Package: comparer (via r-universe)

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Type Package

Title Compare Output and Run Time

Version 0.2.4.9000

Description Quickly run experiments to compare the run time and output of code blocks. The function mbc() can make fast comparisons of code, and will calculate statistics comparing the resulting outputs. It can be used to compare model fits to the same data or see which function runs faster. The R6 class ffexp$new() runs a function using all possible combinations of selected inputs. This is useful for comparing the effect of different parameter values. It can also run in parallel and automatically save intermediate results, which is very useful for long computations.

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Encoding UTF-8

Imports R6

Depends GauPro (>= 0.2.7), mixopt, rmarkdown, plyr, progress

Suggests testthat (>= 2.1.0), covr, knitr, ggplot2, GGally, ggpubr, ContourFunctions, parallel, snow, tibble, lhs, DiceKriging, DiceOptim, microbenchmark

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URL https://github.com/CollinErickson/comparer

BugReports https://github.com/CollinErickson/comparer/issues

VignetteBuilder knitr

Language en-US

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

RemoteUrl https://github.com/collinerickson/comparer

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Contents

`ffexp` *Full factorial experiment*

Description

A class for easily creating and evaluating full factorial experiments.

Usage

```
e1 <- ffexp$new(eval_func=, )

e1$run_all()

e1$plot_run_times()

e1$save_self()
```

Arguments

`eval_func` The function called to evaluate each design point.

`...` Factors and their levels to be evaluated at.

`save_output` Should the output be saved?

`parallel` If `TRUE`, function evaluations are done in parallel.

`parallel_cores` Number of cores to be used in parallel. If `"detect"`, `parallel::detectCores()` is used to determine number. `"detect-1"` may be used so that the computer isn't running at full capacity, which can slow down other tasks.

Methods

`$new()` Initialize an experiment. The preprocessing is done, but no function evaluations are run.

`$run_all()` Run all factor combinations.

`$run_one()` Run a single factor combination.

`$add_result_of_one()` Used to add result of evaluation to data set, don't manually call.

`$plot_run_times()` Plot the run times. Especially useful when they have been run in parallel.

`$save_self()` Save ffexp R6 object.

`$recover_parallel_temp_save()` If you ran the experiment using parallel with `parallel_temp_save=TRUE` and it crashes partway through, call this to recover the runs that were completed. Runs that were stopped mid-execution are not recoverable.

Public fields

`outrawdf` Raw data frame of output.

`outcleandf` Clean output in data frame.

`rungrid` matrix specifying which inputs will be run for each experiment.

`nvars` Number of variables

`allvars` All variables

`varlist` Character vector of objects to pass to a parallel cluster.

`arglist` List of values for each argument

`number_runs` Total number of runs

`completed_runs` Logical vector of whether each run has been completed.

`eval_func` The function that is called for each experiment trial.

`outlist` A list of the output from each run.

`save_output` Logical of whether the output should be saved.

`parallel` Logical whether experiment runs should be run in parallel. Allows for massive speedup.

`parallel_cores` How many cores to use when running in parallel. Can be an integer, or 'detect' will detect how many cores are available, or 'detect-1' will do one less than that.

`parallel_cluster` The parallel cluster being used.

`folder_path` The path to the folder where output will be saved.

`verbose` How much should be printed when running. 0 is none, 2 is average.

`extract_output_to_df` A function to extract the raw output into a data frame. E.g., if the output is a list, but you want a single item to show up in the output data frame.

`hashvalue` A value used to make sure inputs match when reloading.

Methods

Public methods:

- ffexp$new()
- ffexp$run_all()
- ffexp$run_for_time()
- ffexp$run_superbatch()
- ffexp$run_one()
- ffexp$add_result_of_one()
- ffexp$plot_run_times()
- ffexp$plot_pairs()
- ffexp$plot()
- ffexp$calculate_effects()
- ffexp$calculate_effects2()
- ffexp$save_self()
- ffexp$create_save_folder_if_nonexistent()
- ffexp$rename_save_folder()
- ffexp$delete_save_folder_if_empty()
- ffexp$recover_parallel_temp_save()
- ffexp$rungrid2()
- ffexp$add_variable()
- ffexp$add_level()
- ffexp$remove_results()
- ffexp$print()
- ffexp$set_parallel_cores()
- ffexp$stop_cluster()
- ffexp$finalize()
- ffexp$clone()

Method `new()`**:** Create an ‘ffexp‘ object.

Usage:

```
ffexp$new(
  ...,
  eval_func,
  save_output = FALSE,
  parallel = FALSE,
  parallel_cores = "detect",
  folder_path,
  varlist = NULL,
  verbose = 2,
  extract_output_to_df = NULL
)
```

Arguments:

`...` Input arguments for the experiment

`eval_func` The function to be run. It must take named arguments matching the names of ...

`save_output` Should output be saved to file?

`parallel` Should a parallel cluster be used?

`parallel_cores` When running in parallel, how many cores should be used. Not actually the number of cores used, actually the number of clusters created. Can be more than the computer has available, but will hurt performance. Can set to 'detect' to have it detect how many cores are available and use that, or 'detect-1' to use one fewer than there are.

`folder_path` Where the data and files should be stored. If not given, a folder in the existing directory will be created.

`varlist` Character vector of names of objects that need to be passed to the parallel environment.

`verbose` How much should be printed when running. 0 is none, 2 is average.

`extract_output_to_df` A function to extract the raw output into a data frame. E.g., if the output is a list, but you want a single item to show up in the output data frame.

Method `run_all()`**:** Run an experiment. The user can choose to run all rows, or just specified ones, if it should be run in parallel, and what files should be saved.

Usage:

```
ffexp$run_all(
  to_run = NULL,
  random_n = NULL,
  redo = FALSE,
  run_order,
  save_output = self$save_output,
  parallel = self$parallel,
  parallel_cores = self$parallel_cores,
  parallel_temp_save = save_output,
  write_start_files = save_output,
  write_error_files = save_output,
  delete_parallel_temp_save_after = FALSE,
  varlist = self$varlist,
  verbose = self$verbose,
  outfile,
  warn_repeat = TRUE
)
```

Arguments:

`to_run` Which rows should be run? If NULL, then all that haven't been run yet.

`random_n` Randomly selects n trials among those not yet completed and runs them.

`redo` Should already completed rows be run again?

`run_order` In what order should the rows by run? Options: random, in_order, and reverse.

`save_output` Should the output be saved?

`parallel` Should it be run in parallel?

`parallel_cores` When running in parallel, how many cores should be used. Not actually the number of cores used, actually the number of clusters created. Can be more than the computer has available, but will hurt performance. Can set to 'detect' to have it detect how many cores are available and use that, or 'detect-1' to use one fewer than there are.

`parallel_temp_save` Should temp files be written when running in parallel? Prevents losing results if it crashes partway through.

`write_start_files` Should start files be written?

`write_error_files` Should error files be written for rows that fail?

`delete_parallel_temp_save_after` If using parallel temp save files, should they be deleted afterwards?

`varlist` A character vector of names of variables to be passed the the parallel cluster.

`verbose` How much should be printed when running. 0 is none, 2 is average.

`outfile` Where should master output file be saved when running in parallel?

`warn_repeat` Should warnings be given when repeating already completed rows?

Method `run_for_time()`**:** Run the experiment for a given time, not for a specified number of trials. Runs 'batch_size' trials between checking the time elapsed, only needs to be more than 1 when running in parallel. It will complete the current batch before stopping, it does not quit in the middle of the batch when reaching the time limit, so it will go over the time limit given.

Usage:

```
ffexp$run_for_time(
  sec,
  batch_size,
  show_time_in_bar = FALSE,
  save_output = self$save_output,
  parallel = self$parallel,
  parallel_cores = self$parallel_cores,
  parallel_temp_save = save_output,
  write_start_files = save_output,
  write_error_files = save_output,
  delete_parallel_temp_save_after = FALSE,
  varlist = self$varlist,
  verbose = self$verbose,
  warn_repeat = TRUE
)
```

Arguments:

`sec` Number of seconds to run for

`batch_size` Number of trials to run between checking the time elapsed.

`show_time_in_bar` The progress bar can show either the number of runs completed or the time elapsed.

`save_output` Should the output be saved?

`parallel` Should it be run in parallel?

`parallel_cores` When running in parallel, how many cores should be used. Not actually the number of cores used, actually the number of clusters created. Can be more than the computer has available, but will hurt performance. Can set to 'detect' to have it detect how many cores are available and use that, or 'detect-1' to use one fewer than there are.

`parallel_temp_save` Should temp files be written when running in parallel? Prevents losing results if it crashes partway through.

`write_start_files` Should start files be written?

`write_error_files` Should error files be written for rows that fail?

`delete_parallel_temp_save_after` If using parallel temp save files, should they be deleted afterwards?

`varlist` A character vector of names of variables to be passed the the parallel cluster.

`verbose` How much should be printed when running. 0 is none, 2 is average.

`warn_repeat` Should warnings be given when repeating already completed rows?

Method `run_superbatch()`**:** Run batches. Allows for better progress visualization and saving when running in parallel

Usage:

```
ffexp$run_superbatch(
  nsb,
  redo = FALSE,
  run_order,
  save_output = self$save_output,
  parallel = self$parallel,
  parallel_cores = self$parallel_cores,
  parallel_temp_save = save_output,
  write_start_files = save_output,
  write_error_files = save_output,
  delete_parallel_temp_save_after = FALSE,
  varlist = self$varlist,
  verbose = self$verbose,
  warn_repeat = TRUE
)
```

Arguments:

`nsb` Number of super batches

`redo` Should already completed rows be run again?

`run_order` In what order should the rows by run? Options: random, in_order, and reverse.

`save_output` Should the output be saved?

`parallel` Should it be run in parallel?

`parallel_cores` When running in parallel, how many cores should be used. Not actually the number of cores used, actually the number of clusters created. Can be more than the computer has available, but will hurt performance. Can set to 'detect' to have it detect how many cores are available and use that, or 'detect-1' to use one fewer than there are.

`parallel_temp_save` Should temp files be written when running in parallel? Prevents losing results if it crashes partway through.

`write_start_files` Should start files be written?

`write_error_files` Should error files be written for rows that fail?

`delete_parallel_temp_save_after` If using parallel temp save files, should they be deleted afterwards?

`varlist` A character vector of names of variables to be passed the the parallel cluster.

`verbose` How much should be printed when running. 0 is none, 2 is average.

`warn_repeat` Should warnings be given when repeating already completed rows?

`outfile` Where should master output file be saved when running in parallel?

Method `run_one()`**:** Run a single row of the experiment. You can specify which one to run. Generally this should not be used by users, use 'run_all' instead.

Usage:

```
ffexp$run_one(
  irow = NULL,
  save_output = self$save_output,
  write_start_files = save_output,
  write_error_files = save_output,
  warn_repeat = TRUE,
  is_parallel = FALSE,
  return_list_result_of_one = FALSE,
  verbose = self$verbose,
  force_this_as_output
)
```

Arguments:

`irow` Which row should be run?

`save_output` Should the output be saved?

`write_start_files` Should a file be written when starting the experiment?

`write_error_files` Should a file be written if there is an error?

`warn_repeat` Should a warning be given if repeating a row?

`is_parallel` Is this being run in parallel?

`return_list_result_of_one` Should the list of the result of this one be return?

`verbose` How much should be printed when running. 0 is none, 2 is average.

`force_this_as_output` Value to use instead of evaluating function.

Method `add_result_of_one()`**:** Add the result of a single experiment to the object. This shouldn't be used by users.

Usage:

```
ffexp$add_result_of_one(
  output,
  systime,
  irow,
  row_grid,
  row_df,
  start_time,
  end_time,
  save_output,
  hashvalue
)
```

Arguments:

`output` The output of the experiment.

`systime` The time it took to run

`irow` The row of inputs used.

`row_grid` The corresponding row in the run grid.

`row_df` The corresponding row data frame.

`start_time` The start time of the experiment.

`end_time` The end time of the experiment.

`save_output` Should the output be saved?

`hashvalue` Not used.

Method `plot_run_times()`**:** Plot the run times of each trial.

Usage:

```
ffexp$plot_run_times()
```

Method `plot_pairs()`**:** Plot pairs of inputs and outputs. Helps see correlations and distributions.

Usage:

```
ffexp$plot_pairs()
```

Method `plot()`**:** Calling 'plot' on an 'ffexp' object calls 'plot_pairs()'

Usage:

```
ffexp$plot()
```

Method `calculate_effects()`**:** Calculate the effects of each variable as if this was an experiment using a linear model.

Usage:

```
ffexp$calculate_effects()
```

Method `calculate_effects2()`**:** Calculate the effects of each variable as if this was an experiment using a linear model.

Usage:

```
ffexp$calculate_effects2()
```

Method `save_self()`**:** Save this R6 object

Usage:

```
ffexp$save_self(verbose = self$verbose)
```

Arguments:

`verbose` How much should be printed when running. 0 is none, 2 is average.

Method `create_save_folder_if_nonexistent()`**:** Create the save folder if it doesn't already exist.

Usage:

```
ffexp$create_save_folder_if_nonexistent()
```

Method `rename_save_folder()`**:** Rename the save folder

Usage:

```
ffexp$rename_save_folder(new_folder_path, new_folder_name)
```

Arguments:

`new_folder_path` New path for the save folder

new_folder_name If you want the new save folder to be in the current directory, you can use this instead of 'new_folder_path' and just give the folder name.

Method `delete_save_folder_if_empty()`**:** Delete the save folder if it is empty. Used to prevent leaving behind empty folders.

Usage:

```
ffexp$delete_save_folder_if_empty(verbose = self$verbose)
```

Arguments:

verbose How much should be printed when running. 0 is none, 2 is average.

Method `recover_parallel_temp_save()`**:** Running this loads the information saved to files if 'save_parallel_temp_save=TRUE' was used when running. Useful when running long jobs in parallel so that you don't lose all results if it crashes before finishing.

Usage:

```
ffexp$recover_parallel_temp_save(delete_after = FALSE, only_reload_new = FALSE)
```

Arguments:

delete_after Should the temp files be deleted after they are recovered? If TRUE, make sure you save the ffexp object after running this function so you don't lose the data.

only_reload_new Will only reload output from runs that don't show as completed yet. Can make it much faster if there are many saved files, but most have already been loaded to this object.

Method `rungrid2()`**:** Display the input rows of the experiment. rungrid just gives integers, this gives the actual values.

Usage:

```
ffexp$rungrid2(rows = 1:nrow(self$rungrid))
```

Arguments:

rows Which rows to display the inputs for? On big experiments, specifying the rows can be much faster.

Method `add_variable()`**:** Add a variable to the experiment. You must specify the value of the variable for all existing rows, and then also the values of the variable which haven't been run yet.

Usage:

```
ffexp$add_variable(name, existing_value, new_values, suppressMessage = FALSE)
```

Arguments:

name Name of the variable being added.

existing_value Which existing argument is a level being added to?

new_values The values of the new variable which have not been run. This should not include 'arg_name', the name of the new variable at the existing values.

suppressMessage Should the message be suppressed? The message tells the user a new variable was added and it is being returned in a new object. Default FALSE.

Method `add_level()`**:** Add a level to one of the arguments. This returns a new object. The existing object is not changed.

Usage:

```
ffexp$add_level(arg_name, new_values, suppressMessage = FALSE)
```

Arguments:

`arg_name` Which existing argument is a level being added to?

`new_values` The value of the new levels to be added to ‘arg_name‘.

`suppressMessage` Should the message be suppressed? The message tells the user a new level was added and it is being returned in a new object. Default FALSE.

Method `remove_results()`**:** Remove results of completed trials. They will be rerun next time $run_all() is called.

Usage:

```
ffexp$remove_results(to_remove)
```

Arguments:

`to_remove` Indexes of trials to remove

Method `print()`**:** Printing the object shows some summary information.

Usage:

```
ffexp$print()
```

Method `set_parallel_cores()`**:** Set the number of parallel cores to be used when running in parallel. Needed in case user sets "detect"

Usage:

```
ffexp$set_parallel_cores(parallel_cores)
```

Arguments:

`parallel_cores` When running in parallel, how many cores should be used. Not actually the number of cores used, actually the number of clusters created. Can be more than the computer has available, but will hurt performance. Can set to ’detect’ to have it detect how many cores are available and use that, or ’detect-1’ to use one fewer than there are.

Method `stop_cluster()`**:** Stop the parallel cluster.

Usage:

```
ffexp$stop_cluster()
```

Method `finalize()`**:** Cleanup after deleting object.

Usage:

```
ffexp$finalize()
```

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
ffexp$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
# Two factors, both with two levels.
#   The evaluation function simply prints out the combination
cc <- ffexp$new(a=1:2,b=c("A","B"),
                eval_func=function(...) {c(...)})
# View the factor settings it will run (each row).
cc$rungrid
# Evaluate all four settings
cc$run_all()


cc <- ffexp$new(a=1:3,b=2, cd=data.frame(c=3:4,d=5:6),
                eval_func=function(...) {list(...)})
```

---

hype *Hyperparameter optimization*

Description

Hyperparameter optimization

Usage

```
hype(
  eval_func,
  ...,
  X0 = NULL,
  Z0 = NULL,
  n_lhs,
  extract_output_func,
  verbose = 1,
  model = "GauPro",
  covtype = "matern5_2",
  nugget.estim = TRUE
)
```

Arguments

eval_func	The function we evaluate.
...	Pass in hyperparameters, such as par_unif() as unnamed arguments.
X0	A data frame of initial points to include. They must have the same names as the hyperparameters. If Z0 is also passed, it should match the points in X0. If Z0 is not passed, then X0 will be the first points evaluated.
Z0	A vector whose values are the result of applying 'eval_func' to each row of X0.
n_lhs	The number of random points to start with. They are selected using a Latin hypercube sample.

extract_output_func
: A function that takes in the output from 'eval_func' and returns the value we are trying to minimize.

verbose
: How much should be printed? 0 is none, 1 is standard, 2 is more, 5+ is a lot

model
: What kind of model to use.

covtype
: The covariance function to use for the Gaussian process model.

nugget.estim
: Whether a nugget should be estimated when fitting the Gaussian process model.

Examples

```
# Have df output, but only use one value from it
h1 <- hype(
  eval_func = function(a, b) {data.frame(c=a^2+b^2, d=1:2)},
  extract_output_func = function(odf) {odf$c[1]},
  a = par_unif('a', -1, 2),
  b = par_unif('b', -10, 10),
  n_lhs = 10
)
h1$run_all()
h1$add_EI(n = 1)
h1$run_all()
#system.time(h1$run_EI_for_time(sec=3, batch_size = 1))
#system.time(h1$run_EI_for_time(sec=3, batch_size = 3))
h1$plotorder()
h1$plotX()
```

---

mbc *Model benchmark compare*

Description

Compare the run time and output of various code chunks

Usage

```
mbc(
  ...,
  times = 5,
  input,
  inputi,
  evaluator,
  post,
  target,
  targetin,
  metric = "rmse",
  paired,
  kfold
)
```

Arguments

...	Functions to run
times	Number of times to run
input	Object to be passed as input to each function
inputi	Function to be called with the replicate number then passed to each function.
evaluator	An expression that the ... expressions will be passed as "." for evaluation.
post	Function or expression (using ".") to post-process results.
target	Values the functions are expected to (approximately) return.
targetin	Values that will be given to the result of the run to produce output.
metric	c("rmse", "t", "mis90", "sr27") Metric used to compare output values to target. mis90 is the mean interval score for 90% confidence, see Gneiting and Raftery (2007). sr27 is the scoring rule given in Equation 27 of Gneiting and Raftery (2007).
paired	Should the results be paired for comparison?
kfold	First element should be the number of elements that are being split into groups. If the number of folds is different from 'times', then the second argument is the number of folds. Use 'ki' in 'inputi' and 'targeti' to select elements in the current fold.

Value

Data frame of comparison results

References

Gneiting, T., & Raftery, A. E. (2007). Strictly proper scoring rules, prediction, and estimation. Journal of the American Statistical Association, 102(477), 359-378.

Examples

```
# Compare distribution of mean for different sample sizes
mbc(mean(rnorm(1e2)),
    mean(rnorm(1e4)),
    times=20)

# Compare mean and median on same data
mbc(mean(x),
    median(x),
    inputi={x=rexp(1e2)})

# input given, no post
mbc({Sys.sleep(rexp(1, 30));mean(x)},
     {Sys.sleep(rexp(1, 5));median(x)},
    inputi={x=runif(100)})

# input given with post
mbc(mean={Sys.sleep(rexp(1, 30));mean(x)},
```

```
    med={Sys.sleep(rexp(1, 5));median(x)},
    inputi={x=runif(100)},
    post=function(x){c(x+1, x^2)})

# input given with post, 30 times
mbc(mean={Sys.sleep(rexp(1, 30));mean(x)+runif(1)},
    med={Sys.sleep(rexp(1, 50));median(x)+runif(1)},
    inputi={x=runif(100)},
    post=function(x){c(x+1, x^2)}, times=10)

# Name one function and post
mbc({mean(x)+runif(1)},
    a1={median(x)+runif(1)},
    inputi={x=runif(100)},
    post=function(x){c(rr=x+1, gg=x^2)}, times=10)

# No input
m1 <- mbc(mean={x <- runif(100);Sys.sleep(rexp(1, 30));mean(x)},
          med={x <- runif(100);Sys.sleep(rexp(1, 50));median(x)})
```

`par_discretenum` *Parameter with uniform distribution for hyperparameter optimization*

Description

Parameter with uniform distribution for hyperparameter optimization

Usage

```
par_discretenum(name, values)
```

Arguments

`name`	Name of the parameter, must match the input to ‘eval_func‘.
`values`	Values, discrete numeric

Examples

```
p1 <- par_discretenum('x1', 0:2)
class(p1)
print(p1)
```

par_integer *Parameter with uniform distribution over integer range for hyperparameter optimization*

Description

Parameter with uniform distribution over integer range for hyperparameter optimization

Usage

```
par_integer(name, lower, upper)
```

Arguments

name	Name of the parameter, must match the input to 'eval_func'.
lower	Lower bound of the parameter
upper	Upper bound of the parameter

Examples

```
p1 <- par_integer('x1', 3, 8)
class(p1)
print(p1)
table(p1$generate(runif(1000)))
```

par_log10 *Hyperparameter on log10 scale*

Description

Hyperparameter on log10 scale

Usage

```
par_log10(name, lower, upper)
```

Arguments

name	Name of the parameter, must match the input to 'eval_func'.
lower	Lower bound of the parameter
upper	Upper bound of the parameter

Examples

```
p1 <- par_log10('x1', 1e-4, 1e4)
class(p1)
print(p1)
```

par_ordered *Hyperparameter of discrete (factor) variable*

Description

Hyperparameter of discrete (factor) variable

Usage

```
par_ordered(name, values)
```

Arguments

name	Name of the parameter, must match the input to 'eval_func'.
values	Vector of values

Examples

```
p1 <- par_ordered('x1', c('a', 'b', 'c'))
class(p1)
print(p1)
```

par_unif *Uniform parameter*

Description

Parameter with uniform distribution for hyperparameter optimization

Usage

```
par_unif(name, lower, upper)
```

Arguments

name	Name of the parameter, must match the input to 'eval_func'.
lower	Lower bound of the parameter
upper	Upper bound of the parameter

Value

Returns an R6 class generated by R6_par_unif.

Examples

```
p1 <- par_unif('x1', 1, 10)
class(p1)
print(p1)
```

par_unordered *Hyperparameter of discrete (factor) variable*

Description

Hyperparameter of discrete (factor) variable

Usage

```
par_unordered(name, values)
```

Arguments

name	Name of the parameter, must match the input to ‘eval_func‘.
values	Vector of values

Examples

```
p1 <- par_unordered('x1', c('a', 'b', 'c'))
class(p1)
print(p1)
```

plot.mbc *Plot mbc class*

Description

Plot mbc class

Usage

```
## S3 method for class 'mbc'
plot(x, ...)
```

Arguments

x	Object of class mbc
...	Additional parameters

Value

None

Examples

```
m1 <- mbc(mn= {Sys.sleep(rexp(1, 30));mean(x)},
          med={Sys.sleep(rexp(1, 5));median(x)},
          input=runif(100))
plot(m1)
```

---

print.mbc *Print mbc class*

Description

Print mbc class

Usage

```
## S3 method for class 'mbc'
print(x, ...)
```

Arguments

x	Object of class mbc
...	Additional parameters

Value

None

Examples

```
m1 <- mbc({Sys.sleep(rexp(1, 30));mean(x)},
          {Sys.sleep(rexp(1, 5));median(x)},
          input=runif(100))
print(m1)
```

R6_hype *Hyperparameter optimization*

Description

Hyperparameter optimization

Hyperparameter optimization

Public fields

`X` Data frame of inputs that have been evaluated or will be evaluated next.

`Z` Output at X

`runtime` The time it took to evaluate each row of X

`parnames` Names of the parameters

`parlowerraw` Lower bounds for each parameter on raw scale

`parupperraw` Upper bounds for each parameter on raw scale

`parlowertrans` Lower bounds for each parameter on transformed scale

`paruppertrans` Upper bounds for each parameter on transformed scale

`parlist` List of all parameters

`modlist` A list with details about the model. The user shouldn't ever edit this directly.

`ffexp` An ffexp R6 object used to run the experiment and store the results.

`eval_func` The function we evaluate.

`extract_output_func` A function that takes in the output from 'eval_func' and returns the value we are trying to minimize.

`par_all_cts` Are all the parameters continuous?

`verbose` How much should be printed? 0 is none, 1 is standard, 2 is more, 5+ is a lot

Active bindings

`mod` Gaussian process model used to predict what the output will be.

Methods

Public methods:

- `R6_hype$new()`
- `R6_hype$add_data()`
- `R6_hype$add_X()`
- `R6_hype$add_LHS()`
- `R6_hype$convert_trans_to_raw()`
- `R6_hype$convert_raw_to_trans()`
- `R6_hype$change_par_bounds()`
- `R6_hype$add_EI()`
- `R6_hype$fit_mod()`
- `R6_hype$run_all()`
- `R6_hype$run_EI_for_time()`
- `R6_hype$plot()`
- `R6_hype$pairs()`
- `R6_hype$plotorder()`
- `R6_hype$plotX()`
- `R6_hype$plotXorder()`

- R6_hype$plotinteractions()
- R6_hype$print()
- R6_hype$best_params()
- R6_hype$update_mod_userspeclist()
- R6_hype$clone()

Method `new()`**:** Create hype R6 object.

Usage:

```
R6_hype$new(
  eval_func,
  ...,
  X0 = NULL,
  Z0 = NULL,
  n_lhs,
  extract_output_func,
  verbose = 1,
  model = "GauPro",
  covtype = "matern5_2",
  nugget.estim = TRUE
)
```

Arguments:

`eval_func` The function used to evaluate new points.

`...` Hyperparameters to optimize over.

`X0` Data frame of initial points to run, or points already evaluated. If already evaluated, give in outputs in "Z0"

`Z0` Evaluated outputs at "X0".

`n_lhs` The number that should initially be run using a maximin Latin hypercube.

`extract_output_func` A function that takes in the output from ‘eval_func‘ and returns the value we are trying to minimize.

`verbose` How much should be printed? 0 is none, 1 is standard, 2 is more, 5+ is a lot

`model` What package to fit the Gaussian process model with. Either "GauPro" or "DiceKriging"/"DK".

`covtype` Covariance/correlation/kernel function for the GP model.

`nugget.estim` Should the nugget be estimated when fitting the GP model?

Method `add_data()`**:** Add data to the experiment results.

Usage:

```
R6_hype$add_data(X, Z)
```

Arguments:

`X` Data frame with names matching the input parameters

`Z` Output at rows of X matching the experiment output.

Method `add_X()`**:** Add new inputs to run. This allows the user to specify what they want run next.

Usage:

```
R6_hype$add_X(X)
```

Arguments:

`X` Data frame with names matching the input parameters.

Method `add_LHS()`**:** Add new input points using a maximin Latin hypercube. Latin hypercubes are usually more spacing than randomly picking points.

Usage:

```
R6_hype$add_LHS(n, just_return_df = FALSE)
```

Arguments:

`n` Number of points to add.

`just_return_df` Instead of adding to experiment, should it just return the new set of values?

Method `convert_trans_to_raw()`**:** Convert parameters from transformed scale to raw scale.

Usage:

```
R6_hype$convert_trans_to_raw(Xtrans)
```

Arguments:

`Xtrans` Parameters on the transformed scale

Method `convert_raw_to_trans()`**:** Convert parameters from raw scale to transformed scale.

Usage:

```
R6_hype$convert_raw_to_trans(Xraw)
```

Arguments:

`Xraw` Parameters on the raw scale

Method `change_par_bounds()`**:** Change lower/upper bounds of a parameter

Usage:

```
R6_hype$change_par_bounds(parname, lower, upper)
```

Arguments:

`parname` Name of the parameter

`lower` New lower bound. Leave empty if not changing.

`upper` New upper bound. Leave empty if not changing.

Method `add_EI()`**:** Add new inputs to run using the expected information criteria

Usage:

```
R6_hype$add_EI(
  n,
  covtype = NULL,
  nugget.estim = NULL,
  model = NULL,
  eps,
  just_return = FALSE,
  calculate_at
)
```

Arguments:

`n` Number of points to add.

`covtype` Covariance function to use for the Gaussian process model.

`nugget.estim` Should a nugget be estimated?

`model` Which package should be used to fit the model and calculate the EI? Use "DK" for DiceKriging or "GauPro" for GauPro.

`eps` Exploration parameter. The minimum amount of improvement you care about.

`just_return` Just return the EI info, don't actually add the points to the design.

`calculate_at` Calculate the EI at a specific point.

Method `fit_mod()`**:** Fit model to the data collected so far

Usage:

```
R6_hype$fit_mod(covtype = NULL, nugget.estim = NULL, model = NULL)
```

Arguments:

`covtype` Covariance function to use for the Gaussian process model.

`nugget.estim` Should a nugget be estimated?

`model` Which package should be used to fit the model and calculate the EI? Use "DK" for DiceKriging or "GauPro" for GauPro.

Method `run_all()`**:** Run all unevaluated input points.

Usage:

```
R6_hype$run_all(...)
```

Arguments:

`...` Passed into 'ffexp$run_all'. Can set 'parallel=TRUE' to evaluate multiple points simultaneously as long as all needed variables have been passed to 'varlist'

Method `run_EI_for_time()`**:** Add points using the expected information criteria, evaluate them, and repeat until a specified amount of time has passed.

Usage:

```
R6_hype$run_EI_for_time(
  sec,
  batch_size,
  covtype = "matern5_2",
  nugget.estim = TRUE,
  verbose = 0,
  model = "GauPro",
  eps = 0,
  ...
)
```

Arguments:

`sec` Number of seconds to run for. It will go over this time limit, finish the current iteration, then stop.

`batch_size` Number of points to run at once.

`covtype` Covariance function to use for the Gaussian process model.

`nugget.estim` Should a nugget be estimated?

`verbose` Verbose parameter to pass to ffexp$

`model` Which package should be used to fit the model and calculate the EI? Use "DK" for DiceKriging or "GauPro" for GauPro.

`eps` Exploration parameter. The minimum amount of improvement you care about.

`...` Passed into 'ffexp$run_all'.

Method `plot()`**:** Make a plot to summarize the experiment.

Usage:

```
R6_hype$plot()
```

Method `pairs()`**:** Plot pairs of inputs and output

Usage:

```
R6_hype$pairs()
```

Method `plotorder()`**:** Plot the output of the points evaluated in order.

Usage:

```
R6_hype$plotorder()
```

Method `plotX()`**:** Plot the output as a function of each input.

Usage:

```
R6_hype$plotX(
  addlines = TRUE,
  addEIlines = TRUE,
  covtype = NULL,
  nugget.estim = NULL,
  model = NULL
)
```

Arguments:

`addlines` Should prediction mean and 95% interval be plotted?

`addEIlines` Should expected improvement lines be plotted?

`covtype` Covariance function to use for the Gaussian process model.

`nugget.estim` Should a nugget be estimated?

`model` Which package should be used to fit the model and calculate the EI? Use "DK" for DiceKriging or "GauPro" for GauPro.

Method `plotXorder()`**:** Plot each input in the order they were chosen. Colored by quality.

Usage:

```
R6_hype$plotXorder()
```

Method `plotinteractions()`**:** Plot the 2D plots from inputs to the output. All other variables are held at their values for the best input.

Usage:

```
R6_hype$plotinteractions(covtype = "matern5_2", nugget.estim = TRUE)
```

Arguments:

`covtype` Covariance function to use for the Gaussian process model.

`nugget.estim` Should a nugget be estimated?

Method `print()`**:** Print details of the object.

Usage:

```
R6_hype$print(...)
```

Arguments:

`...` not used

Method `best_params()`**:** Returns the best parameters evaluated so far.

Usage:

```
R6_hype$best_params()
```

Method `update_mod_userspeclist()`**:** Updates the specifications for the GP model.

Usage:

```
R6_hype$update_mod_userspeclist(
  model = NULL,
  covtype = NULL,
  nugget.estim = NULL
)
```

Arguments:

`model` What package to fit the Gaussian process model with. Either "GauPro" or "DiceKriging"/"DK".

`covtype` Covariance/correlation/kernel function for the GP model.

`nugget.estim` Should the nugget be estimated when fitting the GP model?

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
R6_hype$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
# Have df output, but only use one value from it
h1 <- hype(
  eval_func = function(a, b) {data.frame(c=a^2+b^2, d=1:2)},
  extract_output_func = function(odf) {odf$c[1]},
  a = par_unif('a', -1, 2),
  b = par_unif('b', -10, 10),
  n_lhs = 10
)
h1$run_all()
h1$add_EI(n = 1)
h1$run_all()
#system.time(h1$run_EI_for_time(sec=3, batch_size = 1))
#system.time(h1$run_EI_for_time(sec=3, batch_size = 3))
h1$plotorder()
h1$plotX()
```

R6_par_discretenum *R6 object for discrete numeric*

Description

R6 object for discrete numeric

R6 object for discrete numeric

Details

Parameter with uniform distribution for hyperparameter optimization

Super class

`comparer::par_hype` -> `par_discretenum`

Public fields

`name` Name of the parameter, must match the input to 'eval_func'.

`values` Values, discrete numeric

`ggtrans` Transformation for ggplot, see ggplot2::scale_x_continuous()

Methods

Public methods:

- `R6_par_discretenum$fromraw()`
- `R6_par_discretenum$toraw()`
- `R6_par_discretenum$generate()`
- `R6_par_discretenum$getseq()`
- `R6_par_discretenum$isvalid()`
- `R6_par_discretenum$convert_to_mopar()`
- `R6_par_discretenum$new()`
- `R6_par_discretenum$print()`
- `R6_par_discretenum$clone()`

Method `fromraw()`**:** Function to convert from raw scale to transformed scale

Usage:

```
R6_par_discretenum$fromraw(x)
```

Arguments:

`x` Value of raw scale

Method `toraw()`**:** Function to convert from transformed scale to raw scale

Usage:

```
R6_par_discretenum$toraw(x)
```

Arguments:

`x` Value of transformed scale

Method `generate()`**:** Generate values in the raw space based on quantiles.

Usage:

```
R6_par_discretenum$generate(q)
```

Arguments:

`q` In [0,1].

Method `getseq()`**:** Get a sequence, uniform on the transformed scale

Usage:

```
R6_par_discretenum$getseq(n)
```

Arguments:

`n` Number of points. Ignored for discrete.

Method `isvalid()`**:** Check if input is valid for parameter

Usage:

```
R6_par_discretenum$isvalid(x)
```

Arguments:

`x` Parameter value

Method `convert_to_mopar()`**:** Convert this to a parameter for the mixopt R package.

Usage:

```
R6_par_discretenum$convert_to_mopar(raw_scale = FALSE)
```

Arguments:

`raw_scale` Should it be on the raw scale?

Method `new()`**:** Create a hyperparameter with uniform distribution

Usage:

```
R6_par_discretenum$new(name, values)
```

Arguments:

`name` Name of the parameter, must match the input to 'eval_func'.

`values` Numeric values, must be in ascending order

Method `print()`**:** Print details of the object.

Usage:

```
R6_par_discretenum$print(...)
```

Arguments:

`...` not used

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
R6_par_discretenum$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
p1 <- R6_par_discretenum$new('x1', 0:2)
class(p1)
print(p1)
```

R6_par_hype *Parameter for hyperparameter optimization*

Description

Parameter for hyperparameter optimization

Parameter for hyperparameter optimization

Public fields

`partrans` The transformation type.

Methods

Public methods:

- `R6_par_hype$getseq()`
- `R6_par_hype$clone()`

Method `getseq()`**:** Get a sequence, uniform on the transformed scale

Usage:

```
R6_par_hype$getseq(n)
```

Arguments:

`n` Number of points. Ignored for discrete.

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
R6_par_hype$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
p1 <- R6_par_hype$new()
class(p1)
print(p1)
```

R6_par_integer *Parameter with uniform distribution over integer range for hyperparameter optimization*

Description

Parameter with uniform distribution over integer range for hyperparameter optimization

Parameter with uniform distribution over integer range for hyperparameter optimization

Super class

`comparer::par_hype` -> `par_integer`

Public fields

`name` Name of the parameter, must match the input to 'eval_func'.

`lower` Lower bound of the parameter

`upper` Upper bound of the parameter

`ggtrans` Transformation for ggplot, see ggplot2::scale_x_continuous()

Methods

Public methods:

- `R6_par_integer$fromraw()`
- `R6_par_integer$toraw()`
- `R6_par_integer$generate()`
- `R6_par_integer$getseq()`
- `R6_par_integer$isvalid()`
- `R6_par_integer$convert_to_mopar()`
- `R6_par_integer$new()`
- `R6_par_integer$print()`
- `R6_par_integer$clone()`

Method `fromraw()`**:** Function to convert from raw scale to transformed scale

Usage:

```
R6_par_integer$fromraw(x)
```

Arguments:

`x` Value of raw scale

Method `toraw()`**:** Function to convert from transformed scale to raw scale

Usage:

```
R6_par_integer$toraw(x)
```

Arguments:

x Value of transformed scale

Method `generate()`**:** Generate values in the raw space based on quantiles.

Usage:

```
R6_par_integer$generate(q)
```

Arguments:

q In [0,1].

Method `getseq()`**:** Get a sequence, uniform on the transformed scale

Usage:

```
R6_par_integer$getseq(n)
```

Arguments:

n Number of points. Ignored for discrete.

Method `isvalid()`**:** Check if input is valid for parameter

Usage:

```
R6_par_integer$isvalid(x)
```

Arguments:

x Parameter value

Method `convert_to_mopar()`**:** Convert this to a parameter for the mixopt R package.

Usage:

```
R6_par_integer$convert_to_mopar(raw_scale = FALSE)
```

Arguments:

raw_scale Should it be on the raw scale?

Method `new()`**:** Create a hyperparameter with uniform distribution

Usage:

```
R6_par_integer$new(name, lower, upper)
```

Arguments:

name Name of the parameter, must match the input to 'eval_func'.

lower Lower bound of the parameter

upper Upper bound of the parameter

Method `print()`**:** Print details of the object.

Usage:

```
R6_par_integer$print(...)
```

Arguments:

... not used,

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
R6_par_integer$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

Examples

```
p1 <- R6_par_integer$new('x1', 0, 2)
class(p1)
print(p1)
```

`R6_par_log10` *R6 class for hyperparameter on log10 scale*

Description

R6 class for hyperparameter on log10 scale

R6 class for hyperparameter on log10 scale

Super class

`comparer::par_hype` -> `par_log10`

Public fields

`name` Name of the parameter, must match the input to 'eval_func'.

`lower` Lower bound of the parameter

`upper` Upper bound of the parameter

`ggtrans` Transformation for ggplot, see ggplot2::scale_x_continuous()

Methods

Public methods:

- `R6_par_log10$fromraw()`
- `R6_par_log10$toraw()`
- `R6_par_log10$generate()`
- `R6_par_log10$isvalid()`
- `R6_par_log10$convert_to_mopar()`
- `R6_par_log10$new()`
- `R6_par_log10$print()`
- `R6_par_log10$clone()`

Method `fromraw()`**:** Function to convert from raw scale to transformed scale

Usage:

```
R6_par_log10$fromraw(x)
```

Arguments:

`x` Value of raw scale

Method `toraw()`**:** Function to convert from transformed scale to raw scale

Usage:

```
R6_par_log10$toraw(x)
```

Arguments:

`x` Value of transformed scale

Method `generate()`**:** Generate values in the raw space based on quantiles.

Usage:

```
R6_par_log10$generate(q)
```

Arguments:

`q` In [0,1].

Method `isvalid()`**:** Check if input is valid for parameter

Usage:

```
R6_par_log10$isvalid(x)
```

Arguments:

`x` Parameter value

Method `convert_to_mopar()`**:** Convert this to a parameter for the mixopt R package.

Usage:

```
R6_par_log10$convert_to_mopar(raw_scale = FALSE)
```

Arguments:

`raw_scale` Should it be on the raw scale?

Method `new()`**:** Create a hyperparameter with uniform distribution

Usage:

```
R6_par_log10$new(name, lower, upper)
```

Arguments:

`name` Name of the parameter, must match the input to 'eval_func'.

`lower` Lower bound of the parameter

`upper` Upper bound of the parameter

Method `print()`**:** Print details of the object.

Usage:

```
R6_par_log10$print(...)
```

Arguments:

`...` not used

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
R6_par_log10$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
p1 <- par_log10('x1', 1e-4, 1e4)
class(p1)
print(p1)
```

`R6_par_ordered` *R6 class for hyperparameter of discrete (factor) variable*

Description

R6 class for hyperparameter of discrete (factor) variable

R6 class for hyperparameter of discrete (factor) variable

Super class

`comparer::par_hype` -> `par_ordered`

Public fields

`name` Name of the parameter, must match the input to 'eval_func'.

`values` Vector of values

`ggtrans` Transformation for ggplot, see ggplot2::scale_x_continuous()

`lower` Lower bound of the parameter

`upper` Upper bound of the parameter

Methods

Public methods:

- `R6_par_ordered$fromraw()`
- `R6_par_ordered$toraw()`
- `R6_par_ordered$fromint()`
- `R6_par_ordered$toint()`
- `R6_par_ordered$generate()`
- `R6_par_ordered$getseq()`
- `R6_par_ordered$isvalid()`
- `R6_par_ordered$convert_to_mopar()`
- `R6_par_ordered$new()`
- `R6_par_ordered$print()`
- `R6_par_ordered$clone()`

Method `fromraw()`**:** Function to convert from raw scale to transformed scale

Usage:

```
R6_par_ordered$fromraw(x)
```

Arguments:

x Value of raw scale

Method `toraw()`**:** Function to convert from transformed scale to raw scale

Usage:

```
R6_par_ordered$toraw(x)
```

Arguments:

x Value of transformed scale

Method `fromint()`**:** Convert from integer index to actual value

Usage:

```
R6_par_ordered$fromint(x)
```

Arguments:

x Integer index

Method `toint()`**:** Convert from value to integer index

Usage:

```
R6_par_ordered$toint(x)
```

Arguments:

x Value

Method `generate()`**:** Generate values in the raw space based on quantiles.

Usage:

```
R6_par_ordered$generate(q)
```

Arguments:

q In [0,1].

Method `getseq()`**:** Get a sequence, uniform on the transformed scale

Usage:

```
R6_par_ordered$getseq(n)
```

Arguments:

n Number of points. Ignored for discrete.

Method `isvalid()`**:** Check if input is valid for parameter

Usage:

```
R6_par_ordered$isvalid(x)
```

Arguments:

x Parameter value

Method `convert_to_mopar()`**:** Convert this to a parameter for the mixopt R package.

Usage:

```
R6_par_ordered$convert_to_mopar(raw_scale = FALSE)
```

Arguments:

`raw_scale` Should it be on the raw scale?

Method `new()`**:** Create a hyperparameter with uniform distribution

Usage:

```
R6_par_ordered$new(name, values)
```

Arguments:

`name` Name of the parameter, must match the input to 'eval_func'.

`values` The values the variable can take on.

Method `print()`**:** Print details of the object.

Usage:

```
R6_par_ordered$print(...)
```

Arguments:

`...` not used

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
R6_par_ordered$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
p1 <- par_ordered('x1', c('a', 'b', 'c'))
class(p1)
print(p1)
```

`R6_par_unif` *R6 class for Uniform parameter*

Description

R6 class for Uniform parameter

R6 class for Uniform parameter

Details

Parameter with uniform distribution for hyperparameter optimization

Super class

`comparer::par_hype` -> `par_unif`

Public fields

`name` Name of the parameter, must match the input to 'eval_func'.

`lower` Lower bound of the parameter

`upper` Upper bound of the parameter

`ggtrans` Transformation for ggplot, see ggplot2::scale_x_continuous()

Methods

Public methods:

- `R6_par_unif$fromraw()`
- `R6_par_unif$toraw()`
- `R6_par_unif$generate()`
- `R6_par_unif$isvalid()`
- `R6_par_unif$convert_to_mopar()`
- `R6_par_unif$new()`
- `R6_par_unif$print()`
- `R6_par_unif$clone()`

Method `fromraw()`**:** Function to convert from raw scale to transformed scale

Usage:

```
R6_par_unif$fromraw(x)
```

Arguments:

`x` Value of raw scale

Method `toraw()`**:** Function to convert from transformed scale to raw scale

Usage:

```
R6_par_unif$toraw(x)
```

Arguments:

`x` Value of transformed scale

Method `generate()`**:** Generate values in the raw space based on quantiles.

Usage:

```
R6_par_unif$generate(q)
```

Arguments:

`q` In [0,1].

Method `isvalid()`**:** Check if input is valid for parameter

Usage:

```
R6_par_unif$isvalid(x)
```

Arguments:

`x` Parameter value

Method `convert_to_mopar()`**:** Convert this to a parameter for the mixopt R package.

Usage:

```
R6_par_unif$convert_to_mopar(raw_scale = FALSE)
```

Arguments:

`raw_scale` Should it be on the raw scale?

Method `new()`**:** Create a hyperparameter with uniform distribution

Usage:

```
R6_par_unif$new(name, lower, upper)
```

Arguments:

`name` Name of the parameter, must match the input to 'eval_func'.

`lower` Lower bound of the parameter

`upper` Upper bound of the parameter

Method `print()`**:** Print details of the object.

Usage:

```
R6_par_unif$print(...)
```

Arguments:

`...` not used,

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
R6_par_unif$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

`R6_par_unordered` *R6 class for hyperparameter of discrete (factor) variable*

Description

R6 class for hyperparameter of discrete (factor) variable

R6 class for hyperparameter of discrete (factor) variable

Super class

`comparer::par_hype` -> `par_unordered`

Public fields

`name` Name of the parameter, must match the input to 'eval_func'.

`values` Vector of values

`ggtrans` Transformation for ggplot, see ggplot2::scale_x_continuous()

`lower` Lower bound of the parameter

`upper` Upper bound of the parameter

Methods

Public methods:

- R6_par_unordered$fromraw()
- R6_par_unordered$toraw()
- R6_par_unordered$fromint()
- R6_par_unordered$toint()
- R6_par_unordered$generate()
- R6_par_unordered$getseq()
- R6_par_unordered$isvalid()
- R6_par_unordered$convert_to_mopar()
- R6_par_unordered$new()
- R6_par_unordered$print()
- R6_par_unordered$clone()

Method `fromraw()`**:** Function to convert from raw scale to transformed scale

Usage:

```
R6_par_unordered$fromraw(x)
```

Arguments:

`x` Value of raw scale

Method `toraw()`**:** Function to convert from transformed scale to raw scale

Usage:

```
R6_par_unordered$toraw(x)
```

Arguments:

`x` Value of transformed scale

Method `fromint()`**:** Convert from integer index to actual value

Usage:

```
R6_par_unordered$fromint(x)
```

Arguments:

`x` Integer index

Method `toint()`**:** Convert from value to integer index

Usage:

```
R6_par_unordered$toint(x)
```

Arguments:

`x` Value

Method `generate()`**:** Generate values in the raw space based on quantiles.

Usage:

```
R6_par_unordered$generate(q)
```

Arguments:

q In [0,1].

Method `getseq()`: Get a sequence, uniform on the transformed scale

Usage:

```
R6_par_unordered$getseq(n)
```

Arguments:

n Number of points. Ignored for discrete.

Method `isvalid()`: Check if input is valid for parameter

Usage:

```
R6_par_unordered$isvalid(x)
```

Arguments:

x Parameter value

Method `convert_to_mopar()`: Convert this to a parameter for the mixopt R package.

Usage:

```
R6_par_unordered$convert_to_mopar(raw_scale = FALSE)
```

Arguments:

raw_scale Should it be on the raw scale?

Method `new()`: Create a hyperparameter with uniform distribution

Usage:

```
R6_par_unordered$new(name, values)
```

Arguments:

name Name of the parameter, must match the input to 'eval_func'.

values The values the variable can take on.

Method `print()`: Print details of the object.

Usage:

```
R6_par_unordered$print(...)
```

Arguments:

... not used

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
R6_par_unordered$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

Examples

```
p1 <- par_unordered('x1', c('a', 'b', 'c'))
class(p1)
print(p1)
```

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