	character (with default): path to the pdf file that will be generated by the function if SavePdf=TRUE. If it is not equal to "", it must be terminated by "/".
SaveEstimates	boolean (with default): if TRUE save Bayes estimates, credible interval at level 68% and 95% and the result of the gelman en Rubin test of convergency, in a csv table named OutputFileName in folder OutputFilePath.
OutputTableName	
	character (with default): name of the table that will be generated by the function if SaveEstimates=TRUE.

OutputTablePath

> character (with default): path to the table that will be generated by the function if SaveEstimates=TRUE. If it is not equal to "", it must be terminated by "/".

StratiConstraints

> numeric matrix or character(with default): input object for the statigraphic relation between samples. If there is stratigraphic relation between samples see the details section for instructions regarding how to correctly fill StratiConstraints; the user can refer to a matrix (numeric matrix) or to a csv file (character). If there is no stratigraphic relation default value is suitable.

sepSC

> character (with default): if StratiConstraints is character, indicate column separator in StratiConstraints csv file.

Model

> character (with default): if **"full"**, error on estimate calibration curve is taken account. If **"naive"** this error is not taken account in the age estimate.

CalibrationCurve

> character (with default): calibration curve choosen. Allowed inputs are

> - **"AtmosphericNorth"** for Northern Hemisphere atmospheric radiocarbon calibration curve,
> - **"Marine"** for Marine radiocarbon calibration curve,
> - **"AtmosphericSouth"** for Southern Hemisphere atmospheric radiocarbon calibration curve
> - **a csv file, with tree columns, the first column is dedicated to "Cal.BP", the second to "X14C.age", the third to "Error". The decimal of this file must be a dot, and the separator must be a comma.**

Iter

> integer (with default): number of iterations for the MCMC computation (for more information see jags.model).

t

> integer (with default): 1 every t iterations of the MCMC is considered for sampling the posterior distribution (for more information see jags.model).

Nb_chaines

> integer (with default): number of independent chains for the model (for more information see jags.model).

quiet

> logical (with default): enables/disables rjags messages

Details

** How to fill StratiConstraints ? **

If there is stratigraphic relations between samples, **14C age in Data_C14Cal must be ordered by order of increasing ages**.

The user can fill the StratiConstraints matrix as follow.

1. **Size of the matrix**: row number of StratiConstraints matrix is equal to Nb_sample+1, and column number is equal to Nb_sample.

2. **First line of the matrix**: for all i in {1,...,Nb_Sample}, StratiConstraints[1,i]=1 that means the lower bound of the sample age (given in PriorAge[2i-1]) for the sample whose number ID is equal to i, is taken into account.

3. **Sample relations**: for all j in {2,...,Nb_Sample+1} and all i in {j,...,Nb_Sample}, StratiConstraints[j,i]=1 if sample age whose number ID is equal to j-1 is lower than sample age whose number ID is equal to i. Otherwise, StratiConstraints[j,i]=0.

Note that StratiConstraints_{2:Nb_sample+1,1:Nb_sample} is a upper triangular matrix.

The user can also use SCMatrix or SC_Ordered (if all samples are ordered) functions to construct the StratiConstraints matrix.

The user can also refer to a .csv file that containts the relation between samples as defined above. The user must take care about the separator used in the csv file using the argument sepSC.

** More precision on Model **

We propose two models "full" or "naive". If Model='full' that means measurement error and error on calibration curve are taken account in the Bayesian model; if Model="naive" that means only error on measurement are taken account in the mode.

More precisely, the model considered here, as the one developed by Christen, JA (1994), assume multiplicative effect of errors to address the problem of outliers. In addition, to not penalise variables that are not outliers and damage theirs estimation, we introduce a structure of mixture, that means only variable that are considered as outlier have in addition a multiplicative error.

Value

NUMERICAL OUTPUT

1. **A list containing the following objects:**
   - **Sampling**: that corresponds to a sample of the posterior distributions of the age parameters;
   - **Outlier**: stating the names of samples that are considered as outliers;
   - **Model**: stating which model was chosen ("full" or "naive");
   - **CalibrationCurve**: stating which radiocarbon calibration curve was chosen;
   - **PriorAge**: stating the priors used for the age parameter;
   - **StratiConstraints**: stating the stratigraphic relations between samples considered in the model.
2. **The Gelman and Rubin test of convergency**: print the result of the Gelman and Rubin test of convergency for the age estimate for each sample. A result close to one is expected.
   In addition, the user must visually assess the convergence of the trajectories by looking at the graph generated by the function (see **PLOT OUTPUT** for more informations).
   If both convergencies (Gelman and Rubin test and plot checking) are satisfactory, the user can consider the estimates as valid. Otherwise, the user may try increasing the number of MCMC interations (Iter) or being more precise if it is possible on the PriorAge parameter to reach convergency.
3. **Credible intervals and Bayes estimates**: prints the Bayes estimates, the credible intervals at 95% and 68% for the age parameters for each sample.

PLOT OUTPUT

1. **MCMC trajectories**: A graph with the MCMC trajectories and posterior distributions of the age parameter is displayed.
   On each line, the plot on the left represents the MCMC trajectories, and the one on the right the posterior distribution of the parameter.
2. **Summary of sample age estimates**: plot credible intervals and Bayes estimate of each sample age on one graph.

To give the results in a publication, we recommend to give the Bayes estimate of the parameters as well as the credible interval at 95% or 68%.

Note

Please note that the initial values for all MCMC are currently all the same for all chains since we rely on the automatic initial value generation of JAGS. This is not optimal and will be changed in future. However, it does not affect the quality of the age estimates if the chains have converged.

Author(s)

Claire Christophe, Anne Philippe, Guillaume Guérin

References

Christen, JA (1994). Summarizing a set of radiocarbon determinations: a robust approach. Applied Statistics, 489-503.

Reimer PJ, Bard E, Bayliss A, Beck JW, Blackwell PC, Bronl Ramsey C, Buck CE, Cheng H, Edwards RL, Friedrich M, Grootes PM, Guilderson TP, Haflidason H, Hajdas I, Hatte C, Heaton TJ, Hoffmann DL, Hogg AG, Hughen KA, Kaiser KF, Kromer B, Manning SW, Niu M, Reimer RW, Richards DA, Scott EM, Southon JR, Staff RA, Turney CSM, van der Plicht J. 2013. IntCal13 ans Marine13 radiocarbon age calibration curves 0-50000 years cal BP. Radiocarbon 55(4)=1869-1887.

Hogg AG, Hua Q, Blackwell PG, Niu M, Buck CE, Guilderson TP, Heaton TJ, Palmer JG, Reimer PJ, Reimer RW, Turney CSM, Zimmerman SRH. 2013. SHCal13 Southern Hemisphere calibration, 0-50000 years cal BP. Radiocarbon 55(4):1889-1903

See Also

rjags, plot_MCMC, SCMatrix

Examples

```
## Load data
data(DATA_C14,envir = environment())
C14Cal=DATA_C14$C14[,1]
SigmaC14Cal=DATA_C14$C14[,2]
Names=DATA_C14$Names
nb_sample=length(Names)

## Age computation of samples without stratigraphic relations
Age <- AgeC14_Computation(
Data_C14Cal = C14Cal,
Data_SigmaC14Cal = SigmaC14Cal,
SampleNames = Names,
Nb_sample = nb_sample,
PriorAge = rep(c(20000,60000),nb_sample),
Iter = 500,
quiet = TRUE)
```

AgeS	*Output of* `AgeS_Computation` *function for the samples: "GDB5" and "GDB3"*

Description

Output of `AgeS_Computation` function for the samples: "GDB5" and "GDB3", there is no stratigraphic relation neither systematic errors.

Usage

```
data("AgeS")
```

Format

A list containing

Sampling MCMC.list that corresponds to a sample of the posterior distributions of the ages (in ka), palaeodoses (in Gy) and equivalent dose dispersions (in Gy) parameters of samples "GDB5" and "GDB3";

Model_GrowthCurve stating which dose response fitting option was chosen to run the function

Distribution stating which distribution was chosen to model the dispersion of individual equivalent dose values around the palaeodose of the sample;

PriorAge stating the priors used for the age parameter (in ka);

StratiConstraints stating the matrix of stratigraphic relations between samples considered in the model;

CovarianceMatrix stating the covariance matrix of error used in the model, highlighting not common errors between samples in our cases (diagonal matrix).

References

Tribolo, C., Asrat, A., Bahain, J. J., Chapon, C., Douville, E., Fragnol, C., Hernandez, M., Hovers, E., Leplongeon, A., Martin, L, Pleurdeau, D, Pearson, O , Puaud, S, Assefa, Z. (2017). Across the Gap: Geochronological and Sedimentological Analyses from the Late Pleistocene-Holocene Sequence of Goda Buticha, Southeastern Ethiopia. PloS one, 12(1), e0169418.

Examples

```
data(AgeS)
str(AgeS)
```

AgeS_Computation   *Bayesian analysis for the OSL age estimation of various samples*

Description

This function computes the age (in ka) of at least two samples according to the model developed in
Combes and Philippe (2017), based on outputs of `Generate_DataFile` or `Generate_DataFile_MG`
or both of them using `combine_DataFiles`.
Samples, for which data is avalilable in several BIN files, can be analysed.
Single-grain or Multi-grain OSL measurements can be analysed simultaneouly.

Usage

```
AgeS_Computation(DATA, SampleNames, Nb_sample, PriorAge = rep(c(0.01, 100),
  Nb_sample), BinPerSample = rep(1, Nb_sample), SavePdf = FALSE,
  OutputFileName = c("MCMCplot", "summary"), OutputFilePath = c(""),
  SaveEstimates = FALSE, OutputTableName = c("DATA"),
  OutputTablePath = c(""), THETA = c(), sepTHETA = c(","),
  StratiConstraints = c(), sepSC = c(","), LIN_fit = TRUE,
  Origin_fit = FALSE, distribution = c("cauchy"), Iter = 50000, t = 5,
  Nb_chaines = 3, quiet = FALSE)
```

Arguments

DATA	list of objects: LT, sLT, ITimes, dLab, ddot_env, regDose, J, K, Nb_measurement, provided by the function `Generate_DataFile` or `Generate_DataFile_MG` or `combine_DataFiles`. DATA contains informations for more than one sample. If there is stratigraphic relations between samples, informations in DATA must be ordered by order of incresing ages. See the details section to for more informations.
SampleNames	character vector: names of samples. The length of this vector is equal to Nb_sample.
Nb_sample	integer : number of samples, Nb_sample>1.
PriorAge	numeric vector (with default): lower and upper bounds for age parameter of each sample (in ka). Note that, length(PriorAge)=2*Nb_sample and PriorAge[2i-1,2i] correponds to the lower and upper bounds of sample whose number ID is equal to i.
BinPerSample	integer vector (with default): vector with the number of BIN files per sample. The length of this vector is equal to Nb_sample. BinPerSample[i] correponds to the number of BIN files for the sample whose number ID is equal to i. For more information to fill this vector, we refer to detatils in `Generate_DataFile` or in `Generate_DataFile_MG`.
SavePdf	boolean (with default): if TRUE save graphs in pdf file named OutputFileName in folder OutputFilePath.
OutputFileName	character (with default): name of the pdf file that will be generated by the function if SavePdf=TRUE; length(OutputFileName)=2, see **PLOT OUTPUT** in **Value** section for more informations.
OutputFilePath	character (with default): path to the pdf file that will be generated by the function if SavePdf=TRUE. If it is not equal to "", it must be terminated by "/".

SaveEstimates boolean (with default): if TRUE save Bayes estimates, credible interval at level 68% and 95% and the result of the gelman en Rubin test of convergency, in a csv table named `OutputFileName` in folder `OutputFilePath`.

OutputTableName

 character (with default): name of the table that will be generated by the function if SaveEstimates=TRUE.

OutputTablePath

 character (with default): path to the table that will be generated by the function if SaveEstimates=TRUE. If it is not equal to "", it must be terminated by "/".

THETA numeric matrix or character (with default): input object for systematic and individual error. If systematic errors are considered, see the details section for instructions regarding how to correctly fill THETA; the user can refer to a matrix (numeric matrix) or to a csv file (character). Otherwise, default value is suitable, and only individual errors are considered.

sepTHETA character (with default): if THETA is character, indicate column separator in THETA csv file.

StratiConstraints

 numeric matrix or character(with default): input object for the statigraphic relation between samples. If there is stratigraphic relation between samples see the details section for instructions regarding how to correctly fill StratiConstraints; the user can refer to a matrix (numeric matrix) or to a csv file (character). If there is no stratigraphic relation default value is suitable.

sepSC character (with default): if StratiConstraints is character, indicate column separator in StratiConstraints .csv file.

LIN_fit logical (with default): if TRUE (default) allows a linear component, on top of the (default) saturating exponential curve, for the fitting of dose response curves. See details section for more informations on the proposed dose response curves.

Origin_fit logical (with default): if TRUE, forces the dose response curves to pass through the origin. See details section for more informations on the proposed growth curves.

distribution character (with default): type of distribution that defines how individual equivalent dose values are distributed around the palaeodose. Allowed inputs are **"cauchy"**, **"gaussian"**, **"lognormal_A"** and **"lognormal_M"**, see details section for more informations.

Iter integer (with default): number of iterations for the MCMC computation (for more information see [jags.model](#)).

t integer (with default): 1 every t iterations of the MCMC is considered for sampling the posterior distribution (for more information see [jags.model](#)).

Nb_chaines integer (with default): number of independent chains for the model (for more information see [jags.model](#)).

quiet [logical](#) (with default): enables/disables [rjags](#) messages

Details

** **How to fill** StratiConstraints **?** **

If there is stratigraphic relations between samples, **informations in DATA must be ordered by order of increasing ages**. To do this the user can either fill right Names in [Generate_DataFile](#) or in

Generate_DataFile_MG (as it is indicated in Details section of these function), or ordered by order of increasing ages outputs of Generate_DataFile or Generate_DataFile_MG in combine_DataFiles.

The user can fill the StratiConstraints matrix as follow.

1. **Size of the matrix**: row number of StratiConstraints matrix is equal to Nb_sample+1, and column number is equal to Nb_sample.

2. **First line of the matrix**: for all i in {1,...,Nb_Sample}, StratiConstraints[1,i]=1 that means the lower bound of the sample age (given in PriorAge[2i-1]) for the sample whose number ID is equal to i, is taken into account.

3. **Sample relations**: for all j in {2,...,Nb_Sample+1} and all i in {j,...,Nb_Sample}, StratiConstraints[j,i]=1 if sample age whose number ID is equal to j-1 is lower than sample age whose number ID is equal to i. Otherwise, StratiConstraints[j,i]=0.

Note that StratiConstraints_{2:Nb_sample+A,1:Nb_sample} is a upper triangular matrix.

The user can also use SCMatrix or SC_Ordered (if all samples are ordered) functions to construct the StratiConstraints matrix.

The user can also refer to a csv file that contaits the relation between samples as defined above. The user must take care about the separator used in the csv file using the argument sepSC.

** How to fill THETA covariance matrix concerning common and individual error? **

If systematic errors are considered, the user can fill the THETA matrix as follow.

- row number of THETA is equal the column number, equal to Nb_sample.
- For all i in {1,...,Nb_sample}, THETA[i,i] contaits individual error plus systematic error of the sample whose number ID is equal to i.
- For all i,j in {1,...,Nb_sample} and i different from j , THETA[i,j] contaits common error between samples whose number ID are equal to i and j.

Note that THETA[i,j] is a symetric matrix.

The user can also refer to a .csv file that contaits the errors as defined above.

** Option on growth curves **

As for Age_Computation and Palaeodose_Computation, the user can choose from 4 dose response curves:

- **Saturating exponential plus linear growth** (AgesMultiCS2_EXPLIN):
  for all x in IR+, f(x)=a(1-exp(-x/b))+cx+d; select
    - LIN_fit=TRUE
    - Origin_fit=FALSE
- **Saturating exponential growth** (AgesMultiCS2_EXP):
  for all x in IR+, f(x)=a(1-exp(-x/b))+d; select
    - LIN_fit=FALSE
    - Origin_fit=FALSE
- **Saturating exponential plus linear growth and fitting through the origin** (AgesMultiCS2_EXPLINZO):
  for all x in IR+, f(x)=a(1-exp(-x/b))+cx; select
    - LIN_fit=TRUE

– Origin_fit=TRUE

- **Saturating exponential growth and fitting through the origin** (AgesMultiCS2_EXPZO):
  for all x in IR+, f(x)=a(1-exp(-x/b)); select
    – LIN_fit=FALSE
    – Origin_fit=TRUE

** Option on equivalent dose distribution around the palaeodose **

The use can choose between :

- cauchy: a Cauchy distribution with location parameter equal to the palaeodose of the sample;

- gaussian: a Gaussian distribution with mean equal to the palaeodose of the sample;

- lognormal_A: a log-normal distribution with mean or **A**verage equal to the palaeodose of the sample:

- lognormal_M: a log-normal distribution with **M**edian equal to the palaeodose of the sample.

Value

NUMERICAL OUTPUT

1. **A list containing the following objects:**
   - **Sampling**: that corresponds to a sample of the posterior distributions of the age (in ka), palaeodose (in Gy) and equivalent dose dispersion (in Gy) parameters for each sample;
   - **Model_GrowthCurve**: stating which dose response fitting option was chosen;
   - **Distribution**: stating which distribution was chosen to model the dispersion of individual equivalent dose values around the palaeodose of the sample;
   - **PriorAge**: stating the priors used for the age parameter (in ka);
   - **StratiConstraints**: stating the stratigraphic relations between samples considered in the model;
   - **CovarianceMatrix**: stating the covariance matrix of error used in the model, highlighting common errors between samples or not.

2. **The Gelman and Rubin test of convergency**: prints the result of the Gelman and Rubin test of convergency for the age, palaeodose and equivalent dose dispersion parameters for each sample. A result close to one is expected.
   In addition, the user must visually assess the convergence of the trajectories by looking at the graph generated by the function (see **PLOT OUTPUT** for more informations).
   If both convergencies (Gelman and Rubin test and plot checking) are satisfactory, the user can consider the estimates as valid. Otherwise, the user may try increasing the number of MCMC interations (Iter) or being more precise on the PriorAge parameter (for example specify if it is a young sample c(0.01,10) an old sample c(10,100)), or changing the parameter distribution or the growth curve, to reach convergency.

3. **Credible intervals and Bayes estimates**: prints the Bayes esitmates, the credible intervals at 95% and 68% for the age, palaeodose and equivalent dose dispersion parameters for each sample.

PLOT OUTPUT

1. **MCMC trajectories**: A graph with the MCMC trajectories and posterior distributions of the age, palaeodose and equivalent dose dispersion parameters is displayed, there is one page per sample.

The first line of the figure correponds to the age parameter, the second to the palaeodose parameter and the third to the equivalent dose dispersion parameter. On each line, the plot on the left represents the MCMC trajectories, and the one on the right the posterior distribution of the parameter.

2. **Summary of sample age estimates**: plot credible intervals and Bayes estimate of each sample age on a same graph.

To give the results in a publication, we recommend to give the Bayes estimate of the parameters as well as the credible interval at 95% or 68%.

Note

Please note that the initial values for all MCMC are currently all the same for all chains since we rely on the automatic initial value generation of JAGS. This is not optimal and will be changed in future. However, it does not affect the quality of the age estimates if the chains have converged.

Author(s)

Claire Christophe, Anne Philippe, Guillaume Guérin

References

Combes, Benoit and Philippe, Anne, 2017. Bayesian analysis of multiplicative Gaussian error for multiple ages estimation in optically stimulated luminescence dating. Quaternary Geochronology (39, 24-34)

Combes, B., Philippe, A., Lanos, P., Mercier, N., Tribolo, C., Guerin, G., Guibert, P., Lahaye, C., 2015. A Bayesian central equivalent dose model for optically stimulated luminescence dating. Quaternary Geochronology 28, 62-70. doi:10.1016/j.quageo.2015.04.001

See Also

Generate_DataFile, Generate_DataFile_MG, rjags, plot_MCMC, SCMatrix Age_Computation, Palaeodose_Computation

Examples

```
## load data
data(DATA1,envir = environment())
data(DATA2,envir = environment())
Data <- combine_DataFiles(DATA2,DATA1)

## Age computation of samples GDB5 and GDB3,
priorage=c(1,10,20,60) # these samples are not young
## without common error and without stratigraphic constraints
Age <- AgeS_Computation(
  DATA = Data,
  Nb_sample = 2,
  SampleNames = c("GDB5","GDB3"),
  PriorAge = priorage,
  Iter = 50,
  Nb_chaines = 2,
  quiet = TRUE
  )

## Age computation of samples GDB5 and GDB3,
```

```
## without common error, assuming GDB5 age younder than GDB3 age
## Not run:
Nb_sample <- 2
SC <- matrix(
  data = c(1,1,0,1,0,0),
  ncol = 2,
  nrow = (Nb_sample+1),byrow = T)

Age <- AgeS_Computation(
 DATA = Data,
 Nb_sample = Nb_sample,
 SampleNames = c("GDB5","GDB3"),
 PriorAge = priorage,
 StratiConstraints = SC,
 Iter = 10000,
 quiet = FALSE)

## End(Not run)
```

Age_Computation   *Bayesian analysis for the OSL age estimation of one sample*

Description

This function computes the age (in ka) of a sample according to the model developed in Combes and Philippe (2017), based on an output of `Generate_DataFile` or `Generate_DataFile_MG`.
A sample, for which data is available in several BIN files, can be analysed.

Usage

```
Age_Computation(DATA, SampleName, PriorAge = c(0.01, 100),
  BinPerSample = c(1), SavePdf = FALSE, OutputFileName = c("MCMCplot"),
  OutputFilePath = c(""), SaveEstimates = FALSE,
  OutputTableName = c("DATA"), OutputTablePath = c(""), LIN_fit = TRUE,
  Origin_fit = FALSE, distribution = c("cauchy"), I = 1, Iter = 50000,
  t = 5, Nb_chaines = 3, quiet = FALSE)
```

Arguments

DATA	list of objects: LT, sLT, ITimes, dLab, ddot_env, regDose, J, K, Nb_measurement, provided by the function `Generate_DataFile` or `Generate_DataFile_MG`. DATA can contain informations for more than one sample.
SampleName	character: name of the sample.
PriorAge	numeric vector (with default): lower and upper bounds for the sample age parameter (in ka). Note that, length(PriorAge)=2.
BinPerSample	integer vector (with default): vector with the number of BIN files per sample. If in DATA there is more than one sample, the BinPerSample vector must be the same as that used to run the function `Generate_DataFile` or in `Generate_DataFile_MG` for generating the DATA object.
SavePdf	boolean (with default): if TRUE save graph in pdf file named OutputFileName in folder OutputFilePath.

OutputFileName	character (with default): name of the pdf file that will be generated by the function if SavePdf=TRUE; length(OutputFileName)=2, see **PLOT OUTPUT** in **Value** section for more informations.
OutputFilePath	character (with default): path to the pdf file that will be generated by the function if SavePdf=TRUE. If it is not equal to "", it must be terminated by "/".
SaveEstimates	boolean (with default): if TRUE save Bayes estimates and credible interval at level 68% and 95% and the result of the gelman en Rubin test of convergency, in a csv table named OutputFileName in folder OutputFilePath.
OutputTableName	
	character (with default): name of the table that will be generated by the function if SaveEstimates=TRUE.
OutputTablePath	
	character (with default): path to the table that will be generated by the function if SaveEstimates=TRUE. If it is not equal to "", it must be terminated by "/".
LIN_fit	logical (with default): if TRUE (default) allows a linear component, on top of the (default) saturating exponential curve, for the fitting of dose response curves. See details section for more informations on the proposed dose response curves.
Origin_fit	logical (with default): if TRUE, forces the dose response curves to pass through the origin. See details section for more informations on the proposed growth curves.
distribution	character (with default): type of distribution that defines how individual equivalent dose values are distributed around the palaeodose. Allowed inputs are **"cauchy"**, **"gaussian"**, **"lognormal_A"** and **"lognormal_M"**, see details section for more informations.
I	integer (with default): if DATA contains data from more than one sample, I indicates the ID number of the sample to be analysed.
Iter	integer (with default): number of iterations for the MCMC computation (for more information see [jags.model](#)).
t	integer (with default): 1 every t iterations of the MCMC is considered for sampling the posterior distribution (for more information see [jags.model](#)).
Nb_chaines	integer (with default): number of independent chains for the model (for more information see [jags.model](#)).
quiet	[logical](#) (with default): enables/disables [rjags](#) messages

Details

** Option on growth curves **

As for [AgeS_Computation](#) and [Palaeodose_Computation](#), the user can choose from 4 dose response curves:

- **Saturating exponential plus linear growth** (AgeMultiBF_EXPLIN):

  for all x in IR+, f(x)=a(1-exp(-x/b))+cx+d; select
  - LIN_fit=TRUE
  - Origin_fit=FALSE

- **Saturating exponential growth** (AgeMultiBF_EXP):

  for all x in IR+, f(x)=a(1-exp(-x/b))+d; select
  - LIN_fit=FALSE

– `Origin_fit=FALSE`

- **Saturating exponential plus linear growth and fitting through the origin** (`AgeMultiBF_EXPLINZO`):
  for all x in IR+, f(x)=a(1-exp(-x/b))+cx; select
    – `LIN_fit=TRUE`
    – `Origin_fit=TRUE`
- **Saturating exponential growth and fitting through the origin** (`AgeMultiBF_EXPZO`):
  for all x in IR+, f(x)=a(1-exp(-x/b)); select
    – `LIN_fit=FALSE`
    – `Origin_fit=TRUE`

** Option on equivalent dose distribution around the palaeodose **

The use can choose between :

- `cauchy`: a Cauchy distribution with location parameter equal to the palaeodose of the sample
- `gaussian`: a Gaussian distribution with mean equal to the palaeodose of the sample
- `lognormal_A`: a log-normal distribution with mean or **A**verage equal to the palaeodose of the sample
- `lognormal_M`: a log-normal distribution with **M**edian equal to the palaeodose of the sample

Value

NUMERICAL OUTPUT

1. **A list containing the following objects**:
    - **Sampling** that corresponds to a sample of the posterior distributions of the age (in ka), palaeodose (in Gy) and equivalent dose dispersion (in Gy) parameters.
    - **Model_GrowthCurve**, stating which dose response fitting option was chosen;
    - **Distribution**, stating which distribution was chosen to model the dispersion of individual equivalent dose values around the palaeodose of the sample;
    - **PriorAge**, stating the priors used for the age parameter (in ka).
2. **The Gelman and Rubin test of convergency**: prints the result of the Gelman and Rubin test of convergency for the age, palaeodose and equivalent dose dispersion parameters. A result close to one is expected.
    In addition, the user must visually assess the convergence of the trajectories by looking at the graph generated by the function (see **PLOT OUTPUT** for more informations).
    If both convergencies (Gelman and Rubin test and plot checking) are satisfactory, the user can consider the printed estimates as valid. Otherwise, the user may try increasing the number of MCMC interations (`Iter`), or being more precise on the `PriorAge` parameter (for example specify if it is a young sample `c(0.01,10)` an old sample `c(10,100)`), or changing the parameter `distribution` or the growth curve, to reach convergency.to reach convergency.
3. **Credible intervals and Bayes estimates**: prints the Bayes esitmates, the credible intervals at 95% and 68% for the age, palaeodose and equivalent dose dispersion parameters of the sample.

PLOT OUTPUT

A graph with the MCMC trajectories and posterior distributions of the age, palaeodose and equivalent dose dispersion parameters is displayed.
The first line of the figure correponds to the age parameter, the second to the palaeodose parameter

and the third to the equivalent dose dispersion parameter. On each line, the plot on the left represents the MCMC trajectories, and the one on the right the posterior distribution of the parameter.

To give the results in a publication, we recommend to give the Bayes estimate of the parameter as well as the credible interval at 95% or 68%.

Note

Please note that the initial values for all MCMC are currently all the same for all chains since we rely on the automatic initial value generation of JAGS. This is not optimal and will be changed in future. However, it does not affect the quality of the age estimates if the chains have converged.

Author(s)

Claire Christophe, Sebastian Kreutzer, Anne Philippe, Guillaume Guérin

References

Combes, Benoit and Philippe, Anne, 2017. Bayesian analysis of multiplicative Gaussian error for multiple ages estimation in optically stimulated luminescence dating. Quaternary Geochronology (39, 24-34)

Combes, B., Philippe, A., Lanos, P., Mercier, N., Tribolo, C., Guerin, G., Guibert, P., Lahaye, C., 2015. A Bayesian central equivalent dose model for optically stimulated luminescence dating. Quaternary Geochronology 28, 62-70. doi:10.1016/j.quageo.2015.04.001

See Also

Generate_DataFile, Generate_DataFile_MG, rjags, plot_MCMC AgeS_Computation, Palaeodose_Computation

Examples

```
## load data file generated by the function Generate_DataFile
data(DATA1,envir = environment())
priorage <- c(10,60) # GDB3 is an old sample
Age <- Age_Computation(
 DATA = DATA1,
 SampleName = "GDB3",
 PriorAge = priorage,
 Iter = 100,
 quiet = TRUE)
```

Age_OSLC14   *Bayesian analysis for age estimation of OSL measerments and 14C ages of various samples*

Description

This function compute an age of OSL data of at least two samples and calibrate 14C ages of samples to get an age (in ka).
Age of OSL data are computed according to the model given in Combes and Philippe (2017). Single-grain or Multi-grain OSL measurements can be analysed simultaneouly (with output of Generate_DataFile or Generate_DataFile_MG or both of them using combine_DataFiles).

Samples, for which data is avalilable in several BIN files, can be analysed.
For C14 data, the user can choose one of the following radiocarbon calibration curve: Northern or Sourthen Hemisphere or marine atmospheric.

Usage

```
Age_OSLC14(DATA, Data_C14Cal, Data_SigmaC14Cal, Nb_sample, SampleNames,
  SampleNature, PriorAge = rep(c(10, 60), Nb_sample), SavePdf = FALSE,
  OutputFileName = c("MCMCplot", "HPD_Cal14CCurve", "summary"),
  OutputFilePath = c(""), SaveEstimates = FALSE,
  OutputTableName = c("DATA"), OutputTablePath = c(""),
  StratiConstraints = c(), sepSC = c(","), BinPerSample = rep(1,
  sum(SampleNature[1, ])), THETA = c(), sepTHETA = c(","), LIN_fit = TRUE,
  Origin_fit = FALSE, distribution = c("cauchy"), Model_C14 = c("full"),
  CalibrationCurve = c("AtmosphericNorth"), Iter = 50000, t = 5,
  Nb_chaines = 3, quiet = FALSE)
```

Arguments

DATA   list of objects: LT, sLT, ITimes, dLab, ddot_env, regDose, J, K, Nb_measurement, provided by the function `Generate_DataFile` or `Generate_DataFile_MG` or `combine_DataFiles`. DATA contains information for more than one sample. If there is stratigraphic relations between samples, informations in DATA must be ordered by order of incresing ages. See the details section to for more informations.

Data_C14Cal   numeric vector: corresponding to 14C age estimate (in years, conversion in ka is automatically donne in the function). If there is stratigraphic relations between samples, `Data_C14Cal` must be ordered by order of incresing ages.

Data_SigmaC14Cal
                    numeric vector: correponding to the error of 14C age estimates.

Nb_sample   integer: number of samples (OSL data and 14C age), (Nb_sample>3, at least to sample of OSL data and one sample of 14C age).

SampleNames   character vector: sample names for both OSL data and C14 data. The length of this vector is equal to Nb_sample. If there is stratigephic relation, this vector must be ordered by increasing order (to mix OSL samples and 14C ages if it is needed).

SampleNature   numeric matrix: states the nature of the sample. Row number of `SampleNature` matrix is equal to 2 and column number is equal to Nb_sample. First line of the matrix: `SampleNature[1,i]` states if sample whose number ID is equal to i, is an OSL sample **1** or not **0**. Second line of the matrix: `SampleNature[2,i]` states if sample whose number ID is equal to i, is an 14C sample **1** or not **0**.

PriorAge   numeric vector (with default): lower and upper bounds for age parameter of each sample **(in ka)**. Note that, length(PriorAge)=2*Nb_sample and PriorAge[2i-1, 2i] correponds to the lower and upper bounds of sample whose number ID is equal to i.

SavePdf   boolean (with default): if TRUE save graphs in pdf file named `OutputFileName` in folder `OutputFilePath`.

OutputFileName   character (with default): name of the pdf file that will be generated by the function if SavePdf=TRUE, length(OutputFileName)=3, see **PLOT OUTPUT** in **Value** section for more informations.

OutputFilePath   character (with default): path to the pdf file that will be generated by the function
                    if SavePdf=TRUE. If it is not equal to "", it must be terminated by "/".

SaveEstimates   boolean (with default): if TRUE save Bayes estimates, credible interval at level
                    68% and 95% and the result of the gelman en Rubin test of convergency, in a
                    csv table named OutputFileName in folder OutputFilePath.

OutputTableName
                    character (with default): name of the table that will be generated by the function
                    if SaveEstimates=TRUE.

OutputTablePath
                    character (with default): path to the table that will be generated by the function
                    if SaveEstimates=TRUE. If it is not equal to "", it must be terminated by "/".

StratiConstraints
                    numeric matrix or character(with default): input object for the statigraphic re-
                    lation between samples. If there is stratigraphic relation between samples see the
                    details section for instructions regarding how to correctly fill StratiConstraints,
                    the user can refer to a matrix (numeric matrix) or to a csv file (character). Oth-
                    erwise, default value is suitable.

sepSC   character (with default): if StratiConstraints is character, indicate column
                    separator in StratiConstraints csv file.

BinPerSample   integer vector (with default): vector with the number of BIN files per OSL
                    sample. The length of this vector is equal to the number of OSL samples.
                    BinPerSample[i] correponds to the number of BIN files for the sample whose
                    number ID is equal to i. For more information to fill this vector, we refer to
                    detatils in Generate_DataFile or in Generate_DataFile_MG.

THETA   numeric matrix or character (with default): input object for systematic and indi-
                    vidual error for OSL samples. If systematic errors are considered, see the details
                    section for instructions regarding how to correctly fill THETA; the user can refer
                    to a matrix (numeric matrix) or to a csv file (character). Otherwise, default value
                    is suitable, and only individual error is considered.

sepTHETA   character (with default): if THETA is character, indicate column separator in
                    THETA csv file.

LIN_fit   logical (with default): if TRUE (default) allows a linear component, on top of the
                    (default) saturating exponential curve, for the fitting of dose response curves, for
                    OSL samples. See details for more informations on the proposed dose response
                    curves.

Origin_fit   logical (with default): if TRUE, forces the dose response curves to pass through
                    the origin. See details for more informations on the proposed growth curves, for
                    OSL samples.

distribution   character (with default): type of distribution that defines how individual equiv-
                    alent dose values are distributed around the palaeodose, for OSL samples. Al-
                    lowed inputs are **"cauchy"**, **"gaussian"**, **"lognormal_A"** and **"lognormal_M"**,
                    see details for more informations.

Model_C14   character (with default): if **"full"**, error on estimate calibration curve is taken
                    account, for 14C samples. If **"naive"** this error is not taken account in the age
                    estimate.

CalibrationCurve
                    character (with default): calibration curve choosen, for 14C samples. Allowed
                    inputs are

                        • **"AtmosphericNorth"** for Northern Hemisphere atmospheric radiocarbon
                          calibration curve,

- **"Marine"** for Marine radiocarbon calibration curve,
- **"AtmosphericSouth"** for Southern Hemisphere atmospheric radiocarbon calibration curve,
- **a csv file, with tree columns, the first column is dedicated to "Cal.BP", the second to "X14C.age", the third to "Error". The decimal of this file must be a dot, and the separator must be a comma.**

Iter   integer (with default): number of iterations for the MCMC computation (for more information see `jags.model`).

t   integer (with default): 1 every `t` iterations of the MCMC is considered for sampling the posterior distribution (for more information see `jags.model`).

Nb_chaines   integer (with default): number of independent chains for the model (for more information see `jags.model`).

quiet   `logical` (with default): enables/disables `rjags` messages

Details

Note that there is tree type of arguments in the previous list. There are arguments for informtations concerning only OSL samples: `DATA`, `BinPerSample`, `THETA`, `sepTHETA`, `LIN_fit`, `Origin_fit`, `distribution`.

There are arguments for informtations concerning only C14 samples: `Data_C14Cal`, `Data_SigmaC14Cal`, `Model_C14`, `CalibrationCurve`.

There are arguments for informtations concerning all the samples: `Nb_sample`, `SampleNames`, `SampleNature`, `PriorAge`, `SavePdf`, `OutputFileName`, `OutputFilePath`, `SaveEstimates`, `OutputTableName`, `OutputTablePath`, `StratiConstraints`, `sepSC`.

** How to fill `StratiConstraints` **? ****

If there is stratigraphic relations between samples, **14C estimate age in** `Data_C14Cal` **must be ordered by order of increasing ages, as informations in** `DATA`. Names in `SampleNames` must be ordered and correponds to the order in `Data_C14Cal` and in `DATA`, also if it is needed to mix names of OSL samples and 14C samples.

The user can fill the `StratiConstraints` matrix as follow.

1. **Size of the matrix**: row number of `StratiConstraints` matrix is equal to `Nb_sample+1`, and column number is equal to `Nb_sample`.

2. **First line of the matrix**: for all `i` in {1,...,Nb_Sample}, `StratiConstraints[1,i]=1` that means the lower bound of the sample age (given in `PriorAge[2i-1]`) for the sample whose number ID is equal to `i`, is taken into account.

3. **Sample relations**: for all `j` in {2,...,Nb_Sample+1} and all `i` in {j,...,Nb_Sample}, `StratiConstraints[j,i]=1` if sample age whose number ID is equal to `j-1` is lower than sample age whose number ID is equal to `i`. Otherwise, `StratiConstraints[j,i]=0`.

Note that `StratiConstraints_{2:Nb_sample+1,1:Nb_sample}` is a upper triangular matrix.

The user can also use `SCMatrix` or `SC_Ordered` (if all samples are ordered) function to construc the `StratiConstraints` matrix.

The user can also refer to a csv file that containts the relation between samples as defined above. The user must take care about the separator used in the csv file using the argument `sepSC`.

** How to fill THETA **covariance matrix concerning common and individual error? ****

If systematic errors are considered, the user can fill the THETA matrix as follow.

- row number of THETA is equal the column number, equal to Nb_sample.
- For all i in {1,...,Nb_sample}, THETA[i,i] contaits individual error plus systematic error of the sample whose number ID is equal to i.
- For all i,j in {1,...,Nb_sample} and i different from j, THETA[i,j] contaits common error between samples whose number ID are equal to i and j.

Note that THETA[i,j] is a symetric matrix.

The user can also refer to a .csv file that contaits the errors as defined above.

** Option on growth curves **

As for Age_Computation and Palaeodose_Computation, the user can choose from 4 dose response curves:

- **Saturating exponential plus linear growth** (AgesMultiCS2_EXPLIN):
  for all x in IR+, f(x)=a(1-exp(-x/b))+cx+d; select
  - LIN_fit=TRUE
  - Origin_fit=FALSE
- **Saturating exponential growth** (AgesMultiCS2_EXP):
  for all x in IR+, f(x)=a(1-exp(-x/b))+d; select
  - LIN_fit=FALSE
  - Origin_fit=FALSE
- **Saturating exponential plus linear growth and fitting through the origin** (AgesMultiCS2_EXPLINZO):
  for all x in IR+, f(x)=a(1-exp(-x/b))+cx; select
  - LIN_fit=TRUE
  - Origin_fit=TRUE
- **Saturating exponential growth and fitting through the origin** (AgesMultiCS2_EXPZO):
  for all x in IR+, f(x)=a(1-exp(-x/b)); select
  - LIN_fit=FALSE
  - Origin_fit=TRUE

** Option on equivalent dose distribution around the palaeodose **

The use can choose between :

- cauchy: a Cauchy distribution with location parameter equal to the palaeodose of the sample
- gaussian: a Gaussian distribution with mean equal to the palaeodose of the sample
- lognormal_A: a log-normal distribution with mean or **A**verage equal to the palaeodose of the sample
- lognormal_M: a log-normal distribution with **M**edian equal to the palaeodose of the sample

** More precision on `Model` ******

We propose two models "full" or "naive". If `Model='full'` that means measurement error and error on calibration curve are taken account in the Bayesian model; if `Model="naive"` that means only error on measurement are taken account in the mode.

More precisely, the model considered here, as the one developed by Christen, JA (1994), assume multiplicative effect of errors to address the problem of outliers. In addition, to not penalyse variables that are not outliers and damage theirs estimation, we introduce a structure of mixture, that means only variable that are considered as outlier have in addition a multiplicative error.

Value

NUMERICAL OUTPUT

1. **A list containing the following objects:**
   - **Sampling**: that corresponds to a sample of the posterior distributions of the age parameters (in ka for both C14 samples and OSL samples);
   - **PriorAge**: stating the priors used for the age parameter;
   - **StratiConstraints**: stating the stratigraphic relations between samples considered in the model;
   - **Model_OSL_GrowthCurve**: stating which dose response fitting option was chosen;
   - **Model_OSL_Distribution**: stating which distribution was chosen to model the dispersion of individual equivalent dose values around the palaeodose of the sample;
   - **Model_C14**: stating which model was chosen (″full″ or ″naive″);
   - **CalibrationCurve**: stating which radiocarbon calibration curve was chosen;
   - **Outlier**: stating the names of samples that must be outliers.

2. **The Gelman and Rubin test of convergency**: prints the result of the Gelman and Rubin test of convergency for the age estimate for each sample. A result close to one is expected.
   In addition, the user must visually assess the convergence of the trajectories by looking at the graph generated by the function (see **PLOT OUTPUT** for more informations).
   If both convergencies (Gelman and Rubin test and plot checking) are satisfactory, the user can consider the estimates as valid. Otherwise, the user may try increasing the number of MCMC interations (`Iter`) or be more precise on the `PriorAge` parameter to reach convergency.

3. **Credible intervals and Bayes estimates**: prints the Bayes esitmates, the credible intervals at 95% and 68% for the age parameters for each sample.

PLOT OUTPUT

1. **MCMC trajectories**: A graph with the MCMC trajectories and posterior distributions of the age parameter is displayed.
   On each line, the plot on the left represents the MCMC trajectories, and the one on the right the posterior distribution of the parameter.

2. **Age estimate and HPD at 95% of 14C samples on calibration curve**: plot age estimate and HPD on calibration plot.

3. **Summary of sample age estimates**: plot credible intervals and Bayes estimate of each sample age on a same graph.

Note

Please note that the initial values for all MCMC are currently all the same for all chains since we rely on the automatic initial value generation of JAGS. This is not optimal and will be changed in future. However, it does not affect the quality of the age estimates if the chains have converged.

Author(s)

Claire Christophe, Anne Philippe, Guillaume Guerin

References

Reimer PJ, Bard E, Bayliss A, Beck JW, Blackwell PC, Bronl Ramsey C, Buck CE, Cheng H, Edwards RL, Friedrich M, Grootes PM, Guilderson TP, Haflidason H, Hajdas I, Hatte C, Heaton TJ, Hoffmann DL, Hogg AG, Hughen KA, Kaiser KF, Kromer B, Manning SW, Niu M, Reimer RW, Richards DA, Scott EM, Southon JR, Staff RA, Turney CSM, van der Plicht J. 2013. IntCal13 ans Marine13 radiocarbon age calibration curves 0-50000 years cal BP. Radiocarbon 55(4)=1869-1887.

Hogg AG, Hua Q, Blackwell PG, Niu M, Buck CE, Guilderson TP, Heaton TJ, Palmer JG, Reimer PJ, Reimer RW, Turney CSM, Zimmerman SRH. 2013. SHCal13 Southern Hemisphere calibration, 0-50000 years cal BP. Radiocarbon 55(4):1889-1903

See Also

rjags, plot_MCMC, SCMatrix

Examples

```
## Load data
# OSL data
data(DATA1,envir = environment())
data(DATA2,envir = environment())
Data <- combine_DataFiles(DATA2,DATA1)

# 14C data
C14Cal <- DATA_C14$C14[1,1]
SigmaC14Cal <- DATA_C14$C14[1,2]
Names <- DATA_C14$Names[1]

# Prior Age
prior=rep(c(1,60),3)
samplenature=matrix(data=c(1,0,1,0,1,0),ncol=3,nrow=2,byrow=TRUE)
SC <- matrix(data=c(1,1,1,0,1,1,0,0,1,0,0,0),ncol=3,nrow=4,byrow=TRUE)

## Age computation of samples
Age <- Age_OSLC14(DATA=Data,Data_C14Cal=C14Cal,Data_SigmaC14Cal=SigmaC14Cal,
    SampleNames=c("GDB5",Names,"GDB3"),Nb_sample=3,SampleNature=samplenature,
    PriorAge=prior,StratiConstraints=SC,Iter=50,Nb_chaines=2)
```

AtmosphericNorth_CalC14

Atmospheric North data for calibration of 14C age

Description

As 14C years is not equal to calendar years because atmospheric 14C concentration varies through time. Hence, data in AtmosphericNorth_CalC14 allows a calibration for mid-latitude Northern Hemisphere atmospher reservoir.

Usage

```
data("AtmosphericNorth_CalC14")
```

Format

A data frame with 5 variables.

CAL.BP a numeric vector correpondig to calendar years befor present

X14C.age a numeric vector correponding to 14C age

Error a numeric vector correponding to error arround 14C age measurement

References

Reimer PJ, Bard E, Bayliss A, Beck JW, Blackwell PC, Bronl Ramsey C, Buck CE, Cheng H, Edwards RL, Friedrich M, Grootes PM, Guilderson TP, Haflidason H, Hajdas I, Hatte C, Heaton TJ, Hoffmann DL, Hogg AG, Hughen KA, Kaiser KF, Kromer B, Manning SW, Niu M, Reimer RW, Richards DA, Scott EM, Southon JR, Staff RA, Turney CSM, van der Plicht J. 2013. IntCal13 ans Marine13 radiocarbon age calibration curves 0-50000 years cal BP. Radiocarbon 55(4)=1869-1887.

Examples

```
data(AtmosphericNorth_CalC14)
## maybe str(AtmosphericNorth_CalC14) ; head(AtmosphericNorth_CalC14) ...
```

AtmosphericSouth_CalC14

Atmospheric South data for calibration of 14C age

Description

As 14C years is not equal to calendar years because atmospheric 14C concentration varies through time. Hence, data in AtmosphericSouth_CalC14 allows a calibration for mid-latitude Southern Hemisphere atmospher reservoir.

Usage

```
data("AtmosphericSouth_CalC14")
```

Format

A data frame with 3 variables.

`CAL.BP` a numeric vector correpondig to calendar years befor present

`X14C.age` a numeric vector correponding to 14C age

`Error` a numeric vector correponding to error arround 14C age measurement

References

Reimer PJ, Bard E, Bayliss A, Beck JW, Blackwell PC, Bronl Ramsey C, Buck CE, Cheng H, Edwards RL, Friedrich M, Grootes PM, Guilderson TP, Haflidason H, Hajdas I, Hatte C, Heaton TJ, Hoffmann DL, Hogg AG, Hughen KA, Kaiser KF, Kromer B, Manning SW, Niu M, Reimer RW, Richards DA, Scott EM, Southon JR, Staff RA, Turney CSM, van der Plicht J. 2013. IntCal13 ans Marine13 radiocarbon age calibration curves 0-50000 years cal BP. Radiocarbon 55(4)=1869-1887.

Examples

```
data(AtmosphericSouth_CalC14)
## maybe str(AtmosphericSouth_CalC14) ; head(AtmosphericSouth_CalC14) ...
```

---

combine_DataFiles   *Combine objects generated by [Generate_DataFile](#) and [Generate_DataFile_MG](#)*

Description

Combine objects generated by Generate_DataFile and Generate_DataFile_MG

Old function Concat_DataFile()

Usage

```
combine_DataFiles(...)

Concat_DataFile(...)
```

Arguments

`...`   list objects generated by Generate_DataFile or Generate_DataFile_MG

Details

The function allows to combine data already generated by Generate_DataFile or Generate_DataFile_MG. The number of input objects is not limited and the function works similar to the standard base R function c(), but preserves the particular structure of the objects imported and generated by 'BayLum'. The elements are combined by list element names.

Combining such data is rather useful in two scenarious:

- The data have been already imported and treated and then stored in RData-files. Using the function combine_DataFiles() will significantly speed up the processing time,

- simultaneous analysis of single and multi-grain OSL measurements.

Value

A nested list combining the input objects.

Function version

0.1.1

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, UMR 5060, CNRS - Université Bordeaux Montaigne (France), adapting the idea from the function 'Concat_DataFile()' by Claire Christophe.

See Also

Generate_DataFile, Generate_DataFile_MG

Examples

```
# load data files
data(DATA1,envir = environment())
data(DATA2,envir = environment())

#combine objects
DATA3 <- combine_DataFiles(DATA1, DATA2)
str(DATA3)
```

DATA1   *DATA of sample named GDB3*

Description

list of objects: LT, sLT, ITimes, dLab, ddot_env, regDose, J,K,Nb_measurement obtained using Generate_DataFile function with single-grain OSL measurementsl of the sample GDB3.

Usage

```
data("DATA1")
```

Format

A list containing:

LT: (one list per sample): each list contains all L/T values for the corresponding sample;

sLT: (one list per sample): each list contains all uncertainties on L/T values for the corresponding sample;

ITimes: (one list per sample): each list contains irradiation time values for the corresponding sample;

dLab= a matrix containing in line i, the laboratory dose rate and its variance for sample i;

ddot_env: a matrix containing in line i, the environmental dose rate and its variance (excluding the common error terms) for sample i;

regDose: (one list per sample): each list contains all regenerated doses;

J: a vector giving, for each BIN file, the number of aliquots selected for the analysis;

K: a vector giving, for each BIN file, the number of regenerative doses in the SAR protocol;

Nb_measurement: a vector giving, for each BIN file, the number of measurements;

References

For more informations on this sample we refer to the following publication:

Tribolo, C., Asrat, A., Bahain, J. J., Chapon, C., Douville, E., Fragnol, C., Hernandez, M., Hovers, E., Leplongeon, A., Martin, L, Pleurdeau, D, Pearson, O , Puaud, S, Assefa, Z. (2017). Across the Gap: Geochronological and Sedimentological Analyses from the Late Pleistocene-Holocene Sequence of Goda Buticha, Southeastern Ethiopia. PloS one, 12(1), e0169418.

Examples

```
data(DATA1)
str(DATA1)
```

DATA2 *DATA on sample named GDB5*

Description

list of objects: LT, sLT, ITimes, dLab, ddot_env, regDose, J,K,Nb_measurement obtained using Generate_DataFile function with single-grain OSL measurementsl of the sample GDB5.

Usage

```
data("DATA2")
```

Format

A data frame containing:

LT: (one list per sample): each list contains all L/T values for the corresponding sample;

sLT: (one list per sample): each list contains all uncertainties on L/T values for the corresponding sample;

ITimes: (one list per sample): each list contains irradiation time values for the corresponding sample;

dLab: a matrix containing in line i, the laboratory dose rate and its variance for sample i;

ddot_env: a matrix containing in line i, the environmental dose rate and its variance (excluding the common error terms) for sample i;

regDose: (one list per sample): each list contains all regenerated doses;

J: a vector giving, for each BIN file, the number of aliquots selected for the analysis;

K: a vector giving, for each BIN file, the number of regenerative doses in the SAR protocol;

Nb_measurement: , a vector giving, for each BIN file, the number of measurements;

References

For more informations on this sample we refer to the following publication:

Tribolo, C., Asrat, A., Bahain, J. J., Chapon, C., Douville, E., Fragnol, C., Hernandez, M., Hovers, E., Leplongeon, A., Martin, L, Pleurdeau, D, Pearson, O , Puaud, S, Assefa, Z. (2017). Across the Gap: Geochronological and Sedimentological Analyses from the Late Pleistocene-Holocene Sequence of Goda Buticha, Southeastern Ethiopia. PloS one, 12(1), e0169418.

Examples

```
data(DATA2)
str(DATA2)
```

DATA3 *DATA of sample named FER1*

Description

list of objects: LT, sLT, ITimes, dLab, ddot_env, regDose, J,K,Nb_measurement obtained using Generate_DataFile function with multi-grain OSL measurementsl of the sample FER1.

Usage

```
data("DATA3")
```

Format

A list containing:

LT: (one list per sample): each list contains all L/T values for the corresponding sample;

sLT: (one list per sample): each list contains all uncertainties on L/T values for the corresponding sample;

ITimes: (one list per sample): each list contains irradiation time values for the corresponding sample;

dLab= a matrix containing in line i, the laboratory dose rate and its variance for sample i;

ddot_env: a matrix containing in line i, the environmental dose rate and its variance (excluding the common error terms) for sample i;

regDose: (one list per sample): each list contains all regenerated doses;

J: a vector giving, for each BIN file, the number of aliquots selected for the analysis;

K: a vector giving, for each BIN file, the number of regenerative doses in the SAR protocol;

Nb_measurement: a vector giving, for each BIN file, the number of measurements;

References

For more informations on this sample we refer to the following publication:

Guerin, G., Frouin, M., Talamo, S., Aldeias, V., Bruxelles, L., Chiotti, L., Goldberg, P., Hublin, J.J., Jain, M., Lahaye, C., Madelaine, S., Maureille, B., McPherron, S., Mercier, N., Murray, A., Sandgathe, D., Steele, T., Thomsen, K., Turq, A. (2015). A multi-method luminescence dating of the Palaeolithic sequence of La Ferrassie based on new excavations adjacent to the La Ferrassie 1 and 2 skeletons. Journal of Archaeological Science, 58, 147-166.

Examples

```
data(DATA3)
str(DATA3)
```

DATA_C14	*C14 cal age estiamte and its error*

Description

C14 cal age estiamtes and theirs error of samples S-EVA-26510, S-EVA-26506, S-EVA-26507, S-EVA-26508.

Usage

```
data("DATA_C14")
```

Format

A list containing:

Names: character vector of the sample names;

C14: numeric matrix, in the first column the 14C Cal age of the samples, and in the second column theirs errors.

References

For more informations on this sample we refer to the following publication:

Guerin, G., Frouin, M., Talamo, S., Aldeias, V., Bruxelles, L., Chiotti, L., Goldberg, P., Hublin, J.J., Jain, M., Lahaye, C., Madelaine, S., Maureille, B., McPherron, S., Mercier, N., Murray, A., Sandgathe, D., Steele, T., Thomsen, K., Turq, A. (2015). A multi-method luminescence dating of the Palaeolithic sequence of La Ferrassie based on new excavations adjacent to the La Ferrassie 1 and 2 skeletons. Journal of Archaeological Science, 58, 147-166.

Examples

```
data(DATA_C14)
(DATA_C14)
```

Generate_DataFile	*Generates, from one (or several) BIN-file(s) of Single-grain OSL measurements, a list of luminescence data and information before statistical analysis*

Description

This function is used to generate, from the BIN file(s), a list of values of: **Single-grain** OSL intensities and associated uncertainties, regenerative doses, etc., which will be the input of the Bayesian models. To be easy-to-use, this function requires a rigorous organisation - all needed files should be arranged in one folder - of informations concerning each BIN file.
It is possible to process data for various samples simultaneously and to consider more than one BIN file per sample.

Usage

```
Generate_DataFile(Path, FolderNames, Nb_sample,
  Nb_binfile = length(FolderNames), BinPerSample = rep(1, Nb_sample),
  sepDP = c(","), sepDE = c(","), sepDS = c(","), sepR = c("="),
  verbose = TRUE, ...)
```

Arguments

Path	character (**required**): the path to the project folder, containing one or more subfolders in which the BIN files are located. If it is not equal to "", it must be terminated by "/".
FolderNames	character (**required**): list of names of the sub-folders containing the BIN files • each subfolder must contain a BIN file and associated csv files. See details for more informations on associated csv files required in the subfolders. If there is more than one BIN file per sample, see the details section for instructions regarding how to correctly fill the FolderNames vector.
Nb_sample	integer (**required**): number of samples.
Nb_binfile	integer (with default): number of BIN files. It must be equal to, or greater than Nb_sample.
BinPerSample	integer vector (with default): vector with the number of BIN files per sample. The length of this vector must be equal to Nb_sample and the sum of entries of this vector must be equal to Nb_binfile. If there is more than one BIN file per sample, see the details section for instructions regarding how to correctly fill BinPerSample vector. Otherwise, this vector must contain a list of 1 values.
sepDP	character (with default): column separator in the DiscPose.csv files.
sepDE	character (with default): column separator in the DoseEnv.csv files.
sepDS	character (with default): column separator in the DoseLab.csv files.
sepR	character (with default): column separator in the Rule.csv files.
verbose	logical (with default): enable/disable verbose mode
...	further arguments that can be passed to Luminescence::read_BIN2R.

Details

With Path and FolderNames, this function goes to the subfolders containing the BIN files and associated information to compute the luminescence data.

** What are the required files in each subfolder? **

Each subfolder can be named, for example, as the sample name followed by a number; it must contain:

- **bin.BIN**: the bin file renamed as bin.BIN (note: the name of all files matters);
- **DiscPos.csv**: a two columns csv file containing the list of disc and grain position number of the previously selected grains (typically this list will include the position of grains based on their sensitivity, recycling or other properties);
- **DoseEnv.csv**: a two columns file containing the observation of the natural (or environmental), dose rate, and its non-shared variance (i.e. after removing all shared errors), both in Gy. Note: the user shall provide the squared value of the error associated with the dose rate experienced by the sample grains in nature;

- **DoseSourve.csv**: a two columns file containing the observation of the laboratory dose rate, and its variance (squared error) both in Gy;

- **rule.csv**: a csv file containing information on
    - `beginSignal=` the first channel for summing the natural or regenerative OSL signal (typically 1 or 6);
    - `endSignal=` the last channel for summing the natural or regenerative OSL signal (typically 5 or 10);
    - `beginBackground=` the first channel for background estimation of the natural or regenerative OSL signal (typically 76 or 81);
    - `endBackground=` the last channel for background estimation of the natural or regenerative OSL signal (typically 95 or 100);
    - `beginTest=`,
    - `endTest=`,
    - `beginTestBackground=`,
    - `endTestBackground=` same values as above, for the test dose response (typically the same values should be used);
    - `inflatePercent=` uncertainty arising from the instrument reproducibility (typically 0.02, i.e. 2%);
    - `nbOfLastCycleToRemove=` number of cycles at the end of the SAR protocol which should not be included in the dose response curve fitting (typically 1 if only a recycling test is performed, or 2 if both recycling and IR depletion are tested).

** How to fill the `FolderNames` **vector? ****

`FolderNames` is a vector of length `Nb_binfile`. `FolderNames[i]` is the name (e.g., Sample1-File1, or successive names separated by "/" signs, if BIN files are in subfolders, e.g. Sample1/File1) of the subfolder containing all informations on the BIN file of ID number `i`. The names in `FolderNames` are ordered following two rules:

- The names in the `FolderNames` vector must be ordered following the sample order (the names of subfolders containing BIN files for the same sample should follow each other in the `FolderNames` vector, e.g. Sample1, Sample2-File1, Sample2-File2, etc.).

- If stratigraphic constraints apply to samples, and so a **Bayesian model with stratigraphic constraints** is implemented, then the names in the `FolderNames` vector must be ordered by order of increasing ages.
  For example, FolderNames=c(noun1,noun2), in which case noun1 (respectively, noun2) corresponds to the subfolder name containing the BIN file of sample 1 (respectively of sample 2). In addition, if we know that sample 1 is younger than sample 2, then FolderNames vector is correctly filled.
  If conversely, FolderNames=c(noun2,noun1), the analysis performed by [AgeS_Computation](#) would not be consistent.

** How to fill the `BinPerSample` **vector? ****

`BinPerSample[i]` correponds to the number of BIN files for the sample whose number ID is equal to `i`.
For example, let us consider a case with two samples (Sample1 and Sample2), with 2 BIN files for Sample1 and 1 for Sample2. In this case, Nb_binfile=3 and Nb_sample=2. The user may then set FolderNames=c("Sample1-File1", "Sample1-File2", "Sample2-File1"), in which

case "Sample1-File1" is the name of the subfolder containing the first BIN file for Sample1, "Sample1-File2" the name of the subfolder for the second BIN file of Sample1; eventually, "Sample2-File1" is the name of the subfolder containing the BIN file for the second sample. In this case, BinPerSample=c(2,1).

For the general BIN-file structure, the reader is referred to the following website: http://www.nutech.dtu.dk/

The function read_BIN2R developped in Luminescence package is used to read the BIN files.

Value

A list containing the following objects:

- **LT** (one list per sample); each list contains all L/T values for the corresponding sample;
- **sLT** (one list per sample); each list contains all uncertainties on L/T values for the corresponding sample;
- **ITimes** (one list per sample); each list contains irradiation time values for the corresponding sample;
- **dLab**, a matrix containing in line i, the laboratory dose rate and its variance for sample i;
- **ddot_env**, a matrix containing in line i, the environmental dose rate and its variance (excluding the common error terms) for sample i;
- **regDose** (one list per sample); each list contains all regenerated doses;
- **J**, a vector giving, for each BIN file, the number of aliquots selected for the analysis;
- **K**, a vector giving, for each BIN file, the number of regenerative doses in the SAR protocol;
- **Nb_measurement**, a vector giving, for each BIN file, the number of measurements.

** How to save this list **

You can save this list in a .RData object. To do this, you can use the fonction save. Then, to load this list you can use the function load (see example section fore more details).

Author(s)

Claire Christophe, Sebastian Kreutzer, Anne Philippe, Guillaume Guerin

See Also

read_BIN2R, combine_DataFiles, Generate_DataFile_MG, LT_RegenDose Age_Computation, AgeS_Computation, Palaeodose_Computation

Examples

```
## Example for one sample with one Bin File
path<- system.file("extdata/samp1", "", package="BayLum")
folder=""
nbsample=1  # give the number of sample
Data <- Generate_DataFile(
 Path = path,
 FolderNames = folder,
 Nb_sample = nbsample,
 verbose = FALSE)
str(Data)
```

```
## to save information in RData object in folder containing bin file
# save(Data,file=c(paste(path,folder,'Data.RData',sep="")))
## to load information containing Data.RData object
# load(file=c(paste(path,folder,"Data.RData",sep="")))
```

Generate_DataFile_MG   *Generates, from one (or several) BIN file(s) of Multi-grain OSL mea-surements, a list of luminescence data and information before statisti-cal analysis*

Description

This function is used to generate, from the BIN file(s), a list of values of: **Multi-grain** OSL inten-sities and associated uncertainties, regenerative doses, etc., which will be the input of the Bayesian models. To be easy-to-use, this function requires a rigorous organisation - all needed files should be arranged in one folder - of informations concerning each BIN file.

It is possible to process data for various samples simultaneously and to consider more than one BIN file per sample.

Usage

```
Generate_DataFile_MG(Path, FolderNames, Nb_sample,
  Nb_binfile = length(FolderNames), BinPerSample = rep(1, Nb_sample),
  sepD = c(","), sepDE = c(","), sepDS = c(","), sepR = c("="),
  verbose = TRUE, ...)
```

Arguments

Path
:   [character](#) (**required**): the path to the project folder, containing one or more subfolders in which the BIN files are located. If it is not equal to "", it must be terminated by "/".

FolderNames
:   [character](#) (**required**) vector: list of names of the sub-folders containing the BIN files

    • each subfolder must contain a BIN file and associated csv files. See details for more informations on associated csv files required in the subfolders. If there is more than one BIN file per sample, see the details section for instructions regarding how to correctly fill the FolderNames vector.

Nb_sample
:   [integer](#) (**required**): number of samples.

Nb_binfile
:   [integer](#) (with default): number of BIN files. It must be equal to, or greater than Nb_sample.

BinPerSample
:   [integer](#) vector (with default): vector with the number of BIN files per sample. The length of this vector must be equal to Nb_sample and the sum of entries of this vector must be equal to Nb_binfile. If there is more than one BIN file per sample, see the details section for instructions regarding how to correctly fill BinPerSample vector. Otherwise, this vector must contain a list of 1 values.

sepD
:   [character](#) (with default): column separator in the DiscPose.csv files.

sepDE
:   [character](#) (with default): column separator in the DoseEnv.csv files.

sepDS
:   [character](#) (with default): column separator in the DoseLab.csv files.

sepR	character (with default): column separator in the Rule.csv files.
verbose	logical (with default): enable/disable verbose mode
...	further arguments that can be passed to Luminescence::read_BIN2R.

Details

With `Path` and `FolderNames`, this function goes to the subfolders containing the BIN files and associated information to compute the luminescence data.

** What are the required files in each subfolder? **

Each subfolder can be named, for example, as the sample name followed by a number; it must contain:

- **bin.BIN**, the bin file renamed as bin.BIN (note: the name of all files matters);
- **Disc.csv**, a one columns csv file containing the list of disc number of the previously selected grains (typically this list will include the position of grains based on their sensitivity, recycling or other properties);
- **DoseEnv.csv**, a two columns file containing the observation of the natural (or environmental), dose rate, and its non-shared variance (i.e. after removing all shared errors), both in Gy. Note: the user shall provide the squared value of the error associated with the dose rate experienced by the sample grains in nature;
- **DoseSourve.csv**, a two columns file containing the observation of the laboratory dose rate, and its variance (squared error), both in Gy;
- **rule.csv**, a csv file containing information on
  - beginSignal= the first channel for summing the natural or regenerative OSL signal (typically 1 or 6);
  - endSignal= the last channel for summing the natural or regenerative OSL signal (typically 5 or 10);
  - beginBackground= the first channel for background estimation of the natural or regenerative OSL signal (typically 76 or 81);
  - endBackground= the last channel for background estimation of the natural or regenerative OSL signal (typically 95 or 100);
  - beginTest,
  - endTest,
  - beginTestBackground,
  - endTestBackground= same values as above, for the test dose response (typically the same values should be used);
  - inflatePercent= uncertainty arising from the instrument reproducibility (typically 0.02, i.e. 2%);
  - nbOfLastCycleToRemove= number of cycles at the end of the SAR protocol which should not be included in the dose response curve fitting (typically 1 if only a recycling test is performed, or 2 if both recycling and IR depletion are tested).

** How to fill the `FolderNames` vector? **

`FolderNames` is a vector of length `Nb_binfile`. `FolderNames[i]` is the name (e.g., Sample1-File1, or successive names separated by "/" signs, if BIN files are in subfolders, e.g. Sample1/File1) of the subfolder containing all informations on the BIN file of ID number i. The names in `FolderNames` are ordered following two rules:

- The names in the `FolderNames` vector must be ordered following the sample order (the names of subfolders containing BIN files for the same sample should follow each other in the `FolderNames` vector, e.g. Sample1, Sample2-File1, Sample2-File2, etc.).

- If stratigraphic constraints apply to samples, and so a **Bayesian model with stratigraphic constraints** is implemented, then the names in the `FolderNames` vector must be ordered by order of increasing ages.

  For example, FolderNames=c(noun1,noun2), in which case noun1 (respectively, noun2) corresponds to the subfolder name containing the BIN file of sample 1 (respectively of sample 2). In addition, if we know that sample 1 is younger than sample 2, then `FolderNames` vector is correctly filled.

  If conversely, FolderNames=c(noun2,noun1), the analysis performed by `AgeS_Computation` would not be consistent.

** How to fill the `BinPerSample` vector? **

`BinPerSample[i]` correponds to the number of BIN files for the sample whose number ID is equal to `i`.

For example, let us consider a case with two samples (Sample1 and Sample2), with 2 BIN files for Sample1 and 1 for Sample2. In this case, Nb_binfile=3 and Nb_sample=2. The user may then set FolderNames=c("Sample1-File1", "Sample1-File2", "Sample2-File1"), in which case "Sample1-1" is the name of the subfolder containing the first BIN file for Sample1, "Sample1-File2" the name of the subfolder for the second BIN file of Sample1; eventually, "Sample2-1" is the name of the subfolder containing the BIN file for the second sample. In this case, BinPerSample=c(2,1).

For the general BIN-file structure, the reader is referred to the following website: `http://www.nutech.dtu.dk/`

The function `read_BIN2R` developped in `Luminescence` package is used to read the BIN files.

Value

A list containing the following objects:

- **LT** (one list per sample); each list contains all L/T values for the corresponding sample;

- **sLT** (one list per sample); each list contains all uncertainties on L/T values for the corresponding sample;

- **ITimes** (one list per sample); each list contains irradiation time values for the corresponding sample;

- **dLab**, a matrix containing in line i, the laboratory dose rate and its variance for sample i;

- **ddot_env**, a matrix containing in line i, the environmental dose rate and its variance (excluding the common error terms) for sample i;

- **regDose** (one list per sample); each list contains all regenerated doses;

- **J**, a vector giving, for each BIN file, the number of aliquots selected for the analysis;

- **K**, a vector giving, for each BIN file, the number of regenerative doses in the SAR protocol;

- **Nb_measurement**, a vector giving, for each BIN file, the number of measurements;

** How to save this list **

You can save this list in a .RData object. To do this, you can use the fonction `save`. Then, to load this list you can use the function `load` (see example section fore more details).

Note

The function imports only BIN-file records which have been previously selected.

Author(s)

Claire Christophe, Sebastian Kreutzer, Anne Philippe, Guillaume Guérin

See Also

[read_BIN2R](#), [combine_DataFiles](#), [LT_RegenDose](#) [Age_Computation](#), [AgeS_Computation](#), [Palaeodose_Computation](#)

Examples

```
path<- system.file("extdata/FER1", "", package="BayLum")
folder=""
# give the number of sample
nbsample=1
DATA=Generate_DataFile_MG(Path=path,FolderNames=folder,Nb_sample=nbsample)
str(DATA)

# to save information in RData object in folder containing bin file
#save(DATA,file=c(paste(path,folder,'DATA.RData',sep="")))
# to load information containing DATA.RData object
#load(file=c(paste(path,folder,"DATA.RData",sep="")))
```

LT_RegenDose   *Plots Lx/Tx as a function of the regenerative dose*

Description

This function plots Lx/Tx values as a function of regenerative dose, for every selected aliquot and
for each sample.

Usage

```
LT_RegenDose(DATA, Path, FolderNames, SampleNames = FolderNames, Nb_sample,
  BinPerSample = rep(1, Nb_sample), SG = rep(TRUE, Nb_sample),
  sepDP = c(","), nrow = 3L, ncol = nrow)
```

Arguments

DATA   [list](#) (**required**): list of objects LT, sLT, ITimes, dLab, ddot_env, regDose, J, K,
                Nb_measurement, provided by [Generate_DataFile](#) or [Generate_DataFile_MG](#)
                or [combine_DataFiles](#). DATA can contain information from more than one sam-
                ple.

Path   [character](#) (**required**): path to the project folder (the same as the one used in
                [Generate_DataFile](#) or [Generate_DataFile_MG](#) to provide DATA)

FolderNames   [character](#) (**required**): vector of names of the sub-folders containing the BIN
                files, which were used by [Generate_DataFile](#) or [Generate_DataFile_MG](#) to
                generate the DATA object.

SampleNames   [character](#) (with default): Names of samples. To use if there is more than one bin
                file per sample.

Nb_sample	integer (**required**): ID number (in [1,Nb_sample]) of the sample selected for plotting L/T as a function of regenerative doses. Required if the DATA object contains information for more than one sample.
BinPerSample	integer (with default): integer vector (with default): vector with the number of BIN files per sample, which was used in Generate_DataFile or Generate_DataFile_MG to generate the DATA object.
SG	logical (with default): vector to set the type of measurement for each sample (length(SG)=Nb_sample). If the sample of number ID equal to i, SG[i]=TRUE if it is a Single-grain OSL measurements, SG[i]=FALSE if it is a Multi-grain OSL measurements.
sepDP	character (with default): column separator in the DiscPose.csv file or in Disc.csv file. It must be the same separator for all samples, for Single-grain OSL measurements or Multi-grain OSL measurements.
nrow	integer (with default): controls the arangment of the plots, here the number of rows. Can be set to NULL.
ncol	integer (with default): controls the arangment of the plots, here the number of columns. Can be set to NULL.

Details

To fill FolderNames and BinPerSample, we refer to the **Detail** section from the Generate_DataFile or Generate_DataFile function. As well for a precise description of input DATA.

Value

Lx/Tx plots; there are as many plots as selected aliquots in the DiscPos.csv file. There are 9 plots per page. There is not interpolation.

Author(s)

Claire Christophe, Sebastian Kreutzer, Anne Philippe, Guillaume Guérin

See Also

Generate_DataFile, Generate_DataFile_MG

Examples

```
## load data file generated by the function Generate_DataFile
data(DATA3,envir = environment())
path<- system.file("extdata/FER1", "", package="BayLum")
folder=""
samplename="FER1"
LT_RegenDose(DATA=DATA3,Path=path,FolderNames=folder,SampleNames=samplename,Nb_sample=1,SG=FALSE)
```

Marine_CalC14 *Marine data for calibration of 14C age*

Description

As 14C years is not equal to calendar years because atmospheric 14C concentration varies through time. Hence, data in marine_CalC14 allows a calibration for hypothetical "global" marine reservoir.

Usage

```
data("Marine_CalC14")
```

Format

A data frame with 3 variables.

CAL.BP a numeric vector correpondig to calendar years befor present

X14C.age a numeric vector correponding to 14C age

Error a numeric vector correponding to error arround 14C age measurement

References

Reimer PJ, Bard E, Bayliss A, Beck JW, Blackwell PC, Bronl Ramsey C, Buck CE, Cheng H, Edwards RL, Friedrich M, Grootes PM, Guilderson TP, Haflidason H, Hajdas I, Hatte C, Heaton TJ, Hoffmann DL, Hogg AG, Hughen KA, Kaiser KF, Kromer B, Manning SW, Niu M, Reimer RW, Richards DA, Scott EM, Southon JR, Staff RA, Turney CSM, van der Plicht J. 2013. IntCal13 ans Marine13 radiocarbon age calibration curves 0-50000 years cal BP. Radiocarbon 55(4)=1869-1887.

Examples

```
data(Marine_CalC14)
## maybe str(Marine_CalC14) ; head(Marine_CalC14) ...
```

MCMCsample *MCMC sample from the posterior distribution of the dataset GDB5*

Description

MCMC samples from the posterior distribution of "A" for age, "D" for palaeodose and "sD" for dispersion of equivalent doses around "D", of the data set GDB5.

Usage

```
data("MCMCsample")
```

Format

It is a matric with 6000 row and tree column.

A The first column of the matrice are sampled from the posterior distribution of the paramete A

D The first column of the matrice are sampled from the posterior distribution of the paramete D

sD The first column of the matrice are sampled from the posterior distribution of the paramete sD

References

Tribolo, C., Asrat, A., Bahain, J. J., Chapon, C., Douville, E., Fragnol, C., Hernandez, M., Hovers, E., Leplongeon, A., Martin, L, Pleurdeau, D, Pearson, O , Puaud, S, Assefa, Z. (2017). Across the Gap: Geochronological and Sedimentological Analyses from the Late Pleistocene-Holocene Sequence of Goda Buticha, Southeastern Ethiopia. PloS one, 12(1), e0169418.

Examples

```
data(MCMCsample)
## maybe str(MCMCsample) ; plot(MCMCsample[,1],type="l") ...
```

ModelC14   *Likelihood of C14 samples for JAGS models use in* Age_OSLC14

Description

A list of models for C14 data to define likelyhood in JAGS models.

Usage

```
data("ModelC14")
```

Format

This list contains:

full a model considering error on calibration curve.

naive a model not considering error on calibration curve.

References

Reimer PJ, Bard E, Bayliss A, Beck JW, Blackwell PC, Bronl Ramsey C, Buck CE, Cheng H, Edwards RL, Friedrich M, Grootes PM, Guilderson TP, Haflidason H, Hajdas I, Hatte C, Heaton TJ, Hoffmann DL, Hogg AG, Hughen KA, Kaiser KF, Kromer B,Manning SW, Niu M, Reimer RW, Richards DA, Scott EM, Southon JR, Staff RA, Turney CSM, van der Plicht J. 2013. IntCal13 ans Marine13 radiocarbon age calibration curves 0-50000 years cal BP. Radiocarbon 55(4)=1869-1887.

Hogg AG, Hua Q, Blackwell PG, Niu M, Buck CE, Guilderson TP, Heaton TJ, Palmer JG, Reimer PJ, Reimer RW, Turney CSM, Zimmerman SRH. 2013. SHCal13 Southern Hemisphere calibration, 0-50000 years cal BP. Radiocarbon 55(4):1889-1903

Examples

```
data(Model_AgeC14)
## ModelC14[[full]]
## ModelC14$full
```

ModelOSL   *Likelihood of OSL samples for JAGS models use in* Age_OSLC14

Description

A list of models for OSL data to define likelyhood in JAGS models.

Usage

```
data("ModelOSL")
```

Format

This list contains:

AgesMultiCS2_EXPLIN a list of 4 models that all consider a saturating exponential plus linear growth. These 4 models have different distribution to describe equivalent dose values around the palaeodose.

AgesMultiCS2_EXP a list of 4 models that all consider a saturating exponential growth. These 4 models have different distribution to describe equivalent dose values around the palaeodose.

AgesMultiCS2_EXPZO a list of 4 models that all consider a saturating exponential plus linear growth and fitting through the origin. These 4 models have different distribution to describe equivalent dose values around the palaeodose.

AgesMultiCS2_EXPLINZO a list of 4 models that all consider a saturating exponential growth and fitting through the origin. These 4 models have different distribution to describe equivalent dose values around the palaeodose.

Details

The different distibutions to describe equivalent dose values around the palaeodose are:

cauchy a Cauchy distribution with postition parameter equal to the palaeodose of the sample

gaussian a Gaussian distribution with mean equal to the palaeodose of the sample

lognormal_A a log-normal distribution with mean or **A**verage equal to the palaeodose of the sample

lognormal_M a log-normal distribution with **M**edian equal to the palaeodose of the sample

For more information we refer to the function AgeS_Computation, section Details.

References

Plummer, M. (2003). JAGS: A program for analysis of Bayesian graphical models using Gibbs sampling. In Proceedings of the 3rd international workshop on distributed statistical computing, volume 124, page 125. Technische Universit at Wien, Austria.

Plummer, M. (2015). JAGS Version 4.0. 0 user manual.

Examples

```
data(ModelOSL)
## The JAGS model of the likelyhood for a saturating exponential plus linear growth
## (a function of the type \code{f(x)=a(1-exp(-x/b))+cx+d})
## and a gaussian distribution of equivalent doses around the palaeodose:
## ModelOSL[[AgesMultiOSL_EXPLIN]][[gaussian]]
```

ModelPrior   *Prior for JAGS models use in* Age_OSLC14

Description

A list to define prior in JAGS models, taking acount OSL data and C14 data in stratigraphic constraint. The difficulty is in the fact that each cases is different. The youngest sample can be a C14 as well as a OSL sample. To resolve this problem we consider diferent cases thanks to this list.

Usage

```
data("ModelPrior")
```

Format

This list contains:

Sample1_C14 model considering that the youngest sample is a C14 sample

Sample1_OSL model considering that the youngest sample is a OSL sample

C14_OSL model considering that the second sample is a C14 sample

OSL_C14 model considering that the second sample is a OSL sample

C14 model considering that the last sample is a C14 sample

OSL model considering that the last sample is a OSL sample

References

Plummer, M. (2003). JAGS: A program for analysis of Bayesian graphical models using Gibbs sampling. In Proceedings of the 3rd international workshop on distributed statistical computing, volume 124, page 125. Technische Universit at Wien, Austria.

Plummer, M. (2015). JAGS Version 4.0. 0 user manual.

Examples

```
data(ModelPrior)
## ModelPrior[[OSL]]
## ModelPrior$OSL
```

Model_Age   *JAGS models use in* Age_Computation

Description

A list of JAGS models use to a Bayesian analysis of OSL age of one sample. There are models for various growth curves and various distrubution to describe equivalent dose distribution around the palaeodose.

Usage

```
data("Model_Age")
```

Format

This list contains:

AgeMultiBF_EXPLIN a list of 4 models that all consider a saturating exponential plus linear growth. These 4 models have different distribution to describe equivalent dose values around the palaeodose.

AgeMultiBF_EXP a list of 4 models that all consider a saturating exponential growth. These 4 models have different distribution to describe equivalent dose values around the palaeodose.

AgeMultiBF_EXPZO a list of 4 models that all consider a saturating exponential plus linear growth and fitting through the origin. These 4 models have different distribution to describe equivalent dose values around the palaeodose.

AgeMultiBF_EXPLINZO a list of 4 models that all consider a saturating exponential growth and fitting through the origin. These 4 models have different distribution to describe equivalent dose values around the palaeodose.

Details

The different distibutions to describe equivalent dose values around the palaeodose are:

cauchy a Cauchy distribution with postition parameter equal to the palaeodose of the sample

gaussian a Gaussian distribution with mean equal to the palaeodose of the sample

lognormal_A a log-normal distribution with mean or **A**verage equal to the palaeodose of the sample

lognormal_M a log-normal distribution with **M**edian equal to the palaeodose of the sample

For more information we refer to the function Age_Computation, section Details.

References

Plummer, M. (2003). JAGS: A program for analysis of Bayesian graphical models using Gibbs sampling. In Proceedings of the 3rd international workshop on distributed statistical computing, volume 124, page 125. Technische Universit at Wien, Austria.

Plummer, M. (2015). JAGS Version 4.0. 0 user manual.

See Also

rjags

Examples

```
data(Model_Age)
## The JAGS model for a saturating exponential plus linear growth
## (a function of the type \code{f(x)=a(1-exp(-x/b))+cx+d})
## and a gaussian distribution of equivalent doses around the palaeodose:
# Model_Age[[AgeMultiBF_EXPLIN]][[gaussian]]
```

Model_AgeC14　　　　　　　　*JAGS models use in* AgeC14_Computation

Description

A list of JAGS models use to a Bayesian analysis of C14 calibration age of various sample. Stratigraphic relations can be taken in count to calibrate C14 ages. This ages take into account that some data can be an outlier.

Usage

```
data("Model_AgeC14")
```

Format

This list contains:

full a model considering error on calibration curve.

naive a model not considering error on calibration curve.

References

Reimer PJ, Bard E, Bayliss A, Beck JW, Blackwell PC, Bronl Ramsey C, Buck CE, Cheng H, Edwards RL, Friedrich M, Grootes PM, Guilderson TP, Haflidason H, Hajdas I, Hatte C, Heaton TJ, Hoffmann DL, Hogg AG, Hughen KA, Kaiser KF, Kromer B,Manning SW, Niu M, Reimer RW, Richards DA, Scott EM, Southon JR, Staff RA, Turney CSM, van der Plicht J. 2013. IntCal13 ans Marine13 radiocarbon age calibration curves 0-50000 years cal BP. Radiocarbon 55(4)=1869-1887.

Hogg AG, Hua Q, Blackwell PG, Niu M, Buck CE, Guilderson TP, Heaton TJ, Palmer JG, Reimer PJ, Reimer RW, Turney CSM, Zimmerman SRH. 2013. SHCal13 Southern Hemisphere calibration, 0-50000 years cal BP. Radiocarbon 55(4):1889-1903

See Also

rjags

Examples

```
data(Model_AgeC14)
## Model_AgeC14[[full]]
## Model_AgeC14$full
```

Model_AgeS   *JAGS models use in* AgeS_Computation

Description

A list of JAGS models use to a Bayesian analysis of OSL age of various samples. There are models for various growth curves and various distrubution to describe equivalent dose distribution around the palaeodose.

Usage

```
data("Model_AgeS")
```

Format

This list contains:

AgesMultiCS2_EXPLIN a list of 4 models that all consider a saturating exponential plus linear growth. These 4 models have different distribution to describe equivalent dose values around the palaeodose.

AgesMultiCS2_EXP a list of 4 models that all consider a saturating exponential growth. These 4 models have different distribution to describe equivalent dose values around the palaeodose.

AgesMultiCS2_EXPZO a list of 4 models that all consider a saturating exponential plus linear growth and fitting through the origin. These 4 models have different distribution to describe equivalent dose values around the palaeodose.

AgesMultiCS2_EXPLINZO a list of 4 models that all consider a saturating exponential growth and fitting through the origin. These 4 models have different distribution to describe equivalent dose values around the palaeodose.

Details

The different distibutions to describe equivalent dose values around the palaeodose are:

cauchy a Cauchy distribution with postition parameter equal to the palaeodose of the sample

gaussian a Gaussian distribution with mean equal to the palaeodose of the sample

lognormal_A a log-normal distribution with mean or **A**verage equal to the palaeodose of the sample

lognormal_M a log-normal distribution with **M**edian equal to the palaeodose of the sample

For more information we refer to the function AgeS_Computation, section Details.

References

Plummer, M. (2003). JAGS: A program for analysis of Bayesian graphical models using Gibbs sampling. In Proceedings of the 3rd international workshop on distributed statistical computing, volume 124, page 125. Technische Universit at Wien, Austria.

Plummer, M. (2015). JAGS Version 4.0. 0 user manual.

See Also

rjags

Examples

```
data(Model_AgeS)
## The JAGS model for a saturating exponential plus linear growth
## (a function of the type \code{f(x)=a(1-exp(-x/b))+cx+d})
## and a gaussian distribution of equivalent doses around the palaeodose:
# Model_Age[[AgesMultiCS2_EXPLIN]][[gaussian]]
```

Model_Palaeodose   *JAGS models use in* Palaeodose_Computation

---

Description

A list of JAGS models use to a Bayesian analysis of OSL palaeodose of one or various samples. There are models for various growth curves and various distrubution to describe equivalent dose distribution around the palaeodose.

Usage

```
data("Model_Palaeodose")
```

Format

This list contains:

PalaeodosesMultiBF_EXPLIN a list of 4 models that all consider a saturating exponential plus linear growth. These 4 models have different distribution to describe equivalent dose values around the palaeodose.

PalaeodosesMultiBF_EXP a list of 4 models that all consider a saturating exponential growth. These 4 models have different distribution to describe equivalent dose values around the palaeodose.

PalaeodosesMultiBF_EXPZO a list of 4 models that all consider a saturating exponential plus linear growth and fitting through the origin. These 4 models have different distribution to describe equivalent dose values around the palaeodose.

PalaeodosesMultiBF_EXPLINZO a list of 4 models that all consider a saturating exponential growth and fitting through the origin. These 4 models have different distribution to describe equivalent dose values around the palaeodose.

Details

The different distibutions to describe equivalent dose values around the palaeodose are:

cauchy a Cauchy distribution with postition parameter equal to the palaeodose of the sample

gaussian a Gaussian distribution with mean equal to the palaeodose of the sample

lognormal_A a log-normal distribution with mean or **A**verage equal to the palaeodose of the sample

lognormal_M a log-normal distribution with **M**edian equal to the palaeodose of the sample

For more information we refer to the function Palaeodose_Computation, section Details.

References

Plummer, M. (2003). JAGS: A program for analysis of Bayesian graphical models using Gibbs sampling. In Proceedings of the 3rd international workshop on distributed statistical computing, volume 124, page 125. Technische Universit at Wien, Austria.

Plummer, M. (2015). JAGS Version 4.0. 0 user manual.

See Also

[rjags](#)

Examples

```
data(Model_Palaeodose)
## The JAGS model for a saturating exponential plus linear growth
## (a function of the type \code{f(x)=a(1-exp(-x/b))+cx+d})
## and a gaussian distribution of equivalent doses around the palaeodose:
# Model_Age[[PalaeodosesMultiBF_EXPLIN]][[gaussian]]
```

Palaeodose_Computation

Bayesian analysis for the palaeodose estimation of various samples

---

Description

This function computes the palaeodose (in Gy) of one or various samples according to the model developed in Combes et al (2015), based on an output of `Generate_DataFile` or `Generate_DataFile_MG` or both of them using `combine_DataFiles`.
Samples, for which data is avalilable in several BIN files, can be analysed.
Single-grain or Multi-grain OSL measurements can be analysed simultaneouly.

Usage

```
Palaeodose_Computation(DATA, SampleNames, Nb_sample, BinPerSample = rep(1,
  Nb_sample), SavePdf = FALSE, OutputFileName = c("MCMCplot"),
  OutputFilePath = c(""), SaveEstimates = FALSE,
  OutputTableName = c("DATA"), OutputTablePath = c(""), LIN_fit = TRUE,
  Origin_fit = FALSE, distribution = c("cauchy"), Iter = 50000, t = 5,
  Nb_chaines = 3)
```

Arguments

DATA	list of objects: LT, sLT, ITimes, dLab, ddot_env, regDose, J, K, Nb_measurement, provided by `Generate_DataFile` or `Generate_DataFile_MG`. DATA contains information for more than one sample.
SampleNames	character vector: names of sample. The length of this vector is equal to Nb_sample.
Nb_sample	integer: number of samples.
BinPerSample	integer vector (with default): vector with the number of BIN files per sample. The length of this vector is equal to Nb_sample. BinPerSample[i] correponds to the number of BIN files for the sample whose number ID is equal to i. For more information to fill this vector, we refer to detatils in `Generate_DataFile` or `Generate_DataFile_MG`.

SavePdf	boolean (with default): if TRUE save graph in pdf file named OutputFileName in folder OutputFilePath.
OutputFileName	character (with default): name of the pdf files that will be generated by the function.
OutputFilePath	character (with default): path to the pdf files that will be generated by the function.
SaveEstimates	boolean (with default): if TRUE save Bayes estimates and credible interval at level 68 in a csv table named OutputFileName in folder OutputFilePath.
OutputTableName	
	character (with default): name of the table that will be generated by the function if SaveEstimates=TRUE.
OutputTablePath	
	character (with default): path to the table that will be generated by the function if SaveEstimates=TRUE.
LIN_fit	logical (with default): if TRUE (default) allows a linear component, on top of the (default) saturating exponential curve, for the fitting of dose response curves. Please see details for more informations on the proposed dose response curves.
Origin_fit	logical (with default): if TRUE, forces the dose response curves to pass through the origin. Please see details for more informations on the proposed growth curves.
distribution	character (with default): type of distribution that defines how individual equivalent dose values are distributed around the palaeodose. Allowed inputs are **"cauchy"**, **"gaussian"**, **"lognormal_A"** and **"lognormal_M"**.
Iter	integer (with default): number of iterations for the MCMC computation (for more information see `jags.model`).
t	integer (with default): 1 every t iterations of the MCMC is considered for sampling the posterior distribution (for more information see `jags.model`).
Nb_chaines	integer (with default): number of independent chains for the model (for more information see `jags.model`).

Details

** Option on growth curves **

As for `Age_Computation` and `AgeS_Computation`, the user can choose from 4 dose response curves:

- **Saturating exponential plus linear growth** (PalaeodosesMultiBF_EXPLIN):
  for all x in IR+, f(x)=a(1-exp(-x/b))+cx+d; select
  - LIN_fit=TRUE
  - Origin_fit=FALSE
- **Saturating exponential growth** (PalaeodosesMultiBF_EXP):
  for all x in IR+, f(x)=a(1-exp(-x/b))+d; select
  - LIN_fit=FALSE
  - Origin_fit=FALSE
- **Saturating exponential plus linear growth and fitting through the origin** (PalaeodosesMultiBF_EXPLINZO):
  for all x in IR+, f(x)=a(1-exp(-x/b))+cx; select
  - LIN_fit=TRUE

– `Origin_fit=TRUE`

- **Saturating exponential growth and fitting through the origin** (`PalaeodosesMultiBF_EXPZO`): for all x in IR+, `f(x)=a(1-exp(-x/b))`; select
    – `LIN_fit=FALSE`
    – `Origin_fit=TRUE`

** Option on equivalent dose distribution around the palaeodose **

The use can choose between :

- `cauchy`: a Cauchy distribution with location parameter equal to the palaeodose of the sample
- `gaussian`: a Gaussian distribution with mean equal to the palaeodose of the sample
- `lognormal_A`: a log-normal distribution with mean or **A**verage equal to the palaeodose of the sample
- `lognormal_M`: a log-normal distribution with **M**edian equal to the palaeodose of the sample

Value

NUMERICAL OUTPUT

1. **A list containing the following objects:**
    - **Sampling** that corresponds to a sample of the posterior distributions of palaeodose and equivalent dose dispersion parameters (both in Gy).
    - **Model_GrowthCurve**, stating which dose response fitting option was chosen;
    - **Distribution**, stating which distribution was chosen to model the dispersion of individual equivalent dose values around the palaeodose of the sample.
2. **The Gelman and Rubin test of convergency**: prints the result of the Gelman and Rubin test of convergency for palaeodose and equivalent dose dispersion parameters for each sample. A result close to one is expected.
    In addition, the user must visually assess the convergency of the trajectories by looking at the pdf file generated by the function (see **PLOT OUTPUT** for more informations).
    If both convergencies (Gelman and Rubin test and plot checking) are satisfactory, the user can consider the printed estimates as valid. Otherwise, the user may try increasing the number of MCMC interations (`Iter`) to reach convergency.
3. **Credible intervals and Bayes estimates**: prints the Bayes esitmates, the credible intervals at 95% and 68% for the palaeodose and equivalent dose dispersion parameters for each sample.

PLOT OUTPUT

1. **MCMC trajectories** A graph with the MCMC trajectories and posterior distributions of the palaeodose and equivalent dose dispersion parameters is displayed, there is one page per sample.
    The first line of the figure correponds to the palaeodose parameter and the second to the equivalent dose dispersion parameter. On each line, the plot on the left represents the MCMC trajectories, and the one on the right the posterior distribution of the parameter.
2. **Summary of palaeodose estimates**: plot credible intervals and Bayes estimate of each sample palaeodose on a same graph.

To give result in a publication, we recommend to give the Bayes estimate of the parameters as well as the credible interval at 95% or 68%.

Note

Please note that the initial values for all MCMC are currently all the same for all chains since we rely on the automatic initial value generation of JAGS. This is not optimal and will be changed in future. However, it does not affect the quality of the age estimates if the chains have converged.

Author(s)

Claire Christophe, Sebastian Kreutzer, Anne Philippe, Guillaume Guérin

References

Combes, B., Philippe, A., Lanos, P., Mercier, N., Tribolo, C., Guerin, G., Guibert, P., Lahaye, C., 2015. A Bayesian central equivalent dose model for optically stimulated luminescence dating. Quaternary Geochronology 28, 62-70. doi:10.1016/j.quageo.2015.04.001

See Also

Generate_DataFile, Generate_DataFile_MG, combine_DataFiles, rjags, plot_MCMC, Age_Computation, AgeS_Computation

Examples

```
## Load data
data(DATA1,envir = environment())
## Palaeodose computation of samples GDB3
P=Palaeodose_Computation(DATA=DATA1,Nb_sample=1,SampleNames=c("GDB5"),Iter=100)
```

---

plot_MCMC   *Plot MCMC trajectories and posterior distributions*

Description

This function uses the output of rjags::jags.model to visualise the traces of the MCMC and the corresponding densities. In particular it displays the posterior distributions of the age, if it is calculated, palaeodose and the equivalent dose dispersion parameters of the sample. The function output is very similar to plot output produced with the 'coda' package, but tailored to meet the needs in the context of the 'BayLum' package.

Usage

```
plot_MCMC(object, sample_names = NULL, variables = c("A", "D", "sD"),
  axes_labels = c(A = "Age (ka)", D = "D (Gy)", sD = "sD (Gy)"),
  n.chains = NULL, n.iter = 1000L, smooth = FALSE, rug = TRUE,
  plot_single = FALSE, ...)
```

Arguments

object   coda::mcmc.list or coda::mcmc (**required**): Output generated by rjags::jags.model, e.g., in Age_Computation

sample_names   character (optional): Names of the used samples. This argument overrides the optional argument mtext.

variables   character (with default): Variables in your coda::mcmc object to be plotted.

axes_labels   character (with default): Axes labels used for the trace and density plots. The labels should be provided as named character vector with the parameter names as the names used to assign the axes labelling. The labelling for the x-axis (trace plots) and y-axis (density plot) cannot be modified.

n.chains   numeric (optional): Set the number of chains to visualise, if nothing is provided the number of chains is determined from the input object

n.iter   integer (with default): Set the number of iterations to be visualised in the trace plots, regardless of the size of the input dataset as long as the real number of iterations is > n.iter. Please note that large numbers impact the plot performance.

smooth   logical (with default): Enable/disables smooth of trace plots using stats::smooth

rug   logical (with default): Enable/disables rug under density plots

plot_single   logical (with default): Enables/disables the single plot mode of the function, i.e. if set to TRUE every plot is returned in a single plot and own par settings can be applied.

...   further arguments that can be passed to modifiy the plot output. Supported arguments are lwd, lty, col, type, cex,mtext, cf. mtext for mtext and plot.default for the other arguments.

Details

The function is used in the function Age_Computation, AgeS_Computation and Palaeodose_Computation, but can be used also as standalone plot function.

Value

Two plots: Traces of the MCMC chains and the corresponding density plots. This plots are similar to coda::traceplot and coda::densplot.

Function version

0.1.1

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Université Bordeaux Montaigne (France). This function is a re-written version of the function MCMC_plot() by Claire Christophe

See Also

Age_Computation, AgeS_Computation, Palaeodose_Computation, rjags::coda.samples and rjags packages.

Examples

```
data(MCMCsample,envir = environment())
object <- coda::as.mcmc(MCMCsample)
plot_MCMC(object)
```

---

plot_Scatterplots   *Display Scatter Plot Matrix of the Bayesian Age Results*

Description

Create a hexbin plot matrix (hexbin::hexplom) of age results returned by the bayesian age calculation.

Old function ScatterPlots()

Usage

```
plot_Scatterplots(object, variables = c("A"), sample_names = NULL,
  sample_selection = NULL, n.chains = NULL, ...)

ScatterSamples(...)
```

Arguments

object	coda::mcmc.list (**required**): mcmc list objects generated by rjags::jags.model in AgeS_Computation, AgeC14_Computation or Age_OSLC14.
variables	character (*with default*): variable to be selected for the scatter plot, e.g., "A". Please note that you can only select one variable at the time
sample_names	character (*optional*): sample names shown in the plot matrix
sample_selection	
	numeric (*with default*): vector of samples to be plotted in the scatter matrix, e.g., c(1,2) will plot the first two samples, c(1,3) will plot samples 1 and 3 and c(1:3) will plot the first three samples
n.chains	integer (*with default*): allows to limit the number of chains shown, by default the results of all chains are plotted.
...	further arguments to control the plot output, supported are main, xlab, colramp, pscales

Value

A scatter plot based on hexbin::hexplom

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, UMR 5060, CNRS - Université Bordeaux Montaigne (France), based on the function ScatterSamples() by Claire Christophe, Anne Philippe, Guillaume Guérin

See Also

Age_Computation, AgeS_Computation, AgeC14_Computation, and rjags packages.

Examples

```
data(AgeS,envir = environment())
plot_Scatterplots(
   object = AgeS$Sampling,
   sample_names = c("GDB5", "GDB3"),
   sample_selection = c(1,2)
 )
```

SCMatrix   *Definition of the stratigraphic constraint matrix*

Description

This function helps to define the stratigraphic relation between samples, with questions. The output of this function can be used in function `AgeS_Computation`.

Usage

```
SCMatrix(Nb_sample, SampleNames)
```

Arguments

Nb_sample   interger: the sample number.

SampleNames   charcater vector: sample names.

Details

Ask if sample i is younger than sample j to construc the stratigraphic constrain matrix.

Value

A Matrix that summarise the ordered relation between samples. This matrix can be intergrate in `AgeS_Computation` function. We refer to detail on `AgeS_Computation` for more information concerning this matrix.

Author(s)

Claire Christophe, Anne Philippe, Guillaume Guerin

See Also

`AgeS_Computation`

Examples

```
## Assume that "sample1" is younger than "sample2"
## That means the expected value is 1.
## It is an interactive function.
## Not run:
SCMatrix(Nb_sample=2,SampleNames=c("sample1","sample2"))
## Enter the value 1

## End(Not run)
```

SC_Ordered   *Create stratigraphically ordered sample matrix*

Description

Construct the stratigraphic matrix used in the functions AgeS_Computation and AgeC14_Computation
for samples that are all ordered by increasing age.

Usage

```
SC_Ordered(Nb_sample)
```

Arguments

Nb_sample   integer (**required**): the number of samples

Value

Stratigraphic matrix where each sample are ordered by increasing order. This matrix can be inter-
grated in the function AgeS_Computation. Please see AgeS_Computation for more information on
this matrix.

Author(s)

Claire Christophe, Anne Philippe, Sebastian Kreutzer, Guillaume Guérin

See Also

AgeS_Computation, SCMatrix

Examples

```
# compute the stratigraphic matrix for 3 samples such that the first sample is younger
# than the second, and the second is younger than the third
SC <- SC_Ordered(Nb_sample = 3)
```

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