Package ‘flashlight’

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Description

The function calls `light_breakdown` for `n_shap` observations and adds the resulting (approximate) SHAP decompositions as static element "shap" to the (multi-)flashlight for further analyses. We offer two approximations to SHAP: For `visit_strategy = "importance"`, the breakdown algorithm (see reference) is used with importance based visit order. Use the default `visit_strategy = "permutation"` to run breakdown for multiple random permutations, averaging the results. This approximation will be closer to exact SHAP values, but very slow. Most available arguments can be chosen to reduce computation time.

Usage

```r
add_shap(x, ...)
```

## Default S3 method:
```
add_shap(x, ...)
```

## S3 method for class 'flashlight'
```
add_shap(
  x,
  v = NULL,
  visit_strategy = c("permutation", "importance", "v"),
  n_shap = 200,
  n_max = Inf,
  n_perm = 12,
  seed = NULL,
  use_linkinv = FALSE,
  verbose = TRUE,
  ...
)
```

## S3 method for class 'multiflashlight'
```
add_shap(x, ...)
```

Arguments

- `x`  
  An object of class `flashlight` or `multiflashlight`.
- `...`  
  Further arguments passed from or to other methods.
- `v`  
  Vector of variables to assess contribution for. Defaults to all except those specified by "y", "w" and "by".
- `visit_strategy`  
  In what sequence should variables be visited? By `n_perm "permutation"` (slow), by "importance" (fast), or as "v" (not recommended).
- `n_shap`  
  Number of SHAP decompositions to calculate.
n_max
Maximum number of rows in data to consider in the reference data. Set to lower value if data is large.

n_perm
Number of permutations of random visit sequences. Only used if visit_strategy = "permutation".

seed
An integer random seed.

use_linkinv
Should retransformation function be applied? We suggest to keep the default (FALSE) as the values can be retransformed later.

verbose
Should progress bar be shown? Default is TRUE.

Value
An object of class flashlight or multiflashlight with additional element "shap" of class "shap" (and "list").

Methods (by class)
• default: Default method not implemented yet.
• flashlight: Variable attribution to single observation for a flashlight.
• multiflashlight: Add SHAP to multiflashlight.

References

Examples
## Not run:
fit <- lm(Sepal.Length ~ . + Petal.Length:Species, data = iris)
x <- flashlight(model = fit, label = "lm", data = iris, y = "Sepal.Length")
x <- add_shap(x)
is.shap(x$shap)
plot(light_importance(x, type = "shap"))
plot(light_scatter(x, type = "shap", v = "Petal.Length"))
plot(light_scatter(x, type = "shap", v = "Petal.Length", by = "Species"))
## End(Not run)
ale_profile

Usage

ale_profile(
  x,
  v,
  breaks = NULL,
  n_bins = 11,
  cut_type = c("equal", "quantile"),
  counts = TRUE,
  counts_weighted = FALSE,
  pred = NULL,
  evaluate_at = NULL,
  indices = NULL,
  n_max = 1000,
  seed = NULL,
  two_sided = FALSE,
  calibrate = TRUE,
  ...
)

Arguments

x An object of class flashlight.
v The variable to be profiled.
breaks Cut breaks for a numeric v. Only used if no evaluate_at is specified.
n_bins Maxium number of unique values to evaluate for numeric v. Only used if no
evaluate_at is specified.
cut_type For the default "equal", bins of equal width are created for v by pretty. Choose
"quantile" to create quantile bins.
counts Should counts be added?
counts_weighted If counts is TRUE: Should counts be weighted by the case weights? If TRUE,
the sum of w is returned by group.
pred Optional vector with predictions.
evaluate_at Vector with values of v used to evaluate the profile. Only relevant for type =
"partial dependence".
indices A vector of row numbers to consider.
n_max Maximum number of ICE profiles to calculate within interval (not within data).
seed Integer random seed passed to light_ice.
two_sided Standard ALE profiles are calculated via left derivatives. Set to TRUE if two-
sided derivatives should be calculated. Only works for continuous v. More
specifically: Usually, local effects at value x are calculated using points between
x-e and x. Set ale_two_sided = TRUE to use points between x-e/2 and x+e/2.
calibrate Should values be calibrated based on average predictions? Default is TRUE.
... Other arguments passed to this function (currently unused).
**Value**

A tibble containing results.

---

**all_identical**

**Description**

Checks if an aspect is identical for all elements in a nested list. The aspect is specified by `fun`, e.g. `[[], followed by the element name to compare.`

**Usage**

```r
all_identical(x, fun, ...)
```

**Arguments**

- `x` A nested list of objects.
- `fun` Function used to extract information of each element of `x`.
- `...` Further arguments passed to `fun`.

**Value**

A logical vector of length one.

**Examples**

```r
x <- list(a = 1, b = 2)
y <- list(a = 1, b = 3)
all_identical(list(x, y), `[[`, "a")
all_identical(list(x, y), `[[`, "b")
```

---

**auto_cut**

**Description**

Discretizes a Vector

This function takes a vector `x` and returns a list with information on discretized version of `x`, see `return` for details on the resulting object.
Usage

```r
auto_cut(
  x,
  breaks = NULL,
  n_bins = 27,
  cut_type = c("equal", "quantile"),
  x_name = "value",
  level_name = "level",
  ...
)
```

Arguments

- `x`: A vector.
- `breaks`: An optional vector of breaks. Only relevant for numeric `x`.
- `n_bins`: If `x` is numeric and no breaks are provided, this is the maximum number of bins allowed or to be created (approximately).
- `cut_type`: For the default type "equal", bins of equal width are created by `pretty`. Choose "quantile" to create quantile bins.
- `x_name`: Column name with the values of `x` in the output.
- `level_name`: Column name with the bin labels of `x` in the output.
- `...`: Further arguments passed to `cut3`.

Details

The construction of level names can be controlled by passing `...` arguments to `formatC`.

Value

A list with the following four elements:

- `data`: A `data.frame` with columns `x_name` and `level_name` each with the same length as `x`. The column `x_name` has values in output `bin_means` while the column `level_name` has values in `bin_labels`.
- `breaks`: A vector of increasing and unique breaks used to cut a numeric `x` with too many distinct levels. NULL otherwise.
- `bin_means`: The midpoints of subsequent breaks, or if there are no breaks in the output, factor levels or distinct values of `x`.
- `bin_labels`: Break labels of the form "(low, high]" if there are breaks in the output, otherwise the same as `bin_means`. Same order as `bin_means`.

Examples

```r
auto_cut(1:10, n_bins = 3)
auto_cut(c(NA, 1:10), n_bins = 3)
auto_cut(1:10, breaks = 3:4, n_bins = 3)
auto_cut(1:10, n_bins = 3, cut_type = "quantile")
```
auto_cut(LETTERS[4:1], n_bins = 2)
auto_cut(factor(LETTERS[1:4], LETTERS[4:1]), n_bins = 2)
auto_cut(900:1100, n_bins = 3, big.mark = ",", format = "fg")
auto_cut(c(0.0001, 0.0002, 0.0003, 0.005), n_bins = 3, format = "fg")

common_breaks  
Common Breaks for multiflashlight

Description
Internal function used to find common breaks from different flashlights.

Usage
  common_breaks(x, v, data = NULL, n_bins, cut_type)

Arguments
  x  An object of class multiflashlight.
  v  The variable to be profiled.
  data  A data.frame.
  n_bins  Maximum number of unique values to evaluate for numeric v.
  cut_type  Cut type

Value
  A vector of breaks

cut3  
Modified cut

Description
Slightly modified version of base::cut.default. Both modifications refer to the construction of break labels. Firstly, ... arguments are passed to formatC in formatting the numbers in the labels. Secondly, a separator between the two numbers can be specified with default ",, ".

Usage

cut3(
  x,
  breaks,
  labels = NULL,
  include.lowest = FALSE,
  right = TRUE,
  dig.lab = 3L,
  ordered_result = FALSE,
  sep = "", ",",
  ...
)

Arguments

x Numeric vector.
breaks Numeric vector of cut points or a single number specifying the number of intervals desired.
labels Labels for the levels of the final categories.
include.lowest Flag if minimum value should be added to intervals of type (,] (or maximum for [, )).
right Flag if intervals should be closed to the right or left.
dig.lab Number of significant digits passed to formatC.
ordered.result Flag if resulting output vector should be ordered.
sep Separator between from-to labels.
... Arguments passed to formatC.

Value

Vector of the same length as x.

Examples

  x <- 998:1001
  cut3(x, breaks = 2)
  cut3(x, breaks = 2, big.mark = "", sep = ":")

Description

Creates or updates a flashlight object. If a flashlight is to be created, all arguments are optional except label. If a flashlight is to be updated, all arguments are optional up to x (the flashlight to be updated).
Usage

`flashlight(x, ...)`

```r
## Default S3 method:
flashlight(
  x,
  model = NULL,
  data = NULL,
  y = NULL,
  predict_function = predict,
  linkinv = function(z) z,
  w = NULL,
  by = NULL,
  metrics = list(rmse = rmse),
  label = NULL,
  shap = NULL,
  ...
)

## S3 method for class 'flashlight'
flashlight(x, check = TRUE, ...)
```

Arguments

- `x`  
  An object of class `flashlight`. If not provided, a new flashlight is created based on further input. Otherwise, `x` is updated based on further input.

- `...`  
  Arguments passed from or to other functions.

- `model`  
  A fitted model of any type. Most models require a customized `predict_function`.

- `data`  
  A data.frame or tibble used as basis for calculations.

- `y`  
  Variable name of response.

- `predict_function`  
  A real valued function with two arguments: A model and a data of the same structure as `data`. Only the order of the two arguments matter, not their names.

- `linkinv`  
  An inverse transformation function applied after `predict_function`.

- `w`  
  A variable name of case weights.

- `by`  
  A character vector with names of grouping variables.

- `metrics`  
  A named list of metrics. Here, a metric is a function with exactly four arguments: actual, predicted, w (case weights) and ... like those in package MetricsWeighted.

- `label`  
  Name of the flashlight. Required.

- `shap`  
  An optional shap object. Typically added by calling `add_shap`.

- `check`  
  When updating the flashlight: Should internal checks be performed? Default is TRUE.
grouped_center

Value

An object of class flashlight (and list) containing each input (except \( x \)) as element.

Methods (by class)

- default: Used to create a flashlight object. No \( x \) has to be passed in this case.
- flashlight: Used to update an existing flashlight object.

See Also

multiflashlight.

Examples

```r
fit <- lm(Sepal.Length ~ ., data = iris)
(fl <- flashlight(model = fit, data = iris, y = "Sepal.Length", label = "ols"))
(fl_updated <- flashlight(fl, linkinv = exp))
```

---

grouped_center  

Grouped, weighted mean centering

Description

Centers a numeric variable within optional groups and optional weights. The order of values is unchanged.

Usage

```
grouped_center(data, x, w = NULL, by = NULL, ...)
```

Arguments

- **data**: A data.frame.
- **x**: Variable name in data to center.
- **w**: Optional name of the column in data with case weights.
- **by**: An optional vector of column names in data used to group the results.
- **...**: Additional arguments passed to mean calculation (e.g. `na.rm = TRUE`).

Value

A numeric vector with centered values in column \( x \).

Examples

```r
ir <- data.frame(iris, w = 1)
mean(grouped_center(ir, "Sepal.Width"))
rowsum(grouped_center(ir, "Sepal.Width", by = "Species"), ir$Species)
mean(grouped_center(ir, "Sepal.Width", w = "w"))
rowsum(grouped_center(ir, "Sepal.Width", by = "Species", w = "w"), ir$Species)
```
grouped_counts  

**Description**

Calculates weighted counts grouped by optional columns.

**Usage**

```r
grouped_counts(data, by = NULL, w = NULL, value_name = "n", ...)
```

**Arguments**

- `data` A data.frame.
- `by` An optional vector of column names in data used to group the results.
- `w` Optional name of the column in data with case weights.
- `value_name` Name of the resulting column with counts.
- `...` Arguments passed to `sum` (only if weights are provided).

**Value**

A data.frame with columns `by` and `value_name`.

**Examples**

```r
grouped_counts(iris)
grouped_counts(iris, by = "Species")
grouped_counts(iris, w = "Petal.Length")
grouped_counts(iris, by = "Species", w = "Petal.Length")
```

grouped_stats  

**Description**

Calculates weighted means, quartiles, or variances (and counts) of a variable grouped by optional columns. By default, counts are not weighted, even if there is a weighting variable.
grouped_stats

Usage

grouped_stats(
  data,
  x,
  w = NULL,
  by = NULL,
  stats = c("mean", "quartiles", "variance"),
  counts = TRUE,
  counts_weighted = FALSE,
  counts_name = "counts",
  value_name = x,
  q1_name = "q1",
  q3_name = "q3",
  ...
)

Arguments

data A data.frame.
x Variable name in data to summarize.
w Optional name of the column in data with case weights.
by An optional vector of column names in data used to group the results.
stats Statistic to calculate: "mean", "quartiles", or "variance".
counts Should group counts be added?
counts_weighted Should counts be weighted by the case weights? If TRUE, the sum of w is returned by group.
counts_name Name of column in the resulting data.frame containing the counts.
value_name Name of the resulting column with mean, median, or variance.
q1_name Name of the resulting column with first quartile values. Only relevant for stats "quartiles".
q3_name Name of the resulting column with third quartile values. Only relevant for stats "quartiles".
... Additional arguments passed to MetricsWeighted::weighted_mean, MetricsWeighted::weighted_quartiles or MetricsWeighted::weighted_var.

Value

A data.frame with columns by, x and optionally counts_name.

Examples

grouped_stats(iris, "Sepal.Width")
grouped_stats(iris, "Sepal.Width", stats = "quartiles")
grouped_stats(iris, "Sepal.Width", stats = "variance")
grouped_stats(iris, "Sepal.Width", w = "Petal.Width", counts_weighted = TRUE)
grouped_stats(iris, "Sepal.Width", by = "Species")
grouped_weighted_mean  

Fast Grouped Weighted Mean

Description

Fast version of grouped_stats(..., counts = FALSE). Works if there is at most one "by" variable.

Usage

grouped_weighted_mean(
  data,    # A data.frame.
x,        # Variable name in data to summarize.
w = NULL,  # Optional name of the column in data with case weights.
by = NULL, # An optional vector of column names in data used to group the results.
na.rm = TRUE, # Should missing values in x be removed?
value_name = x # Name of the resulting column with means.
)

Arguments

data    # A data.frame.
x        # Variable name in data to summarize.
w        # Optional name of the column in data with case weights.
by       # An optional vector of column names in data used to group the results.
na.rm    # Should missing values in x be removed?
value_name # Name of the resulting column with means.

Value

A data.frame with grouped weighted means.

Examples

n <- 100
data <- data.frame(x = rnorm(n), w = runif(n), group = factor(sample(1:3, n, TRUE)))
grouped_weighted_mean(data, x = "x", w = "w", by = "group")
Description

Checks if an object inherits specific class relevant for the flashlight package.

Usage

```r
is.flashlight(x)

is.multiflashlight(x)

is.light(x)

is.light_performance(x)

is.light_performance_multi(x)

is.light_importance(x)

is.light_importance_multi(x)

is.light_breakdown(x)

is.light_breakdown_multi(x)

is.light_ice(x)

is.light_ice_multi(x)

is.light_profile(x)

is.light_profile_multi(x)

is.light_profile2d(x)

is.light_profile2d_multi(x)

is.light_effects(x)

is.light_effects_multi(x)

is.shap(x)

is.light_scatter(x)
```
is.light_scatter_multi(x)

is.light_global_surrogate(x)

is.light_global_surrogate_multi(x)

**Arguments**

x  
Any object.

**Value**

A logical vector of length one.

**Functions**

- is.multiflashlight: Check for multiflashlight object.
- is.light: Check for light object.
- is.light_performance: Check for light_performance object.
- is.light_performance_multi: Check for light_performance_multi object.
- is.light_importance: Check for light_importance object.
- is.light_importance_multi: Check for light_importance_multi object.
- is.light_breakdown: Check for light_breakdown object.
- is.light_breakdown_multi: Check for light_breakdown_multi object.
- is.light_ice: Check for light_ice object.
- is.light_ice_multi: Check for light_ice_multi object.
- is.light_profile: Check for light_profile object.
- is.light_profile_multi: Check for light_profile_multi object.
- is.light_profile2d: Check for light_profile2d object.
- is.light_profile2d_multi: Check for light_profile2d_multi object.
- is.light_effects: Check for light_effects object.
- is.light_effects_multi: Check for light_effects_multi object.
- is.shap: Check for shap object.
- is.light_scatter: Check for light_scatter object.
- is.light_scatter_multi: Check for light_scatter_multi object.
- is.light_global_surrogate: Check for light_global_surrogate object.
- is.light_global_surrogate_multi: Check for light_global_surrogate_multi object.

**Examples**

```r
a <- flashlight(label = "a")
is.flashlight(a)
is.flashlight("a")
```
**Description**

Calculates sequential additive variable contributions (approximate SHAP) to the prediction of a single observation, see Gosiewska and Biecek (see reference) and the details below.

**Usage**

```r
light_breakdown(x, ...)  
## Default S3 method:
light_breakdown(x, ...)  
## S3 method for class 'flashlight'
light_breakdown(  
  x,  
  new_obs,  
  data = x$data,  
  by = x$by,  
  v = NULL,  
  visit_strategy = c("importance", "permutation", "v"),  
  n_max = Inf,  
  n_perm = 20,  
  seed = NULL,  
  use_linkinv = FALSE,  
  description = TRUE,  
  digits = 2,  
  ...  
)
```

```r
## S3 method for class 'multiflashlight'
light_breakdown(x, ...)
```

**Arguments**

- `x`: An object of class `flashlight` or `multiflashlight`.
- `...`: Further arguments passed to `prettyNum` to format numbers in description text.
- `new_obs`: One single new observation to calculate variable attribution for. Needs to be a `data.frame` of same structure as `data`.
- `data`: An optional `data.frame`.
- `by`: An optional vector of column names used to filter data for rows with equal values in "by" variables as `new_obs`.
- `v`: Vector of variable names to assess contribution for. Defaults to all except those specified by "y", "w" and "by".
**visit_strategy**  In what sequence should variables be visited? By "importance", by n_perm "permutation" or as "v" (see Details).

**n_max**  Maximum number of rows in data to consider in the reference data. Set to lower value if data is large.

**n_perm**  Number of permutations of random visit sequences. Only used if visit_strategy = "permutation".

**seed**  An integer random seed used to shuffle rows if n_max is smaller than the number of rows in data.

**use_linkinv**  Should retransformation function be applied? Default is FALSE.

**description**  Should descriptions be added? Default is TRUE.

**digits**  Passed to prettyNum to format numbers in description text.

**Details**

The breakdown algorithm works as follows: First, the visit order (x_1, ..., x_m) of the variables v is specified. Then, in the query data, the column x_1 is set to the value of x_1 of the single observation new_obs to be explained. The change in the (weighted) average prediction on data measures the contribution of x_1 on the prediction of new_obs. This procedure is iterated over all x_i until eventually, all rows in data are identical to new_obs. A complication with this approach is that the visit order is relevant, at least for non-additive models. Ideally, the algorithm could be repeated for all possible permutations of v and its results averaged per variable. This is basically what SHAP values do, see the reference below for an explanation. Unfortunately, there is no efficient way to do this in a model agnostic way. We offer two visit strategies to approximate SHAP. The first one uses the short-cut described in the reference below: The variables are sorted by the size of their contribution in the same way as the breakdown algorithm but without iteration, i.e. starting from the original query data for each variable $x_i$. We call this visit strategy "importance". The second strategy "permutation" averages contributions from a small number of random permutations of v. Note that the minimum required elements in the (multi-) flashlight are a "predict_function", "model", and "data". The latter can also directly be passed to light_breakdown. Note that by default, no retransformation function is applied.

**Value**

An object of class light_breakdown with the following elements.

- **data** A tibble with results. Can be used to build fully customized visualizations. Column names can be controlled by options(flashlight.column_name).

- **by** Same as input by.

**Methods (by class)**

- **default**: Default method not implemented yet.

- **flashlight**: Variable attribution to single observation for a flashlight.

- **multiflashlight**: Variable attribution to single observation for a multiflashlight.
References


See Also

plot.light_breakdown.

Examples

```r
fit <- lm(Sepal.Length ~ . + Petal.Length:Species, data = iris)
fl <- flashlight(model = fit, label = "lm", data = iris, y = "Sepal.Length")
light_breakdown(fl, new_obs = iris[1, ])
```

Description

Checks if an object of class flashlight or multiflashlight is consistently defined.

Usage

```r
light_check(x, ...)
```

Arguments

- `x` An object of class flashlight or multiflashlight.
- `...` Further arguments passed from or to other methods.

Value

The input `x` or an error message.

Methods (by class)

- default: Default check method not implemented yet.
- flashlight: Checks if a flashlight object is consistently defined.
- multiflashlight: Checks if a multiflashlight object is consistently defined.
Examples

```r
fit <- lm(Sepal.Length ~ ., data = iris)
fit_log <- lm(log(Sepal.Length) ~ ., data = iris)
fl <- flashlight(fit, data = iris, y = "Sepal.Length", label = "ols")
fl_log <- flashlight(fit_log, y = "Sepal.Length", label = "ols", linkinv = exp)
light_check(fl)
light_check(fl_log)
```

**light_combine**

Combine Objects

Description

Combines a list of similar objects each of class `light` by row binding `data.frame` slots and retaining the other slots from the first list element.

Usage

```r
light_combine(x, ...)
```

### Default S3 method:
```r
light_combine(x, ...)
```

### S3 method for class 'light'
```r
light_combine(x, new_class = NULL, ...)
```

### S3 method for class 'list'
```r
light_combine(x, new_class = NULL, ...)
```

Arguments

- **x**
  - A list of objects of the same class.

- **...**
  - Further arguments passed from or to other methods.

- **new_class**
  - An optional vector with additional class names to be added to the output.

Value

If `x` is a list, an object like each element but with unioned rows in data slots.

Methods (by class)

- **default**: Default method not implemented yet.
- **light**: Since there is nothing to combine, the input is returned except for additional classes.
- **list**: Combine a list of similar light objects.
Examples

```r
fit_lm <- lm(Sepal.Length ~ ., data = iris)
fit_glm <- glm(Sepal.Length ~ ., family = Gamma(link = "log"), data = iris)
mod_lm <- flashlight(model = fit_lm, label = "lm", data = iris, y = "Sepal.Length")
mod_glm <- flashlight(model = fit_glm, label = "glm", data = iris, y = "Sepal.Length",
                      predict_function = function(object, newdata)
                      predict(object, newdata, type = "response"))
mods <- multiflashlight(list(mod_lm, mod_glm))
perf_lm <- light_performance(mod_lm)
perf_glm <- light_performance(mod_glm)
manual_comb <- light_combine(list(perf_lm, perf_glm),
                             new_class = "light_performance_multi")
auto_comb <- light_performance(mods)
all.equal(manual_comb, auto_comb)
```

---

**Description**

Calculates response-, prediction-, partial dependence, and ALE profiles of a (multi-)flashlight with respect to a covariable \( v \).

**Usage**

```r
light_effects(x, ...)
```

---

**light_effects**  
Combination of Response, Predicted, Partial Dependence, and ALE profiles.
light_effects

## S3 method for class 'multiflashlight'
light_effects(
  x,
  v,
  data = NULL,
  breaks = NULL,
  n_bins = 11,
  cut_type = c("equal", "quantile"),
  ...)

### Arguments

- **x**: An object of class `flashlight` or `multiflashlight`.
- **...**: Further arguments passed to `cut3` resp. `formatC` in forming the cut breaks of the `v` variable.
- **v**: The variable name to be profiled.
- **data**: An optional `data.frame`.
- **by**: An optional vector of column names used to additionally group the results.
- **stats**: Statistic to calculate for the response profile: "mean" or "quartiles".
- **breaks**: Cut breaks for a numeric `v`. Used to overwrite automatic binning via `n_bins` and `cut_type`. Ignored if `v` is not numeric.
- **n_bins**: Approximate number of unique values to evaluate for numeric `v`. Ignored if `v` is not numeric or if `breaks` is specified.
- **cut_type**: Should a numeric `v` be cut into "equal" or "quantile" bins? Ignored if `v` is not numeric or if `breaks` is specified.
- **use_linkinv**: Should retransformation function be applied? Default is TRUE.
- **counts_weighted**: Should counts be weighted by the case weights? If TRUE, the sum of `w` is returned by group.
- **v_labels**: If FALSE, return group centers of `v` instead of labels. Only relevant if `v` is numeric with many distinct values. In that case useful if e.g. different flashlights use different data sets.
- **pred**: Optional vector with predictions (after application of inverse link). Can be used to avoid recalculation of predictions over and over if the functions is to be repeatedly called for different `v` and predictions are computationally expensive to make. Not implemented for multiflashlight.
- **pd_indices**: A vector of row numbers to consider in calculating partial dependence and ALE profiles. Useful to force all flashlights to use the same basis for calculations of partial dependence and ALE.
**pd_n_max**

Maximum number of ICE profiles to consider for partial dependence and ALE calculation (will be randomly picked from data).

**pd_seed**

An integer random seed used to sample ICE profiles for partial dependence and ALE.

**ale_two_sided**

If TRUE, v is continuous and breaks are passed or being calculated, then two-sided derivatives are calculated for ALE instead of left derivatives. This aligns the results better with the x labels. More specifically: Usually, local effects at value x are calculated using points between x-e and x. Set ale_two_sided = TRUE to use points between x-e/2 and x+e/2.

**Details**

Note that ALE profiles are being calibrated by (weighted) average predictions. The resulting level might be quite different from the one of the partial dependence profiles.

**Value**

An object of class `light_effects` with the following elements.

- **response** A tibble containing the response profiles. Column names can be controlled by options(flashlight.column_name).
- **predicted** A tibble containing the prediction profiles.
- **pd** A tibble containing the partial dependence profiles.
- **ale** A tibble containing the ALE profiles.
- **by** Same as input by.
- **v** The variable(s) evaluated.
- **stats** Same as input stats.

**Methods (by class)**

- **default**: Default method.
- **flashlight**: Profiles for a flashlight object.
- **multiflashlight**: Effect profiles for a multiflashlight object.

**See Also**

`light_profile`, `plot.light_effects`.

**Examples**

```r
fit <- lm(Sepal.Length ~ ., data = iris)
fl <- flashlight(model = fit, label = "iris", data = iris, y = "Sepal.Length")
light_effects(fl, v = "Species")
```
Description

Model predictions are modelled by a single decision tree, serving as an easy to interprete surrogate to the original model. As suggested in Molnar (see reference below), the quality of the surrogate tree can be measured by its R-squared.

Usage

light_global_surrogate(x, ...)

## Default S3 method:
light_global_surrogate(x, ...)

## S3 method for class 'flashlight'
light_global_surrogate(
x,
data = x$data,
by = x$by,
v = NULL,
use_linkinv = TRUE,
n_max = Inf,
seed = NULL,
keep_max_levels = 4,
...
)

## S3 method for class 'multiflashlight'
light_global_surrogate(x, ...)

Arguments

x An object of class flashlight or multiflashlight.
...
Arguments passed to rpart, such as maxdepth.
data An optional data.frame.
by An optional vector of column names used to additionally group the results. For each group, a separate tree is grown.
v Vector of variables used in the surrogate model. Defaults to all variables in data except "by", "w" and "y".
use_linkinv Should retransformation function be applied? Default is TRUE.
n_max Maximum number of data rows to consider to build the tree.
An integer random seed used to select data rows if n_max is lower than the number of data rows.

Number of levels of categorical and factor variables to keep. Other levels are combined to a level "Other". This prevents rpart to take too long to split non-numeric variables with many levels.

The size of the tree can be modified by passing ... arguments to rpart.

An object of class light_global_surrogate with the following elements.

- data A tibble with results. Can be used to build fully customized visualizations. Column names can be controlled by options(flashlight.column_name).
- by Same as input by.

Default method not implemented yet.

Surrogate model for a flashlight.

Surrogate model for a multiflashlight.


plot.light_global_surrogate.

fit <- lm(Sepal.Length ~ ., data = iris)
x <- flashlight(model = fit, label = "lm", data = iris)
light_global_surrogate(x)
Description

Generates Individual Conditional Expectation (ICE) profiles. An ICE profile shows how the prediction of an observation changes if one or multiple variables are systematically changed across its ranges, holding all other values fixed (see the reference below for details). The curves can be centered in order to increase visibility of interaction effects.

Usage

light_ice(x, ...)

## Default S3 method:
light_ice(x, ...)

## S3 method for class 'flashlight'
light_ice(
  x,
  v = NULL,
  data = x$data,
  by = x$by,
  evaluate_at = NULL,
  breaks = NULL,
  grid = NULL,
  n_bins = 27,
  cut_type = c("equal", "quantile"),
  indices = NULL,
  n_max = 20,
  seed = NULL,
  use_linkinv = TRUE,
  center = c("no", "first", "middle", "last", "mean", "0"),
  ...
)

## S3 method for class 'multiflashlight'
light_ice(x, ...)

Arguments

x An object of class flashlight or multiflashlight.
...
Further arguments passed to or from other methods.
v The variable name to be profiled.
data An optional data.frame.
by An optional vector of column names used to additionally group the results.
evaluate_at: Vector with values of v used to evaluate the profile.
breaks: Cut breaks for a numeric v. Used to overwrite automatic binning via n_bins and cut_type. Ignored if v is not numeric or if grid or evaluate_at are specified.
grid: A data.frame with evaluation grid. Can e.g. be generated by expand.grid.
n_bins: Approximate number of unique values to evaluate for numeric v. Ignored if v is not numeric or if breaks, grid or evaluate_at are specified.
cut_type: Should a numeric v be cut into "equal" or "quantile" bins? Ignored if v is not numeric or if breaks, grid or evaluate_at are specified.
indices: A vector of row numbers to consider.
n_max: If indices is not given, maximum number of rows to consider. Will be randomly picked from data if necessary.
seed: An integer random seed.
use_linkinv: Should retransformation function be applied? Default is TRUE.
center: How should curves be centered? Default is "no". Choose "first", "middle", or "last" to 0-center at specific evaluation points. Choose "mean" to center all profiles at the within-group means. Choose "0" to mean-center curves at 0.

Details

There are two ways to specify the variable(s) to be profiled. The first option is to pass the variable name via v and an optional vector with evaluation points evaluate_at (or breaks). This works for dependence on a single variable. The second option is much more general: You can specify any grid as a data.frame with one or more columns. It can e.g. be generated by a call to expand.grid. The minimum required elements in the (multi-)flashlight are "predict_function", "model", "linkinv" and "data", where the latest can be passed on the fly. Which rows in data are profiled? This is specified by indices. If not given and n_max is smaller than the number of rows in data, then row indices will be sampled randomly from data. If the same rows should be used for all flashlights in a multiflashlight, there are two options: Either pass a seed (with potentially undesired consequences for subsequent code) or a vector of indices used to select rows. In both cases, data should be the same for all flashlights considered.

Value

An object of class light_ice with the following elements.
- data: A tibble containing the results. Can be used to build fully customized visualizations. Column names can be controlled by options(flashlight.column_name).
- by: Same as input by.
- v: The variable(s) evaluated.
- center: How centering was done.

Methods (by class)

- default: Default method not implemented yet.
- flashlight: ICE profiles for a flashlight object.
- multiflashlight: ICE profiles for a multiflashlight object.
References


See Also

light_profile, plot.light_ice.

Examples

```r
fit <- lm(Sepal.Length ~ ., data = iris)
f1 <- flashlight(model = fit, label = "lm", data = iris)
light_ice(f1, v = "Species")
```

<table>
<thead>
<tr>
<th>light_importance</th>
<th>Variable Importance</th>
</tr>
</thead>
</table>

Description

Two algorithms to calculate variable importance are available: (a) Permutation importance and (b) SHAP importance. Algorithm (a) measures importance of variable v as the drop in performance by permuting the values of v, see Fisher et al. 2018 (reference below). Algorithm (b) measures variable importance by averaging absolute SHAP values.

Usage

```r
light_importance(x, ...)
```

## Default S3 method:

```
light_importance(x, ...)
```

## S3 method for class 'flashlight'

```
light_importance(
x,
data = x$data,
by = x$by,
type = c("permutation", "shap"),
v = NULL,
n_max = Inf,
seed = NULL,
m_repetitions = 1,
metric = x$metrics[1],
lower_is_better = TRUE,
use_linkinv = FALSE,
...)
```
light_importance

## S3 method for class 'multiflashlight'
light_importance(x, ...)

### Arguments

- **x**
  An object of class flashlight or multiflashlight.

- **...**
  Further arguments passed to `light_performance`. Not used for `type = "shap"`.

- **data**
  An optional data frame. Not used for `type = "shap"`.

- **by**
  An optional vector of column names used to additionally group the results.

- **type**
  Type of importance: "permutation" (default) or "shap". "shap" is only available if a "shap" object is contained in `x`.

- **v**
  Vector of variable names to assess importance for. Defaults to all variables in `data` except "by" and "y".

- **n_max**
  Maximum number of rows to consider. Not used for `type = "shap"`.

- **seed**
  An integer random seed used to select and shuffle rows. Not used for `type = "shap"`.

- **m_repetitions**
  Number of permutations. Defaults to 1. A value above 1 provides more stable estimates of variable importance and allows the calculation of standard errors measuring the uncertainty from permuting. Not used for `type = "shap"`.

- **metric**
  An optional named list of length one with a metric as element. Defaults to the first metric in the flashlight. The metric needs to be a function with at least four arguments: actual, predicted, case weights `w` and 

- **lower_is_better**
  Logical flag indicating if lower values in the metric are better or not. If set to `FALSE`, the increase in metric is multiplied by -1. Not used for `type = "shap"`.

- **use_linkinv**
  Should retransformation function be applied? Default is `FALSE`. Not uses for `type = "shap"`.

### Details

For algorithm (a), the minimum required elements in the (multi-) flashlight are "y", "predict_function", "model", "data" and "metrics". For algorithm (b), the only required element is "shap". Call `add_shap` once to add such object. Note: The values of the permutation algorithm (a) are on the scale of the selected metric. For shap algorithm (b), the values are on the scale of absolute values of the predictions.

### Value

An object of class `light_importance` with the following elements.

- **data**
  A tibble with results. Can be used to build fully customized visualizations. Column names can be controlled by `options(flashlight.column_name)`.

- **by**
  Same as input `by`.

- **type**
  Same as input `type`. For information only.
Methods (by class)

- default: Default method not implemented yet.
- flashlight: Variable importance for a flashlight.
- multiflashlight: Variable importance for a multiflashlight.

References

Fisher A., Rudin C., Dominici F. (2018). All Models are Wrong but many are Useful: Variable Importance for Black-Box, Proprietary, or Misspecified Prediction Models, using Model Class Reliability. Arxiv.

See Also

most_important, plot.light_importance.

Examples

```r
fit <- lm(Sepal.Length ~ Petal.Length, data = iris)
fl <- flashlight(model = fit, label = "full", data = iris, y = "Sepal.Length")
light_importance(fl)
```

<table>
<thead>
<tr>
<th>light_interaction</th>
<th>Interaction Strength</th>
</tr>
</thead>
</table>

Description

This function provides Friedman’s H statistic for overall interaction strength per covariable as well as its version for pairwise interactions, see the reference below. As a fast alternative to assess overall interaction strength, with `type = "ice"`, the function offers a method based on centered ICE curves: The corresponding H* statistic measures how much of the variability of a c-ICE curve is unexplained by the main effect. As for Friedman’s H statistic, it can be useful to consider unnormalized or squared values (see Details below).

Usage

```r
light_interaction(x, ...)
```

## Default S3 method:
```
light_interaction(x, ...)
```

## S3 method for class 'flashlight'
```
light_interaction(x,
    data = x$data,
    by = x$by,
    v = NULL,
    pairwise = FALSE,
)```
light_interaction

```r
  type = c("H", "ice"),
  normalize = TRUE,
  take_sqrt = TRUE,
  grid_size = 200,
  n_max = 1000,
  seed = NULL,
  use_linkinv = FALSE,
  ...
)

## S3 method for class 'multiflashlight'
light_interaction(x, ...)
```

### Arguments

- **x**: An object of class `flashlight` or `multiflashlight`.
- **...**: Further arguments passed to or from other methods.
- **data**: An optional `data.frame`.
- **by**: An optional vector of column names used to additionally group the results.
- **v**: Vector of variable names to be assessed.
- **pairwise**: Should overall interaction strength per variable be shown or pairwise interactions? Defaults to `FALSE`.
- **type**: Are measures based on Friedman’s H statistic ("H") or on "ice" curves? Option "ice" is available only if pairwise = `FALSE`.
- **normalize**: Should the variances explained be normalized? Default is `TRUE` in order to reproduce Friedman’s H statistic.
- **take_sqrt**: In order to reproduce Friedman’s H statistic, resulting values are root transformed. Set to `FALSE` if squared values should be returned.
- **grid_size**: Grid size used to form the outer product. Will be randomly picked from data (after limiting to n_max).
- **n_max**: Maximum number of data rows to consider. Will be randomly picked from data if necessary.
- **seed**: An integer random seed used for subsampling.
- **use_linkinv**: Should retransformation function be applied? Default is `FALSE`.

### Details

Friedman’s H statistic relates the interaction strength of a variable (pair) to the total effect strength of that variable (pair) based on partial dependence curves. Due to this normalization step, even variables with low importance can have high values for H. The function `light_interaction` offers the option to skip normalization in order to have a more direct comparison of the interaction effects across variable (pairs). The values of such unnormalized H statistics are on the scale of the response variable. Use `take_sqrt = FALSE` to return squared values of H. Note that in general, for each variable (pair), predictions are done on a data set with grid_size * n_max, so be cautious with increasing the defaults too much. Still, even with larger grid_size and n_max, there might be...
considerable variation across different runs, thus setting a seed might be required for reproducibility. The minimum required elements in the (multi-) flashlight are a "predict_function", "model", and "data".

Value

An object of class light_importance with the following elements.

- data A tibble containing the results. Can be used to build fully customized visualizations. Column names can be controlled by options(flashlight.column_name).
- by Same as input by.
- type Same as input type. For information only.

Methods (by class)

- default: Default method not implemented yet.
- flashlight: Interaction strengths for a flashlight object.
- multiflashlight: for a multiflashlight object.

References


See Also

light_ice.

Examples

```r
fit_additive <- lm(Sepal.Length ~ Petal.Length + Petal.Width + Species, data = iris)
fitted_nonadditive <- lm(Sepal.Length ~ Petal.Length * Petal.Width + Species, data = iris)
fl_additive <- flashlight(model = fit_additive, label = "additive")
fl_nonadditive <- flashlight(model = fit_nonadditive, label = "nonadditive")
fls <- multiflashlight(list(fl_additive, fl_nonadditive), data = iris)
plot(st <- light_interaction(fls), fill = "darkgreen")
plot(light_interaction(fls, pairwise = TRUE), fill = "darkgreen")
```

Model Performance of Flashlight

Calculates performance of a flashlight with respect to one or more performance measure.
Usage

light_performance(x, ...)

## Default S3 method:
light_performance(x, ...)

## S3 method for class 'flashlight'
light_performance(
x,
data = x$data,
by = x$by,
metrics = x$metrics,
use_linkinv = FALSE,
...  
)

## S3 method for class 'multiflashlight'
light_performance(x, ...)

Arguments

x  An object of class flashlight or multiflashlight.

...  Arguments passed from or to other functions.

data  An optional data.frame.

by  An optional vector of column names used to additionally group the results. Will overwrite x$by.

metrics  An optional named list with metrics. Each metric takes at least four arguments: actual, predicted, case weights w and ....

use_linkinv  Should retransformation function be applied? Default is FALSE.

Details

The minimal required elements in the (multi-) flashlight are "y", "predict_function", "model", "data" and "metrics". The latter two can also directly be passed to light_performance. Note that by default, no retransformation function is applied.

Value

An object of class light_performance with the following elements.

- data  A tibble containing the results. Can be used to build fully customized visualizations. Column names can be controlled by options(flashlight.column_name).

- by  Same as input by.
Methods (by class)

- default: Default method not implemented yet.
- flashlight: Model performance of flashlight object.
- multiflashlight: Model performance of multiflashlight object.

See Also

plot.light_performance.

Examples

```r
fit <- lm(Sepal.Length ~ ., data = iris)
fl <- flashlight(model = fit, label = "lm", data = iris, y = "Sepal.Length")
light_performance(fl)
light_performance(fl, by = "Species")
```

Description

Calculates different types of profiles across covariable values. By default, partial dependence profiles are calculated (see Friedman). Other options are profiles of ALE (accumulated local effects, see Apley), response, predicted values ("M plots" or "marginal plots", see Apley), residuals, and shap. The results are aggregated either by (weighted) means or by (weighted) quartiles. Note that ALE profiles are calibrated by (weighted) average predictions. In contrast to the suggestions in Apley, we calculate ALE profiles of factors in the same order as the factor levels. They are not being reordered based on similarity of other variables.

Usage

```r
light_profile(x, ...)
```

## Default S3 method:
```
light_profile(x, ...)
```

## S3 method for class 'flashlight'
```
light_profile(
  x,
  v = NULL,
  data = NULL,
  by = x$by,
  type = c("partial dependence", "ale", "predicted", "response", "residual", "shap"),
  stats = c("mean", "quartiles"),
  breaks = NULL,
  n_bins = 11,
)```
light_profile

cut_type = c("equal", "quantile"),
use_linkinv = TRUE,
counts = TRUE,
counts_weighted = FALSE,
v_labels = TRUE,
pred = NULL,
pd_evaluate_at = NULL,
pd_grid = NULL,
pd_indices = NULL,
pd_n_max = 1000,
pd_seed = NULL,
pd_center = c("no", "first", "middle", "last", "mean", "0"),
ale_two_sided = FALSE,
...)

## S3 method for class 'multiflashlight'
light_profile(
x,
v = NULL,
data = NULL,
type = c("partial dependence", "ale", "predicted", "response", "residual", "shap"),
breaks = NULL,
n_bins = 11,
cut_type = c("equal", "quantile"),
pd_evaluate_at = NULL,
pd_grid = NULL,
...)

Arguments

x An object of class flashlight or multiflashlight.
...
Further arguments passed to cut3 resp. formatC in forming the cut breaks of the v variable. Not relevant for partial dependence and ALE profiles.
v The variable name to be profiled.
data An optional data.frame. Not used for type = "shap".
by An optional vector of column names used to additionally group the results.
type Type of the profile: Either "partial dependence", "ale", "predicted", "response", "residual", or "shap".
stats Statistic to calculate: "mean" or "quartiles". For ALE profiles, only "mean" makes sense.
breaks Cut breaks for a numeric v. Used to overwrite automatic binning via n_bins and cut_type. Ignored if v is not numeric.
n_bins Approximate number of unique values to evaluate for numeric v. Ignored if v is not numeric or if breaks is specified.
**light_profile**

**cut_type**  Should a numeric \( v \) be cut into "equal" or "quantile" bins? Ignored if \( v \) is not numeric or if \( \text{breaks} \) is specified.

**use_linkinv**  Should retransformation function be applied? Default is TRUE. Not used for type "shap".

**counts**  Should observation counts be added?

**counts_weighted**  If counts is TRUE: Should counts be weighted by the case weights? If TRUE, the sum of \( w \) is returned by group.

**v_labels**  If FALSE, return group centers of \( v \) instead of labels. Only relevant for types "response", "predicted" or "residual" and if \( v \) is being binned. In that case useful if e.g. different flashlight use different data sets and bin labels would not match.

**pred**  Optional vector with predictions (after application of inverse link). Can be used to avoid recalculation of predictions over and over if the functions is to be repeatedly called for different \( v \) and predictions are computationally expensive to make. Only relevant for type = "predicted" and type = "ale". Not implemented for multiflashlight.

**pd_evaluate_at**  Vector with values of \( v \) used to evaluate the profile. Only relevant for type = "partial dependence" and "ale".

**pd_grid**  A data.frame with grid values, e.g. generated by expand.grid. Only used for type = "partial dependence".

**pd_indices**  A vector of row numbers to consider in calculating partial dependence profiles. Only used for type = "partial dependence" and "ale".

**pd_n_max**  Maximum number of ICE profiles to calculate (will be randomly picked from \( \text{data} \)). Only used for type = "partial dependence" and "ale".

**pd_seed**  Integer random seed used to select ICE profiles. Only used for type = "partial dependence".

**pd_center**  How should ICE curves be centered? Default is "no". Choose "first", "middle", or "last" to 0-center at specific evaluation points. Choose "mean" to center all profiles at the within-group means. Choose "0" to mean-center curves at 0. Only relevant for partial dependence.

**ale_two_sided**  If TRUE, \( v \) is continuous and \( \text{breaks} \) are passed or being calculated, then two-sided derivatives are calculated for ALE instead of left derivatives. More specifically: Usually, local effects at value \( x \) are calculated using points between \( x-e \) and \( x \). Set \( \text{ale_two_sided} = \text{TRUE} \) to use points between \( x-e/2 \) and \( x+e/2 \).

**Details**

Numeric covariables \( v \) with more than \( n\_bins \) disjoint values are binned into \( n\_bins \) bins. Alternatively, \( \text{breaks} \) can be provided to specify the binning. For partial dependence profiles (and partly also ALE profiles), this behaviour can be overwritten either by providing a vector of evaluation points (\( \text{pd_evaluate_at} \)) or an evaluation \( \text{pd_grid} \). By the latter we mean a data frame with column name(s) with a (multi-)variate evaluation grid. For partial dependence, ALE, and prediction profiles, "model", "predict_function", linkinv" and "data" are required. For response profiles its "y", "linkinv" and "data" and for shap profiles it is just "shap". "data" can be passed on the fly.
An object of class `light_profile` with the following elements.

- **data**: A tibble containing results. Can be used to build fully customized visualizations. Column names can be controlled by `options(flashlight.column_name)`.
- **by**: Names of group by variable.
- **v**: The variable(s) evaluated.
- **type**: Same as input type. For information only.
- **stats**: Same as input stats.

### Methods (by class)

- **default**: Default method not implemented yet.
- **flashlight**: Profiles for flashlight.
- **multiflashlight**: Profiles for multiflashlight.

### References


### See Also

- `light_effects`
- `plot.light_profile`

### Examples

```r
fit <- lm(Sepal.Length ~ ., data = iris)
fl <- flashlight(model = fit, label = "iris", data = iris, y = "Sepal.Length")
light_profile(fl, v = "Species")
light_profile(fl, v = "Petal.Width", type = "residual")
```

### Description

Calculates different types of 2D-profiles across two variables. By default, partial dependence profiles are calculated (see Friedman). Other options are response, predicted values, residuals, and shap. The results are aggregated by (weighted) means.
Usage

light_profile2d(x, ...)

## Default S3 method:
light_profile2d(x, ...)

## S3 method for class 'flashlight'
light_profile2d(
    x,
    v = NULL,
    data = NULL,
    by = x$by,
    type = c("partial dependence", "predicted", "response", "residual", "shap"),
    breaks = NULL,
    n_bins = 11,
    cut_type = "equal",
    use_linkinv = TRUE,
    counts = TRUE,
    counts_weighted = FALSE,
    pd_evaluate_at = NULL,
    pd_grid = NULL,
    pd_indices = NULL,
    pd_n_max = 1000,
    pd_seed = NULL,
    ...
)

## S3 method for class 'multiflashlight'
light_profile2d(
    x,
    v = NULL,
    data = NULL,
    type = c("partial dependence", "predicted", "response", "residual", "shap"),
    breaks = NULL,
    n_bins = 11,
    cut_type = "equal",
    pd_evaluate_at = NULL,
    pd_grid = NULL,
    ...
)

Arguments

x An object of class flashlight or multiflashlight.

... Further arguments passed to cut3 resp. formatC in forming the cut breaks of the v variables. Not relevant for partial dependence profiles.

v A vector of exactly two variable names to be profiled.
data  An optional data.frame. Not used for type = "shap".
by   An optional vector of column names used to additionally group the results.
type Type of the profile: Either "partial dependence", "predicted", "response", "residual", or "shap".
b breaks Named list of cut breaks specifying how to bin one or more numeric variables. Used to overwrite automatic binning via n_bins and cut_type. Ignored for non-numeric v.
n_bins Approximate number of unique values to evaluate for numeric v. Can be an unnamed vector of length 2 to distinguish between v.
cut_type Should numeric v be cut into "equal" or "quantile" bins? Can be an unnamed vector of length 2 to distinguish between v.
use_linkinv Should retransformation function be applied? Default is TRUE. Not used for type "shap".
counts Should observation counts be added? counts_weighted If counts is TRUE: Should counts be weighted by the case weights? If TRUE, the sum of w is returned by group.
pd_evaluate_at An named list of evaluation points for one or more variables. Only relevant for type = "partial dependence".
pd_grid An evaluation data.frame with exactly two columns, e.g. generated by expand.grid. Only used for type = "partial dependence". Offers ultimate flexibility.
pd_indices A vector of row numbers to consider in calculating partial dependence profiles. Only used for type = "partial dependence".
pd_n_max Maximum number of ICE profiles to calculate (will be randomly picked from data). Only used for type = "partial dependence".
pd_seed Integer random seed used to select ICE profiles. Only used for type = "partial dependence".

Details

Different binning options are available, see arguments below. For high resolution partial dependence plots, it might be necessary to specify breaks, pd_evaluate_at or pd_grid in order to avoid empty parts in the plot. A high value of n_bins might not have the desired effect as it internally capped at the number of distinct values of a variable.

For partial dependence and prediction profiles, "model", "predict_function", linkinv" and "data" are required. For response profiles it is "y", "linkinv" and "data" and for shap profiles it is just "shap". "data" can be passed on the fly.

Value

An object of class light_profile2d with the following elements.

  • data A tibble containing results. Can be used to build fully customized visualizations. Column names can be controlled by options(flashlight.column_name).
  • by Names of group by variables.
  • v The two variable names evaluated.
  • type Same as input type. For information only.
Methods (by class)

- default: Default method not implemented yet.
- flashlight: 2D profiles for flashlight.
- multiflashlight: 2D profiles for multiflashlight.

References


See Also

light_profile, plot.light_profile2d.

Examples

```r
fit <- lm(Sepal.Length ~ ., data = iris)
fl <- flashlight(model = fit, label = "iris", data = iris, y = "Sepal.Length")
light_profile2d(fl, v = c("Petal.Length", "Species"))
```

Description

Recodes factor levels of columns in data slots of an object of class light.

Usage

```r
light_recode(x, ...)
```

## Default S3 method:
```r
light_recode(x, ...)
```

## S3 method for class 'light'
```r
light_recode(x, what, levels, labels, ...)
```

Arguments

- `x`: An object of class light.
- `...`: Further arguments passed to `factor`.
- `what`: Column identifier to be recoded, e.g. "type". For backward compatibility, also the option identifier (e.g. "type_name") can be passed.
- `levels`: Current levels/values of `type_name` column (in desired order).
- `labels`: New levels of `type_name` column in same order as `levels`. 
Value

x with new factor levels of type_name column.

Methods (by class)

- default: Default method not implemented yet.
- light: Recoding factors in data slots of light object.

See Also

plot.light_effects.

Examples

```r
fit_full <- lm(Sepal.Length ~ ., data = iris)
fit_part <- lm(Sepal.Length ~ Petal.Length, data = iris)
mod_full <- flashlight(model = fit_full, label = "full", data = iris, y = "Sepal.Length")
mod_part <- flashlight(model = fit_part, label = "part", data = iris, y = "Sepal.Length")
mods <- multiflashlight(list(mod_full, mod_part))
eff <- light_effects(mods, v = "Species")
eff <- light_recode(eff, what = "type_name",
                   levels = c("response", "predicted", "partial dependence", "ale"),
                   labels = c("Observed", "Fitted", "PD", "ALE"))
plot(eff, use = "all")
```

Description

This function prepares values for drawing a scatter plot of predicted values, responses, residuals, or SHAP values against a selected variable.

Usage

```r
light_scatter(x, ...)
```

```r
## Default S3 method:
light_scatter(x, ...)
```

```r
## S3 method for class 'flashlight'
light_scatter(
  x,
  v,
  data = x$data,
  by = x$by,
  type = c("predicted", "response", "residual", "shap"),
  use_linkinv = TRUE,
```
light_scatter

```r
n_max = 400,
seed = NULL,
...
)
```

```r
## S3 method for class 'multiflashlight'
light_scatter(x, ...)
```

**Arguments**

- `x` An object of class `flashlight` or `multiflashlight`.
- `...` Further arguments passed from or to other methods.
- `v` The variable name to be shown on the x-axis.
- `data` An optional `data.frame`. Not relevant for `type = "shap"`.
- `by` An optional vector of column names used to additionally group the results.
- `type` Type of the profile: Either "predicted", "response", "residual", or "shap".
- `use_linkinv` Should retransformation function be applied? Default is TRUE. Not used for `type = "shap"`.
- `n_max` Maximum number of data rows to select. Will be randomly picked from the relevant data.
- `seed` An integer random seed used for subsampling.

**Value**

An object of class `light_scatter` with the following elements.

- `data` A tibble with results. Can be used to build fully customized visualizations. Column names can be controlled by `options(flashlight.column_name)`.
- `by` Same as input `by`.
- `v` The variable evaluated.
- `type` Same as input `type`. For information only.

**Methods (by class)**

- `default`: Default method not implemented yet.
- `flashlight`: Variable profile for a flashlight.
- `multiflashlight`: `light_scatter` for a multiflashlight.

**See Also**

`plot.light_scatter`. 

---

n_max = 400,
seed = NULL,
... 

```r
## S3 method for class 'multiflashlight'
light_scatter(x, ...)
```

**Arguments**

- `x` An object of class `flashlight` or `multiflashlight`.
- `...` Further arguments passed from or to other methods.
- `v` The variable name to be shown on the x-axis.
- `data` An optional `data.frame`. Not relevant for `type = "shap"`.
- `by` An optional vector of column names used to additionally group the results.
- `type` Type of the profile: Either "predicted", "response", "residual", or "shap".
- `use_linkinv` Should retransformation function be applied? Default is TRUE. Not used for `type = "shap"`.
- `n_max` Maximum number of data rows to select. Will be randomly picked from the relevant data.
- `seed` An integer random seed used for subsampling.

**Value**

An object of class `light_scatter` with the following elements.

- `data` A tibble with results. Can be used to build fully customized visualizations. Column names can be controlled by `options(flashlight.column_name)`.
- `by` Same as input `by`.
- `v` The variable evaluated.
- `type` Same as input `type`. For information only.

**Methods (by class)**

- `default`: Default method not implemented yet.
- `flashlight`: Variable profile for a flashlight.
- `multiflashlight`: `light_scatter` for a multiflashlight.

**See Also**

`plot.light_scatter`. 

**Examples**

```r
fit_a <- lm(Sepal.Length ~ . - Petal.Length, data = iris)
fit_b <- lm(Sepal.Length ~ ., data = iris)
fl_a <- flashlight(model = fit_a, label = "without Petal.Length")
fl_b <- flashlight(model = fit_b, label = "all")
fls <- multiflashlight(list(fl_a, fl_b), data = iris, y = "Sepal.Length")
pr <- light_scatter(fls, v = "Petal.Length")
plot(light_scatter(fls, "Petal.Length", by = "Species", type = "residual"), alpha = 0.2)
```

---

**Description**

Returns the most important variable names sorted descendingly.

**Usage**

```r
most_important(x, top_m = Inf)
```

```r
# Default S3 method:
most_important(x, top_m = Inf)

# S3 method for class 'light_importance'
most_important(x, top_m = Inf)
```

**Arguments**

- `x` An object of class `light_importance`.
- `top_m` Maximum number of important variables to be returned. Defaults to `Inf`, i.e. return all variables in descending order of importance.

**Value**

A character vector of variable names sorted in descending order by importance.

**Methods (by class)**

- `default`: Default method not implemented yet.
- `light_importance`: Extracts most important variables from an object of class `light_importance`.

**See Also**

`light_importance`.
Examples

```r
fit <- lm(Sepal.Length ~ ., data = iris)
fl <- flashlight(model = fit, label = "ols", data = iris, y = "Sepal.Length")
(imp <- light_importance(fl, seed = 4))
most_important(imp)
most_important(imp, 2)
```

---

multiflashlight

Create or Update a multiflashlight

Description

Combines a list of flashlights to an object of class multiflashlight and/or updates a multiflashlight.

Usage

```r
multiflashlight(x, ...)
```

## Default S3 method:
```r
multiflashlight(x, ...)
```

## S3 method for class 'flashlight'
```r
multiflashlight(x, ...)
```

## S3 method for class 'list'
```r
multiflashlight(x, ...)
```

## S3 method for class 'multiflashlight'
```r
multiflashlight(x, ...)
```

Arguments

- `x` An object of class multiflashlight, flashlight or a list of flashlights.
- `...` Optional arguments in the flashlights to update, see examples.

Value

An object of class multiflashlight. This is a named list of flashlight objects.

Methods (by class)

- default: Used to create a flashlight object. No x has to be passed in this case.
- flashlight: Updates an existing flashlight object and turns into a multiflashlight.
- list: Creates (and updates) a multiflashlight from a list of flashlights.
- multiflashlight: Updates an object of class multiflashlight.
plot.light_breakdown

See Also

flashlight.

Examples

```r
fit_lm <- lm(Sepal.Length ~ ., data = iris)
fit_glm <- glm(Sepal.Length ~ ., family = Gamma(link = log), data = iris)
mod_lm <- flashlight(model = fit_lm, label = "lm")
mod_glm <- flashlight(model = fit_glm, label = "glm")
(mods <- multiflashlight(list(mod_lm, mod_glm)))
```

Description

Minimal visualization of an object of class `light_breakdown` as waterfall plot. The object returned
is of class `ggplot` and can be further customized.

Usage

```r
## S3 method for class 'light_breakdown'
plot(x, facet_scales = "free", facet_ncol = 1, rotate_x = FALSE, ...)
```

Arguments

- `x` An object of class `light_breakdown`.
- `facet_scales` Scales argument passed to `facet_wrap`.
- `facet_ncol` ncol argument passed to `facet_wrap`.
- `rotate_x` Should x axis labels be rotated by 45 degrees? Default is FALSE.
- `...` Further arguments passed to `geom_label`.

Details

The waterfall plot is to be read from top to bottom. The first line describes the (weighted) average
prediction in the query data used to start with. Then, each additional line shows how the prediction
changes due to the impact of the corresponding variable. The last line finally shows the original
prediction of the selected observation. Multiple flashlights are shown in different facets. Positive
and negative impacts are visualized with different colors.

Value

An object of class `ggplot2`.

See Also

`light_importance`. 
Examples

```r
fit <- lm(Sepal.Length ~ . + Petal.Length:Species, data = iris)
fl <- flashlight(model = fit, label = "lm", data = iris, y = "Sepal.Length")
plot(light_breakdown(fl, new_obs = iris[1, ]))
```

---

**plot.light_effects**  
*Visualize Multiple Types of Profiles Together*

**Description**

Visualizes response-, prediction-, partial dependence, and/or ALE profiles of a (multi-)flashlight with respect to a covariable \( v \). Different flashlights or a single flashlight with one "by" variable are separated by a facet wrap.

**Usage**

```r
## S3 method for class 'light_effects'
plot(
x,  
use = c("response", "predicted", "pd"),
zero_counts = TRUE,
size_factor = 1,
facet_scales = "free_x",
facet_nrow = 1L,
rotate_x = TRUE,
show_points = TRUE,
...
)
```

**Arguments**

- **x**  
  An object of class `light_effects`.
- **use**  
  A vector of elements to show. Any subset of ("response", "predicted", "pd", "ale") or "all". Defaults to all except "ale"
- **zero_counts**  
  Logical flag if 0 count levels should be shown on the x axis.
- **size_factor**  
  Factor used to enlarge default size in `geom_point` and `geom_line`.
- **facet_scales**  
  Scales argument passed to `facet_wrap`.
- **facet_nrow**  
  Number of rows in `facet_wrap`. Must be 1 if `plot_counts` should be used.
- **rotate_x**  
  Should x axis labels be rotated by 45 degrees?
- **show_points**  
  Should points be added to the line (default is TRUE).
- **...**  
  Further arguments passed to geoms.

**Value**

An object of class `ggplot2`. 
See Also  

*light_effects, plot_counts*.  

Examples  

```r  
fit <- lm(Sepal.Length ~ ., data = iris)  
fl <- flashlight(model = fit, label = "iris", data = iris, y = "Sepal.Length")  
plot(light_effects(fl, v = "Species"))  
```

---

**plot.light_global_surrogate**  

*Plot Global Surrogate Trees*  

**Description**  

Using rpart.plot, trees fitted by light_global_surrogate are visualized.  

**Usage**  

```r  
## S3 method for class 'light_global_surrogate'  
plot(x, type = 5, auto_main = TRUE, mfrow = NULL, ...)  
```

**Arguments**  

- `x`  
  An object of class `light_global_surrogate`.  
- `type`  
  Plot type, see help of `rpart.plot`. Default is 5.  
- `auto_main`  
  Automatic plot titles (only if multiple trees are shown in the same figure).  
- `mfrow`  
  If multiple trees are shown in the same figure: what value of `mfrow` to use in `par`?  
- `...`  
  Further arguments passed to `rpart.plot`.  

**Value**  

An object of class ggplot2.  

**See Also**  

*light_global_surrogate*.  

**Examples**  

```r  
fit <- lm(Sepal.Length ~ ., data = iris)  
x <- flashlight(model = fit, label = "lm", data = iris)  
plot(light_global_surrogate(x))  
```
Description

Minimal visualization of an object of class `light_ice` as `geom_line`. The object returned is of class `ggplot` and can be further customized.

Usage

```r
## S3 method for class 'light_ice'
plot(x, facet_scales = "fixed", rotate_x = FALSE, ...)
```

Arguments

- `x` An object of class `light_ice`.
- `facet_scales` Scales argument passed to `facet_wrap`.
- `rotate_x` Should x axis labels be rotated by 45 degrees? Default is FALSE.
- `...` Further arguments passed to `geom_line`.

Details

Each observation is visualized by a line. The first "by" variable is represented by the color, a second "by" variable or a `multiflashlight` by facets.

Value

An object of class `ggplot2`.

See Also

`light_ice`.

Examples

```r
fit_full <- lm(Sepal.Length ~ ., data = iris)
fit_part <- lm(Sepal.Length ~ Petal.Length, data = iris)
mod_full <- flashlight(model = fit_full, label = "full", data = iris)
mod_part <- flashlight(model = fit_part, label = "part", data = iris)
mods <- multiflashlight(list(mod_full, mod_part))
plot(light_ice(mod_full, v = "Species"), alpha = 0.2)
indices <- (1:15) * 10
plot(light_ice(mods, v = "Species", indices = indices))
plot(light_ice(mods, v = "Species", indices = indices, center = "first"))
plot(light_ice(mods, v = "Petal.Width", by = "Species", n_bins = 5, indices = indices))
```
plot.light_importance  Visualize Variable Importance

Description

Minimal visualization of an object of class light_importance as geom_bar. If available, standard errors are added as geom_errorbar. The object returned is of class ggplot and can be further customized.

Usage

```r
## S3 method for class 'light_importance'
plot(
x,  
top_m = Inf,
swap_dim = FALSE,
facet_scales = "fixed",
rotate_x = FALSE,
error_bars = TRUE,
...
)
```

Arguments

- `x`  
  An object of class light_importance.
- `top_m`  
  Maximum number of important variables to be returned.
- `swap_dim`  
  If multiflashlight and one "by" variable or single flashlight with two "by" variables, swap the role of dodge/fill variable and facet variable. If multiflashlight or one "by" variable, use facets instead of colors.
- `facet_scales`  
  Scales argument passed to facet_wrap.
- `rotate_x`  
  Should x axis labels be rotated by 45 degrees? Default is FALSE.
- `error_bars`  
  Should error bars be added? Defaults to TRUE. Only available if light_importance was run with multiple permutations, i.e. by setting m_repetitions > 1.
- `...`  
  Further arguments passed to geom_bar.

Details

The plot is organized as a bar plot with variable names as x-aesthetic. Up to two additional dimensions (multiflashlight and one "by" variable or single flashlight with two "by" variables) can be visualized by facetting and dodge/fill. Set swap_dim = FALSE to revert the role of these two dimensions. One single additional dimension is visualized by a facet wrap, or - if swap_dim = FALSE - by dodge/fill.

Value

An object of class ggplot2.
plot.light_performance

Visualize Model Performance

Description

Minimal visualization of an object of class `light_performance` as `geom_bar`. The object returned has class `ggplot` and can be further customized.

Usage

```r
## S3 method for class 'light_performance'
plot(
  x,
  swap_dim = FALSE,
  geom = c("bar", "point"),
  facet_scales = "free_y",
  rotate_x = FALSE,
  ...
)
```

Arguments

- **x**: An object of class `light_performance`.
- **swap_dim**: Should representation of dimensions (either two "by" variables or one "by" variable and multiflashlight) of x aesthetic and dodge fill aesthetic be swapped? Default is `FALSE`.
- **geom**: Geometry of plot (either "bar" or "point")
- **facet_scales**: Scales argument passed to `facet_wrap`.
- **rotate_x**: Should x axis labels be rotated by 45 degrees? Default is `FALSE`.
- **...**: Further arguments passed to `geom_bar` or `geom_point`.

See Also

- `light_importance`

Examples

```r
fit_full <- lm(Sepal.Length ~ ., data = iris)
fit_part <- lm(Sepal.Length ~ Petal.Length, data = iris)
mod_full <- flashlight(model = fit_full, label = "full", data = iris, y = "Sepal.Length")
mod_part <- flashlight(model = fit_part, label = "part", data = iris, y = "Sepal.Length")
mods <- multiflashlight(list(mod_full, mod_part), by = "Species")
plot(light_importance(mod_part, m_repetitions = 4), fill = "darkred")
plot(light_importance(mods), swap_dim = TRUE)
```
plot.light_profile

Visualize Profiles, e.g. of Partial Dependence

Description

Minimal visualization of an object of class light_profile. The object returned is of class ggplot and can be further customized.

Usage

```r
## S3 method for class 'light_profile'
plot(
  x,
  swap_dim = FALSE,
  facet_scales = "free_x",
  rotate_x = x$type != "partial dependence",
  show_points = TRUE,
  ...
)
```
Arguments

x  An object of class light_profile.
swap_dim  If multiflashlight and one "by" variable or single flashlight with two "by" variables, swap the role of dodge/fill variable and facet variable. If multiflashlight or one "by" variable, use facets instead of colors.
facet_scales  Scales argument passed to facet_wrap.
rotate_x  Should x axis labels be rotated by 45 degrees? TRUE, except for type "partial dependence".
show_points  Should points be added to the line (default is TRUE).
...  Further arguments passed to geom_point and geom_line.

Details

Either lines and points are plotted (if stats = "mean") or quartile boxes. If there is a "by" variable or a multiflashlight, this first dimension is taken care by color (or if swap_dim = TRUE by facets). If there are two "by" variables or a multiflashlight with one "by" variable, the first "by" variable is visualized as color, the second one or the multiflashlight via facet (change with swap_dim).

Value

An object of class ggplot2.

See Also

light_profile, plot.light_effects.

Examples

```r
fit <- lm(Sepal.Length ~ ., data = iris)
fl <- flashlight(model = fit, label = "iris", data = iris, y = "Sepal.Length")
plot(light_profile(fl, v = "Species"))
plot(light_profile(fl, v = "Petal.Width", by = "Species", evaluate_at = 2:4))
plot(light_profile(fl, v = "Petal.Width", type = "predicted"))
```

plot.light_profile2d  Visualize 2D-Profiles, e.g. of Partial Dependence

Description

Minimal visualization of an object of class light_profile2d. The object returned is of class ggplot2 and can be further customized.

Usage

```r
## S3 method for class 'light_profile2d'
plot(x, swap_dim = FALSE, rotate_x = TRUE, numeric_as_factor = FALSE, ...)
```
Arguments

- **x**: An object of class light_profile2d.
- **swap_dim**: Swap the facet_grid dimensions.
- **rotate_x**: Should x axis labels be rotated by 45 degrees? Default is TRUE.
- **numeric_as_factor**: Should numeric x and y values be converted to factors first? Default is FALSE. Useful if cut_type was not set to "equal".

Further arguments passed to geom_tile.

Details

The main geometry is geom_tile. Additional dimensions ("by" variable(s) and/or multiflashlight) are represented by facet_wrap/grid. For all types of profiles except "partial dependence", it is natural to see empty parts in the plot. These are combinations of the v variables that do not appear in the data. Even for type "partial dependence", gaps can occur, e.g. for cut_type = "quantile" or if n_bins are larger than the number of distinct values of a v variable. Such gaps can be suppressed by setting numeric_as_factor = TRUE or by using the arguments breaks, pd_evaluate_at or pd_grid in light_profile2d().

Value

An object of class ggplot2.

See Also

- light_profile2d.

Examples

```r
fit <- lm(Sepal.Length ~ ., data = iris)
fl <- flashlight(model = fit, label = "iris", data = iris, y = "Sepal.Length")
plot(light_profile2d(fl, v = c("Petal.Length", "Species")))
pr <- light_profile2d(fl, v = c("Petal.Length", "Sepal.Width"),
  type = "predicted", by = "Species", n_bins=c(2, 3), sep = ";")
plot(pr)
```

---

**plot.light_scatter  Scatter Plot**

Description

Values are plotted against a variable. The object returned is of class ggplot and can be further customized. To avoid overplotting, pass e.g. alpha = 0.2 or position = "jitter".

Usage

```r
## S3 method for class 'light_scatter'
plot(x, swap_dim = FALSE, facet_scales = "free_x", rotate_x = FALSE, ...)
```
Add Counts to Effects Plot

**Description**

Add counts as labelled bar plot on top of light_effects plot.

**Usage**

```r
plot_counts(p, x, text_size = 3, facet_scales = "free_x", show_labels = TRUE, big.mark = ",", scientific = FALSE, digits = 0, ...)
```
predict.flashlight

Arguments

- **p**: The result of `plot.light_effects`.
- **x**: An object of class `light_effects`.
- **text_size**: Size of count labels.
- **facet_scales**: Scales argument passed to `facet_wrap`.
- **show_labels**: Should count labels be added as text?
- **big.mark**: Parameter passed to `format` the labels. Default is "".
- **scientific**: Parameter passed to `format` the labels. Default is `FALSE`.
- **digits**: Used to round the labels. Default is 0.
- **...**: Further arguments passed to `geom_bar`.

Details

Experimental. Uses package `ggpubr` to rearrange the figure. Thus, the resulting plot cannot be easily modified. Furthermore, adding counts only works if the legend in `plot.light_effects` is not placed on the left or right side of the plot. It has to be placed inside or at the bottom.

Value

An object of class `ggplot2`.

See Also

`plot.light_effects`.

Examples

```r
fit <- lm(Sepal.Length ~ ., data = iris)
fl <- flashlight(model = fit, label = "iris", data = iris, y = "Sepal.Length")
x <- light_effects(fl, v = "Species")
plot_counts(plot(x), x, width = 0.3, alpha = 0.2)
```

Description

Predict method for an object of class `flashlight`. Pass additional elements to update the flashlight, typically data.

Usage

```r
## S3 method for class 'flashlight'
predict(object, ...)
```
Arguments

object  
An object of class flashlight.

...  
Arguments used to update the flashlight.

Value

A vector with predictions.

Examples

```r
fit <- lm(Sepal.Length ~ ., data = iris)
(fl <- flashlight(model = fit, data = iris, y = "Sepal.Length", label = "ols"))
predict(fl)[1:5]
predict(fl, data = iris[1:5, ])
predict(fl, data = iris[1:5, ], linkinv = exp)
```

---

Predictions for multiflashlight

Description

Predict method for an object of class multiflashlight. Pass additional elements to update the flashlight, typically data.

Usage

```r
## S3 method for class 'multiflashlight'
predict(object, ...)
```

Arguments

object  
An object of class multiflashlight.

...  
Arguments used to update the multiflashlight.

Value

A named list of prediction vectors.

Examples

```r
fit_part <- lm(Sepal.Length ~ Petal.Length, data = iris)
fit_full <- lm(Sepal.Length ~ ., data = iris)
mod_full <- flashlight(model = fit_full, label = "full")
mod_part <- flashlight(model = fit_part, label = "part")
mods <- multiflashlight(list(mod_full, mod_part), data = iris, y = "Sepal.Length")
predict(mods, data = iris[1:5, ])
```
print.flashlight  

Prints a flashlight

Description
Print method for an object of class flashlight.

Usage

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

Arguments

x A on object of class flashlight.
...
Further arguments passed from other methods.

Value
Invisibly, the input is returned.

See Also
flashlight.

Examples

fit <- lm(Sepal.Length ~ ., data = iris)
flashlight(model = fit, label = "lm", y = "Sepal.Length", data = iris)

print.light  

Prints light Object

Description
Print method for an object of class light.

Usage

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

Arguments

x A on object of class light.
...
Further arguments passed from other methods.
Value

Invisibly, the input is returned.

Examples

```r
fit <- lm(Sepal.Length ~ ., data = iris)
fl <- flashlight(model = fit, label = "lm", y = "Sepal.Length", data = iris)
light_performance(fl, v = "Species")
light_effects(fl, v = "Sepal.Length")
```

Description

Print method for an object of class `multiflashlight`.

Usage

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

Arguments

- `x` An object of class `multiflashlight`.
- `...` Further arguments passed to `print.flashlight`.

Value

Invisibly, the input is returned.

See Also

- `multiflashlight`

Examples

```r
fit_lm <- lm(Sepal.Length ~ ., data = iris)
fit_glm <- glm(Sepal.Length ~ ., family = Gamma(link = log), data = iris)
fl_lm <- flashlight(model = fit_lm, label = "lm")
fl_glm <- flashlight(model = fit_glm, label = "glm")
multiflashlight(list(fl_lm, fl_glm), data = iris)
```
residuals.flashlight  

Description

Residuals method for an object of class `flashlight`. Pass additional elements to update the flashlight before calculation of residuals.

Usage

```r
## S3 method for class 'flashlight'
residuals(object, ...)
```

Arguments

- **object**: An object of class `flashlight`.
- **...**: Arguments used to update the flashlight before calculating the residuals.

Value

A numeric vector with residuals.

Examples

```r
fit <- lm(Sepal.Length ~ ., data = iris)
(fl <- flashlight(model = fit, data = iris, y = "Sepal.Length", label = "ols"))
residuals(fl)[1:5]
residuals(fl, data = iris[1:5, ])
residuals(fl, data = iris[1:5, ], linkinv = exp)
resid(fl)[1:5]
```

residuals.multiflashlight  

Description

Residuals method for an object of class `multiflashlight`. Pass additional elements to update the multiflashlight before calculation of residuals.

Usage

```r
## S3 method for class 'multiflashlight'
residuals(object, ...)
```
Arguments

object An object of class multiflashlight.
...
Arguments used to update the multiflashlight before calculating the residuals.

Value

A named list with residuals per flashlight.

Examples

```r
fit_part <- lm(Sepal.Length ~ Petal.Length, data = iris)
fit_full <- lm(Sepal.Length ~ ., data = iris)
mod_full <- flashlight(model = fit_full, label = "full")
mod_part <- flashlight(model = fit_part, label = "part")
mods <- multiflashlight(list(mod_full, mod_part), data = iris, y = "Sepal.Length")
residuals(mods, data = head(iris))
```

Description

Extracts response from object of class flashlight.

Usage

```r
response(object, ...)
```

## Default S3 method:

response(object, ...)

## S3 method for class "flashlight"

response(object, ...)

## S3 method for class "multiflashlight"

response(object, ...)

Arguments

object An object of class flashlight.
...
Arguments used to update the flashlight before extracting the response.

Value

A numeric vector of responses.
Methods (by class)

- default: Default method not implemented yet.
- flashlight: Extract response from flashlight object.
- multiflashlight: Extract responses from multiflashlight object.

Examples

```r
fit <- lm(Sepal.Length ~ ., data = iris)
(fl <- flashlight(model = fit, data = iris, y = "Sepal.Length", label = "ols"))
response(fl)[1:5]
response(fl, data = iris[1:5, ])
response(fl, data = iris[1:5, ], linkinv = exp)
```
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