

Package ‘iraceplot’

March 10, 2023

Title Plots for Visualizing the Data Produced by the 'irace' Package

Version 1.1

Description Graphical visualization tools for analyzing the data produced by 'irace'. The 'iraceplot' package enables users to analyze the performance and the parameter space data sampled by the configuration during the search process. It provides a set of functions that generate different plots to visualize the configurations sampled during the execution of 'irace' and their performance. The functions just require the log file generated by 'irace' and, in some cases, they can be used with user-provided data.

License MIT + file LICENSE

Encoding UTF-8

RoxygenNote 7.2.3

Depends R (>= 3.4)

Imports irace (>= 3.5), cli, dplyr, DT, forcats, ggforce, ggplot2 (>= 3.3.6), gridExtra, knitr, matrixStats (>= 0.55), plotly, rlang, rmarkdown (>= 2.7), stats, tibble, tidyr, truncnorm, utils, viridisLite, withr

Suggests testthat (>= 3.0.0)

VignetteBuilder knitr

URL <https://auto-optimization.github.io/iraceplot/>,
<https://github.com/auto-optimization/iraceplot/>

BugReports <https://github.com/auto-optimization/iraceplot/issues>

Config/testthat/edition 3

NeedsCompilation no

Author Manuel López-Ibáñez [aut, cre]
(<<https://orcid.org/0000-0001-9974-1295>>),
Pablo Oñate Marín [aut],
Leslie Pérez Cáceres [aut] (<<https://orcid.org/0000-0001-5553-6150>>)

Maintainer Manuel López-Ibáñez <manuel.lopez-ibanez@manchester.ac.uk>

Repository CRAN

Date/Publication 2023-03-10 20:00:02 UTC

R topics documented:

| | |
|--|-----------|
| ablation_plot | 2 |
| boxplot_performance | 3 |
| boxplot_test | 5 |
| boxplot_training | 6 |
| configurations_display | 7 |
| distance_config | 8 |
| has_testing_data | 9 |
| parallel_cat | 9 |
| parallel_coord | 10 |
| parallel_coord2 | 12 |
| plot_experiments_matrix | 13 |
| plot_model | 14 |
| read_ablogfile | 15 |
| report | 15 |
| sampling_distance | 16 |
| sampling_frequency | 17 |
| sampling_frequency_iteration | 19 |
| sampling_heatmap | 20 |
| sampling_heatmap2 | 21 |
| sampling_pie | 22 |
| scatter_performance | 23 |
| summarise_by_configuration | 24 |
| summarise_by_instance | 25 |
| summarise_by_iteration | 26 |
| Index | 27 |

| | |
|---------------|---|
| ablation_plot | <i>Create plot from an ablation log</i> |
|---------------|---|

Description

Create plot from an ablation log

Usage

```
ablation_plot(
  ablog,
  type = c("mean", "boxplot", "rank"),
  n = 0L,
  ylab = "Mean configuration cost",
  ylim = NULL,
  rotate_labs = TRUE,
  filename = NULL
)
```

Arguments

| | |
|-------------|---|
| ablog | (list() character(1)) Ablation log object returned by <code>irace::ablation()</code> . Alternatively, the path to an .Rdata file, e.g., "log-ablation.Rdata", from which the object will be loaded. |
| type | Type of plot. Supported values are "mean" and "boxplot". Adding "rank" will plot rank per instance instead of raw cost value. |
| n | (integer(1)) Number of steps included in the plot. By default all steps from source to target are included. |
| ylab | Label of y-axis. |
| ylim | Numeric vector of length 2 giving the y-axis range. |
| rotate_labs | (logical(1)) Whether to rotate labels in x-axis. They are rotated by default because they are typically large. |
| filename | (character(1)) File name to save the plot, for example "~/path/example/filename.png". |

Value

`ggplot2::ggplot()` boxplot object

Author(s)

Manuel López-Ibáñez

See Also

`irace::ablation()`, `irace::plotAblation()`

Examples

```
ablog <- read_ablogfile(system.file(package="irace", "exdata", "log-ablation.Rdata"))
ablation_plot(ablog)
ablation_plot(ablog, type="boxplot", rotate_labs = FALSE)
ablation_plot(ablog, type="mean,boxplot", rotate_labs = FALSE)
ablation_plot(ablog, type="rank,mean,boxplot", n = 4, rotate_labs = FALSE)
ablog <- system.file(package="iraceplot", "exdata", "log-ablation-autoMOPSODTLZ.Rdata")
ablation_plot(ablog, type="rank,mean,boxplot")
```

boxplot_performance *Box Plot of the performance of a set of configurations*

Description

Creates a box plot that displays the performance of a set of configurations which can be displayed by iteration.

Usage

```

boxplot_performance(
  experiments,
  allElites = NULL,
  type = c("all", "ibest"),
  first_is_best = TRUE,
  rpd = TRUE,
  show_points = TRUE,
  best_color = "#08bfaa",
  xlab = "Configurations",
  boxplot = FALSE,
  filename = NULL,
  interactive = base::interactive()
)

```

Arguments

| | |
|---------------|--|
| experiments | Experiment matrix obtained from irace training or testing data. Configurations in columns and instances in rows. As in irace, column names (configurations ids) should be characters. |
| allElites | List or vector of configuration ids, (default NULL). These configurations should be included in the plot. If the argument is not provided all configurations in experiments are included. If allElites is a vector all configurations are assumed without iteration unless argument type="ibest" is provided, in which case each configuration is assumed to be from a different iteration. If allElites is a list, each element of the list is assumed as an iteration. |
| type | String, (default "all") possible values are "all" or "ibest". "all" shows all the selected configurations showing iterations if the information is provided. "ibest" shows the elite configurations of each iteration, note that the best configuration is always assumed to be first in the vector of each iteration. |
| first_is_best | Boolean (default TRUE) Enables the display in a different color the best configuration identified as the first one in a vector. If FALSE, all configurations are shown in the same color. |
| rpd | (logical(1)) TRUE to plot performance as the relative percentage deviation to best results per instance, FALSE to plot raw performance. |
| show_points | Logical, (default TRUE) TRUE to plot performance points together with the box plot. |
| best_color | String, (default "#08bfaa") color to display best configurations. |
| xlab | String, (default "Configurations") label for the x axis. |
| boxplot | By default, display a violin plot (<code>ggplot2::geom_violin()</code>). If TRUE, show a classical boxplot. |
| filename | (character(1)) File name to save the plot, for example "~/path/example/filename.png". |
| interactive | (logical(1)) TRUE if the report may use interactive features (using <code>plotly::ggplotly()</code> , <code>plotly::plot_ly()</code> and <code>DT::renderDataTable()</code>) or FALSE if such features must be disabled. Defaults to the value returned by <code>interactive()</code> , |

Details

The performance data is obtained from the experiment matrix provided in the `experiments` argument. The configurations can be selected using the `allElites` argument and this argument can be also used to define the iteration of each elite configuration was evaluated.

Value

`ggplot2::ggplot()` boxplot object

See Also

`boxplot_test()` `boxplot_training()`

Examples

```
iraceResults <- read_logfile(system.file(package="irace", "exdata",
                                       "irace-acotsp.Rdata", mustWork = TRUE))
boxplot_performance(iraceResults$experiments, iraceResults$allElites)

boxplot_performance(iraceResults$testing$experiments, iraceResults$iterationElites)
```

 boxplot_test

Box Plot Testing Performance

Description

Creates a box plot that displays the performance of a set of configurations on the test instances.

Usage

```
boxplot_test(irace_results, type = c("all", "ibest", "best"), ...)
```

Arguments

| | |
|----------------------------|--|
| <code>irace_results</code> | The data generated when loading the <code>.Rdata</code> file created by <code>irace</code> (or the filename of that file). |
| <code>type</code> | String, (default <code>"all"</code>) possible values are <code>"all"</code> , <code>"ibest"</code> or <code>"best"</code> . <code>"all"</code> shows all the configurations included in the test, <code>"best"</code> shows the elite configurations of the last iteration and <code>"ibest"</code> shows the elite configurations of each iteration (requires that <code>irace</code> includes the iteration elites in the testing). |
| <code>...</code> | Other arguments passed to <code>boxplot_performance()</code> . |

Details

The performance data is obtained from the test evaluations performed by `irace`. Note that the testing is not a default feature in `irace` and should be enabled in the setup (see the `irace` package user guide for more details).

Value

`ggplot2::ggplot()` boxplot object

See Also

`boxplot_training()` `boxplot_performance()`

Examples

```
iraceResults <- read_logfile(system.file(package="iraceplot", "exdata",
                                        "guide-example.Rdata", mustWork = TRUE))
boxplot_test(iraceResults)
```

boxplot_training *Box Plot Training*

Description

Creates a box plot that displays the performance of a set of configurations on the training instances. Performance data is obtained from the evaluations performed by irace during the execution process. This implies that the number of evaluations can differ between configurations.

Usage

```
boxplot_training(
  irace_results,
  iteration = NULL,
  id_configurations = NULL,
  ...
)
```

Arguments

`irace_results` The data generated when loading the .Rdata file created by irace (or the file-name of that file).

`iteration` Numeric, iteration number that should be included in the plot (example: `iteration = 5`) When no iteration and no `id_configurations` are provided, the iterations is assumed to be the last one performed by irace. The performance data is obtained from the evaluations performed by irace during the execution process. This implies that the number of evaluations can differ between configurations due to the elimination process applied by irace. This plot, consequently, does not provide a complete comparison of two configurations, for a fair comparison use the test data plot.

`id_configurations` Numeric vector, configurations ids whose performance should be included in the plot. If no ids are provided, the configurations ids are set as the elite configuration ids of the selected iteration (last iteration by default) (example: `id_configurations = c(20, 50, 100, 300, 500, 600, 700)`).

... Other arguments passed to `boxplot_performance()`.

Value

`ggplot2::ggplot()` boxplot object

See Also

`boxplot_test()` `boxplot_performance()`

Examples

```
iraceResults <- read_logfile(system.file(package="irace", "exdata",
                                         "irace-acotsp.Rdata", mustWork = TRUE))
boxplot_training(iraceResults)

boxplot_training(iraceResults, iteration = 5)
boxplot_training(iraceResults, id_configurations = c(23,28,29))
```

configurations_display

The configurations by iteration and instance

Description

A graph is created with all the settings and instance of the training data

Usage

```
configurations_display(
  irace_results,
  rpd = TRUE,
  filename = NULL,
  interactive = base::interactive()
)
```

Arguments

| | |
|----------------------------|--|
| <code>irace_results</code> | The data generated when loading the .Rdata file created by irace (or the file-name of that file). |
| <code>rpd</code> | (logical(1)) TRUE to plot performance as the relative percentage deviation to best results per instance, FALSE to plot raw performance. |
| <code>filename</code> | (character(1)) File name to save the plot, for example "~/path/example/filename.png". |
| <code>interactive</code> | (logical(1)) TRUE if the report may use interactive features (using <code>plotly::ggplotly()</code> , <code>plotly::plot_ly()</code> and <code>DT::renderDataTable()</code>) or FALSE if such features must be disabled. Defaults to the value returned by <code>interactive()</code> , |

Value

ggplot2::ggplot() object

Examples

```
iraceResults <- read_logfile(system.file(package="iraceplot", "exdata",  
                                       "guide-example.Rdata", mustWork = TRUE))  
configurations_display(iraceResults)
```

| | |
|-----------------|--|
| distance_config | <i>Distance between configurations</i> |
|-----------------|--|

Description

Calculate the difference between a configuration and the others in the irace data.

Usage

```
distance_config(irace_results, id_configuration, t = 0.05)
```

Arguments

`irace_results` The data generated when loading the .Rdata file created by irace (or the file-name of that file).

`id_configuration` Numeric, configuration id which should be compared to others (example: `id_configuration = c(806,809)`)

`t` Numeric, (default 0.05) threshold that defines the distance (percentage of the domain size) to consider a parameter value equal to other.

Value

numeric

Examples

NULL

| | |
|------------------|---|
| has_testing_data | <i>Check if the results object generated by irace has data about the testing phase.</i> |
|------------------|---|

Description

Check if the results object generated by irace has data about the testing phase.

Usage

```
has_testing_data(irace_results)
```

Arguments

`irace_results` The data generated when loading the .Rdata file created by irace (or the filename of that file).

Value

```
logical(1)
```

| | |
|--------------|--------------------------------------|
| parallel_cat | <i>Parallel Coordinates Category</i> |
|--------------|--------------------------------------|

Description

Parallel categories plot of selected configurations. Numerical parameters are discretized to maximum `n_bins` intervals. To visualize configurations of other iterations these must be provided setting the argument `iterations`, groups of configurations of different iterations are shown in different colors. Specific configurations can be selected providing their ids in the `id_configurations` argument.

Usage

```
parallel_cat(  
  irace_results,  
  id_configurations = NULL,  
  param_names = NULL,  
  iterations = NULL,  
  by_n_param = NULL,  
  n_bins = 3,  
  filename = NULL  
)
```

Arguments

| | |
|-------------------|--|
| irace_results | The data generated when loading the .Rdata file created by irace (or the file-name of that file). |
| id_configurations | Configuration ids to be included in the plot. Example: <code>c(20, 50, 100, 300, 500, 600, 700)</code> |
| param_names | (<code>character()</code>) Parameters to be included in the plot. Example: <code>c("algorithm", "alpha", "rho", "q0",</code> |
| iterations | Numeric vector, iterations from which configuration should be obtained (example: <code>iterations = c(1,4,5)</code>) |
| by_n_param | Numeric (optional), maximum number of parameters to be displayed. |
| n_bins | Numeric (default 3), number of intervals to generate for numerical parameters. |
| filename | (<code>character(1)</code>) File name to save the plot, for example <code>"~/path/example/filename.png"</code> . |

Details

The parameters to be included in the plot can be selected with the `param_names` argument. Additionally, the maximum number of parameters to be displayed in one plot. A list of plots is returned by this function in several plots are required to display the selected data.

Value

parallel categories plot

See Also

[parallel_coord\(\)](#) [parallel_coord2\(\)](#)

Examples

```
iraceResults <- read_logfile(system.file(package="irace", "exdata",
                                       "irace-acotsp.Rdata", mustWork = TRUE))
parallel_cat(iraceResults)

parallel_cat(iraceResults, by_n_param = 6)
parallel_cat(iraceResults, id_configurations = c(20, 50, 100))
parallel_cat(iraceResults, param_names = c("algorithm", "alpha", "rho", "q0", "rasrank"))
parallel_cat(iraceResults, iterations = c(1, 4, 6), n_bins=4)
```

Description

Parallel coordinates plot of a set of selected configurations. Each line in the plot represents a configuration. By default, the final elite configurations are shown. To visualize configurations of other iterations these must be provided setting the argument `iterations`, configurations of different iterations are shown in different colors. Setting the `only_elites` argument to `FALSE` allows to display all configurations in the selected iterations, specific configurations can be selected providing their ids in the `id_configuration` argument.

Usage

```
parallel_coord(
  irace_results,
  id_configurations = NULL,
  param_names = NULL,
  iterations = NULL,
  only_elite = TRUE,
  by_n_param = NULL,
  color_by_instances = TRUE,
  filename = NULL
)
```

Arguments

| | |
|---------------------------------|--|
| <code>irace_results</code> | The data generated when loading the <code>.Rdata</code> file created by <code>irace</code> (or the filename of that file). |
| <code>id_configurations</code> | Configuration ids to be included in the plot. Example: <code>c(20, 50, 100, 300, 500, 600, 700)</code> |
| <code>param_names</code> | (<code>character()</code>) Parameters to be included in the plot. Example: <code>c("algorithm", "alpha", "rho", "q0",</code> |
| <code>iterations</code> | Numeric vector, iteration number that should be included in the plot (example: <code>iterations = c(1,4,5)</code>) |
| <code>only_elite</code> | logical (default <code>TRUE</code>), only print elite configurations (argument ignored when <code>id_configurations</code> is provided) |
| <code>by_n_param</code> | Numeric (optional), maximum number of parameters to be displayed. |
| <code>color_by_instances</code> | Logical (default <code>TRUE</code>), choose how to color the lines. <code>TRUE</code> shows the number of instances evaluated by the configuration in the colores. <code>FALSE</code> to show the iteration number where the configuration was sampled. |
| <code>filename</code> | (<code>character(1)</code>) File name to save the plot, for example <code>"~/path/example/filename.png"</code> . |

Details

The parameters to be included in the plot can be selected with the `param_names` argument. Additionally, the maximum number of parameters to be displayed in one plot. A list of plots is returned by this function in several plots are required to display the selected data.

To export the plot to a file, it is possible to do it so manually using the functionality provided by `plotly` in the plot. If a filename is provided, `orca` server will be used to export the plots and thus, it requires the library to be installed (<https://github.com/plotly/orca>).

Value

parallel coordinates plot

Examples

```
iraceResults <- read_logfile(system.file(package="irace", "exdata",
                                         "irace-acotsp.Rdata", mustWork = TRUE))

parallel_coord(iraceResults)

parallel_coord(iraceResults, by_n_param = 5)
parallel_coord(iraceResults, only_elite = FALSE)
parallel_coord(iraceResults, id_configurations = c(20, 30, 40, 50, 100))
parallel_coord(iraceResults, param_names = c("algorithm", "alpha", "rho", "q0", "rasrank"))
parallel_coord(iraceResults, iterations = c(1, 4, 6))
```

parallel_coord2 *Parallel Coordinates Plot (configurations)*

Description

Parallel coordinates plot of a set of provided configurations. Each line in the plot represents a configuration. The parameters to be included in the plot can be selected with the `param_names` argument. Additionally, the maximum number of parameters to be displayed in one plot. A list of plots is returned by this function in several plots are required to display the selected data.

Usage

```
parallel_coord2(
  configurations,
  parameters,
  param_names = parameters$names,
  by_n_param = NULL,
  filename = NULL
)
```

Arguments

| | |
|-----------------------------|---|
| <code>configurations</code> | Data frame, configurations in irace format (example: <code>configurations = iraceResults\$allConfigurations</code>) |
| <code>parameters</code> | List, parameter object in irace format (example: <code>parameters = iraceResults\$parameters</code>) |
| <code>param_names</code> | (<code>character()</code>) Parameters to be included in the plot. Example: <code>c("algorithm", "alpha", "rho", "q0", "rasrank")</code> |
| <code>by_n_param</code> | Numeric (optional), maximum number of parameters to be displayed |
| <code>filename</code> | (<code>character(1)</code>) File name to save the plot, for example <code>"~/path/example/filename.png"</code> . |

Details

To export the plot to a file, it is possible to do it so manually using the functionality provided by plotly in the plot. If a filename is provided, orca server will be used to export the plots and thus, it requires the library to be installed (<https://github.com/plotly/orca>).

Value

parallel coordinates plot

Examples

```
iraceResults <- read_logfile(system.file(package="irace", "exdata",
                                       "irace-acotsp.Rdata", mustWork = TRUE))
parallel_coord2(iraceResults$allConfigurations[iraceResults$iterationElites,],
               iraceResults$parameters)
parallel_coord2(iraceResults$allConfigurations[iraceResults$iterationElites,],
               iraceResults$parameters,
               param_names = c("algorithm", "alpha", "rho", "q0", "rasrank"))
parallel_coord2(iraceResults$allConfigurations[iraceResults$iterationElites,],
               iraceResults$parameters, by_n_param = 5)
```

plot_experiments_matrix

Heat Map Plot

Description

Creates a heatmap plot that shows all performance data seen by irace. Configurations are shown in the x-axis in the order in which they are created in the configuration process. Instances are shown in the y-axis in the order in which they were seen during the configuration run. This plot gives a general idea of the configuration process progression, the number of evaluations of each configuration show how long they survived in the iterated racing procedure.

Usage

```
plot_experiments_matrix(
  irace_results,
  filename = NULL,
  metric = c("raw", "rpd", "rank"),
  show_conf_ids = FALSE,
  interactive = base::interactive()
)
```

Arguments

| | |
|---------------|--|
| irace_results | The data generated when loading the .Rdata file created by irace (or the file-name of that file). |
| filename | (character(1)) File name to save the plot, for example "~/path/example/filename.png". |
| metric | Cost metric shown in the plot: "raw" shows the raw values, "rpd" shows relative percentage deviation per instance and "rank" shows rank per instance. |
| show_conf_ids | If TRUE, it shows the configuration IDs in the x-axis. Usually there are too many configurations, thus the default is FALSE. |
| interactive | (logical(1)) TRUE if the report may use interactive features (using <code>plotly::ggplotly()</code> , <code>plotly::plot_ly()</code> and <code>DT::renderDataTable()</code>) or FALSE if such features must be disabled. Defaults to the value returned by <code>interactive()</code> , |

Value

`ggplot2::ggplot()` object

Examples

```
iraceResults <- read_logfile(system.file(package="irace", "exdata",
                                       "irace-acotsp.Rdata", mustWork = TRUE))
plot_experiments_matrix(iraceResults)
```

plot_model

Plot the sampling models used by irace

Description

Display the sampling models from which irace generated parameter values for new configurations during the configurations process.

For categorical parameters a stacked bar plot is created. This plot shows the sampling probabilities of the parameter values for the elite configurations in the iterations of the configuration process.

For numerical parameters a sampling distributions plot of the numerical parameters for the elite configurations of an iteration. This plot shows the density function of the truncated normal distributions associated to each parameter for each elite configuration on each iteration.

Usage

```
plot_model(irace_results, param_name, filename = NULL)
```

Arguments

| | |
|---------------|---|
| irace_results | The data generated when loading the .Rdata file created by irace (or the file-name of that file). |
| param_name | String, parameter to be included in the plot, e.g., param_name = "algorithm" |
| filename | (character(1)) File name to save the plot, for example "~/path/example/filename.png". |

Value

sampling model plot

Examples

```
iraceResults <- read_logfile(system.file(package="irace", "exdata",  
                                       "irace-acotsp.Rdata", mustWork = TRUE))  
plot_model(iraceResults, param_name="algorithm")  
  
plot_model(iraceResults, param_name="alpha")
```

| | |
|----------------|--|
| read_ablogfile | <i>Read the log file (log-ablation.Rdata) produced by irace::ablation().</i> |
|----------------|--|

Description

Read the log file (log-ablation.Rdata) produced by [irace::ablation\(\)](#).

Usage

```
read_ablogfile(filename)
```

Arguments

| | |
|----------|---|
| filename | Filename that contains the log file saved by irace::ablation() . Example: log-ablation.Rdata. |
|----------|---|

Value

(list())

| | |
|--------|---|
| report | <i>Create HTML Report from irace data</i> |
|--------|---|

Description

This function creates an HTML report of the most relevant irace data. This report provides general statistics and plots that show the best configurations and their performance. Example: https://auto-optimization.github.io/iraceplot/articles/example/report_example.html

Usage

```
report(
  irace_results,
  filename = "report",
  sections = list(experiments_matrix = NULL),
  interactive = base::interactive()
)
```

Arguments

| | |
|----------------------------|--|
| <code>irace_results</code> | The data generated when loading the .Rdata file created by irace (or the filename of that file). |
| <code>filename</code> | (character(1)) Filename indicating where to save the report (example: "~/path-to/filename"). |
| <code>sections</code> | (list()) List of sections to enable/disable. This is useful for disabling sections that may cause problems, such as out-of-memory errors. NA means automatically enable/disable a section depending on the memory required. |
| <code>interactive</code> | (logical(1)) TRUE if the report may use interactive features (using <code>plotly::ggplotly()</code> , <code>plotly::plot_ly()</code> and <code>DT::renderDataTable()</code>) or FALSE if such features must be disabled. Defaults to the value returned by <code>interactive()</code> , |

Value

filename where the report was created or it opens the report in the default browser (interactive).

Examples

```
withr::with_tempdir({
  iraceResults <- read_logfile(system.file(package="irace", "exdata",
                                          "irace-acotsp.Rdata", mustWork = TRUE))
  report(iraceResults, filename = file.path(getwd(), "report"))
}, clean = !base::interactive())
```

| | |
|-------------------|-------------------------------|
| sampling_distance | <i>Sampling distance Plot</i> |
|-------------------|-------------------------------|

Description

The `sampling_distance` function creates a plot that displays the mean of the distance between the configurations that were executed in each iteration.

For categorical parameters the distance is calculated as the hamming distance, for numerical parameters a equality interval is defined by a threshold specified by argument `t` and hamming distance is calculated using this interval.

Usage

```
sampling_distance(
  irace_results,
  type = c("boxplot", "line", "both"),
  t = 0.05,
  filename = NULL
)
```

Arguments

| | |
|----------------------------|--|
| <code>irace_results</code> | The data generated when loading the .Rdata file created by irace (or the filename of that file). |
| <code>type</code> | String, (default "boxplot") Type of plot to be produced, either "line", "boxplot" or "both". The "boxplot" setting shows a boxplot of the mean distance of all configurations, "line" shows the mean distance of the solution population in each iteration, "both" shows both plots. |
| <code>t</code> | Numeric, (default 0.05) percentage factor that will determine a distance to define equal numerical parameter values. If the numerical parameter values to be compared are v_1 and v_2 they are considered equal if $ v_1 - v_2 \leq ub - lb * t$. |
| <code>filename</code> | (character(1)) File name to save the plot, for example "~/path/example/filename.png". |

Value

line or box plot

Examples

```
iraceResults <- read_logfile(system.file(package="irace", "exdata",
                                         "irace-acotsp.Rdata", mustWork = TRUE))
sampling_distance(iraceResults)

sampling_distance(iraceResults, type = "boxplot", t=0.07)
```

sampling_frequency *Parameter Frequency and Density Plot*

Description

Frequency or density plot that depicts the sampling performed by irace across the iterations of the configuration process. For categorical parameters a frequency plot is created, while for numerical parameters a histogram and density plots are created. The plots are shown in groups of maximum 9, the parameters included in the plot can be specified by setting the `param_names` argument.

Usage

```
sampling_frequency(
  configurations,
  parameters,
  param_names = NULL,
  n = NULL,
  filename = NULL
)
```

Arguments

configurations Data frame, configurations in irace format. Example: `iraceResults$allConfigurations`.

parameters List, parameters object in irace format. If this argument is missing, the first parameter is taken as the `iraceResults` data generated when loading the `.Rdata` file created by `irace` and `configurations=iraceResults$allConfigurations` and `parameters = iraceResults$parameters`.

param_names `(character())` Parameters to be included in the plot. Example: `c("algorithm", "alpha", "rho", "q0",`

n Numeric, for scenarios with large parameter sets, it selects a subset of 9 parameters. For example, `n=1` selects the first 9 (1 to 9) parameters, `n=2` selects the next 9 (10 to 18) parameters and so on.

filename `(character(1))` File name to save the plot, for example `"~/path/example/filename.png"`.

Value

Frequency and/or density plot

Note

If there are more than 9 parameters, a pdf file extension is recommended as it allows to create a multi-page document. Otherwise, you can use the `n` argument of the function to generate the plot of a subset of the parameters.

Examples

```
# Either use iraceResults
iraceResults <- read_logfile(system.file(package="iraceplot", "exdata",
                                         "guide-example.Rdata", mustWork = TRUE))

sampling_frequency(iraceResults)

sampling_frequency(iraceResults, n = 2)
sampling_frequency(iraceResults, param_names = c("alpha"))
sampling_frequency(iraceResults, param_names = c("algorithm", "alpha", "rho", "q0", "rasrank"))

# Or explicitly specify the configurations and parameters.
sampling_frequency(iraceResults$allConfigurations, iraceResults$parameters)

sampling_frequency(iraceResults$allConfigurations, iraceResults$parameters, n = 2)
sampling_frequency(iraceResults$allConfigurations, iraceResults$parameters,
  param_names = c("alpha"))
```

```
sampling_frequency(iraceResults$allConfigurations, iraceResults$parameters,
  param_names = c("algorithm", "alpha", "rho", "q0", "rasrank"))
```

sampling_frequency_iteration

Frequency and Density plot based on its iteration

Description

The function will return a frequency plot used for categorical data (its values are string, show a bar plot) or numeric data (show a histogram and density plot) by each iteration

Usage

```
sampling_frequency_iteration(
  irace_results,
  param_name,
  numerical_type = "both",
  filename = NULL
)
```

Arguments

| | |
|----------------|--|
| irace_results | The data generated when loading the .Rdata file created by irace (or the file-name of that file). |
| param_name | String, name of the parameter to be included (example: param_name = "algorithm") |
| numerical_type | String, (default "both") Indicates the type of plot to be displayed for numerical parameters. "density" shows a density plot, "frequency" shows a frequency plot and "both" show both frequency and density. |
| filename | (character(1)) File name to save the plot, for example "~/path/example/filename.png". |

Value

Frequency and/or density plot

Examples

```
iraceResults <- read_logfile(system.file(package="irace", "exdata",
  "irace-acotsp.Rdata", mustWork = TRUE))
sampling_frequency_iteration(iraceResults, param_name = "alpha")

sampling_frequency_iteration(iraceResults, param_name = "alpha", numerical_type="density")
```

| | |
|------------------|-------------------------------|
| sampling_heatmap | <i>Sampling heat map plot</i> |
|------------------|-------------------------------|

Description

Heatmap that displays the frequency of sampling values of two parameters.

Usage

```
sampling_heatmap(
  irace_results,
  param_names,
  sizes = c(0, 0),
  iterations = NULL,
  only_elite = TRUE,
  filename = NULL
)
```

Arguments

| | |
|----------------------------|--|
| <code>irace_results</code> | The data generated when loading the .Rdata file created by irace (or the file-name of that file). |
| <code>param_names</code> | (character()) Parameters to be included in the plot. Example: <code>c("algorithm", "alpha", "rho", "q0",</code> |
| <code>sizes</code> | Numeric vector that indicated the number of intervals to be considered for numerical parameters. This argument is positional with respect to <code>param_names</code> . By default, numerical parameters are displayed using 10 intervals. (example <code>sizes = c(0,10)</code>) |
| <code>iterations</code> | Numeric vector, iteration number that should be included in the plot (example: <code>iterations = c(1,4,5)</code>) |
| <code>only_elite</code> | logical (default TRUE), only print elite configurations. |
| <code>filename</code> | (character(1)) File name to save the plot, for example <code>"~/path/example/filename.png"</code> . |

Value

sampling heat map plot

Examples

```
iraceResults <- read_logfile(system.file(package="irace", "exdata",
                                         "irace-acotsp.Rdata", mustWork = TRUE))
sampling_heatmap(iraceResults, param_names=c("beta", "alpha"))
sampling_heatmap(iraceResults, param_names=c("beta", "alpha"), iterations = c(3,4))
sampling_heatmap(iraceResults, param_names=c("beta", "alpha"), only_elite = FALSE)
```

sampling_heatmap2 *Sampling heat map plot*

Description

Heatmap that displays the frequency of sampling values of two parameters.

Usage

```
sampling_heatmap2(  
  configurations,  
  parameters,  
  param_names,  
  sizes = c(0, 0),  
  filename = NULL  
)
```

Arguments

configurations Data frame, configurations in irace format (example: configurations = iraceResults\$allConfigurations)

parameters List, parameter object in irace format (example: configurations = iraceResults\$parameters)

param_names String vector of size 2, names of the parameters that should be included in the plot (example: param_names = c("beta", "alpha"))

sizes Numeric vector that indicated the number of intervals to be considered for numerical parameters. This argument is positional with respect to param_names. By default, numerical parameters are displayed using 10 intervals. (example sizes = c(0,10))

filename (character(1)) File name to save the plot, for example "~/path/example/filename.png".

Value

sampling heat map plot

Examples

```
iraceResults <- read_logfile(system.file(package="irace", "exdata",  
                                       "irace-acotsp.Rdata", mustWork = TRUE))  
sampling_heatmap2(iraceResults$allConfigurations, iraceResults$parameters,  
                  param_names=c("beta", "alpha"))
```

| | |
|--------------|--------------------------|
| sampling_pie | <i>Sampling pie plot</i> |
|--------------|--------------------------|

Description

This function creates a pie plot of the values sampled of a set of selected parameters. Numerical parameters are discretized to maximum `n_bins` intervals. The size of the slices are proportional to the number of configurations that have assigned a parameter value within the rank or the value assigned to that slice. Parameters can be selected by providing their names in the `param_names` argument.

Usage

```
sampling_pie(irace_results, param_names = NULL, n_bins = 3, filename = NULL)
```

Arguments

| | |
|----------------------------|--|
| <code>irace_results</code> | The data generated when loading the .Rdata file created by <code>irace</code> (or the file-name of that file). |
| <code>param_names</code> | String vector, A set of parameters to be included (example: <code>param_names = c("algorithm","dlb")</code>) |
| <code>n_bins</code> | Numeric (default 3), number of intervals to generate for numerical parameters. |
| <code>filename</code> | (<code>character(1)</code>) File name to save the plot, for example <code>"~/path/example/filename.png"</code> . |

Value

Sampling pie plot

Examples

```
iraceResults <- read_logfile(system.file(package="irace", "exdata",  
                                       "irace-acotsp.Rdata", mustWork = TRUE))  
sampling_pie(iraceResults)  
  
sampling_pie(iraceResults, param_names = c("algorithm", "dlb", "ants"))
```

 scatter_performance *Performance Scatter Plot of Two Configurations*

Description

Create a scatter plot that displays the performance of two configurations on a provided experiment matrix. Each point in the plot represents an instance and the color of the points indicates if one configuration is better than the other.

Usage

```
scatter_performance(
  experiments,
  x_id,
  y_id,
  rpd = TRUE,
  filename = NULL,
  interactive = base::interactive(),
  instance_names = NULL
)

scatter_training(irace_results, ...)

scatter_test(irace_results, ...)
```

Arguments

| | |
|----------------|--|
| experiments | Experiment matrix obtained from irace training or testing data. Configurations in columns and instances in rows. As in irace, column names (configurations ids) should be characters. Row names will be used as instance names. |
| x_id, y_id | Configuration IDs for x-axis and y-axis, respectively. |
| rpd | (logical(1)) TRUE to plot performance as the relative percentage deviation to best results per instance, FALSE to plot raw performance. |
| filename | (character(1)) File name to save the plot, for example "~/path/example/filename.png". |
| interactive | (logical(1)) TRUE if the report may use interactive features (using <code>plotly::ggplotly()</code> , <code>plotly::plot_ly()</code> and <code>DT::renderDataTable()</code>) or FALSE if such features must be disabled. Defaults to the value returned by <code>interactive()</code> , |
| instance_names | Either a character vector of instance names in the same order as <code>rownames(experiments)</code> or a function that takes <code>rownames(experiments)</code> as input. |
| irace_results | The data generated when loading the .Rdata file created by irace (or the filename of that file). |
| ... | Other arguments passed to <code>scatter_performance()</code> . |

Details

The performance matrix is assumed to be provided in the format of the irace experiment matrix thus, NA values are allowed. Consequently the number of evaluations can differ between configurations due to the elimination process applied by irace. This plot only shows performance data only for instances in which both configurations are executed.

`scatter_training()` compares the performance of two configurations on the training instances. The performance data is obtained from the evaluations performed by irace during the execution process.

`scatter_test()` compares the performance of two configurations on the test instances. The performance data is obtained from the test evaluations performed by irace. Note that testing is not enabled by default in irace and should be enabled in the scenario setup. Moreover, configuration ids provided in `x_id` and `y_id` should belong to elite configuration set evaluated in the test (see the irace package user guide for more details).

Value

`ggplot2::ggplot()` object

Examples

```
iraceResults <- read_logfile(system.file(package="irace", "exdata",
                                       "irace-acotsp.Rdata", mustWork = TRUE))
best_id <- iraceResults$iterationElites[length(iraceResults$iterationElites)]
scatter_performance(iraceResults$experiments, x_id = 1, y_id = best_id)
iraceResults <- read_logfile(system.file(package="iraceplot", "exdata",
                                       "guide-example.Rdata", mustWork = TRUE))
scatter_training(iraceResults, x_id = 806, y_id = 809)

scatter_training(iraceResults, x_id = 806, y_id = 809, rpd = FALSE)

iraceResults <- read_logfile(system.file(package="iraceplot", "exdata",
                                       "guide-example.Rdata", mustWork = TRUE))
scatter_test(iraceResults, x_id = 92, y_id = 119)

scatter_test(iraceResults, x_id = 92, y_id = 119, rpd=FALSE)
```

summarise_by_configuration

Summarise by configuration

Description

Summarise by configuration

Usage

```
summarise_by_configuration(  
  irace_results,  
  elites_only = FALSE,  
  instances = c("both", "train", "test")  
)
```

Arguments

`irace_results` The data generated when loading the .Rdata file created by irace (or the file-name of that file).

`elites_only` (logical(1)) If TRUE, only report the final elite configurations.

`instances` (character(1)) Select data from the training instances ("train") or from the test instances if available ("test"). The default is from both ("both").

Value

tibble

Examples

```
irace_results <- read_logfile(system.file(package="irace", "exdata",  
                                         "irace-acotsp.Rdata", mustWork = TRUE))  
summarise_by_configuration(irace_results, instances = "train", elites_only = TRUE)
```

summarise_by_instance *Summarise by instance*

Description

Summarise by instance

Usage

```
summarise_by_instance(irace_results)
```

Arguments

`irace_results` The data generated when loading the .Rdata file created by irace (or the file-name of that file).

Value

tibble

Examples

```
irace_result <- read_logfile(system.file(package="irace", "exdata",  
                                     "irace-acotsp.Rdata", mustWork = TRUE))  
summarise_by_instance(irace_result)
```

summarise_by_iteration

Summarise by iteration

Description

Summarise by iteration

Usage

```
summarise_by_iteration(irace_results)
```

Arguments

`irace_results` The data generated when loading the .Rdata file created by irace (or the file-name of that file).

Value

tibble

Examples

```
irace_result <- read_logfile(system.file(package="irace", "exdata",  
                                     "irace-acotsp.Rdata", mustWork = TRUE))  
summarise_by_iteration(irace_result)
```

Index

ablation_plot, 2

boxplot_performance, 3
boxplot_performance(), 5–7
boxplot_test, 5
boxplot_test(), 5, 7
boxplot_training, 6
boxplot_training(), 5, 6

configurations_display, 7

distance_config, 8
DT::renderDataTable(), 4, 7, 14, 16, 23

ggplot2::geom_violin(), 4
ggplot2::ggplot(), 3, 5–8, 14, 24

has_testing_data, 9

irace::ablation(), 3, 15
irace::plotAblation(), 3

parallel_cat, 9
parallel_coord, 10
parallel_coord(), 10
parallel_coord2, 12
parallel_coord2(), 10
plot_experiments_matrix, 13
plot_model, 14
plotly::ggplotly(), 4, 7, 14, 16, 23
plotly::plot_ly(), 4, 7, 14, 16, 23

read_ablogfile, 15
report, 15

sampling_distance, 16
sampling_frequency, 17
sampling_frequency_iteration, 19
sampling_heatmap, 20
sampling_heatmap2, 21
sampling_pie, 22

scatter_performance, 23
scatter_performance(), 23
scatter_test (scatter_performance), 23
scatter_test(), 24
scatter_training (scatter_performance),
23
scatter_training(), 24
summarise_by_configuration, 24
summarise_by_instance, 25
summarise_by_iteration, 26