Package ‘clhs’

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Type Package

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Description Conditioned Latin hypercube sampling, as published by Minasny and McBratney (2006) <DOI:10.1016/j.cageo.2005.12.009>. 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, <DOI:10.1201/b12728>).

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Imports utils, methods, grid, ggplot2, sp, raster, reshape2, plyr, cluster, Rcpp

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License GPL (>= 2)

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LazyLoad yes

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

RoxygenNote 7.1.2

Collate 'RcppExports.R' 'clhs-internal.R' 'clhs-data.frame.R'
  'clhs-package.R' 'clhs-raster.R' 'utils.R' 'clhs.R' 'clhs-sf.R'
  'clhs-sp.R' 'plot.R' 'similarity.R'

NeedsCompilation yes

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Description

This package implements the conditioned Latin hypercube sampling, as published by Minasny and McBratney (2006) and the DLHS variant method (Minasny and McBratney, 2010). This method proposes to stratify sampling in presence of ancillary data.

Details

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)

Pierre Roudier

References

* For the initial cLHS method:

* For the DLHS variant method:

* For the cost-constrained implementation:

* For the similarity buffer prediction:

Brungard, C. and Johanson, J. 2015. The gate’s locked! I can’t get to the exact sampling spot... can I sample nearby? Pedometron, 37:8–10.

See Also

sample

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## clhs

**Conditioned Latin Hypercube Sampling**

### Description

Implementation of the conditioned Latin hypercube sampling, as published by Minasny and McBratney (2006) and the DLHS variant method (Minasny and McBratney, 2010). These methods propose 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

```r
clhs(
  x,
  size,
  must.include,
  can.include,
  cost,
  iter,
  use.cpp,
  temp,
  tdecrease,
  weights,
  eta,
  obj.limit,
  length.cycle,
  simple,
  progress,
  track,
  use.coords,
  ...
)
```

Arguments

\( x \)  A data.frame, SpatialPointsDataFrame, sf, or Raster object.

\( \text{size} \)  A non-negative integer giving the total number of items to select

\( \text{must.include} \)  A numeric vector giving the indices of the rows from \( x \) that must be included in the selected items. For the cost-constrained cLHS method, cost of these mandatory samples is set to 0. If NULL (default), all data are randomly chosen according to the classic cLHS method. If \( \text{must.include} \) is not NULL, argument \( \text{size} \) must include the total size of the final sample i.e. the size of mandatory samples given by \( \text{must.include} \) plus the size of the randomly chosen samples to pick.

\( \text{can.include} \)  A numeric vector giving indices of the rows from \( x \) that are allowed to be sampled from. The algorithm will use all of \( x \) as the reference distribution, but will only select samples from \( \text{possible.sample} \). The option is only available in the C++ version; if use.cpp == FALSE, this parameter will be ignored.

\( \text{cost} \)  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.

\( \text{iter} \)  A positive number, giving the number of iterations for the Metropolis-Hastings annealing process. Defaults to 10000.

\( \text{use.cpp} \)  TRUE or FALSE. If set to TRUE, annealing process uses C++ code. This is ~ 150 times faster than the R version, but is less stable and currently doesn’t accept track or obj.limit parameters. Default to TRUE.

\( \text{temp} \)  The initial temperature at which the simulated annealing begins. Defaults to 1.

\( \text{tdecrease} \)  A number between 0 and 1, giving the rate at which temperature decreases in the simulated annealing process. Defaults to 0.95.

\( \text{weights} \)  A list a length 3, giving the relative weights for continuous data, categorical data, and correlation between variables. Defaults to \( \text{list(numeric = 1, factor = 1, correlation = 1)} \).

\( \text{eta} \)  Either a number equal 1 to perform a classic cLHS or a constrained cLHS or a matrix to perform a cLHS that samples more on the edge of the distribtions (DLHS, see details)

\( \text{obj.limit} \)  The minimal value at which the optimisation is stopped. Defaults to ~Inf.

\( \text{length.cycle} \)  The duration (number of iterations) of the isoltemperature steps. Defaults to 10.

\( \text{simple} \)  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 \( \text{plot.cLHS_result} \)).

\( \text{progress} \)  TRUE or FALSE, displays a progress bar.

\( \text{track} \)  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 process will not be constrained by this attribute. If NULL (default), this option is not used.

\( \text{use.coords} \)  Logical, if TRUE the spatial coordinates of supported spatial objects (either a ‘SpatialPointsDataFrame’ object if using ‘sp’, or a ‘sf’ object if using ‘sf’) are included in the Latin hypercube calculations. Defaults to FALSE.

\( \ldots \)  additional parameters passed to clhs
Details

For the DLHS method, the original paper defines parameter $b$ as the importance of the edge of the distributions. A matrix $\eta$ (size $N \times K$, where $N$ is the size of the final sample and $K$ the number of continuous variables) is defined, to compute the objective function of the algorithm, where each column equal the vector $(b, 1, \ldots, 1, b)$ in order to give the edge of the distribution a probability $b$ times higher to be sampled. In our function, instead of define the $b$ parameter, users can defined their own $\eta$ matrix so that they can give more complex probability design of sampling each strata of the distribution instead of just be able to give more importance to both edges of the distribution.

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 Metropolis-Hastings iterations.
  - `cost`: a vector giving the evolution of the cost function throughout the Metropolis-Hastings iterations (if available).

Author(s)

Pierre Roudier

References

*For the initial cLHS method:


*For the DLHS 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, progress = FALSE, simple = TRUE)
str(res)

# Returning a clhs_result object for plotting using C++
res <- clhs(df, size = 50, use.cpp = TRUE, iter = 5000, progress = FALSE, simple = FALSE)
str(res)
plot(res)

# Method DLHS with a linear increase of the strata weight (i.e. probability to be sampled)
# from 1 for the middle strata to 3 for the edge of the distribution
linear_increase <- 1+(2/24)*0:24
ta <- matrix(c(rev(linear_increase), linear_increase), ncol = 2, nrow = 50)
set.seed(1)
res <- clhs(df, size = 50, iter = 100, eta = ta, progress = FALSE, simple = FALSE)
str(res)
plot(res)
```

---

cLHS_result

*Conditioned Latin Hypercube Sampling result*

**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 Meropolis-Hastings iterations, if available, otherwise NULL.

**Author(s)**

Pierre Roudier
See Also
clhs

CppLHS

This is the internal Cpp function used to run the metropolis hasting algorithm if use.cpp = T. In general, it shouldn’t be used as a stand alone function, because some preprocessing is done in R

Description

This is the internal Cpp function used to run the metropolis hasting algorithm if use.cpp = T. In general, it shouldn’t be used as a stand alone function, because some preprocessing is done in R

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>xA</td>
<td>matrix of data - must be numeric (factors are converted to numeric in R)</td>
</tr>
<tr>
<td>cost</td>
<td>cost vector (0 if no cost)</td>
</tr>
<tr>
<td>strata</td>
<td>matrix of continuous strata</td>
</tr>
<tr>
<td>include</td>
<td>matrix of included data</td>
</tr>
<tr>
<td>idx</td>
<td>integer vector of rows from which sampling is allowed</td>
</tr>
<tr>
<td>factors</td>
<td>boolean factor flag</td>
</tr>
<tr>
<td>i_fact</td>
<td>indices of factors in xA</td>
</tr>
<tr>
<td>nsample</td>
<td>number of samples</td>
</tr>
<tr>
<td>cost_mode</td>
<td>bool cost flag</td>
</tr>
<tr>
<td>iter</td>
<td>number of iterations</td>
</tr>
<tr>
<td>wCont</td>
<td>continuous weight</td>
</tr>
<tr>
<td>wFact</td>
<td>factor weights</td>
</tr>
<tr>
<td>wCorr</td>
<td>correlation weights</td>
</tr>
<tr>
<td>etaMat</td>
<td>eta matrix - either all 1, or user input</td>
</tr>
<tr>
<td>temperature</td>
<td>initial temperature</td>
</tr>
<tr>
<td>tdecrease</td>
<td>temperature decrease every length_cycle iterations</td>
</tr>
<tr>
<td>length_cycle</td>
<td>number of iterations between temperature decrease</td>
</tr>
</tbody>
</table>

Value

list with sampled data, indices, objective values, cost value, and final continuous weights for each sample
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 `mode` 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

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

res <- clhs(df, size = 50, iter = 1000, use.cpp = FALSE, 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"))

---

**similarity_buffer**  
**Gower similarity analysis**

**Description**
Calculates Gower’s similarity index for every pixel within an given radius buffer of each sampling point.

**Usage**

```r
similarity_buffer(
  covs,
  pts,
  buffer,
  fac = NA,
  metric = "gower",
  stand = FALSE,
  ...
)
```

**Arguments**
- `covs`: raster stack of environmental covariates
- `pts`: sampling points, object of class SpatialPointsDataFrame
- `buffer`: Radius of the disk around each point that similarity will be calculated
- `fac`: numeric, can be > 1, (e.g., fac = c(2,3)). Raster layer(s) which are categorical variables. Set to NA if no factor is present
- `metric`: character string specifying the similarity metric to be used. The currently available options are "euclidean", "manhattan" and "gower" (the default). See daisy from the cluster package for more details
- `stand`: logical flag: if TRUE, then the measurements in x are standardized before calculating the dissimilarities.
- `...`: passed to plyr::llply

**Value**
a RasterStack
Author(s)

Colby Brungard

References

Brungard, C. and Johanson, J. 2015. The gate’s locked! I can’t get to the exact sampling spot... can I sample nearby? Pedometron, 37:8–10.

Examples

```r
library(raster)
library(sp)

data(meuse.grid)
coordinates(meuse.grid) = ~x+y
proj4string(meuse.grid) <- CRS("+init=epsg:28992")
gridded(meuse.grid) = TRUE
ms <- stack(meuse.grid)

suppressWarnings(RNGversion("3.5.0"))
set.seed(1)
pts <- clhs(ms, size = 3, iter = 100, progress = FALSE, simple = FALSE)
gw <- similarity_buffer(ms, pts$sampled_data, buffer = 500)
plot(gw)
```
Index

* sampling
  clhs-package, 2

clhs, 3, 8
clhs-package, 2
cLHS_result, 6
CppLHS, 7

plot.cLHS_result, 5, 8

similarity_buffer, 9