Package: PEcAn.MA (via r-universe)

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Type Package

Title PEcAn Functions Used for Meta-Analysis

Version 1.7.2

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Description The Predictive Ecosystem Carbon Analyzer (PEcAn) is a scientific workflow management tool that is designed to simplify the management of model parameterization, execution, and analysis. The goal of PECAn is to streamline the interaction between data and models, and to improve the efficacy of scientific investigation. The PEcAn.MA package contains the functions used in the Bayesian meta-analysis of trait data.

Imports coda (>= 0.18), lattice, PEcAn.utils, PEcAn.DB, PEcAn.logger, MASS, PEcAn.settings, rjags

Suggests ggmcmc, ggplot2, knitr (>= 1.42), rmarkdown (>= 2.19), testthat (>= 1.0.2)

SystemRequirements JAGS

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VignetteBuilder knitr

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LazyData FALSE

Encoding UTF-8

RoxygenNote 7.3.1

Roxygen list(markdown = TRUE)

Repository https://pecanproject.r-universe.dev

RemoteUrl https://github.com/PecanProject/pecan

RemoteRef HEAD

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Contents

`approx.posterior` *Approximate posterior*

Description

Approximate the posterior MCMC with a closed form pdf

Usage

```
approx.posterior(
  trait.mcmc,
  priors,
  trait.data = NULL,
  outdir = NULL,
  filename.flag = ""
)
```

Arguments

`trait.mcmc`	meta analysis outputs
`priors`	dataframe of priors used in meta analysis
`trait.data`	data used in meta-analysis (used for plotting)
`outdir`	directory in which to plot results
`filename.flag`	text to be included in the posteriors.pdf filename to make unique

Details

returns priors where posterior MCMC are missing

NOTE: this function is similar to PEcAn.priors::fit.dist

Value

posteriors data frame, similar to priors, but with closed form pdfs fit to meta-analysis results

Author(s)

David LeBauer, Carl Davidson, Mike Dietze

Examples

```
## Not run:
  data('trait.mcmc', package = 'PEcAn.utils')
  data('prior.distns', package = 'PEcAn.utils')
  approx.posterior(trait.mcmc, priors = prior.distns)

## End(Not run)
```

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jagify *Prepare trait data for JAGS meta-analysis*

Description

Convert queried data to format required by JAGS meta-analysis model

Usage

```
jagify(result, use_ghs = TRUE)
```

Arguments

result	input trait data
use_ghs	(Logical) If FALSE, exclude all greenhouse data. If TRUE, use all data, including greenhouse data.

Value

result transformed to meet requirements of PEcAn meta-analysis model

Author(s)

David LeBauer

p.point.in.prior *find quantile of point within prior distribution*

Description

compare point to prior distribution

Usage

```
p.point.in.prior(point, prior)
```

Arguments

point	quantile of given prior to return
prior	list of distn, parama, paramb

Details

used to compare data to prior, meta analysis posterior to prior

Value

result of p<distn>(point, parama, paramb)

Author(s)

David LeBauer

pecan.ma *Trait Meta-analysis*

Description

Runs heirarchical meta-analysis of plant trait data

Usage

```
pecan.ma(
  trait.data,
  prior.distns,
  taupriors,
  j.iter,
  outdir,
  random = FALSE,
  overdispersed = TRUE,
  logfile = file.path(outdir, "meta-analysis.log)"),
  verbose = TRUE
)
```

Arguments

trait.data	list of data.frames, one per trait for which data is available, generated by call to PEcAn.DB::query.traits(), and post-processed by jagify().
prior.distns	data.frame of prior distributions generated by call to PEcAn.DB::query.priors()
taupriors	priors on variance parameters, can be scaled as needed with data mean
j.iter	number of MCMC samples
outdir	output directory
random	use random effects, FALSE by default
overdispersed	TRUE by default, if set to FALSE, data mean will be used as starting point for MCMC chains (use with caution)
logfile	Path to file for sinking meta analysis output. If NULL, only print output to console.
verbose	Logical. If TRUE (default), print progress messages.
data	data frame generated by jagify function with indexed values for greenhouse, treatment, and site (ghs, trt, site) as well as Y, SE, and n for each observation or summary statistic.

Details

pecan.ma runs a hierarchical Bayesian meta-analytical model. This model combines prior information with data from studies on the particular species or group of interest. Data that is incorporated into the meta-analysis include the mean (Y), sample size (n), and precision (obs.prec). Where a set of data includes more than one level of treatment, comes from more than one site, or comes from both field and greenhouse studies, these variables are included as random (treatment, site) or fixed (greenhouse) effects. The pecan.ma function writes a model for each specific data set and prior using the write.ma.model() function to modify the ma.model.template.bug generic model.

Value

four chains with 5000 total samples from posterior

Author(s)

David LeBauer, Michael C. Dietze, Alexey Shiklomanov

Examples

```
## Not run:
  # Setup
  con <- PEcAn.DB::db.open(...)
  pft <- "temperate.Early_Hardwood"
  pft_id <- PEcAn.DB::db.query("SELECT id FROM pfts WHERE name = $1", con,
  values = list(pft))[[1]]
  traits <- c("SLA", "Vcmax")
  trait_string <- paste(shQuote(traits), collapse = ",")
```

```
  # Load traits and priors from BETY
  species <- PEcAn.DB::query.pft_species(pft, con = con)
  trait.data <- PEcAn.DB::query.traits(species[["id"]], c("SLA", "Vcmax"), con = con)
  prior.distns <- PEcAn.DB::query.priors(pft_id, trait_string, con = con)

  # Pre-process data
  jagged.data <- lapply(trait.data, PEcAn.MA::jagify)
  taupriors <- list(tauA = 0.01,
  tauB = c(SLA = 1000, Vcmax = 1000))
  result <- pecan.ma(jagged.data, prior.distns, taupriors,
                     j.iter = 5000, outdir = tempdir())

## End(Not run)
```

`pecan.ma.summary` *Generate summary statistics and diagnostics for PEcAn meta.analysis*

Description

Generate summary statistics and diagnostics for PEcAn meta.analysis

Usage

```
pecan.ma.summary(mcmc.object, pft, outdir, threshold = 1.2, gg = FALSE)
```

Arguments

`mcmc.object`	JAGS mcmc output from `pecan.ma`
`pft`	plant functional type
`outdir`	output directory
`threshold`	Gelman-Rubin convergence diagnostic (MGPRF) default = 1.2 following Bolker 2008 Ecological Models and Data in R
`gg`	produce extra diagnostic plots using the "ggmcmc" package? Caution: very slow!

Author(s)

David LeBauer, Shawn Serbin

Examples

```
## Not run:
summary <- pecan.ma.summary(
 trait.mcmc,
 settings$pfts$pft,
 settings$outdir,
 settings$meta.analysis$threshold)

## End(Not run)
```

rename_jags_columns *renames the variables within output data frame trait.data*

Description

renames the variables within output data frame trait.data

Usage

```
rename_jags_columns(data)
```

Arguments

data	data frame to with variables to rename

Author(s)

David LeBauer

See Also

used with jagify;

run.meta.analysis *Run meta analysis*

Description

This will use the following items from setings:

- settings$pfts
- settings$database$bety
- settings$database$dbfiles
- settings$meta.analysis$update

Usage

```
run.meta.analysis(
  pfts,
  iterations,
  random = TRUE,
  threshold = 1.2,
  dbfiles,
  database,
  use_ghs = TRUE,
  update = FALSE
)
```

Arguments

pfts	the list of pfts to get traits for
iterations	the number of iterations for the mcmc analysis
random	should random effects be used?
threshold	Gelman-Rubin convergence diagnostic, passed on to pecan.ma.summary
dbfiles	location where previous results are found
database	database connection parameters
use_ghs	do not exclude greenhouse data if TRUE
update	logical: Rerun the meta-analysis if result files already exist?

Value

nothing, as side effect saves trait.mcmc created by pecan.ma and post.distns created by approx.posterior(trait.mcmc, ...) to trait.mcmc.Rdata and post.distns.Rdata, respectively

Author(s)

Shawn Serbin, David LeBauer

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runModule.run.meta.analysis

Run meta-analysis on all PFTs in a (list of) PEcAn settings

Description

Run meta-analysis on all PFTs in a (list of) PEcAn settings

Usage

```
runModule.run.meta.analysis(settings)
```

Arguments

settings	a PEcAn settings or MultiSettings object

Value

list of PFTs, invisibly; saves MA results to settingspftoutdir as a side effect

`single.MA` *Single MA*

Description

Individual Meta-analysis

Usage

```
single.MA(
  data,
  j.chains,
  j.iter,
  tauA,
  tauB,
  prior,
  jag.model.file,
  overdispersed = TRUE
)
```

Arguments

`data`	data frame generated by jagify function with indexed values for greenhouse, treatment, and site (ghs, trt, site) as well as Y, SE, and n for each observation or summary statistic.
`j.chains`	number of chains in meta-analysis
`j.iter`	number of mcmc samples
`tauA`	prior on variance parameters
`tauB`	prior on variance parameters
`prior`	data.frame with columns named 'distn', 'parama', 'paramb' e.g. `prior <- data.frame(distn = 'weibull', parama = 0.5, paramb = 10, n = 1)`
`jag.model.file`	file to which model will be written
`overdispersed`	if TRUE (default), chains start at overdispersed locations in parameter space (recommended)

Details

Individual meta-analysis for a specific trait and PFT is run by the function single.MA. This will allow power analysis to run repeated MA outside of the full loop over traits and PFTs.

Value

jags.out, an mcmc.object with results of meta-analysis

Author(s)

David LeBauer, Michael C. Dietze

transform.nas *Function to remove NA values from database queries*

Description

Transform NA values in data exported from BETYdb

Usage

```
## S3 method for class 'nas'
transform(data)
```

Arguments

data	input data

Value

A data frame NAs sensibly replaced

write.ma.model *write.ma.model*

Description

Convert template ma.model.template.R to a JAGS model.

Usage

```
write.ma.model(
  modelfile,
  outfile,
  reg.model,
  pr.dist,
  pr.param.a,
  pr.param.b,
  n,
  trt.n,
  site.n,
  ghs.n,
  tauA,
  tauB
)
```

Arguments

modelfile	model template file (ma.model.template.R)
outfile	file name of model created
reg.model	structure of regression model
pr.dist	A string representing the root distribution name used by R, e.g. 'norm', 'lnorm', 'gamma', 'beta', etc.
pr.param.a	first parameter value accepted by pr.dist
pr.param.b	second parameter value accepted by pr.dist
n	number of observations in data
trt.n	number of distinct treatments in data
site.n	number of distinct sites in data
ghs.n	= 1 if only non-greenhouse or greenhouse studies included, 2 if both
tauA	parameter a for gamma prior on precision
tauB	parameter b for gamma prior on precision

Details

Writes a meta-analysis model based on available data and prior specification. Inspired by the R2WinBUGS::write.model by Jouni Kerman and Uwe Ligges.

Value

Nothing, but as a side effect, the model is written

Author(s)

David LeBauer and Mike Dietze.

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