

Package: PEcAn.uncertainty (via r-universe)

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Type Package

Title PEcAn Functions Used for Propagating and Partitioning
Uncertainties in Ecological Forecasts and Reanalysis

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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.

Imports dplyr, ggplot2, gridExtra, PEcAn.DB, PEcAn.emulator,
PEcAn.logger, PEcAn.priors, PEcAn.settings, PEcAn.utils, plyr
(>= 1.8.4), purrr, randtoolbox, rlang

Suggests testthat (>= 1.0.2),

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ensemble.filename	<i>Generate ensemble filenames</i>
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Description

Generates a vector of filenames to be used for PEcAn ensemble output files. All paths start from directory 'settings\$outdir', which will be created if it does not exist.

Usage

```
ensemble.filename(  
  settings,  
  prefix = "ensemble.samples",  
  suffix = "Rdata",  
  all.var.yr = TRUE,  
  ensemble.id = settings$ensemble$ensemble.id,  
  variable = settings$ensemble$variable,  
  start.year = settings$ensemble$start.year,  
  end.year = settings$ensemble$end.year  
)
```

Arguments

settings	list of PEcAn settings.
prefix	string to appear at the beginning of the filename
suffix	file extension: string to appear at the end of the filename
all.var.yr	logical: does ensemble include all vars and years? If FALSE, filename will include years and vars
ensemble.id	ensemble ID(s)
variable	variable(s) included in the ensemble.
start.year, end.year	first and last year simulated.

Details

Typically used by passing only a settings object, but all values can be overridden for manual use.

If only a single variable or a subset of years are needed, the generated filename will identify these in the form If all vars and years are included, set 'all.yr.var' to TRUE to get a filename of the form 'prefix.ensemble_id.suffix'. All elements are recycled vectorwise.

Value

a vector of filenames, each in the form '[settings\$outdir]/[prefix].[ensemble.ID].[variable].[start.year].[end.year][suffix]'.

Author(s)

Ryan Kelly

ensemble.ts	<i>Plots an ensemble time-series from PEcAn for the selected target variable</i>
-------------	--

Description

Plots an ensemble time-series from PEcAn for the selected target variable

Usage

```
ensemble.ts(ensemble.ts, observations = NULL, window = 1, ...)
```

Value

nothing, generates an ensemble time-series plot

Author(s)

Michael Dietze, Ryan Kelly

flux.uncertainty	<i>Calculate parameters for heteroskedastic flux uncertainty</i>
------------------	--

Description

Calculate parameters for heteroskedastic flux uncertainty

Usage

```
flux.uncertainty(  
  measurement,  
  QC = 0,  
  flags = TRUE,  
  bin.num = 10,  
  transform = identity,  
  minBin = 5,  
  ...  
)
```

Arguments

- measurement = flux time-series
- QC = quality control flag time series (0 = best)
- flags = additional flags on flux filtering of PAIRS (length = 1/2 that of the time series, TRUE = use).
- bin.num = number of bins (default = 10)
- transform = transformation of magnitude (default = identity)
- minBin = minimum number of points allowed in a bin

Value

return.list List of parameters from the fitted uncertainty model

Author(s)

Mike Dietze, Carl Davidson

get.change *Get delta between sequential flux datapoints*

Description

Get delta between sequential flux datapoints

Usage

get.change(measurement)

Value

Difference between consecutive measurements

Author(s)

Mike Dietze, Carl Davidson

<code>get.coef.var</code>	<i>Get coefficient of variance</i>
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Description

Given a set of numbers (a numeric vector), this returns the set's coefficient of variance.

Usage

```
get.coef.var(set)
```

Arguments

set	numeric vector of trait values
-----	--------------------------------

Value

coefficient of variance

<code>get.elasticity</code>	<i>Get Elasticity</i>
-----------------------------	-----------------------

Description

Generic function for the elasticity

Usage

```
get.elasticity(sensitivity, samples, outputs)
```

Arguments

sensitivity	univariate sensitivity of model to a parameter, can be calculated by get.sensitivity
samples	samples from trait distribution
outputs	model output from ensemble runs

Details

Given the sensitivity, samples, and outputs for a single trait, return elasticity

Value

elasticity = normalized sensitivity

get.ensemble.samples *Get Ensemble Samples*

Description

Get parameter values used in ensemble

Usage

```
get.ensemble.samples(  
  ensemble.size,  
  pft.samples,  
  env.samples,  
  method = "uniform",  
  param.names = NULL,  
  ...  
)
```

Arguments

ensemble.size	number of runs in model ensemble
pft.samples	random samples from parameter distribution, e.g. from a MCMC chain
env.samples	env samples
method	the method used to generate the ensemble samples. Random generators: uniform, uniform with latin hypercube permutation. Quasi-random generators: halton, sobol, torus. Random generation draws random variates whereas quasi-random generation is deterministic but well equidistributed. Default is uniform. For small ensemble size with relatively large parameter number (e.g ensemble size < 5 and # of traits > 5) use methods other than halton.
param.names	a list of parameter names that were fitted either by MA or PDA, important argument, if NULL parameters will be resampled independently
...	Other arguments passed on to the sampling method

Details

Returns a matrix of randomly or quasi-randomly sampled trait values to be assigned to traits over several model runs. given the number of model runs and a list of sample distributions for traits The model run is indexed first by model run, then by trait

Value

matrix of (quasi-)random samples from trait distributions

Author(s)

David LeBauer, Istem Fer

get.gi.phii	<i>Get $g_i(\phi_i)$</i>
-------------	-------------------------------------

Description

Calculate distribution of function of a variable

Usage

```
get.gi.phii(splinefuncs, trait.samples, maxn = NULL)
```

Arguments

splinefuncs	univariate spline functions created for each trait, e.g. by the sensitivity.analysis function.
trait.samples	$n \times m$ matrix (or list with m vectors of length n) of n parameter sets, each with a sample from m traits
maxn	maximum number of parameter sets to evaluate

Details

Transform trait parameter through trait-specific univariate model emulator spline function Given a matrix of parameter sets, calculates a matrix of model output by applying appropriate spline function to each parameter. Output is used with [plot.variance.decomposition](#) and [spline.ensemble](#)

Value

matrix of spline estimates of model output for each of n parameter sets

Author(s)

David LeBauer

get.parameter.samples	<i>Sample from priors or posteriors</i>
-----------------------	---

Description

Convert priors / MCMC samples to chains that can be sampled for model parameters

Usage

```
get.parameter.samples(
  settings,
  posterior.files = rep(NA, length(settings$pfts)),
  ens.sample.method = "uniform"
)
```


Arguments

`pfts` the pfts node of the list of pecan settings

Author(s)

David LeBauer, Shawn Serbin, Istem Fer

get.results *Reads model output and runs sensitivity and ensemble analyses*

Description

Output is placed in model output directory (`settings$outdir`).

Usage

```
get.results(  
  settings,  
  sa.ensemble.id = NULL,  
  ens.ensemble.id = NULL,  
  variable = NULL,  
  start.year = NULL,  
  end.year = NULL  
)
```

Arguments

`settings` list, read from settings file (xml) using [read.settings](#)

`sa.ensemble.id, ens.ensemble.id`
ensemble IDs for the sensitivity analysis and ensemble analysis. If not provided, they are first looked up from 'settings', then if not found they are not used and the most recent set of results is read from `samples.Rdata` in directory `settings$outdir`

`variable` variables to retrieve, as vector of names or expressions

`start.year, end.year`
first and last years to retrieve

Author(s)

David LeBauer, Shawn Serbin, Mike Dietze, Ryan Kelly

get.sensitivity	<i>Calculate Sensitivity</i>
-----------------	------------------------------

Description

Calculate the sensitivity of a function at the median

Usage

```
get.sensitivity(trait.samples, sa.splinefun)
```

Arguments

```
trait.samples
sa.splinefun
```

Details

This function evaluates the sensitivity of a model to a parameter. This is done by evaluating the first derivative of the univariate spline estimate of the model response at the parameter median.

Value

numeric estimate of model sensitivity to parameter

input.ens.gen	<i>Function for generating samples based on sampling method, parent or etc</i>
---------------	--

Description

Function for generating samples based on sampling method, parent or etc

Usage

```
input.ens.gen(settings, input, method = "sampling", parent_ids = NULL)
```

Arguments

settings	list of PEcAn settings
method	Method for sampling - For now looping or sampling with replacement is implemented
parent_ids	This is basically the order of the paths that the parent is sampled. See Details.

Details

If for example met was a parent and it's sampling method resulted in choosing the first, third and fourth samples, these are the ids that need to be sent as parent_ids to this function.

Value

For a given input/tag in the pecan xml and a method, this function returns a list with \$id showing the order of sampling and \$samples with samples of that input.

Examples

```
## Not run: input.ens.gen(settings,"met","sampling")
```

kurtosis	<i>Calculate excess kurtosis from a vector</i>
----------	--

Description

Calculates the excess kurtosis of a vector

Usage

```
kurtosis(x)
```

Arguments

x vector of values

Details

Note that this calculates the 'excess kurtosis', which is defined as kurtosis - 3. This statistic is used in the calculation of the standard deviation of sample variance in the function [sd.var](#). Additional details

Value

numeric value of kurtosis

Author(s)

David LeBauer

References

NIST/SEMATECH e-Handbook of Statistical Methods, <http://www.itl.nist.gov/div898/handbook/eda/section3/eda35b.htm>, 2011-06-20.

plot_flux_uncertainty *Plot fit for heteroskedastic flux uncertainty*

Description

Plot fit for heteroskedastic flux uncertainty

Usage

```
plot_flux_uncertainty(f, ...)
```

Arguments

f output of flux.uncertainty functions
 ... optional graphical paramters

Author(s)

Mike Dietze, Carl Davidson

plot_sensitivities *Plot Sensitivities*

Description

Plot functions and quantiles used in sensitivity analysis

Usage

```
plot_sensitivities(  
  sensitivity.plot.inputs,  
  prior.sensitivity.plot.inputs = NULL,  
  ...  
)
```

Arguments

sensitivity.plot.inputs
 inputs
 prior.sensitivity.plot.inputs
 priors
 ... arguments passed to [plot_sensitivity](#)
 sensitivity.results
 list containing sa.samples and sa.splines

Details

Generates a plot using `plot_sensitivity` for multiple traits.

Value

list of plots, one per trait

plot_sensitivity	<i>Sensitivity plot</i>
------------------	-------------------------

Description

Plot univariate response of model output to a trait parameter.

Usage

```
plot_sensitivity(
  sa.sample,
  sa.spline,
  trait,
  y.range = c(0, 50),
  median.i = 4,
  prior.sa.sample = NULL,
  prior.sa.spline = NULL,
  fontsize = list(title = 12, axis = 8),
  linesize = 1,
  dotsize = 2
)
```

Arguments

sa.sample	trait quantiles used in sensitivity analysis
sa.spline	spline function estimated from sensitivity analysis
trait	trait name for title
y.range	
median.i	index of median value in sa.sample; median.i == which(as.numeric(rownames(sa.sample)) == 50)
prior.sa.sample	similar to sa.sample, but for prior distribution. If given, plots sensitivity for prior run
prior.sa.spline	similar to sa.spline, but for prior trait distribution.
fontsize	(optional) list with three arguments that can be set to vary the fontsize of the title, axis labels, and axis title in the sensitivity plots

Details

Plots for a single trait; called by `plot_sensitivities` to plot sensitivity plots for multiple traits.

Value

object of class `ggplot`

plot_variance_decomposition
Variance Decomposition Plots

Description

Plots variance decomposition tryptich

Usage

```
plot_variance_decomposition(  
  plot.inputs,  
  fontsize = list(title = 18, axis = 14)  
)
```

Arguments

<code>plot.inputs</code>	Output from a sensitivity analysis. Output must be of the form given by <code>sensitivity.results\$variance.decomposition.output</code> in model output
<code>fontsize</code>	list specifying the font size of the titles and axes of the graph

Author(s)

David LeBauer, Carl Davidson

Examples

```
x <- list(trait.labels = c('a', 'b', 'c'),  
         coef.vars = c(a=1,b=0.5, c=0.1),  
         elasticities = c(a=1,b=2,c=0.5),  
         variances = c(a = 20, b=30, c = 10))  
do.call(gridExtra::grid.arrange, c(plot_variance_decomposition(x), ncol = 4))
```

read.ameriflux.L2 *Read Ameriflux L2 Data*

Description

Read Ameriflux L2 Data

Usage

```
read.ameriflux.L2(file.name, year)
```

Value

Ameriflux L2 data read from file

Author(s)

Mike Dietze, Carl Davidson

read.ensemble.output *Read ensemble output*

Description

Reads output from model ensemble

Usage

```
read.ensemble.output(  
  ensemble.size,  
  pecandir,  
  outdir,  
  start.year,  
  end.year,  
  variable,  
  ens.run.ids = NULL  
)
```

Arguments

ensemble.size	the number of ensemble members run
pecandir	specifies where pecan writes its configuration files
outdir	directory with model output to use in ensemble analysis
start.year	first year to include in ensemble analysis
end.year	last year to include in ensemble analysis

variable target variables for ensemble analysis

ens.run.ids dataframe. Must contain a column named "id" giving the run IDs to be read. If NULL, will attempt to read IDs from a file named "samples.Rdata" in pecandir

Details

Reads output for an ensemble of length specified by ensemble.size and bounded by start.year and end.year

Value

a list of ensemble model output

Author(s)

Ryan Kelly, David LeBauer, Rob Kooper

read.ensemble.ts	<i>Reads an ensemble time-series from PEcAn for the selected target variable</i>
------------------	--

Description

Reads ensemble time-series from PEcAn for the selected target variable

Usage

```
read.ensemble.ts(  
  settings,  
  ensemble.id = NULL,  
  variable = NULL,  
  start.year = NULL,  
  end.year = NULL  
)
```

Value

list

Author(s)

Michael Dietze, Ryan Kelly

read.sa.output *Read Sensitivity Analysis output*

Description

Reads output of sensitivity analysis runs

Usage

```
read.sa.output(
  traits,
  quantiles,
  pecandir,
  outdir,
  pft.name = "",
  start.year,
  end.year,
  variable,
  sa.run.ids = NULL,
  per.pft = FALSE
)
```

Arguments

traits	model parameters included in the sensitivity analysis
quantiles	quantiles selected for sensitivity analysis
pecandir	specifies where pecan writes its configuration files
outdir	directory with model output to use in sensitivity analysis
pft.name	name of PFT used in sensitivity analysis (Optional)
start.year	first year to include in sensitivity analysis
end.year	last year to include in sensitivity analysis
variable	variables to be read from model output
sa.run.ids	list of run ids to read. If NULL, will look in 'pecandir' for a file named 'samples.Rdata' and read from that
per.pft	flag to determine whether we want SA on pft-specific variables

Value

dataframe with one col per quantile analysed and one row per trait, each cell is a list of AGB over time

Author(s)

Ryan Kelly, David LeBauer, Rob Kooper, Mike Dietze, Istem Fer
 Ryan Kelly, David LeBauer, Rob Kooper, Mike Dietze

`run.ensemble.analysis` *run ensemble.analysis*

Description

`run ensemble.analysis`

Usage

```
run.ensemble.analysis(  
  settings,  
  plot.timeseries = NA,  
  ensemble.id = NULL,  
  variable = NULL,  
  start.year = NULL,  
  end.year = NULL,  
  ...  
)
```

Arguments

`plot.timeseries`
if TRUE plots a modeled timeseries of target variable(s) with CIs

Value

nothing, creates ensemble plots as `ensemble.analysis.pdf`

Author(s)

David LeBauer, Shawn Serbin, Ryan Kelly

`run.sensitivity.analysis`
run sensitivity.analysis

Description

Runs the sensitivity analysis module on a finished run

Usage

```
run.sensitivity.analysis(
  settings,
  plot = TRUE,
  ensemble.id = NULL,
  variable = NULL,
  start.year = NULL,
  end.year = NULL,
  pfts = NULL,
  ...
)
```

Arguments

settings	a PEcAn settings object
plot	logical. Option to generate sensitivity analysis and variance decomposition plots (plot=TRUE) or to turn these plots off (plot=FALSE).
ensemble.id	ensemble ID
variable	which variable(s) to do sensitivity analysis for. Defaults to all specified in 'settings'
start.year	defaults to what is specified in 'settings'
end.year	defaults to what is specified in 'settings'
pfts	a vector of PFT names found in 'settings' to run sensitivity analysis on
...	currently unused

Value

nothing, saves sensitivity.results as sensitivity.results.Rdata, sensitivity plots as sensitivity-analysis.pdf, and variance decomposition 'popsicle plot' as variancedecomposition.pdf a side effect (OPTIONAL)

Author(s)

David LeBauer, Shawn Serbin, Ryan Kelly

Examples

```
## Not run:
library(PEcAn.settings)
library(PEcAn.uncertainty)
settings <- read.settings("path/to/pecan.xml")
run.sensitivity.analysis(settings)

## End(Not run)
```

runModule.get.results *Apply get.results to each of a list of settings*

Description

Apply get.results to each of a list of settings

Usage

```
runModule.get.results(settings)
```

Arguments

settings a PEcAn Settings or MultiSettings object

See Also

get.results

sa.splinefun *Sensitivity spline function*

Description

Spline estimate of univariate relationship between parameter value and model output

Usage

```
sa.splinefun(quantiles.input, quantiles.output)
```

Arguments

quantiles.input

quantiles.output

Details

Creates a spline function using the splinefun function that estimates univariate response of parameter input to model output

Value

function

sd.var *Standard deviation of sample variance*

Description

Calculates the standard deviation of the variance estimate

Usage

```
sd.var(x)
```

Arguments

x sample

Details

Uses the equation $\sigma^4 \left(\frac{2}{n-1} + \frac{\kappa}{n} \right)$

Value

estimate of standard deviation of the sample variance

Author(s)

David LeBauer

References

Mood, Graybill, Boes 1974 'Introduction to the Theory of Statistics' 3rd ed. p 229; Casella and Berger 'Statistical Inference' p 364 ex. 7.45; 'Reference for Var(s^2)' CrossValidated <http://stats.stackexchange.com/q/29905/1381>, 'Calculating required sample size, precision of variance estimate' CrossValidated <http://stats.stackexchange.com/q/7004/1381>, 'Variance of Sample Variance?' Mathematics - Stack Exchange <http://math.stackexchange.com/q/72975/3733>

sensitivity.analysis *Sensitivity Analysis*

Description

Performs univariate sensitivity analysis and variance decomposition

Usage

```
sensitivity.analysis(trait.samples, sa.samples, sa.output, outdir)
```

Arguments

trait.samples	list of vectors, one per trait, representing samples of the trait value, with length equal to the mcmc chain length. Samples are taken from either the prior distribution or meta-analysis results
sa.samples	data.frame with one column per trait and one row for the set of quantiles used in sensitivity analysis. Each cell contains the value of the trait at the given quantile.
sa.output	list of data.frames, similar to sa.samples, except cells contain the results of a model run with that trait x quantile combination and all other traits held at their median value
outdir	directory to which plots are written

Details

This function estimates the univariate responses of a model to a parameter for a set of traits, calculates the model sensitivity at the median, and performs a variance decomposition. This function results in a set of sensitivity plots (one per variable) and plot_variance_decomposition.

Value

results of sensitivity analysis

Author(s)

David LeBauer

Examples

```
## Not run:
sensitivity.analysis(
  trait.samples[[pft$name]],
  sa.samples[[pft$name]],
  sa.agb[[pft$name]],
  pft$outdir
)

## End(Not run)
```

sensitivity.filename *Generate sensitivity analysis filenames*

Description

Generate sensitivity analysis filenames

Usage

```
sensitivity.filename(  
  settings,  
  prefix = "sensitivity.samples",  
  suffix = "Rdata",  
  all.var.yr = TRUE,  
  pft = NULL,  
  ensemble.id = settings$sensitivity.analysis$ensemble.id,  
  variable = settings$sensitivity.analysis$variable,  
  start.year = settings$sensitivity.analysis$start.year,  
  end.year = settings$sensitivity.analysis$end.year  
)
```

Arguments

settings	list of PEcAn settings.
prefix	string to appear at the beginning of the filename
suffix	file extension: string to appear at the end of the filename
all.var.yr	logical: does ensemble include all vars and years? If FALSE, filename will include years and vars
pft	name of PFT used for analysis. If NULL, assumes all PFTs in run are used and does not add them to the filename
ensemble.id	ensemble ID(s)
variable	variable(s) included in the ensemble.
start.year, end.year	first and last year simulated.

Details

Generally uses values in settings, but can be overwritten for manual uses

Value

a filename

Author(s)

Ryan Kelly

spline.ensemble *Spline Ensemble*

Description

Estimate model output based on univariate splines

Usage

```
spline.ensemble(gi.phii, median)
```

Arguments

gi.phii	matrix given as output from get.gi.phii
median	median value around which variance will be calculated

Details

Accepts output from [get.gi.phii](#) (the matrix $g(\phi_i)$) and produces spline estimate of $f(\phi)$ for use in estimating closure term associated with spline approximation

Author(s)

David LeBauer

spline.truncate *Truncate spline*

Description

Truncate spline at zero if..

Usage

```
spline.truncate(x, min.quantile = stats::pnorm(-3))
```

Arguments

x	vector
min.quantile	threshold quantile for testing lower bound on variable

Details

Truncate spline at zero if $P[x < 0] < \text{pnorm}(-3)$ $\text{pnorm}(-3)$ chosen as default value for min quantile because this is the default low end of range for the sensitivity analysis. This parameter could be determined based on minimum value in `settings$sensitivity.analysis$quantiles`

Value

either x or a vector with values < 0 converted to zero

Author(s)

David LeBauer

Examples

```
set.seed(0)
x <- c(rgamma(998,1,1), rnorm(10))
min(x) # -0.5238
min(PeCAn.uncertainty::spline.truncate(x))
```

variance.stats

variance statistics

Description

Variance and SD(variance)

Usage

```
variance.stats(x)
```

Arguments

x numeric vector

Details

calculates variance and sd of variance using the `var` from base R and [sd.var](#) from PeCAn.

Value

list with variance and sd of variance

Author(s)

David LeBauer

```
write.ensemble.configs
```

Write ensemble config files

Description

Writes config files for use in meta-analysis and returns a list of run ids. Given a pft.xml object, a list of lists as supplied by get.sa.samples, a name to distinguish the output files, and the directory to place the files.

Usage

```
write.ensemble.configs(
  defaults,
  ensemble.samples,
  settings,
  model,
  clean = FALSE,
  write.to.db = TRUE,
  restart = NULL,
  rename = FALSE
)
```

Arguments

defaults	pft
ensemble.samples	list of lists supplied by get.ensemble.samples
settings	list of PEcAn settings
model	name of model to be run, e.g. "ED2" or "SIPNET"
clean	remove old output first?
write.to.db	logical: Record this run in BETY?
restart	In case this is a continuation of an old simulation. restart needs to be a list with name tags of runid, inputs, new.params (parameters), new.state (initial condition), ensemble.id (ensemble id), start.time and stop.time. See Details.
rename	Decide if we want to rename previous output files, for example convert from sipnet.out to sipnet.2020-07-16.out.

Details

The restart functionality is developed using model specific functions by calling write_restart.modelname function. First, you need to make sure that this function already exist for your desired model. See here <https://pecanproject.github.io/pecan-documentation/master/pecan-models.html> new state is a dataframe with a different column for each state variable. The number of the rows in this dataframe needs to be the same as the ensemble size. State variables that you can use for

setting up the initial conditions differs for different models. You may check the documentation of the `write_restart.modelname` your model. The units for the state variables need to be in the PEEAn standard units which can be found in [standard_vars](#). `new.params` also has similar structure to `ensemble.samples` which is sent as an argument.

Value

list, containing `$runs` = data frame of runids, `$ensemble.id` = the ensemble ID for these runs and `$samples` with ids and samples used for each tag. Also writes sensitivity analysis configuration files as a side effect

Author(s)

David LeBauer, Carl Davidson, Hamze Dokoochaki

`write.sa.configs` *Write sensitivity analysis config files*

Description

Writes config files for use in sensitivity analysis.

Usage

```
write.sa.configs(
  defaults,
  quantile.samples,
  settings,
  model,
  clean = FALSE,
  write.to.db = TRUE
)
```

Arguments

<code>defaults</code>	named list with default parameter values
<code>quantile.samples</code>	list of lists supplied by get.sa.samples
<code>settings</code>	list of settings
<code>model</code>	name of model to be run
<code>clean</code>	logical: Delete any existing contents of the directory specified by <code>settings\$rundir</code> before writing to it?
<code>write.to.db</code>	logical: Record this run to BETY? If TRUE, uses connection settings specified in <code>settings\$database</code>

Value

list, containing \$runs = data frame of runids, and \$ensemble.id = the ensemble ID for these runs.
Also writes sensitivity analysis configuration files as a side effect

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