

Package: shapviz (via r-universe)

September 14, 2024

Title SHAP Visualizations

Version 0.9.5

Description Visualizations for SHAP (SHapley Additive exPlanations), such as waterfall plots, force plots, various types of importance plots, dependence plots, and interaction plots. These plots act on a 'shapviz' object created from a matrix of SHAP values and a corresponding feature dataset. Wrappers for the R packages 'xgboost', 'lightgbm', 'fastshap', 'shapr', 'h2o', 'treeshap', 'DALEX', and 'kernelshap' are added for convenience. By separating visualization and computation, it is possible to display factor variables in graphs, even if the SHAP values are calculated by a model that requires numerical features. The plots are inspired by those provided by the 'shap' package in Python, but there is no dependency on it.

License GPL (>= 2)

Depends R (>= 3.6.0)

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

Imports ggfittext (>= 0.8.0), gggenes, ggplot2 (>= 3.4.0), ggrepel, grid, patchwork, rlang (>= 0.3.0), stats, utils, xgboost

Enhances fastshap, h2o, lightgbm

LazyData true

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

URL <https://github.com/ModelOriented/shapviz>,
<https://modeloriented.github.io/shapviz/>

BugReports <https://github.com/ModelOriented/shapviz/issues>

Repository <https://modeloriented.r-universe.dev>

RemoteUrl <https://github.com/modeloriented/shapviz>

RemoteRef HEAD

RemoteSha 96da9527820f08a5d8214f4743c018cac1c394e8

Contents

shapviz-package	2
+shapviz	3
c.shapviz	4
collapse_shap	5
dim.shapviz	6
dimnames.shapviz	6
dimnames<-shapviz	7
extractors	8
format_max	9
is.mshapviz	10
is.shapviz	11
miami	12
mshapviz	13
potential_interactions	13
print.mshapviz	15
print.shapviz	15
rbind.shapviz	16
shapviz	17
split.shapviz	22
summary.shapviz	23
sv_dependence	23
sv_dependence2D	26
sv_force	28
sv_importance	30
sv_interaction	33
sv_waterfall	35
[.shapviz	37
Index	39

shapviz-package

shapviz: SHAP Visualizations

Description

Visualizations for SHAP (SHapley Additive exPlanations), such as waterfall plots, force plots, various types of importance plots, dependence plots, and interaction plots. These plots act on a 'shapviz' object created from a matrix of SHAP values and a corresponding feature dataset. Wrappers for the R packages 'xgboost', 'lightgbm', 'fastshap', 'shapr', 'h2o', 'treeshap', 'DALEX', and 'kernelshap' are added for convenience. By separating visualization and computation, it is possible to display

factor variables in graphs, even if the SHAP values are calculated by a model that requires numerical features. The plots are inspired by those provided by the 'shap' package in Python, but there is no dependency on it.

Author(s)

Maintainer: Michael Mayer <mayermichael79@gmail.com>

Other contributors:

- Adrian Stando <adrian.j.stando@gmail.com> [contributor]

See Also

Useful links:

- <https://github.com/ModelOriented/shapviz>
- <https://modeloriented.github.io/shapviz/>
- Report bugs at <https://github.com/ModelOriented/shapviz/issues>

+.shapviz

Rowbinds two "shapviz" Objects

Description

Rowbinds two "shapviz" objects using +.

Usage

```
## S3 method for class 'shapviz'  
e1 + e2
```

```
## S3 method for class 'mshapviz'  
e1 + e2
```

Arguments

e1 The first object of class "shapviz".
e2 The second object of class "shapviz".

Value

A new object of class "shapviz".

See Also

[shapviz\(\)](#), [rbind.shapviz\(\)](#)

Examples

```

S <- matrix(c(1, -1, -1, 1), ncol = 2, dimnames = list(NULL, c("x", "y")))
X <- data.frame(x = c("a", "b"), y = c(100, 10))
s1 <- shapviz(S, X, baseline = 4)[1]
s2 <- shapviz(S, X, baseline = 4)[2]
s <- s1 + s2
s
# mshapviz
S <- matrix(c(1, -1, -1, 1), ncol = 2, dimnames = list(NULL, c("x", "y")))
X <- data.frame(x = c("a", "b"), y = c(100, 10))
s1 <- shapviz(S, X, baseline = 4)[1L]
s2 <- shapviz(S, X, baseline = 4)[2L]
s <- mshapviz(c(shp1 = s1, shp2 = s2))
s + s

```

c.shapviz

Concatenates "shapviz" Objects

Description

This function combines two or more (usually named) "shapviz" objects to an object of class "mshapviz".

Usage

```

## S3 method for class 'shapviz'
c(...)

```

Arguments

... Any number of (optionally named) "shapviz" objects.

Value

A "mshapviz" object.

See Also

[mshapviz\(\)](#)

Examples

```

S <- matrix(c(1, -1, -1, 1), ncol = 2, dimnames = list(NULL, c("x", "y")))
X <- data.frame(x = c("a", "b"), y = c(100, 10))
s1 <- shapviz(S, X, baseline = 4)[1]
s2 <- shapviz(S, X, baseline = 4)[2]
s <- c(shp1 = s1, shp2 = s2)
s

```

collapse_shap	<i>Collapse SHAP values</i>
---------------	-----------------------------

Description

This function sums up SHAP values (or SHAP interaction values) of feature groups. Typical application: SHAP values have been generated by a model with one or multiple one-hot encoded variables, but the explanations should be done using the original factor.

Usage

```
collapse_shap(S, collapse = NULL, ...)
```

Arguments

S	Either a (n x p) matrix of SHAP values or a (n x p x p) array of SHAP interaction values.
collapse	A named list of character vectors. Each vector specifies the feature names whose SHAP values need to be summed up. The names determine the resulting collapsed column/dimension names.
...	Currently unused.

Value

A matrix of SHAP values, or an array of SHAP interaction values.

Examples

```
S <- cbind(
  x = c(0.1, 0.1, 0.1),
  `age low` = c(0.2, -0.1, 0.1),
  `age mid` = c(0, 0.2, -0.2),
  `age high` = c(1, -1, 0)
)
collapse <- list(age = c("age low", "age mid", "age high"))
collapse_shap(S, collapse)

# Arrays (as with SHAP interactions)
S_inter <- array(1, dim = c(2, 4, 4), dimnames = list(NULL, letters[1:4], letters[1:4]))
collapse_shap(S_inter, collapse = list(cd = c("c", "d"), ab = c("a", "b")))
```

dim.shapviz *Dimensions of "shapviz" Object*

Description

Dimensions of "shapviz" Object

Usage

```
## S3 method for class 'shapviz'
dim(x)
```

Arguments

x An object of class "shapviz".

Value

A numeric vector of length two providing the number of rows and columns of the SHAP matrix stored in x.

See Also

[shapviz\(\)](#)

Examples

```
S <- matrix(c(1, -1, -1, 1), ncol = 2, dimnames = list(NULL, c("x", "y")))
X <- data.frame(x = c("a", "b"), y = c(100, 10))
x <- shapviz(S, X)
dim(x)
nrow(x)
ncol(x)
```

dimnames.shapviz *Dimnames of "shapviz" Object*

Description

This implies to use `colnames(x)` to get the column names of the SHAP and feature matrix (and optional SHAP interaction values).

Usage

```
## S3 method for class 'shapviz'
dimnames(x)
```

Arguments

`x` An object of class "shapviz".

Value

Dimnames of the SHAP matrix.

See Also

[shapviz\(\)](#)

Examples

```
S <- matrix(c(1, -1, -1, 1), ncol = 2, dimnames = list(NULL, c("x", "y")))
X <- data.frame(x = c("a", "b"), y = c(100, 10))
x <- shapviz(S, X, baseline = 4)
dimnames(x)
colnames(x)
```

`dimnames<-.shapviz` *Dimnames (Replacement Method) of "shapviz" Object*

Description

This implies `colnames(x) <-`

Usage

```
## S3 replacement method for class 'shapviz'
dimnames(x) <- value
```

Arguments

`x` An object of class "shapviz".
`value` A list with rownames and column names compliant with SHAP matrix.

Value

Like `x`, but with replaced dimnames.

See Also

[shapviz\(\)](#)

Examples

```

S <- matrix(c(1, -1, -1, 1), ncol = 2, dimnames = list(NULL, c("x", "y")))
X <- data.frame(x = c("a", "b"), y = c(100, 10))
x <- shapviz(S, X, baseline = 4)
dimnames(x) <- list(1:2, c("a", "b"))
dimnames(x)
colnames(x) <- c("x", "y")
colnames(x)

```

 extractors

Extractor Functions

Description

Functions to extract SHAP values, feature values, the baseline, or SHAP interactions from a "(m)shapviz" object.

Usage

```

get_shap_values(object, ...)

## S3 method for class 'shapviz'
get_shap_values(object, ...)

## S3 method for class 'mshapviz'
get_shap_values(object, ...)

## Default S3 method:
get_shap_values(object, ...)

get_feature_values(object, ...)

## S3 method for class 'shapviz'
get_feature_values(object, ...)

## S3 method for class 'mshapviz'
get_feature_values(object, ...)

## Default S3 method:
get_feature_values(object, ...)

get_baseline(object, ...)

## S3 method for class 'shapviz'
get_baseline(object, ...)

## S3 method for class 'mshapviz'

```



```

get_baseline(object, ...)

## Default S3 method:
get_baseline(object, ...)

get_shap_interactions(object, ...)

## S3 method for class 'shapviz'
get_shap_interactions(object, ...)

## S3 method for class 'mshapviz'
get_shap_interactions(object, ...)

## Default S3 method:
get_shap_interactions(object, ...)

```

Arguments

object	Object to extract something.
...	Currently unused.

Value

- `get_shap_values()` returns the matrix of SHAP values,
- `get_feature_values()` the data.frame of feature values,
- `get_baseline()` the numeric baseline value, and
- `get_shap_interactions()` the SHAP interactions of the input.

For objects of class "mshapviz", these functions return lists of those elements.

Examples

```

S <- matrix(c(1, -1, -1, 1), ncol = 2, dimnames = list(NULL, c("x", "y")))
X <- data.frame(x = c("a", "b"), y = c(100, 10))
shp <- shapviz(S, X, baseline = 4)
get_shap_values(shp)

```

format_max

Number Formatter

Description

Formats a numeric vector in a way that its largest absolute value determines the number of digits after the decimal separator. This function is helpful in perfectly aligning numbers on plots. Does not use scientific formatting.

Usage

```
format_max(x, digits = 4L, ...)
```

Arguments

<code>x</code>	A numeric vector to be formatted.
<code>digits</code>	Number of significant digits of the largest absolute value.
<code>...</code>	Further arguments passed to <code>format()</code> , e.g., <code>big.mark = ""</code> .

Value

A character vector of formatted numbers.

Examples

```
x <- c(100, 1, 0.1)
format_max(x)

y <- c(100, 1.01)
format_max(y)
format_max(y, digits = 5)
```

is.mshapviz

Check for mshapviz

Description

Is object of class "mshapviz"?

Usage

```
is.mshapviz(object)
```

Arguments

<code>object</code>	An R object.
---------------------	--------------

Value

Returns TRUE if object has "mshapviz" among its classes, and FALSE otherwise.

See Also

[mshapviz\(\)](#)

Examples

```
S <- matrix(c(1, -1, -1, 1), ncol = 2, dimnames = list(NULL, c("x", "y")))
X <- data.frame(x = c("a", "b"), y = c(100, 10))
s1 <- shapviz(S, X, baseline = 4)[1]
s2 <- shapviz(S, X, baseline = 4)
x <- c(s1 = s1, s2 = s2)
is.mshapviz(x)
is.mshapviz(s1)
```

is.shapviz

Check for shapviz

Description

Is object of class "shapviz"?

Usage

```
is.shapviz(object)
```

Arguments

object An R object.

Value

Returns TRUE if object has "shapviz" among its classes, and FALSE otherwise.

See Also

[shapviz\(\)](#)

Examples

```
S <- matrix(c(1, -1, -1, 1), ncol = 2, dimnames = list(NULL, c("x", "y")))
X <- data.frame(x = c("a", "b"), y = c(100, 10))
shp <- shapviz(S, X)
is.shapviz(shp)
is.shapviz("a")
```

 miami

Miami-Dade County House Prices

Description

The dataset contains information on 13,932 single-family homes sold in Miami-Dade County in 2016. Besides publicly available information, the dataset creator Steven C. Bourassa has added distance variables, aviation noise as well as latitude and longitude.

More information can be found open-access on <https://www.mdpi.com/1595920>.

The dataset can also be downloaded via `miami <- OpenML::getOMLDataSet(43093)$data`.

Usage

```
miami
```

Format

A data frame with 13,932 rows and 17 columns:

PARCELNO unique identifier for each property. About 1% appear multiple times.

SALE_PRC sale price (\$)

LND_SQFOOT land area (square feet)

TOT_LVG_AREA floor area (square feet)

SPEC_FEAT_VAL value of special features (e.g., swimming pools) (\$)

RAIL_DIST distance to the nearest rail line (an indicator of noise) (feet)

OCEAN_DIST distance to the ocean (feet)

WATER_DIST distance to the nearest body of water (feet)

CNTR_DIST distance to the Miami central business district (feet)

SUBCNTR_DI distance to the nearest subcenter (feet)

HWY_DIST distance to the nearest highway (an indicator of noise) (feet)

age age of the structure

avno60plus dummy variable for airplane noise exceeding an acceptable level

structure_quality quality of the structure

month_sold sale month in 2016 (1 = jan)

LATITUDE, LONGITUDE Coordinates

mshapviz	<i>Combines compatible "shapviz" Objects</i>
----------	--

Description

This function combines a list of compatible "shapviz" objects to an object of class "mshapviz". The elements can be named.

Usage

```
mshapviz(object, ...)
```

Arguments

object	List of "shapviz" objects to be concatenated.
...	Not used.

Value

A "mshapviz" object.

Examples

```
S <- matrix(c(1, -1, -1, 1), ncol = 2, dimnames = list(NULL, c("x", "y")))
X <- data.frame(x = c("a", "b"), y = c(100, 10))
s1 <- shapviz(S, X, baseline = 4)[1L]
s2 <- shapviz(S, X, baseline = 4)[2L]
s <- mshapviz(c(shp1 = s1, shp2 = s2))
s
```

potential_interactions

Interaction Strength

Description

Returns a vector of interaction strengths between variable *v* and all other variables, see Details.

Usage

```
potential_interactions(
  obj,
  v,
  nbins = NULL,
  color_num = TRUE,
  scale = FALSE,
  adjusted = FALSE
)
```

Arguments

obj	An object of class "shapviz".
v	Variable name to calculate potential SHAP interactions for.
nbins	Into how many quantile bins should a numeric v be binned? The default NULL equals the smaller of $n/20$ and \sqrt{n} (rounded up), where n is the sample size. Ignored if obj contains SHAP interactions.
color_num	Should other ("color") features v' be converted to numeric, even if they are factors/characters? Default is TRUE. Ignored if obj contains SHAP interactions.
scale	Should adjusted R-squared be multiplied with the sample variance of within-bin SHAP values? If TRUE, bins with stronger vertical scatter will get higher weight. The default is FALSE. Ignored if obj contains SHAP interactions.
adjusted	Should <i>adjusted</i> R-squared be used? Default is FALSE.

Details

If SHAP interaction values are available, the interaction strength between feature v and another feature v' is measured by twice their mean absolute SHAP interaction values.

Otherwise, we use a heuristic calculated as follows:

1. If v is numeric, it is binned into nbins bins.
2. Per bin, the SHAP values of v are regressed onto v, and the R-squared is calculated. Rows with missing v' are discarded.
3. The R-squared are averaged over bins, weighted by the number of non-missing v' values.

This measures how much variability in the SHAP values of v is explained by v', after accounting for v.

Set scale = TRUE to multiply the R-squared by the within-bin variance of the SHAP values. This will put higher weight to bins with larger scatter.

Set color_num = FALSE to *not* turn the values of the "color" feature v' to numeric.

Finally, set adjusted = TRUE to use *adjusted* R-squared.

The algorithm does not consider observations with missing v' values.

Value

A named vector of decreasing interaction strengths.

See Also

[sv_dependence\(\)](#)

print.mshapviz	<i>Prints "mshapviz" Object</i>
----------------	---------------------------------

Description

Prints "mshapviz" Object

Usage

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

Arguments

x	An object of class "mshapviz".
...	Further arguments passed from other methods.

Value

Invisibly, the input is returned.

See Also

[mshapviz\(\)](#)

Examples

```
S <- matrix(c(1, -1, -1, 1), ncol = 2, dimnames = list(NULL, c("x", "y")))  
X <- data.frame(x = c("a", "b"), y = c(100, 10))  
s1 <- shapviz(S, X, baseline = 4)[1]  
s2 <- shapviz(S, X, baseline = 4)  
x <- c(s1 = s1, s2 = s2)  
x
```

print.shapviz	<i>Prints "shapviz" Object</i>
---------------	--------------------------------

Description

Prints "shapviz" Object

Usage

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

Arguments

x An object of class "shapviz".
... Further arguments passed from other methods.

Value

Invisibly, the input is returned.

See Also

[shapviz\(\)](#)

Examples

```
S <- matrix(c(1, -1, -1, 1), ncol = 2, dimnames = list(NULL, c("x", "y")))
X <- data.frame(x = c("a", "b"), y = c(100, 10))
x <- shapviz(S, X, baseline = 4)
x
```

rbind.shapviz

Rowbinds Multiple "shapviz" or "mshapviz" Objects

Description

Rowbinds multiple "shapviz" objects based on the + operator.

Usage

```
## S3 method for class 'shapviz'
rbind(...)
```

```
## S3 method for class 'mshapviz'
rbind(...)
```

Arguments

... Any number of "shapviz" or "mshapviz" objects.

Value

A new object of class "shapviz" or "mshapviz".

See Also

[shapviz\(\)](#), [mshapviz\(\)](#)

Examples

```
S <- matrix(c(1, -1, -1, 1), ncol = 2, dimnames = list(NULL, c("x", "y")))
X <- data.frame(x = c("a", "b"), y = c(100, 10))
s1 <- shapviz(S, X, baseline = 4)[1]
s2 <- shapviz(S, X, baseline = 4)[2]
s <- rbind(s1, s2)
s
# mshapviz
S <- matrix(c(1, -1, -1, 1), ncol = 2, dimnames = list(NULL, c("x", "y")))
X <- data.frame(x = c("a", "b"), y = c(100, 10))
s1 <- shapviz(S, X, baseline = 4)[1L]
s2 <- shapviz(S, X, baseline = 4)[2L]
s <- mshapviz(c(shp1 = s1, shp2 = s2))
rbind(s, s)
```

shapviz

Initialize "shapviz" Object

Description

This function creates an object of class "shapviz" from a matrix of SHAP values, or from a fitted model of type

- XGBoost,
- LightGBM, or
- H2O (tree-based regression or binary classification model).

Furthermore, `shapviz()` can digest the results of

- `fastshap::explain()`,
- `shapr::explain()`,
- `treeshap::treeshap()`,
- `DALEX::predict_parts()`,
- `kernelshap::kernelshap()`,
- `kernelshap::permshap()`, and
- `kernelshap::additive_shap()`,

check the vignettes for examples.

Usage

```
shapviz(object, ...)  
  
## Default S3 method:  
shapviz(object, ...)  
  
## S3 method for class 'matrix'  
shapviz(object, X, baseline = 0, collapse = NULL, S_inter = NULL, ...)  
  
## S3 method for class 'xgb.Booster'  
shapviz(  
  object,  
  X_pred,  
  X = X_pred,  
  which_class = NULL,  
  collapse = NULL,  
  interactions = FALSE,  
  ...  
)  
  
## S3 method for class 'lgb.Booster'  
shapviz(object, X_pred, X = X_pred, which_class = NULL, collapse = NULL, ...)  
  
## S3 method for class 'explain'  
shapviz(object, X = NULL, baseline = NULL, collapse = NULL, ...)  
  
## S3 method for class 'treeshap'  
shapviz(  
  object,  
  X = object[["observations"]],  
  baseline = 0,  
  collapse = NULL,  
  ...  
)  
  
## S3 method for class 'predict_parts'  
shapviz(object, ...)  
  
## S3 method for class 'shapr'  
shapviz(object, X = object[["x_test"]], collapse = NULL, ...)  
  
## S3 method for class 'kernelshap'  
shapviz(object, X = object[["X"]], which_class = NULL, collapse = NULL, ...)  
  
## S3 method for class 'H2ORegressionModel'  
shapviz(object, X_pred, X = as.data.frame(X_pred), collapse = NULL, ...)  
  
## S3 method for class 'H2OBinomialModel'
```

```
shapviz(object, X_pred, X = as.data.frame(X_pred), collapse = NULL, ...)

## S3 method for class 'H2OModel'
shapviz(object, X_pred, X = as.data.frame(X_pred), collapse = NULL, ...)
```

Arguments

object	For XGBoost, LightGBM, and H2O, this is the fitted model used to calculate SHAP values from X_pred. In the other cases, it is the object containing the SHAP values.
...	Parameters passed to other methods (currently only used by the predict() functions of XGBoost, LightGBM, and H2O).
X	Matrix or data.frame of feature values used for visualization. Must contain at least the same column names as the SHAP matrix represented by object/X_pred (after optionally collapsing some of the SHAP columns).
baseline	Optional baseline value, representing the average response at the scale of the SHAP values. It will be used for plot methods that explain single predictions.
collapse	A named list of character vectors. Each vector specifies the feature names whose SHAP values need to be summed up. The names determine the resulting collapsed column/dimension names.
S_inter	Optional 3D array of SHAP interaction values. If object has shape n x p, then S_inter needs to be of shape n x p x p. Summation over the second (or third) dimension should yield the usual SHAP values. Furthermore, dimensions 2 and 3 are expected to be symmetric. Default is NULL.
X_pred	Data set as expected by the predict() function of XGBoost, LightGBM, or H2O. For XGBoost, a matrix or xgb.DMatrix, for LightGBM a matrix, and for H2O a data.frame or an H2OFrame. Only used for XGBoost, LightGBM, or H2O objects.
which_class	In case of a multiclass or multioutput setting, which class/output (>= 1) to explain. Currently relevant for XGBoost, LightGBM, kernelshap, and permshap.
interactions	Should SHAP interactions be calculated (default is FALSE)? Only available for XGBoost.

Details

Together with the main input, a data set X of feature values is required, used only for visualization. It can therefore contain character or factor variables, even if the SHAP values were calculated from a purely numerical feature matrix. In addition, to improve visualization, it can sometimes be useful to truncate gross outliers, logarithmize certain columns, or replace missing values with an explicit value.

SHAP values of dummy variables can be combined using the convenient collapse argument. Multi-output models created from XGBoost, LightGBM, "kernelshap", or "permshap" return a "mshapviz" object, containing a "shapviz" object per output.

Value

An object of class "shapviz" with the following elements:

- `S`: Numeric matrix of SHAP values.
- `X`: data.frame containing the feature values corresponding to `S`.
- `baseline`: Baseline value, representing the average prediction at the scale of the SHAP values.
- `S_inter`: Numeric array of SHAP interaction values (or NULL).

Methods (by class)

- `shapviz(default)`: Default method to initialize a "shapviz" object.
- `shapviz(matrix)`: Creates a "shapviz" object from a matrix of SHAP values.
- `shapviz(xgb.Booster)`: Creates a "shapviz" object from an XGBoost model.
- `shapviz(lgb.Booster)`: Creates a "shapviz" object from a LightGBM model.
- `shapviz(explain)`: Creates a "shapviz" object from `fastshap::explain()`.
- `shapviz(treeshap)`: Creates a "shapviz" object from `treeshap::treeshap()`.
- `shapviz(predict_parts)`: Creates a "shapviz" object from `DALEX::predict_parts()`.
- `shapviz(shapr)`: Creates a "shapviz" object from `shapr::explain()`.
- `shapviz(kernelshap)`: Creates a "shapviz" object from an object of class 'kernelshap'. This includes results of `kernelshap()`, `permshap()`, and `additive_shap()`.
- `shapviz(H2ORegressionModel)`: Creates a "shapviz" object from a (tree-based) H2O regression model.
- `shapviz(H2OBinomialModel)`: Creates a "shapviz" object from a (tree-based) H2O binary classification model.
- `shapviz(H2OModel)`: Creates a "shapviz" object from a (tree-based) H2O model (base class).

See Also

[sv_importance\(\)](#), [sv_dependence\(\)](#), [sv_dependence2D\(\)](#), [sv_interaction\(\)](#), [sv_waterfall\(\)](#), [sv_force\(\)](#), [collapse_shap\(\)](#)

Examples

```
S <- matrix(c(1, -1, -1, 1), ncol = 2, dimnames = list(NULL, c("x", "y")))
X <- data.frame(x = c("a", "b"), y = c(100, 10))
shapviz(S, X, baseline = 4)
# XGBoost models
X_pred <- data.matrix(iris[, -1])
dtrain <- xgboost::xgb.DMatrix(X_pred, label = iris[, 1], nthread = 1)
fit <- xgboost::xgb.train(data = dtrain, nrounds = 10, nthread = 1)

# Will use numeric matrix "X_pred" as feature matrix
x <- shapviz(fit, X_pred = X_pred)
x
sv_dependence(x, "Species")
```

```

# Will use original values as feature matrix
x <- shapviz(fit, X_pred = X_pred, X = iris)
sv_dependence(x, "Species")

# "X_pred" can also be passed as xgb.DMatrix, but only if X is passed as well!
x <- shapviz(fit, X_pred = dtrain, X = iris)

# Multiclass setting
params <- list(objective = "multi:softprob", num_class = 3)
X_pred <- data.matrix(iris[, -5])
dtrain <- xgboost::xgb.DMatrix(
  X_pred, label = as.integer(iris[, 5]) - 1, nthread = 1
)
fit <- xgboost::xgb.train(params = params, data = dtrain, nrounds = 10, nthread = 1)

# Select specific class
x <- shapviz(fit, X_pred = X_pred, which_class = 3)
x

# Or combine all classes to "mshapviz" object
x <- shapviz(fit, X_pred = X_pred)
x

# What if we would have one-hot-encoded values and want to explain the original column?
X_pred <- stats::model.matrix(~ . -1, iris[, -1])
dtrain <- xgboost::xgb.DMatrix(X_pred, label = as.integer(iris[, 1]), nthread = 1)
fit <- xgboost::xgb.train(data = dtrain, nrounds = 10, nthread = 1)
x <- shapviz(
  fit,
  X_pred = X_pred,
  X = iris,
  collapse = list(Species = c("Speciessetosa", "Speciesversicolor", "Speciesvirginica"))
)
summary(x)

# Similarly with LightGBM
if (requireNamespace("lightgbm", quietly = TRUE)) {
  fit <- lightgbm::lgb.train(
    params = list(objective = "regression", num_thread = 1),
    data = lightgbm::lgb.Dataset(X_pred, label = iris[, 1]),
    nrounds = 10,
    verbose = -2
  )

  x <- shapviz(fit, X_pred = X_pred)
  x

# Multiclass
params <- list(objective = "multiclass", num_class = 3, num_thread = 1)
X_pred <- data.matrix(iris[, -5])
dtrain <- lightgbm::lgb.Dataset(X_pred, label = as.integer(iris[, 5]) - 1)
fit <- lightgbm::lgb.train(params = params, data = dtrain, nrounds = 10)

```

```

# Select specific class
x <- shapviz(fit, X_pred = X_pred, which_class = 3)
x

# Or combine all classes to a "mshapviz" object
mx <- shapviz(fit, X_pred = X_pred)
mx
all.equal(mx[[3]], x)
}

```

split.shapviz

Splits "shapviz" Object

Description

Splits "shapviz" object along a vector `f` into an object of class "mshapviz".

Usage

```

## S3 method for class 'shapviz'
split(x, f, ...)

```

Arguments

<code>x</code>	Object of class "shapviz".
<code>f</code>	Vector used to split feature values and SHAP (interaction) values. Empty factor levels are dropped.
<code>...</code>	Arguments passed to <code>split()</code> .

Value

A "mshapviz" object.

See Also

[shapviz\(\)](#), [rbind.shapviz\(\)](#)

Examples

```

## Not run:
dtrain <- xgboost::xgb.DMatrix(data.matrix(iris[, -1]), label = iris[, 1])
fit <- xgboost::xgb.train(data = dtrain, nrounds = 10, nthread = 1)
sv <- shapviz(fit, X_pred = dtrain, X = iris)
mx <- split(sv, f = iris$Species)
sv_dependence(mx, "Petal.Length")

## End(Not run)

```

summary.shapviz	<i>Summarizes "shapviz" Object</i>
-----------------	------------------------------------

Description

Summarizes "shapviz" Object

Usage

```
## S3 method for class 'shapviz'
summary(object, n = 2L, ...)
```

Arguments

object	An object of class "shapviz".
n	Maximum number of rows of SHAP values and feature values to show.
...	Further arguments passed from other methods.

Value

Invisibly, the input is returned.

See Also

[shapviz\(\)](#)

Examples

```
S <- matrix(c(1, -1, -1, 1), ncol = 2, dimnames = list(NULL, c("x", "y")))
X <- data.frame(x = c("a", "b"), y = c(100, 10))
object <- shapviz(S, X, baseline = 4)
summary(object)
```

sv_dependence	<i>SHAP Dependence Plot</i>
---------------	-----------------------------

Description

Scatterplot of the SHAP values of a feature against its feature values. If SHAP interaction values are available, setting `interactions = TRUE` allows to focus on pure interaction effects (multiplied by two) or on pure main effects. By default, the feature on the color scale is selected via SHAP interactions (if available) or an interaction heuristic, see [potential_interactions\(\)](#).

Usage

```
sv_dependence(object, ...)

## Default S3 method:
sv_dependence(object, ...)

## S3 method for class 'shapviz'
sv_dependence(
  object,
  v,
  color_var = "auto",
  color = "#3b528b",
  viridis_args = getOption("shapviz.viridis_args"),
  jitter_width = NULL,
  interactions = FALSE,
  ih_nbins = NULL,
  ih_color_num = TRUE,
  ih_scale = FALSE,
  ih_adjusted = FALSE,
  ...
)

## S3 method for class 'mshapviz'
sv_dependence(
  object,
  v,
  color_var = "auto",
  color = "#3b528b",
  viridis_args = getOption("shapviz.viridis_args"),
  jitter_width = NULL,
  interactions = FALSE,
  ih_nbins = NULL,
  ih_color_num = TRUE,
  ih_scale = FALSE,
  ih_adjusted = FALSE,
  ...
)
```

Arguments

object	An object of class "(m)shapviz".
...	Arguments passed to <code>ggplot2::geom_jitter()</code> .
v	Column name of feature to be plotted. Can be a vector/list if object is of class "shapviz".
color_var	Feature name to be used on the color scale to investigate interactions. The default ("auto") uses SHAP interaction values (if available), or a heuristic to select the strongest interacting feature. Set to NULL to not use the color axis. Can be a vector/list if object is of class "shapviz".

color	Color to be used if color_var = NULL. Can be a vector/list if v is a vector.
viridis_args	List of viridis color scale arguments, see <code>?ggplot2::scale_color_viridis_c</code> . The default points to the global option <code>shapviz.viridis_args</code> , which corresponds to <code>list(begin = 0.25, end = 0.85, option = "inferno")</code> . These values are passed to <code>ggplot2::scale_color_viridis_*</code> . For example, to switch to a standard viridis scale, you can either change the default via <code>options(shapviz.viridis_args = list())</code> , or set <code>viridis_args = list()</code> . Only relevant if color_var is not NULL.
jitter_width	The amount of horizontal jitter. The default (NULL) will use a value of 0.2 in case v is discrete, and no jitter otherwise. (Numeric variables are considered discrete if they have at most 7 unique values.) Can be a vector/list if v is a vector.
interactions	Should SHAP interaction values be plotted? Default is FALSE. Requires SHAP interaction values. If color_var = NULL (or it is equal to v), the pure main effect of v is visualized. Otherwise, twice the SHAP interaction values between v and the color_var are plotted.
ih_nbins, ih_color_num, ih_scale, ih_adjusted	Interaction heuristic (ih) parameters used to select the color variable, see potential_interactions() . Only used if color_var = "auto" and if there are no SHAP interaction values.

Value

An object of class "ggplot" (or "patchwork") representing a dependence plot.

Methods (by class)

- `sv_dependence(default)`: Default method.
- `sv_dependence(shapviz)`: SHAP dependence plot for "shapviz" object.
- `sv_dependence(mshapviz)`: SHAP dependence plot for "mshapviz" object.

See Also

[potential_interactions\(\)](#)

Examples

```
dtrain <- xgboost::xgb.DMatrix(
  data.matrix(iris[, -1]), label = iris[, 1], nthread = 1
)
fit <- xgboost::xgb.train(data = dtrain, nrounds = 10, nthread = 1)
x <- shapviz(fit, X_pred = dtrain, X = iris)
sv_dependence(x, "Petal.Length")
sv_dependence(x, "Petal.Length", color_var = "Species")
sv_dependence(x, "Petal.Length", color_var = NULL)
sv_dependence(x, c("Species", "Petal.Length"))
sv_dependence(x, "Petal.Width", color_var = c("Species", "Petal.Length"))

# SHAP interaction values/main effects
x2 <- shapviz(fit, X_pred = dtrain, X = iris, interactions = TRUE)
sv_dependence(x2, "Petal.Length", interactions = TRUE)
```

```
sv_dependence(
  x2, c("Petal.Length", "Species"), color_var = NULL, interactions = TRUE
)
```

sv_dependence2D *2D SHAP Dependence Plot*

Description

Scatterplot of two features, showing the sum of their SHAP values on the color scale. This allows to visualize the combined effect of two features, including interactions. A typical application are models with latitude and longitude as features (plus maybe other regional features that can be passed via `add_vars`).

If SHAP interaction values are available, setting `interactions = TRUE` allows to focus on pure interaction effects (multiplied by two). In this case, `add_vars` has no effect.

Usage

```
sv_dependence2D(object, ...)

## Default S3 method:
sv_dependence2D(object, ...)

## S3 method for class 'shapviz'
sv_dependence2D(
  object,
  x,
  y,
  viridis_args = getOption("shapviz.viridis_args"),
  jitter_width = NULL,
  jitter_height = NULL,
  interactions = FALSE,
  add_vars = NULL,
  ...
)

## S3 method for class 'mshapviz'
sv_dependence2D(
  object,
  x,
  y,
  viridis_args = getOption("shapviz.viridis_args"),
  jitter_width = NULL,
  jitter_height = NULL,
  interactions = FALSE,
  add_vars = NULL,
  ...
)
```

Arguments

object	An object of class "(m)shapviz".
...	Arguments passed to <code>ggplot2::geom_jitter()</code> .
x	Feature name for x axis. Can be a vector/list if object is of class "shapviz".
y	Feature name for y axis. Can be a vector/list if object is of class "shapviz".
viridis_args	List of viridis color scale arguments, see <code>?ggplot2::scale_color_viridis_c</code> . The default points to the global option <code>shapviz.viridis_args</code> , which corresponds to <code>list(begin = 0.25, end = 0.85, option = "inferno")</code> . These values are passed to <code>ggplot2::scale_color_viridis_*</code> . For example, to switch to a standard viridis scale, you can either change the default via <code>options(shapviz.viridis_args = list())</code> , or set <code>viridis_args = list()</code> . Only relevant if <code>color_var</code> is not <code>NULL</code> .
jitter_width	The amount of horizontal jitter. The default (<code>NULL</code>) will use a value of 0.2 in case <code>v</code> is discrete, and no jitter otherwise. (Numeric variables are considered discrete if they have at most 7 unique values.) Can be a vector/list if <code>v</code> is a vector.
jitter_height	Similar to <code>jitter_width</code> for vertical scatter.
interactions	Should SHAP interaction values be plotted? The default (<code>FALSE</code>) will show the rowwise sum of the SHAP values of <code>x</code> and <code>y</code> . If <code>TRUE</code> , will use twice the SHAP interaction value (requires SHAP interactions).
add_vars	Optional vector of feature names, whose SHAP values should be added to the sum of the SHAP values of <code>x</code> and <code>y</code> (only if <code>interactions = FALSE</code>). A use case would be a model with geographic <code>x</code> and <code>y</code> coordinates, along with some additional locational features like distance to the next train station.

Value

An object of class "ggplot" (or "patchwork") representing a dependence plot.

Methods (by class)

- `sv_dependence2D(default)`: Default method.
- `sv_dependence2D(shapviz)`: 2D SHAP dependence plot for "shapviz" object.
- `sv_dependence2D(mshapviz)`: 2D SHAP dependence plot for "mshapviz" object.

See Also

[sv_dependence\(\)](#)

Examples

```
dtrain <- xgboost::xgb.DMatrix(
  data.matrix(iris[, -1]), label = iris[, 1], nthread = 1
)
fit <- xgboost::xgb.train(data = dtrain, nrounds = 10, nthread = 1)
sv <- shapviz(fit, X_pred = dtrain, X = iris)
sv_dependence2D(sv, x = "Petal.Length", y = "Species")
```

```

sv_dependence2D(sv, x = c("Petal.Length", "Species"), y = "Sepal.Width")

# SHAP interaction values
sv2 <- shapviz(fit, X_pred = dtrain, X = iris, interactions = TRUE)
sv_dependence2D(sv2, x = "Petal.Length", y = "Species", interactions = TRUE)
sv_dependence2D(
  sv2, x = "Petal.Length", y = c("Species", "Petal.Width"), interactions = TRUE
)

# mshapviz object
mx <- split(sv, f = iris$Species)
sv_dependence2D(mx, x = "Petal.Length", y = "Sepal.Width")

```

sv_force

SHAP Force Plot

Description

Creates a force plot of SHAP values of one observation. If multiple observations are selected, their SHAP values and predictions are averaged.

Usage

```

sv_force(object, ...)

## Default S3 method:
sv_force(object, ...)

## S3 method for class 'shapviz'
sv_force(
  object,
  row_id = 1L,
  max_display = 6L,
  fill_colors = c("#f7d13d", "#a52c60"),
  format_shap = getOption("shapviz.format_shap"),
  format_feat = getOption("shapviz.format_feat"),
  contrast = TRUE,
  bar_label_size = 3.2,
  show_annotation = TRUE,
  annotation_size = 3.2,
  ...
)

## S3 method for class 'mshapviz'
sv_force(
  object,
  row_id = 1L,
  max_display = 6L,

```

```

fill_colors = c("#f7d13d", "#a52c60"),
format_shap = getOption("shapviz.format_shap"),
format_feat = getOption("shapviz.format_feat"),
contrast = TRUE,
bar_label_size = 3.2,
show_annotation = TRUE,
annotation_size = 3.2,
...
)

```

Arguments

object	An object of class "(m)shapviz".
...	Arguments passed to <code>ggfittext::geom_fit_text()</code> . For example, <code>size = 9</code> will use fixed text size in the bars and <code>size = 0</code> will altogether suppress adding text to the bars.
row_id	Subset of observations to plot, typically a single row number. If more than one row is selected, SHAP values are averaged, and feature values are shown only when they are unique.
max_display	Maximum number of features (with largest absolute SHAP values) should be plotted? If there are more features, they will be collapsed to one feature. Set to <code>Inf</code> to show all features.
fill_colors	A vector of exactly two fill colors: the first for positive SHAP values, the other for negative ones.
format_shap	Function used to format SHAP values. The default uses the global option <code>shapviz.format_shap</code> , which equals to <code>function(z) prettyNum(z, digits = 3, scientific = FALSE)</code> by default.
format_feat	Function used to format numeric feature values. The default uses the global option <code>shapviz.format_feat</code> , which equals to <code>function(z) prettyNum(z, digits = 3, scientific = FALSE)</code> by default.
contrast	Logical flag that determines whether to use white text in dark arrows. Default is <code>TRUE</code> .
bar_label_size	Size of text used to describe bars (via <code>ggrepel::geom_text_repel()</code>).
show_annotation	Should " $f(x)$ " and " $E(f(x))$ " be plotted? Default is <code>TRUE</code> .
annotation_size	Size of the annotation text ($f(x)=...$ and $E(f(x))=...$).

Details

$f(x)$ denotes the prediction on the SHAP scale, while $E(f(x))$ refers to the baseline SHAP value.

Value

An object of class "ggplot" (or "patchwork") representing a force plot.

Methods (by class)

- `sv_force(default)`: Default method.
- `sv_force(shapviz)`: SHAP force plot for object of class "shapviz".
- `sv_force(mshapviz)`: SHAP force plot for object of class "mshapviz".

See Also

[sv_waterfall\(\)](#)

Examples

```
dtrain <- xgboost::xgb.DMatrix(
  data.matrix(iris[, -1]), label = iris[, 1], nthread = 1
)
fit <- xgboost::xgb.train(data = dtrain, nrounds = 20, nthread = 1)
x <- shapviz(fit, X_pred = dtrain, X = iris[, -1])
sv_force(x)
sv_force(x, row_id = 65, max_display = 3, size = 9, fill_colors = 4:5)

# Aggregate over all observations with Petal.Length == 1.4
sv_force(x, row_id = x$X$Petal.Length == 1.4)
```

sv_importance

SHAP Importance Plots

Description

This function provides two types of SHAP importance plots: a bar plot and a beeswarm plot (sometimes called "SHAP summary plot"). The two types of plots can also be combined.

Usage

```
sv_importance(object, ...)

## Default S3 method:
sv_importance(object, ...)

## S3 method for class 'shapviz'
sv_importance(
  object,
  kind = c("bar", "beeswarm", "both", "no"),
  max_display = 15L,
  fill = "#fca50a",
  bar_width = 2/3,
  bee_width = 0.4,
  bee_adjust = 0.5,
  viridis_args = getOption("shapviz.viridis_args"),
```

```

    color_bar_title = "Feature value",
    show_numbers = FALSE,
    format_fun = format_max,
    number_size = 3.2,
    sort_features = TRUE,
    ...
)

## S3 method for class 'mshapviz'
sv_importance(
  object,
  kind = c("bar", "beeswarm", "both", "no"),
  max_display = 15L,
  fill = "#fca50a",
  bar_width = 2/3,
  bar_type = c("dodge", "stack", "facets", "separate"),
  bee_width = 0.4,
  bee_adjust = 0.5,
  viridis_args = getOption("shapviz.viridis_args"),
  color_bar_title = "Feature value",
  show_numbers = FALSE,
  format_fun = format_max,
  number_size = 3.2,
  sort_features = TRUE,
  ...
)

```

Arguments

object	An object of class "(m)shapviz".
...	Arguments passed to <code>ggplot2::geom_bar()</code> (if kind = "bar") or to <code>ggplot2::geom_point()</code> otherwise. For instance, passing <code>alpha = 0.2</code> will produce semi-transparent beeswarms, and setting <code>size = 3</code> will produce larger dots.
kind	Should a "bar" plot (the default), a "beeswarm" plot, or "both" be shown? Set to "no" in order to suppress plotting. In that case, the sorted SHAP feature importances of all variables are returned.
max_display	How many features should be plotted? Set to Inf to show all features. Has no effect if kind = "no".
fill	Color used to fill the bars (only used if bars are shown).
bar_width	Relative width of the bars (only used if bars are shown).
bee_width	Relative width of the beeswarms.
bee_adjust	Relative bandwidth adjustment factor used in estimating the density of the beeswarms.
viridis_args	List of viridis color scale arguments. The default points to the global option <code>shapviz.viridis_args</code> , which corresponds to <code>list(begin = 0.25, end = 0.85, option = "inferno")</code> . These values are passed to <code>ggplot2::scale_color_viridis_c()</code> . For example, to switch to standard viridis, either change the default with <code>options(shapviz.viridis_args = list())</code> or set <code>viridis_args = list()</code> .

color_bar_title	Title of color bar of the beeswarm plot. Set to NULL to hide the color bar altogether.
show_numbers	Should SHAP feature importances be printed? Default is FALSE.
format_fun	Function used to format SHAP feature importances (only if show_numbers = TRUE). To change to scientific notation, use <code>function(x) = prettyNum(x, scientific = TRUE)</code> .
number_size	Text size of the numbers (if show_numbers = TRUE).
sort_features	Should features be sorted or not? The default is TRUE.
bar_type	For "mshapviz" objects with kind = "bar": How should bars be represented? The default is "dodge" for dodged bars. Other options are "stack", "wrap", or "separate" (via "patchwork"). Note that "separate" is currently the only option that supports show_numbers = TRUE.

Details

The bar plot shows SHAP feature importances, calculated as the average absolute SHAP value per feature. The beeswarm plot displays SHAP values per feature, using min-max scaled feature values on the color axis. Non-numeric features are transformed to numeric by calling `data.matrix()` first. For both types of plots, the features are sorted in decreasing order of importance.

Value

A "ggplot" (or "patchwork") object representing an importance plot, or - if kind = "no" - a named numeric vector of sorted SHAP feature importances (or a matrix in case of an object of class "mshapviz").

Methods (by class)

- `sv_importance(default)`: Default method.
- `sv_importance(shapviz)`: SHAP importance plot for an object of class "shapviz".
- `sv_importance(mshapviz)`: SHAP importance plot for an object of class "mshapviz".

See Also

[sv_interaction](#)

Examples

```
X_train <- data.matrix(iris[, -1])
dtrain <- xgboost::xgb.DMatrix(X_train, label = iris[, 1], nthread = 1)
fit <- xgboost::xgb.train(data = dtrain, nrounds = 10, nthread = 1)
x <- shapviz(fit, X_pred = X_train)
sv_importance(x)
sv_importance(x, kind = "no")
sv_importance(x, kind = "beeswarm", show_numbers = TRUE)
```

sv_interaction	<i>SHAP Interaction Plot</i>
----------------	------------------------------

Description

Plots a beeswarm plot for each feature pair. Diagonals represent the main effects, while off-diagonals show interactions (multiplied by two due to symmetry). The colors on the beeswarm plots represent min-max scaled feature values. Non-numeric features are transformed to numeric by calling `data.matrix()` first. The features are sorted in decreasing order of usual SHAP importance.

Usage

```
sv_interaction(object, ...)

## Default S3 method:
sv_interaction(object, ...)

## S3 method for class 'shapviz'
sv_interaction(
  object,
  kind = c("beeswarm", "no"),
  max_display = 7L,
  alpha = 0.3,
  bee_width = 0.3,
  bee_adjust = 0.5,
  viridis_args = getOption("shapviz.viridis_args"),
  color_bar_title = "Row feature value",
  sort_features = TRUE,
  ...
)

## S3 method for class 'mshapviz'
sv_interaction(
  object,
  kind = c("beeswarm", "no"),
  max_display = 7L,
  alpha = 0.3,
  bee_width = 0.3,
  bee_adjust = 0.5,
  viridis_args = getOption("shapviz.viridis_args"),
  color_bar_title = "Row feature value",
  sort_features = TRUE,
  ...
)
```

Arguments

object	An object of class "(m)shapviz" containing element S_inter.
...	Arguments passed to <code>ggplot2::geom_point()</code> . For instance, passing <code>size = 1</code> will produce smaller dots.
kind	Set to "no" to return the matrix of average absolute SHAP interactions (or a list of such matrices in case of object of class "mshapviz"). Due to symmetry, off-diagonals are multiplied by two. The default is "beeswarm".
max_display	How many features should be plotted? Set to <code>Inf</code> to show all features. Has no effect if <code>kind = "no"</code> .
alpha	Transparency of the beeswarm dots. Defaults to 0.3.
bee_width	Relative width of the beeswarms.
bee_adjust	Relative bandwidth adjustment factor used in estimating the density of the beeswarms.
viridis_args	List of viridis color scale arguments. The default points to the global option <code>shapviz.viridis_args</code> , which corresponds to <code>list(begin = 0.25, end = 0.85, option = "inferno")</code> . These values are passed to <code>ggplot2::scale_color_viridis_c()</code> . For example, to switch to standard viridis, either change the default with <code>options(shapviz.viridis_args = list())</code> or set <code>viridis_args = list()</code> .
color_bar_title	Title of color bar of the beeswarm plot. Set to <code>NULL</code> to hide the color bar altogether.
sort_features	Should features be sorted or not? The default is <code>TRUE</code> .

Value

A "ggplot" (or "patchwork") object, or - if `kind = "no"` - a named numeric matrix of average absolute SHAP interactions sorted by the average absolute SHAP values (or a list of such matrices in case of "mshapviz" object).

Methods (by class)

- `sv_interaction(default)`: Default method.
- `sv_interaction(shapviz)`: SHAP interaction plot for an object of class "shapviz".
- `sv_interaction(mshapviz)`: SHAP interaction plot for an object of class "mshapviz".

See Also

[sv_importance\(\)](#)

Examples

```
dtrain <- xgboost::xgb.DMatrix(
  data.matrix(iris[, -1]), label = iris[, 1], nthread = 1
)
fit <- xgboost::xgb.train(data = dtrain, nrounds = 10, nthread = 1)
x <- shapviz(fit, X_pred = dtrain, X = iris, interactions = TRUE)
sv_interaction(x, kind = "no")
sv_interaction(x, max_display = 2, size = 3)
```

`sv_waterfall`*SHAP Waterfall Plot*

Description

Creates a waterfall plot of SHAP values of one observation. If multiple observations are selected, their SHAP values and predictions are averaged.

Usage

```
sv_waterfall(object, ...)

## Default S3 method:
sv_waterfall(object, ...)

## S3 method for class 'shapviz'
sv_waterfall(
  object,
  row_id = 1L,
  max_display = 10L,
  order_fun = function(s) order(abs(s)),
  fill_colors = c("#f7d13d", "#a52c60"),
  format_shap = getOption("shapviz.format_shap"),
  format_feat = getOption("shapviz.format_feat"),
  contrast = TRUE,
  show_connection = TRUE,
  show_annotation = TRUE,
  annotation_size = 3.2,
  ...
)

## S3 method for class 'mshapviz'
sv_waterfall(
  object,
  row_id = 1L,
  max_display = 10L,
  order_fun = function(s) order(abs(s)),
  fill_colors = c("#f7d13d", "#a52c60"),
  format_shap = getOption("shapviz.format_shap"),
  format_feat = getOption("shapviz.format_feat"),
  contrast = TRUE,
  show_connection = TRUE,
  show_annotation = TRUE,
  annotation_size = 3.2,
  ...
)
```

Arguments

object	An object of class "(m)shapviz".
...	Arguments passed to <code>ggfittext::geom_fit_text()</code> . For example, <code>size = 9</code> will use fixed text size in the bars and <code>size = 0</code> will altogether suppress adding text to the bars.
row_id	Subset of observations to plot, typically a single row number. If more than one row is selected, SHAP values are averaged, and feature values are shown only when they are unique.
max_display	Maximum number of features (with largest absolute SHAP values) should be plotted? If there are more features, they will be collapsed to one feature. Set to <code>Inf</code> to show all features.
order_fun	Function specifying the order of the variables/SHAP values. It maps the vector <code>s</code> of SHAP values to sort indices from 1 to <code>length(s)</code> . The default is <code>function(s) order(abs(s))</code> . To plot without sorting, use <code>function(s) 1:length(s)</code> or <code>function(s) length(s):1</code> .
fill_colors	A vector of exactly two fill colors: the first for positive SHAP values, the other for negative ones.
format_shap	Function used to format SHAP values. The default uses the global option <code>shapviz.format_shap</code> , which equals to <code>function(z) prettyNum(z, digits = 3, scientific = FALSE)</code> by default.
format_feat	Function used to format numeric feature values. The default uses the global option <code>shapviz.format_feat</code> , which equals to <code>function(z) prettyNum(z, digits = 3, scientific = FALSE)</code> by default.
contrast	Logical flag that determines whether to use white text in dark arrows. Default is <code>TRUE</code> .
show_connection	Should connecting lines be shown? Default is <code>TRUE</code> .
show_annotation	Should "f(x)" and "E(f(x))" be plotted? Default is <code>TRUE</code> .
annotation_size	Size of the annotation text (f(x)=... and E(f(x))=...).

Details

$f(x)$ denotes the prediction on the SHAP scale, while $E(f(x))$ refers to the baseline SHAP value.

Value

An object of class "ggplot" (or "patchwork") representing a waterfall plot.

Methods (by class)

- `sv_waterfall(default)`: Default method.
- `sv_waterfall(shapviz)`: SHAP waterfall plot for an object of class "shapviz".
- `sv_waterfall(mshapviz)`: SHAP waterfall plot for an object of class "mshapviz".

See Also[sv_force\(\)](#)**Examples**

```
dtrain <- xgboost::xgb.DMatrix(
  data.matrix(iris[, -1]), label = iris[, 1], nthread = 1
)
fit <- xgboost::xgb.train(data = dtrain, nrounds = 20, nthread = 1)
x <- shapviz(fit, X_pred = dtrain, X = iris[, -1])
sv_waterfall(x)
sv_waterfall(x, row_id = 123, max_display = 2, size = 9, fill_colors = 4:5)

# Ordered by colnames(x), combined with max_display
sv_waterfall(
  x[, sort(colnames(x))], order_fun = function(s) length(s):1, max_display = 3
)

# Aggregate over all observations with Petal.Length == 1.4
sv_waterfall(x, row_id = x$X$Petal.Length == 1.4)
```

[.shapviz

*Subsets "shapviz" Object***Description**

Use standard square bracket subsetting to select rows and/or columns of SHAP values, feature values, and SHAP interaction values of a "shapviz" object.

Usage

```
## S3 method for class 'shapviz'
x[i, j, ...]
```

Arguments

x	An object of class "shapviz".
i	Row subsetting.
j	Column subsetting.
...	Currently unused.

Value

A new object of class "shapviz".

See Also[shapviz\(\)](#)

Examples

```
S <- matrix(c(1, -1, -1, 1), ncol = 2, dimnames = list(NULL, c("x", "y")))
X <- data.frame(x = c("a", "b"), y = c(100, 10))
x <- shapviz(S, X, baseline = 4)
x[1, "x"]
x[1]
x[c(FALSE, TRUE), ]
x[, "x"]
```

Index

- * **datasets**
 - miami, 12
- + .mshapviz (+.shapviz), 3
- + .shapviz, 3
- [.shapviz, 37

- c.shapviz, 4
- collapse_shap, 5
- collapse_shap(), 20

- data.matrix(), 32, 33
- dim.shapviz, 6
- dimnames.shapviz, 6
- dimnames<- .shapviz, 7

- extractors, 8

- format(), 10
- format_max, 9

- get_baseline (extractors), 8
- get_feature_values (extractors), 8
- get_shap_interactions (extractors), 8
- get_shap_values (extractors), 8
- ggfittext::geom_fit_text(), 29, 36
- ggplot2::geom_bar(), 31
- ggplot2::geom_jitter(), 24, 27
- ggplot2::geom_point(), 31, 34
- ggplot2::scale_color_viridis_c(), 31, 34
- ggrepel::geom_text_repel(), 29

- is.mshapviz, 10
- is.shapviz, 11

- miami, 12
- mshapviz, 13
- mshapviz(), 4, 10, 15, 16

- potential_interactions, 13
- potential_interactions(), 23, 25

- print.mshapviz, 15
- print.shapviz, 15

- rbind.mshapviz (rbind.shapviz), 16
- rbind.shapviz, 16
- rbind.shapviz(), 3, 22

- shapviz, 17
- shapviz(), 3, 6, 7, 11, 16, 17, 22, 23, 37
- shapviz-package, 2
- split.shapviz, 22
- summary.shapviz, 23
- sv_dependence, 23
- sv_dependence(), 14, 20, 27
- sv_dependence2D, 26
- sv_dependence2D(), 20
- sv_force, 28
- sv_force(), 20, 37
- sv_importance, 30
- sv_importance(), 20, 34
- sv_interaction, 32, 33
- sv_interaction(), 20
- sv_waterfall, 35
- sv_waterfall(), 20, 30