Package ‘clhs’

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Description Conditioned Latin hypercube sampling, as published by Minasny and McBratney (2006). This method proposes to stratify sampling in presence of ancillary data. An extension of this method, which propose to associate a cost to each individual and take it into account during the optimisation process, is also proposed (Roudier et al., 2012).
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Description

This package implements the conditioned Latin hypercube sampling, as published by Minasny and McBratney (2006). This method proposes to stratify sampling in presence of ancillary data.

An extension of this method, which propose to associate a cost to each individual and take it into account during the optimisation process, is also proposed (Roudier et al., 2012).

Author(s)

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References

*For the initial cLHS method:


*For the cost-constrained implementation:


See Also

sample

Examples

df <- data.frame(
a = runif(1000),
b = rnorm(1000),
c = sample(LETTERS[1:5], size = 1000, replace = TRUE)
)
res <- clhs(df, size = 50, iter = 2000, progress = FALSE)
str(res)
Conditioned Latin Hypercube Sampling

Description

Implementation of the conditioned Latin hypercube sampling, as published by Minasny and McBratney (2006). This method proposes to stratify sampling in presence of ancillary data. An extension of this method, which propose to associate a cost to each individual and take it into account during the optimisation process, is also proposed (Roudier et al., 2012).

Usage

clhs(x, ...)

Arguments

x A data.frame, SpatialPointsDataFrame or Raster object.
...
Additional arguments, see under Details.

Details

Below are the additional arguments that can be used:
- size: A non-negative integer giving the number of samples to pick.
- cost: A character giving the name or an integer giving the index of the attribute in x that gives a cost that can be use to constrain the cLHS sampling. If NULL (default), the cost-constrained implementation is not used.
- track: A character giving the name or an integer giving the index of the attribute in x that gives a cost associated with each individual. However, this method will only track the cost - the sampling prrocess will not be constrained by this attribute. If NULL (default), this option is not used.
- iter: A positive number, giving the number of iterations for the Metropolis-Hastings annealing process. Defaults to 10000.
- temp: The initial temperature at which the simulated annealing begins. Defaults to 1.
- tdecrease: A number between 0 and 1, giving the rate at which temperature decreases in the simulated annealing process. Defaults to 0.95.
- weights: A list a length 3, giving the relative weights for continuous data, categorical data, and correlation between variables. Defaults to list(numeric = 1, factor = 1, correlation = 1).
- obj.limit: The minimal value at which the optimisation is stopped. Defaults to -Inf.
- length.cycle: The duration (number of iterations) of the isotemperature steps. Defaults to 10.
- progress: TRUE or FALSE, displays a progress bar.
- simple: TRUE or FALSE. If set to TRUE, only the indices of the selected samples are returned, as a numeric vector. If set to FALSE, a cLHS_result object is returned (takes more memory but allows to make use of cLHS_results methods such as plot.cLHS_result).
Value

* If the `simple` option is set to TRUE (default behaviour): A numeric vector containing the indices of the selected samples is returned

* If the `simple` option is set to FALSE: An object of class `clhs_result`, with the following elements:

  - `index_samples` a vector giving the indices of the chosen samples.
  - `sampled_data` the sampled data.frame.
  - `obj` a vector giving the evolution of the objective function throughout the Meropolis-Hastings iterations.
  - `cost` a vector giving the evolution of the cost function throughout the Meropolis-Hastings iterations (if available).

Author(s)

Pierre Roudier

References

*For the initial cLHS method:


*For the cost-constrained implementation:


See Also

  `plot.clhs_result`

Examples

```r
df <- data.frame(
  a = runif(1000),
  b = rnorm(1000),
  c = sample(LETTERS[1:5], size = 1000, replace = TRUE)
)

# Returning the indices of the sampled points
res <- clhs(df, size = 50, iter = 100, progress = FALSE, simple = TRUE)
str(res)

# Returning a clhs_result object for plotting
res <- clhs(df, size = 50, iter = 100, progress = FALSE, simple = FALSE)
str(res)
plot(res)
```
Description

A S3 class describing a cLHS result.

Value

An object of class `cLHS_result` contains the following slots:

- `index_samples`: a vector giving the indices of the chosen samples.
- `sampled_data`: the sampled data.frame.
- `obj`: a vector giving the evolution of the objective function throughout the Metropolis-Hastings iterations.
- `cost`: a vector giving the evolution of the cost function throughout the Metropolis-Hastings iterations, if available, otherwise NULL.

Author(s)

Pierre Roudier

See Also

clhs

plot.cLHS_result

Plot cLHS results

Description

Produces a plot illustrating the result of a cLHS sampling procedure.

Usage

```r
## S3 method for class 'cLHS_result'
plot(x, modes = "obj", ...)
```

Arguments

- `x`: Object of class “cLHS_result”.
- `modes`: A character vector describing the plot to produce (see Details)
- `...`: Other ggplot2 plotting parameters.
Details

The subplots to be included in the final illustration are controlled by the `mdoe` option: - "obj" adds the evolution of the objective function over the iterations - "cost" adds the evolution of the cost function over the iterations (if available in `x`) - "hist" adds the comparison of the distributions of each variables in both the original object and the sampled result using histogram plots (for continuous variables). - "dens" adds the comparison of the distributions of each variables in both the original object and the sampled result using density plots (for continuous variables). - "box" adds the comparison of the distributions of each variables in both the original object and the sampled result using boxplots (for continuous variables).

Author(s)

Pierre Roudier

See Also

clhs

Examples

df <- data.frame(
  a = runif(1000),
  b = rnorm(1000),
  c = sample(LETTERS[1:5], size = 1000, replace = TRUE)
)
res <- clhs(df, size = 50, iter = 2000, progress = FALSE, simple = FALSE)
# You can plot only the objective function
plot(res, mode = "obj")
# Or you can compare the distribution in the original object
# and in the sampled result
plot(res, mode = c("obj", "box"))
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