

# Package ‘xplainfi’

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**Title** Feature Importance Methods for Global Explanations

**Version** 1.0.0

**Description** Provides a consistent interface for common feature importance methods as described in Ewald et al. (2024)  [<doi:10.1007/978-3-031-63797-1\\_22>](https://doi.org/10.1007/978-3-031-63797-1_22), including permutation feature importance (PFI), conditional and relative feature importance (CFI, RFI), leave one covariate out (LOCO), and Shapley additive global importance (SAGE), as well as feature sampling mechanisms to support conditional importance methods.

**License** LGPL (>= 3)

**URL** <https://mlr-org.github.io/xplainfi/>,  
<https://github.com/mlr-org/xplainfi>

**BugReports** <https://github.com/mlr-org/xplainfi/issues>

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CFI

*Conditional Feature Importance*

---

### Description

Implementation of CFI using modular sampling approach

### Super classes

`xplainfi::FeatureImportanceMethod` -> `xplainfi::PerturbationImportance` -> CFI

**Methods****Public methods:**

- [CFI\\$new\(\)](#)
- [CFI\\$compute\(\)](#)
- [CFI\\$clone\(\)](#)

**Method** `new()`: Creates a new instance of the CFI class

*Usage:*

```
CFI$new(
  task,
  learner,
  measure = NULL,
  resampling = NULL,
  features = NULL,
  groups = NULL,
  relation = "difference",
  n_repeats = 1L,
  batch_size = NULL,
  sampler = NULL
)
```

*Arguments:*

`task`, `learner`, `measure`, `resampling`, `features`, `groups`, `relation`, `n_repeats`, `batch_size`  
Passed to [PerturbationImportance](#).

`sampler` ([ConditionalSampler](#)) Optional custom sampler. Defaults to instantiating `ConditionalARFSampler` internally with default parameters.

**Method** `compute()`: Compute CFI scores

*Usage:*

```
CFI$compute(
  n_repeats = NULL,
  batch_size = NULL,
  store_models = TRUE,
  store_backends = TRUE
)
```

*Arguments:*

`n_repeats` (`integer(1)`) Number of permutation iterations. If `NULL`, uses stored value.

`batch_size` (`integer(1) | NULL: NULL`) Maximum number of rows to predict at once. If `NULL`, uses stored value.

`store_models`, `store_backends` (`logical(1): TRUE`) Whether to store fitted models / data backends, passed to [mlr3::resample](#) internally for the initial fit of the learner. This may be required for certain measures and is recommended to leave enabled unless really necessary.

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

*Usage:*

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

*Arguments:*

`deep` Whether to make a deep clone.

## References

Blesch K, Koenen N, Kapar J, Golchian P, Burk L, Loecher M, Wright M (2025). “Conditional Feature Importance with Generative Modeling Using Adversarial Random Forests.” *Proceedings of the AAAI Conference on Artificial Intelligence*, **39**(15), 15596–15604. doi:10.1609/aaai.v39i15.33712.

## Examples

```
library(mlr3)
library(mlr3learners)

task <- sim_dgp_correlated(n = 500)

# Using default ConditionalARFSampler
cfi <- CFI$new(
  task = task,
  learner = lrn("regr.ranger", num.trees = 10),
  measure = msr("regr.mse")
)
cfi$compute()
cfi$importance()
```

---

check\_groups

*Check group specification*

---

## Description

Check group specification

## Usage

```
check_groups(groups, all_features)
```

## Arguments

groups (list) A (named) list of groups  
all\_features (character()) All available feature names from the task.

## Value

The input list group, with each element now named.

**Examples**

```

task <- sim_dgp_interactions(n = 100)
task$feature_names

# Intended use
groups1 = list(effects = c("x1", "x2", "x3"), noise = c("noise1", "noise2"))
check_groups(groups1, task$feature_names)

# Names are auto-generated where needed
check_groups(list(a = "x1", c("x2", "x1")), task$feature_names)

# Examples for cases that throw errors:

# Unexpected features
groups2 = list(effects = c("x1", "foo", "bar", "x1"))
try(check_groups(groups2, task$feature_names))
# Too deeply nested
groups3 = list(effects = c("x1", "x2", "x3"), noise = c("noise1", list(c("noise2"))))
try(check_groups(groups2, task$feature_names))

```

---

ConditionalARFSampler *ARF-based Conditional Sampler*

---

**Description**

Implements conditional sampling using Adversarial Random Forests (ARF). ARF can handle mixed data types (continuous and categorical) and provides flexible conditional sampling by modeling the joint distribution.

**Details**

The ConditionalARFSampler fits an [Adversarial Random Forest](#) model on the task data, then uses it to generate samples from  $P(X_j|X_{-j})$  where  $X_j$  is the feature of interest and  $X_{-j}$  are the conditioning features.

**Super classes**

`xplainfi::FeatureSampler` -> `xplainfi::ConditionalSampler` -> `ConditionalARFSampler`

**Public fields**

`feature_types` (`character()`) Feature types supported by the sampler. Will be checked against the provided `mlr3::Task` to ensure compatibility.

`arf_model` Adversarial Random Forest model created by `arf::adversarial_rf`.

`psi` Distribution parameters estimated from by `arf::forde`.

## Methods

### Public methods:

- [ConditionalARFSampler\\$new\(\)](#)
- [ConditionalARFSampler\\$sample\(\)](#)
- [ConditionalARFSampler\\$sample\\_newdata\(\)](#)
- [ConditionalARFSampler\\$clone\(\)](#)

**Method new():** Creates a new instance of the ConditionalARFSampler class. To fit the ARF in parallel, register a parallel backend first (see [arf::arf](#)) and set `parallel = TRUE`.

#### Usage:

```
ConditionalARFSampler$new(
  task,
  conditioning_set = NULL,
  num_trees = 10L,
  min_node_size = 20L,
  finite_bounds = "no",
  epsilon = 1e-15,
  round = TRUE,
  stepsize = 0,
  verbose = FALSE,
  parallel = FALSE,
  ...
)
```

#### Arguments:

`task` ([mlr3::Task](#)) Task to sample from.

`conditioning_set` (character | NULL) Default conditioning set to use in `$sample()`. This parameter only affects the sampling behavior, not the ARF model fitting.

`num_trees` (integer(1): 10L) Number of trees for ARF. Passed to [arf::adversarial\\_rf](#).

`min_node_size` (integer(1): 20L) Minimum node size for ARF. Passed to [arf::adversarial\\_rf](#) and in turn to [ranger::ranger](#). This is increased to 20 to mitigate overfitting.

`finite_bounds` (character(1): "no") How to handle variable bounds. Passed to [arf::forde](#). Default is "no" for compatibility. "local" may improve extrapolation but can cause issues with some data.

`epsilon` (numeric(1): 0) Slack parameter for when `finite_bounds != "no"`. Passed to [arf::forde](#).

`round` (logical(1): TRUE) Whether to round continuous variables back to their original precision in sampling. Can be overridden in `$sample()` calls.

`stepsize` (numeric(1): 0) Number of rows of evidence to process at a time when `parallel` is TRUE. Default (0) spreads evidence evenly over registered workers. Can be overridden in `$sample()` calls.

`verbose` (logical(1): FALSE) Whether to print progress messages. Default is FALSE (`arf`'s default is TRUE). Can be overridden in `$sample()` calls.

`parallel` (logical(1): FALSE) Whether to use parallel processing via `foreach`. See examples in [arf::forge\(\)](#). Can be overridden in `$sample()` calls.

... Additional arguments passed to [arf::adversarial\\_rf](#).

**Method** `sample()`: Sample from stored task. Parameters use hierarchical resolution: function argument > stored param\_set value > hard-coded default.

*Usage:*

```
ConditionalARFSampler$sample(  
  feature,  
  row_ids = NULL,  
  conditioning_set = NULL,  
  round = NULL,  
  stepsize = NULL,  
  verbose = NULL,  
  parallel = NULL  
)
```

*Arguments:*

`feature` (character) Feature(s) to sample.  
`row_ids` (integer() | NULL) Row IDs to use. If NULL, uses all rows.  
`conditioning_set` (character | NULL) Features to condition on.  
`round` (logical(1) | NULL) Round continuous variables.  
`stepsize` (numeric(1) | NULL) Batch size for parallel processing.  
`verbose` (logical(1) | NULL) Print progress messages.  
`parallel` (logical(1) | NULL) Use parallel processing.

*Returns:* Modified copy with sampled feature(s).

**Method** `sample_newdata()`: Sample from external data. See `$sample()` for parameter details.

*Usage:*

```
ConditionalARFSampler$sample_newdata(  
  feature,  
  newdata,  
  conditioning_set = NULL,  
  round = NULL,  
  stepsize = NULL,  
  verbose = NULL,  
  parallel = NULL  
)
```

*Arguments:*

`feature` (character) Feature(s) to sample.  
`newdata` ([data.table](#)) External data to use.  
`conditioning_set` (character | NULL) Features to condition on.  
`round` (logical(1) | NULL) Round continuous variables.  
`stepsize` (numeric(1) | NULL) Batch size for parallel processing.  
`verbose` (logical(1) | NULL) Print progress messages.  
`parallel` (logical(1) | NULL) Use parallel processing.

*Returns:* Modified copy with sampled feature(s).

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

*Usage:*

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

*Arguments:*

deep Whether to make a deep clone.

**References**

Watson D, Blesch K, Kapar J, Wright M (2023). “Adversarial Random Forests for Density Estimation and Generative Modeling.” In *Proceedings of The 26th International Conference on Artificial Intelligence and Statistics*, 5357–5375. <https://proceedings.mlr.press/v206/watson23a.html>.

Blesch K, Koenen N, Kapar J, Golchian P, Burk L, Loecher M, Wright M (2025). “Conditional Feature Importance with Generative Modeling Using Adversarial Random Forests.” *Proceedings of the AAAI Conference on Artificial Intelligence*, **39**(15), 15596–15604. doi:10.1609/aaai.v39i15.33712.

**Examples**

```
library(mlr3)
task = tgen("2dnormals")$generate(n = 100)
# Create sampler with default parameters
sampler = ConditionalARFSampler$new(task, conditioning_set = "x2", verbose = FALSE)
# Sample using row_ids from stored task
sampled_data = sampler$sample("x1", row_ids = 1:10)
# Or use external data
data = task$data()
sampled_data_ext = sampler$sample_newdata("x1", newdata = data, conditioning_set = "x2")

# Example with custom ARF parameters
sampler_custom = ConditionalARFSampler$new(
  task,
  min_node_size = 10L,
  finite_bounds = "local",
  verbose = FALSE
)
sampled_custom = sampler_custom$sample("x1", conditioning_set = "x2")
```

---

ConditionalCtreeSampler

*(experimental) Conditional Inference Tree Conditional Sampler*

---

**Description**

Implements conditional sampling using conditional inference trees (ctree). Builds a tree predicting target features from conditioning features, then samples from the terminal node corresponding to each test observation.



## Details

This sampler approximates the conditional distribution  $P(X_B|X_A = x_A)$  by:

1. Building a conditional inference tree with  $X_B$  as response and  $X_A$  as predictors
2. For each test observation, finding its terminal (leaf) node in the tree
3. Sampling uniformly from training observations in that same terminal node

Conditional inference trees (ctree) use permutation tests to determine splits, which helps avoid overfitting and handles mixed feature types naturally. The tree partitions the feature space based on the conditioning variables, creating local neighborhoods that respect the conditional distribution structure.

### Key advantages over other samplers:

- Handles mixed feature types (continuous and categorical)
- Non-parametric (no distributional assumptions)
- Automatic feature selection (splits only on informative features)
- Can capture non-linear conditional relationships
- Statistically principled splitting criteria

### Hyperparameters control tree complexity:

- `mincriterion`: Significance level for splits (higher = fewer splits)
- `minsplit`: Minimum observations required for a split
- `minbucket`: Minimum observations in terminal nodes

This implementation is inspired by shapr's ctree approach but simplified for our use case (we build trees on-demand rather than pre-computing all subsets).

### Advantages:

- Works with any feature types
- Robust to outliers
- Interpretable tree structure
- Handles high-dimensional conditioning

### Limitations:

- Requires model fitting (slower than kNN)
- Can produce duplicates if terminal nodes are small
- Tree building time increases with data size

## Super classes

```
xplainfi::FeatureSampler -> xplainfi::ConditionalSampler -> ConditionalCtreeSampler
```

**Public fields**

feature\_types (character()) Feature types supported by the sampler. Will be checked against the provided `mlr3::Task` to ensure compatibility.

tree\_cache (environment) Cache for fitted ctree models.

**Methods****Public methods:**

- `ConditionalCtreeSampler$new()`
- `ConditionalCtreeSampler$clone()`

**Method** `new()`: Creates a new `ConditionalCtreeSampler`.

*Usage:*

```
ConditionalCtreeSampler$new(
  task,
  conditioning_set = NULL,
  mincriterion = 0.95,
  minsplit = 20L,
  minbucket = 7L,
  use_cache = TRUE
)
```

*Arguments:*

task (`mlr3::Task`) Task to sample from.

conditioning\_set (character | NULL) Default conditioning set to use in `$sample()`.

mincriterion (numeric(1): 0.95) Significance level threshold for splitting (1 - p-value).  
Higher values result in fewer splits (simpler trees).

minsplit (integer(1): 20L) Minimum number of observations required for a split.

minbucket (integer(1): 7L) Minimum number of observations in terminal nodes.

use\_cache (logical(1): TRUE) Whether to cache fitted trees.

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

*Usage:*

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

*Arguments:*

deep Whether to make a deep clone.

**References**

Hothorn T, Hornik K, Zeileis A (2006). “Unbiased Recursive Partitioning: A Conditional Inference Framework.” *Journal of Computational and Graphical Statistics*, **15**(3), 651–674. doi:10.1198/106186006X133933.

Aas K, Jullum M, Løland A (2021). “Explaining Individual Predictions When Features Are Dependent: More Accurate Approximations to Shapley Values.” *Artificial Intelligence*, **298**, 103502. doi:10.1016/j.artint.2021.103502.

**Examples**

```

library(mlr3)
task = tgen("friedman1")$generate(n = 100)

# Create sampler with default parameters
sampler = ConditionalCtreeSampler$new(task)

# Sample features conditioned on others
test_data = task$data(rows = 1:5)
sampled = sampler$sample_newdata(
  feature = c("important2", "important3"),
  newdata = test_data,
  conditioning_set = "important1"
)

```

---

ConditionalGaussianSampler

*Gaussian Conditional Sampler*


---

**Description**

Implements conditional sampling assuming features follow a multivariate Gaussian distribution. Computes conditional distributions analytically using standard formulas for multivariate normal distributions.

**Details**

For a joint Gaussian distribution  $X \sim N(\mu, \Sigma)$ , partitioned as  $X = (X_A, X_B)$ , the conditional distribution is:

$$X_B | X_A = x_A \sim N(\mu_{B|A}, \Sigma_{B|A})$$

where:

$$\mu_{B|A} = \mu_B + \Sigma_{BA} \Sigma_{AA}^{-1} (x_A - \mu_A)$$

$$\Sigma_{B|A} = \Sigma_{BB} - \Sigma_{BA} \Sigma_{AA}^{-1} \Sigma_{AB}$$

This is equivalent to the regression formulation used by fippy:

$$\beta = \Sigma_{BA} \Sigma_{AA}^{-1}$$

$$\mu_{B|A} = \mu_B + \beta(x_A - \mu_A)$$

$$\Sigma_{B|A} = \Sigma_{BB} - \beta \Sigma_{AB}$$

**Assumptions:**

- Features are approximately multivariate normal

- Only continuous features are supported

#### Advantages:

- Very fast (closed-form solution)
- Deterministic (given seed)
- No hyperparameters
- Memory efficient

#### Limitations:

- Strong distributional assumption
- May produce out-of-range values for bounded features
- Cannot handle categorical features
- Integer features are treated as continuous and rounded back to integers

#### Super classes

`xplainfi::FeatureSampler` -> `xplainfi::ConditionalSampler` -> `ConditionalGaussianSampler`

#### Public fields

`feature_types` (`character()`) Feature types supported by the sampler.

`mu` (`numeric()`) Mean vector estimated from training data.

`sigma` (`matrix()`) Covariance matrix estimated from training data.

#### Methods

##### Public methods:

- `ConditionalGaussianSampler$new()`
- `ConditionalGaussianSampler$clone()`

**Method** `new()`: Creates a new `ConditionalGaussianSampler`.

*Usage:*

```
ConditionalGaussianSampler$new(task, conditioning_set = NULL)
```

*Arguments:*

`task` (`mlr3::Task`) Task to sample from. Must have only numeric/integer features.

`conditioning_set` (`character` | `NULL`) Default conditioning set to use in `$sample()`.

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

*Usage:*

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

*Arguments:*

`deep` Whether to make a deep clone.

## References

Anderson T (2003). *An Introduction to Multivariate Statistical Analysis*, 3rd edition. Wiley-Interscience, Hoboken, NJ. ISBN 9780471360919.

## Examples

```
library(mlr3)
task = tgen("friedman1")$generate(n = 100)
sampler = ConditionalGaussianSampler$new(task)

# Sample x2, x3 conditioned on x1
test_data = task$data(rows = 1:5)
sampled = sampler$sample_newdata(
  feature = c("important2", "important3"),
  newdata = test_data,
  conditioning_set = "important1"
)
```

---

ConditionalKNNSampler *k-Nearest Neighbors Conditional Sampler*

---

## Description

Implements conditional sampling using k-nearest neighbors (kNN). For each observation, finds the k most similar observations based on conditioning features, then samples the target features from these neighbors.

## Details

This sampler approximates the conditional distribution  $P(X_B|X_A = x_A)$  by:

1. Finding the k nearest neighbors of  $x_A$  in the training data
2. Sampling uniformly from the target feature values  $X_B$  of these k neighbors

This is a simple, non-parametric approach that:

- Requires no distributional assumptions
- Handles mixed feature types (numeric, integer, factor, ordered, logical)
- Is computationally efficient (no model fitting required)
- Adapts locally to the data structure

The method is related to hot-deck imputation and kNN imputation techniques used in missing data problems. As  $k \rightarrow \infty$  and  $k/n \rightarrow 0$ , the kNN conditional distribution converges to the true conditional distribution under mild regularity conditions (Lipschitz continuity).

### Distance Metrics:

The sampler supports two distance metrics:

- **Euclidean:** For numeric/integer features only. Standardizes features before computing distances.
- **Gower:** For mixed feature types. Handles numeric, factor, ordered, and logical features. Numeric features are range-normalized, categorical features use exact matching (0/1).

The distance parameter controls which metric to use:

- "auto" (default): Automatically selects Euclidean for all-numeric features, Gower otherwise
- "euclidean": Forces Euclidean distance (errors if non-numeric features present)
- "gower": Forces Gower distance (works with any feature types)

#### Advantages:

- Very fast (no model training)
- Works with any feature types
- Automatic distance metric selection
- Naturally respects local data structure

#### Limitations:

- Sensitive to choice of k
- The full task data is required for prediction
- Can produce duplicates if k is small
- May not extrapolate well to new regions

#### Super classes

```
xplainfi::FeatureSampler -> xplainfi::ConditionalSampler -> ConditionalKNNsampler
```

#### Public fields

feature\_types (character()) Feature types supported by the sampler.

#### Methods

##### Public methods:

- `ConditionalKNNsampler$new()`
- `ConditionalKNNsampler$sample()`
- `ConditionalKNNsampler$sample_newdata()`
- `ConditionalKNNsampler$clone()`

**Method** `new()`: Creates a new `ConditionalKNNsampler`.

*Usage:*

```
ConditionalKNNsampler$new(task, conditioning_set = NULL, k = 5L)
```

*Arguments:*

task (`mlr3::Task`) Task to sample from.

conditioning\_set (character | NULL) Default conditioning set to use in `$sample()`.

k (integer(1): 5L) Number of nearest neighbors to sample from.

**Method** sample(): Sample features from their kNN-based conditional distribution.

*Usage:*

```
ConditionalKNNsampler$sample(  
  feature,  
  row_ids = NULL,  
  conditioning_set = NULL,  
  k = NULL  
)
```

*Arguments:*

feature (character()) Feature name(s) to sample.

row\_ids (integer() | NULL) Row IDs from task to use as conditioning values.

conditioning\_set (character() | NULL) Features to condition on. If NULL, samples from marginal distribution (random sampling from training data).

k (integer(1) | NULL) Number of neighbors. If NULL, uses stored parameter.

*Returns:* Modified copy with sampled feature(s).

**Method** sample\_newdata(): Sample from external data conditionally.

*Usage:*

```
ConditionalKNNsampler$sample_newdata(  
  feature,  
  newdata,  
  conditioning_set = NULL,  
  k = NULL  
)
```

*Arguments:*

feature (character()) Feature(s) to sample.

newdata ([data.table](#)) External data to use.

conditioning\_set (character() | NULL) Features to condition on.

k (integer(1) | NULL) Number of neighbors. If NULL, uses stored parameter.

*Returns:* Modified copy with sampled feature(s).

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

*Usage:*

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

*Arguments:*

deep Whether to make a deep clone.

## References

Little R, Rubin D (2019). *Statistical Analysis with Missing Data*, 3rd edition. John Wiley & Sons, Hoboken, NJ. ISBN 9780470526798.

Troyanskaya O, Cantor M, Sherlock G, Brown P, Hastie T, Tibshirani R, Botstein D, Altman R (2001). "Missing Value Estimation Methods for DNA Microarrays." *Bioinformatics*, **17**(6), 520–525. doi:[10.1093/bioinformatics/17.6.520](https://doi.org/10.1093/bioinformatics/17.6.520).

**Examples**

```

library(mlr3)
task = tgen("friedman1")$generate(n = 100)
sampler = ConditionalKNNsampler$new(task, k = 5)

# Sample features conditioned on others
test_data = task$data(rows = 1:5)
sampled = sampler$sample_newdata(
  feature = c("important2", "important3"),
  newdata = test_data,
  conditioning_set = "important1"
)

```

---

 ConditionalSAGE

*Conditional SAGE*


---

**Description**

**SAGE** with conditional sampling (features are "marginalized" conditionally). Uses [ConditionalARFSampler](#) as default [ConditionalSampler](#).

**Super classes**

[xplainfi::FeatureImportanceMethod](#) -> [xplainfi::SAGE](#) -> ConditionalSAGE

**Public fields**

sampler ([ConditionalSampler](#)) Sampler for conditional marginalization.

**Methods****Public methods:**

- [ConditionalSAGE\\$new\(\)](#)
- [ConditionalSAGE\\$clone\(\)](#)

**Method** `new()`: Creates a new instance of the ConditionalSAGE class.

*Usage:*

```

ConditionalSAGE$new(
  task,
  learner,
  measure = NULL,
  resampling = NULL,
  features = NULL,
  n_permutations = 10L,
  sampler = NULL,
  batch_size = 5000L,

```



```

    n_samples = 100L,
    early_stopping = FALSE,
    se_threshold = 0.01,
    min_permutations = 10L,
    check_interval = 1L
  )

```

*Arguments:*

task, learner, measure, resampling, features, n\_permutations, batch\_size, n\_samples, early\_stopping, Passed to [SAGE](#).

sampler ([ConditionalSampler](#)) Optional custom sampler. Defaults to [ConditionalARFSampler](#).

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

*Usage:*

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

*Arguments:*

deep Whether to make a deep clone.

**See Also**

[MarginalSAGE](#)

**Examples**

```

library(mlr3)
task = tgen("friedman1")$generate(n = 100)

# Using default ConditionalARFSampler (also handles all mixed data)
sage = ConditionalSAGE$new(
  task = task,
  learner = lrn("regr.ranger", num.trees = 50),
  measure = msr("regr.mse"),
  n_permutations = 3L,
  n_samples = 20
)
sage$compute()

# For alternative conditional samplers:
custom_sampler = ConditionalGaussianSampler$new(
  task = task
)
sage_custom = ConditionalSAGE$new(
  task = task,
  learner = lrn("regr.ranger", num.trees = 50),
  measure = msr("regr.mse"),
  n_permutations = 5L,
  n_samples = 20,
  sampler = custom_sampler
)

```

```
)
sage_custom$compute()
```

---

ConditionalSampler      *Conditional Feature Sampler*

---

## Description

Base class for conditional sampling methods where features are sampled conditionally on other features. This is an abstract class that should be extended by concrete implementations.

## Super class

```
xplainfi::FeatureSampler -> ConditionalSampler
```

## Methods

### Public methods:

- `ConditionalSampler$new()`
- `ConditionalSampler$sample()`
- `ConditionalSampler$sample_newdata()`
- `ConditionalSampler$clone()`

**Method** `new()`: Creates a new instance of the ConditionalSampler class

*Usage:*

```
ConditionalSampler$new(task, conditioning_set = NULL)
```

*Arguments:*

`task` (`mlr3::Task`) Task to sample from

`conditioning_set` (`character` | `NULL`) Default conditioning set to use in `$sample()`.

**Method** `sample()`: Sample from stored task conditionally on other features.

*Usage:*

```
ConditionalSampler$sample(
  feature,
  row_ids = NULL,
  conditioning_set = NULL,
  ...
)
```

*Arguments:*

`feature` (`character`) Feature(s) to sample.

`row_ids` (`integer()` | `NULL`) Row IDs to use. If `NULL`, uses all rows.

`conditioning_set` (`character` | `NULL`) Features to condition on.

... Additional arguments passed to the sampler implementation.

*Returns:* Modified copy with sampled feature(s).

**Method** `sample_newdata()`: Sample from external data conditionally.

*Usage:*

```
ConditionalSampler$sample_newdata(
  feature,
  newdata,
  conditioning_set = NULL,
  ...
)
```

*Arguments:*

`feature` (character) Feature(s) to sample.

`newdata` ([data.table](#)) External data to use.

`conditioning_set` (character | NULL) Features to condition on.

... Additional arguments passed to the sampler implementation.

*Returns:* Modified copy with sampled feature(s).

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

*Usage:*

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

*Arguments:*

`deep` Whether to make a deep clone.

---

FeatureImportanceMethod

*Feature Importance Method Class*

---

## Description

Feature Importance Method Class

Feature Importance Method Class

## Public fields

`label` (character(1)) Method label.

`task` ([mlr3::Task](#))

`learner` ([mlr3::Learner](#))

`measure` ([mlr3::Measure](#))

`resampling` ([mlr3::Resampling](#)), instantiated upon construction.

`resample_result` ([mlr3::ResampleResult](#)) of the original learner and task, used for baseline scores.

`features` (character: NULL) Features of interest. By default, importances will be computed for each feature in task, but optionally this can be restricted to at least one feature. Ignored if `groups` is specified.

`groups` (list: NULL) A (named) list of features (names or indices as in task). If `groups` is specified, `features` is ignored. Importances will be calculated for group of features at a time, e.g., in [PFI](#) not one but the group of features will be permuted at each step. Analogously in [WVIM](#), each group of features will be left out (or in) for each model refit. Not all methods support groups (e.g., [SAGE](#)).

`param_set` ([paradox::ps\(\)](#))

`predictions` ([data.table](#)) Feature-specific prediction objects provided for some methods ([PFI](#), [WVIM](#)). Contains columns for feature of interest, resampling iteration, refit or perturbation iteration, and [mlr3::Prediction](#) objects.

## Methods

### Public methods:

- [FeatureImportanceMethod\\$new\(\)](#)
- [FeatureImportanceMethod\\$compute\(\)](#)
- [FeatureImportanceMethod\\$importance\(\)](#)
- [FeatureImportanceMethod\\$obs\\_loss\(\)](#)
- [FeatureImportanceMethod\\$reset\(\)](#)
- [FeatureImportanceMethod\\$print\(\)](#)
- [FeatureImportanceMethod\\$scores\(\)](#)
- [FeatureImportanceMethod\\$clone\(\)](#)

**Method** `new()`: Creates a new instance of this [R6](#) class. This is typically intended for use by derived classes.

*Usage:*

```
FeatureImportanceMethod$new(
  task,
  learner,
  measure = NULL,
  resampling = NULL,
  features = NULL,
  groups = NULL,
  param_set = paradox::ps(),
  label
)
```

*Arguments:*

`task`, `learner`, `measure`, `resampling`, `features`, `groups`, `param_set`, `label` Used to set fields

**Method** `compute()`: Compute feature importance scores

*Usage:*

```
FeatureImportanceMethod$compute(store_backends = TRUE)
```

*Arguments:*

store\_backends (logical(1): TRUE) Whether to store backends.

**Method importance():** Get aggregated importance scores. The stored `measure` object's aggregator (default: mean) will be used to aggregated importance scores across resampling iterations and, depending on the method use, permutations ([PerturbationImportance](#) or refits [LOCO](#)).

*Usage:*

```
FeatureImportanceMethod$importance(
  relation = NULL,
  standardize = FALSE,
  ci_method = c("none", "raw", "nadeau_bengio", "quantile"),
  conf_level = 0.95,
  ...
)
```

*Arguments:*

relation (character(1)) How to relate perturbed scores to originals ("difference" or "ratio"). If NULL, uses stored parameter value. This is only applicable for methods where importance is based on some relation between baseline and post-modification loss, i.e. [PerturbationImportance](#) methods such as [PFI](#) or [WVIM / LOCO](#). Not available for [SAGE](#) methods.

standardize (logical(1): FALSE) If TRUE, importances are standardized by the highest score so all scores fall in [-1, 1].

ci\_method (character(1): "none") Which confidence interval estimation method to use, defaulting to omitting variance estimation ("none"). If "raw", uncorrected (too narrow) CIs are provided purely for informative purposes. If "nadeau\_bengio", variance correction is performed according to Nadeau & Bengio (2003) as suggested by Molnar et al. (2023). If "quantile", empirical quantiles are used to construct confidence-like intervals. These methods are model-agnostic and rely on suitable resamplings, e.g. subsampling with 15 repeats for "nadeau\_bengio". See details.

conf\_level (numeric(1): 0.95) Confidence level to use for confidence interval construction when ci\_method != "none".

... Additional arguments passed to specialized methods, if any.

*Details:* Variance estimates for importance scores are biased due to the resampling procedure. Molnar et al. (2023) suggest to use the variance correction factor proposed by Nadeau & Bengio (2003) of  $n_2/n_1$ , where  $n_2$  and  $n_1$  are the sizes of the test- and train set, respectively. This should then be combined with approx. 15 iterations of either bootstrapping or subsampling.

The use of bootstrapping in this context can lead to problematic information leakage when combined with learners that perform bootstrapping themselves, e.g., Random Forest learners. In such cases, observations may be used as train- and test instances simultaneously, leading to erroneous performance estimates.

An approach leading to still imperfect, but improved variance estimates could be:

```
PFI$new(
  task = sim_dgp_interactions(n = 1000),
  learner = lrn("regr.ranger", num.trees = 100),
  measure = msr("regr.mse"),
  # Subsampling instead of bootstrapping due to RF
  resampling = rsmpl("subsampling", repeats = 15),
```

```
n_repeats = 5
)
```

`n_repeats = 5` in this context only improves the stability of the PFI estimate within the resampling iteration, whereas `rsmp("subsampling", repeats = 15)` is used to account for learner variance and necessitates variance correction.

This approach can in principle also be applied to CFI and RFI, but beware that a conditional sample such as [ConditionalARFSampler](#) also needs to be trained on data, which would need to be taken account by the variance estimation method. Analogously, the "nadeau\_bengio" correction was recommended for the use with [PFI](#) by Molnar et al., so its use with other methods like [LOCO](#) or [SAGE](#) is experimental.

Note that even if `measure` uses an aggregator function that is not the mean, variance estimation currently will always use `mean()` and `var()`.

*Returns:* ([data.table](#)) Aggregated importance scores with columns "feature", "importance", and depending on `ci_method` also "se", "conf\_lower", "conf\_upper".

**Method** `obs_loss()`: Calculate observation-wise importance scores.

Requires that `$compute()` was run and that `measure` is decomposable and has an observation-wise loss (`Measure$obs_loss()`) associated with it. This is not the case for `measure` like `classif_auc`, which is not decomposable.

*Usage:*

```
FeatureImportanceMethod$obs_loss(relation = NULL)
```

*Arguments:*

`relation` (`character(1)`) How to relate perturbed scores to originals ("difference" or "ratio"). If `NULL`, uses stored parameter value. This is only applicable for methods where importance is based on some relation between baseline and post-modification loss, i.e. [PerturbationImportance](#) methods such as [PFI](#) or [WVIM / LOCO](#). Not available for [SAGE](#) methods.

*Returns:* ([data.table](#)) Observation-wise losses and importance scores with columns "feature", "iter\_rsmp", "iter\_repeat" (if applicable), "row\_ids", "loss\_baseline", "loss\_post", and "obs\_importance".

**Method** `reset()`: Resets all stored fields populated by `$compute`: `$resample_result`, `$scores`, `$obs_losses`, and `$predictions`.

*Usage:*

```
FeatureImportanceMethod$reset()
```

**Method** `print()`: Print importance scores

*Usage:*

```
FeatureImportanceMethod$print(...)
```

*Arguments:*

... Passed to `print()`

**Method** `scores()`: Calculate importance scores for each resampling iteration and sub-iterations (`iter_rsmp` in [PFI](#) for example).

Iteration-wise importance are computed on the fly depending on the chosen relation (difference or ratio) to avoid re-computation if only a different relation is needed.

*Usage:*

```
FeatureImportanceMethod$scores(relation = NULL)
```

*Arguments:*

`relation` (character(1)) How to relate perturbed scores to originals ("difference" or "ratio"). If NULL, uses stored parameter value. This is only applicable for methods where importance is based on some relation between baseline and post-modification loss, i.e. [PerturbationImportance](#) methods such as [PFI](#) or [WVIM / LOCO](#). Not available for [SAGE](#) methods.

*Returns:* ([data.table](#)) Iteration-wise importance scores with columns for "feature", iteration indices, baseline and post-modification scores, and "importance".

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

*Usage:*

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

*Arguments:*

`deep` Whether to make a deep clone.

**References**

Nadeau C, Bengio Y (2003). "Inference for the Generalization Error." *Machine Learning*, **52**(3), 239–281. [doi:10.1023/A:1024068626366](https://doi.org/10.1023/A:1024068626366).  
 Molnar C, Freiesleben T, König G, Herbringer J, Reisinger T, Casalicchio G, Wright M, Bischl B (2023). "Relating the Partial Dependence Plot and Permutation Feature Importance to the Data Generating Process." In Longo L (ed.), *Explainable Artificial Intelligence*, 456–479. ISBN 978-3-031-44064-9, [doi:10.1007/9783031440649\\_24](https://doi.org/10.1007/9783031440649_24).

---

 FeatureSampler

*Feature Sampler Class*


---

**Description**

Base class for implementing different sampling strategies for feature importance methods like PFI and CFI

**Public fields**

`task` ([mlr3::Task](#)) Original task.

`label` (character(1)) Name of the sampler.

`feature_types` (character()) Feature types supported by the sampler. Will be checked against the provided [mlr3::Task](#) to ensure compatibility.

`param_set` ([paradox::ParamSet](#)) Parameter set for the sampler.

## Methods

### Public methods:

- [FeatureSampler\\$new\(\)](#)
- [FeatureSampler\\$sample\(\)](#)
- [FeatureSampler\\$sample\\_newdata\(\)](#)
- [FeatureSampler\\$print\(\)](#)
- [FeatureSampler\\$clone\(\)](#)

**Method** `new()`: Creates a new instance of the FeatureSampler class

*Usage:*

```
FeatureSampler$new(task)
```

*Arguments:*

task ([mlr3::Task](#)) Task to sample from

**Method** `sample()`: Sample values for feature(s) from stored task

*Usage:*

```
FeatureSampler$sample(feature, row_ids = NULL)
```

*Arguments:*

feature (character) Feature name(s) to sample (can be single or multiple). Must match those in the stored [Task](#).

row\_ids (integer(): NULL) Row IDs of the stored [Task](#) to use as basis for sampling.

*Returns:* Modified copy of the input features with the feature(s) sampled: A [data.table](#) with same number of columns and one row matching the supplied row\_ids

**Method** `sample_newdata()`: Sample values for feature(s) using external data

*Usage:*

```
FeatureSampler$sample_newdata(feature, newdata)
```

*Arguments:*

feature (character) Feature name(s) to sample (can be single or multiple)

newdata ([data.table](#)) External data to use for sampling.

**Method** `print()`: Print sampler

*Usage:*

```
FeatureSampler$print(...)
```

*Arguments:*

... Ignored.

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

*Usage:*

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

*Arguments:*

deep Whether to make a deep clone.



---

 KnockoffGaussianSampler

*Gaussian Knockoff Conditional Sampler*


---

## Description

A [KnockoffSampler](#) defaulting to second-order Gaussian knockoffs as created by [knockoff::create.second\\_order](#).

## Details

This is equivalent to [KnockoffSampler](#) using the default `knockoff_fun`.

## Super classes

[xplainfi::FeatureSampler](#) -> [xplainfi::KnockoffSampler](#) -> [KnockoffGaussianSampler](#)

## Public fields

`feature_types` (`character()`) Feature types supported by the sampler. Will be checked against the provided [mlr3::Task](#) to ensure compatibility.

`x_tilde` Knockoff matrix

## Methods

### Public methods:

- [KnockoffGaussianSampler\\$new\(\)](#)
- [KnockoffGaussianSampler\\$clone\(\)](#)

**Method** `new()`: Creates a new instance using Gaussian knockoffs via [knockoff::create.second\\_order](#).

*Usage:*

```
KnockoffGaussianSampler$new(task, iters = 1)
```

*Arguments:*

`task` ([mlr3::Task](#)) Task to sample from.

`iters` (`integer(1): 1`) Number of repetitions the `knockoff_fun` is applied to create multiple `x_tilde` instances per observation.

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

*Usage:*

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

*Arguments:*

`deep` Whether to make a deep clone.

## References

Watson D, Wright M (2021). “Testing Conditional Independence in Supervised Learning Algorithms.” *Machine Learning*, **110**(8), 2107–2129. doi:10.1007/s10994021060306.

Blesch K, Watson D, Wright M (2023). “Conditional Feature Importance for Mixed Data.” *AStA Advances in Statistical Analysis*, **108**(2), 259–278. doi:10.1007/s10182023004779.

## Examples

```
library(mlr3)
task = tgen("2dnormals")$generate(n = 100)
# Create sampler
sampler = KnockoffGaussianSampler$new(task)
# Sample using row_ids from stored task
sampled_data = sampler$sample("x1")
```

---

KnockoffSampler

*Knockoff Sampler*

---

## Description

Implements conditional sampling using Knockoffs.

## Details

The KnockoffSampler samples [Knockoffs](#) based on the task data. This class allows arbitrary knockoff\_fun, which also means that no input checking against supported feature types can be done. Use [KnockoffGaussianSampler](#) for the Gaussian knockoff sampler for numeric features. Alternative knockoff samplers include knockoff\_seq() from the seqknockoff package available on GitHub: <https://github.com/kormama1/seqknockoff>.

Knockoffs are related to the ConditionalSampler family, with key differences: They do not allow specifying a conditioning\_set

## Super class

xplainfi::FeatureSampler -> KnockoffSampler

## Public fields

x\_tilde Knockoff matrix with one (or iters) row(s) per original observation in task.

## Methods

### Public methods:

- [KnockoffSampler\\$new\(\)](#)
- [KnockoffSampler\\$sample\(\)](#)
- [KnockoffSampler\\$clone\(\)](#)

**Method** `new()`: Creates a new instance of the `KnockoffSampler` class.

*Usage:*

```
KnockoffSampler$new(
  task,
  knockoff_fun = function(x) knockoff::create.second_order(as.matrix(x)),
  iters = 1
)
```

*Arguments:*

`task` (`mlr3::Task`) Task to sample from

`knockoff_fun` (function) Function used to create knockoff matrix. Default are second-order Gaussian knockoffs (`knockoff::create.second_order()`)

`iters` (`integer(1): 1`) Number of repetitions the `knockoff_fun` is applied to create multiple `x_tilde` instances per observation.

**Method** `sample()`: Sample from stored task using knockoff values. Replaces specified feature(s) with their knockoff counterparts from the pre-generated knockoff matrix.

*Usage:*

```
KnockoffSampler$sample(feature, row_ids = NULL)
```

*Arguments:*

`feature` (character) Feature(s) to sample.

`row_ids` (`integer() | NULL`) Row IDs to use. If `NULL`, uses all rows.

*Returns:* Modified copy with knockoff feature(s).

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

*Usage:*

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

*Arguments:*

`deep` Whether to make a deep clone.

## References

- Watson D, Wright M (2021). “Testing Conditional Independence in Supervised Learning Algorithms.” *Machine Learning*, **110**(8), 2107–2129. doi:10.1007/s10994021060306.
- Blesch K, Watson D, Wright M (2023). “Conditional Feature Importance for Mixed Data.” *AStA Advances in Statistical Analysis*, **108**(2), 259–278. doi:10.1007/s10182023004779.

**Examples**

```
library(mlr3)
task = tgen("2dnormals")$generate(n = 100)
# Create sampler with default parameters
sampler = KnockoffSampler$new(task)
# Sample using row_ids from stored task
sampled_data = sampler$sample("x1")
```

---

 LOCO

*Leave-One-Covariate-Out (LOCO)*


---

**Description**

Calculates Leave-One-Covariate-Out (LOCO) scores.

**Details**

LOCO measures feature importance by comparing model performance with and without each feature. For each feature, the model is retrained without that feature and the performance difference (reduced\_model\_loss - full\_model\_loss) indicates the feature's importance. Higher values indicate more important features.

**Super classes**

`xplainfi::FeatureImportanceMethod` -> `xplainfi::WVIM` -> LOCO

**Methods****Public methods:**

- `LOCO$new()`
- `LOCO$compute()`
- `LOCO$clone()`

**Method** `new()`: Creates a new instance of this R6 class.

*Usage:*

```
LOCO$new(
  task,
  learner,
  measure = NULL,
  resampling = NULL,
  features = NULL,
  n_repeats = 1L
)
```

*Arguments:*

`task` (`mlr3::Task`) Task to compute importance for.

learner (`mlr3::Learner`) Learner to use for prediction.  
 measure (`mlr3::Measure`: `NULL`) Measure to use for scoring. Defaults to `classif.ce` for classification and `regr.mse` for regression.  
 resampling (`mlr3::Resampling`) Resampling strategy. Defaults to `holdout`.  
 features (`character()`) Features to compute importance for. Defaults to all features.  
 n\_repeats (`integer(1)`: `1L`) Number of refit iterations per resampling iteration.

**Method** `compute()`: Compute LOCO importances.

*Usage:*

```
LOCO$compute(store_models = TRUE, store_backends = TRUE)
```

*Arguments:*

`store_models`, `store_backends` (`logical(1)`: `TRUE`) Whether to store fitted models / data backends, passed to `mlr3::resample` internally

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

*Usage:*

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

*Arguments:*

`deep` Whether to make a deep clone.

## References

Lei J, G'Sell M, Rinaldo A, Tibshirani R, Wasserman L (2018). "Distribution-Free Predictive Inference for Regression." *Journal of the American Statistical Association*, **113**(523), 1094–1111. [doi:10.1080/01621459.2017.1307116](https://doi.org/10.1080/01621459.2017.1307116).

## Examples

```

library(mlr3)
library(mlr3learners)

task <- sim_dgp_correlated(n = 500)

loco <- LOCO$new(
  task = task,
  learner = lrn("regr.ranger", num.trees = 10),
  measure = msr("regr.mse")
)
loco$compute()
loco$importance()

```

---

MarginalPermutationSampler

*Marginal Permutation Sampler*

---

## Description

Implements marginal permutation-based sampling for Permutation Feature Importance (PFI). Each specified feature is randomly shuffled (permuted) independently, breaking the relationship between the feature and the target as well as between rows.

## Details

The permutation sampler randomly shuffles feature values across observations:

- Each feature is permuted **independently** within its column
- The association between feature values and target values is broken
- The association between feature values **across rows** is broken
- The marginal distribution of each feature is preserved

### Important distinction from SAGE's "marginal" approach:

- MarginalPermutationSampler: Shuffles features independently, breaking row structure
- MarginalSAGE: Uses reference data but keeps rows intact (features in coalition stay together)

This is the classic approach used in Permutation Feature Importance (PFI) and assumes features are independent.

## Super classes

`xplainfi::FeatureSampler` -> `xplainfi::MarginalSampler` -> MarginalPermutationSampler

## Methods

### Public methods:

- `MarginalPermutationSampler$new()`
- `MarginalPermutationSampler$clone()`

**Method** `new()`: Creates a new instance of the MarginalPermutationSampler class.

*Usage:*

`MarginalPermutationSampler$new(task)`

*Arguments:*

`task` (`mlr3::Task`) Task to sample from.

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

*Usage:*

`MarginalPermutationSampler$clone(deep = FALSE)`

*Arguments:*

`deep` Whether to make a deep clone.

**Examples**

```

library(mlr3)
task = tgen("2dnormals")$generate(n = 10)
task$data()
sampler = MarginalPermutationSampler$new(task)

# Sample using row_ids from stored task
sampler$sample("x1")

# Or use external data
data = task$data()
sampler$sample_newdata("x1", newdata = data)

```

---

MarginalReferenceSampler

*Marginal Reference Sampler*


---

**Description**

Samples complete observations from reference data to replace feature values. This approach samples from the marginal distribution while preserving within-row feature dependencies.

**Details**

This sampler implements what is called "marginal imputation" in the SAGE literature (Covert et al. 2020). For each observation, it samples a complete row from reference data and takes the specified feature values from that row. This approach:

- Samples from the marginal distribution  $P(X_S)$  where S is the set of features
- Preserves dependencies **within** the sampled reference row
- Breaks dependencies **between** test and reference data

**Terminology note:** In SAGE literature, this is called "marginal imputation" because features outside the coalition are "imputed" by sampling from their marginal distribution. We use MarginalReferenceSampler to avoid confusion with missing data imputation and to clarify that it samples from reference data.

**Comparison with other samplers:**

- MarginalPermutationSampler: Shuffles each feature independently, breaking all row structure
- MarginalReferenceSampler: Samples complete rows, preserving within-row dependencies
- ConditionalSampler: Samples from  $P(X_S|X_{-S})$ , conditioning on other features

**Use in SAGE:**

This is the default approach for MarginalSAGE. For a test observation  $x$  and features to marginalize  $S$ , it samples a reference row  $x_{ref}$  and creates a "hybrid" observation combining  $x$ 's coalition features with  $x_{ref}$ 's marginalized features.

**Super classes**

`xplainfi::FeatureSampler` -> `xplainfi::MarginalSampler` -> `MarginalReferenceSampler`

**Public fields**

`reference_data` (`data.table`) Reference data to sample from for marginalization.

**Methods****Public methods:**

- `MarginalReferenceSampler$new()`
- `MarginalReferenceSampler$clone()`

**Method** `new()`: Creates a new instance of the `MarginalReferenceSampler` class.

*Usage:*

```
MarginalReferenceSampler$new(task, n_samples = NULL)
```

*Arguments:*

`task` (`mlr3::Task`) Task to sample from.

`n_samples` (`integer(1) | NULL`) Number of reference samples to use. If `NULL`, uses all task data as reference.

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

*Usage:*

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

*Arguments:*

`deep` Whether to make a deep clone.

**References**

Covert I, Lundberg S, Lee S (2020). "Understanding Global Feature Contributions With Additive Importance Measures." In *Advances in Neural Information Processing Systems*, volume 33, 17212–17223. <https://proceedings.neurips.cc/paper/2020/hash/c7bf0b7c1a86d5eb3be2c722cf2cf746-Abstract.html>.

**Examples**

```
library(mlr3)
task = tgen("friedman1")$generate(n = 100)

# Default: uses all task data as reference
sampler = MarginalReferenceSampler$new(task)
sampled = sampler$sample("important1", row_ids = 1:10)

# Subsample reference data to 50 rows
sampler_subsampled = MarginalReferenceSampler$new(task, n_samples = 50L)
sampled2 = sampler_subsampled$sample("important1", row_ids = 1:10)
```



---

MarginalSAGE

*Marginal SAGE*


---

### Description

[SAGE](#) with marginal sampling (features are marginalized independently). This is the standard SAGE implementation.

### Super classes

[xplainfi::FeatureImportanceMethod](#) -> [xplainfi::SAGE](#) -> MarginalSAGE

### Methods

#### Public methods:

- [MarginalSAGE\\$new\(\)](#)
- [MarginalSAGE\\$clone\(\)](#)

**Method** `new()`: Creates a new instance of the MarginalSAGE class.

*Usage:*

```
MarginalSAGE$new(
  task,
  learner,
  measure = NULL,
  resampling = NULL,
  features = NULL,
  n_permutations = 10L,
  batch_size = 5000L,
  n_samples = 100L,
  early_stopping = FALSE,
  se_threshold = 0.01,
  min_permutations = 10L,
  check_interval = 1L
)
```

*Arguments:*

task, learner, measure, resampling, features, n\_permutations, batch\_size, n\_samples, early\_stopping,  
Passed to [SAGE](#).

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

*Usage:*

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

*Arguments:*

deep Whether to make a deep clone.

**See Also**[ConditionalSAGE](#)**Examples**

```

library(mlr3)
task = tgen("friedman1")$generate(n = 100)
sage = MarginalSAGE$new(
  task = task,
  learner = lrn("regr.ranger", num.trees = 50),
  measure = msr("regr.mse"),
  n_permutations = 3L,
  n_samples = 20
)
sage$compute()

```

---

MarginalSampler

*Marginal Sampler Base Class*


---

**Description**

Abstract base class for marginal sampling strategies that do not condition on other features. Marginal samplers sample from  $P(X_S)$ , the marginal distribution of features  $S$ , ignoring any dependencies with other features.

**Details**

This class provides a common interface for different marginal sampling approaches:

- **MarginalPermutationSampler**: Shuffles features independently within the dataset
- **MarginalReferenceSampler**: Samples complete rows from reference data

Both approaches sample from the marginal distribution  $P(X_S)$ , but differ in how they preserve or break within-row dependencies:

- Permutation breaks ALL dependencies (both with target and between features)
- Reference sampling preserves WITHIN-row dependencies but breaks dependencies with test data

**Comparison with ConditionalSampler:**

- MarginalSampler: Samples from  $P(X_S)$  - no conditioning
- ConditionalSampler: Samples from  $P(X_S|X_{-S})$ - conditions on other features

This base class implements the public `$sample()` and `$sample_newdata()` methods, delegating to private `.sample_marginal()` which subclasses must implement.

**Super class**

xplainfi::FeatureSampler -> MarginalSampler

**Methods****Public methods:**

- MarginalSampler\$sample()
- MarginalSampler\$sample\_newdata()
- MarginalSampler\$clone()

**Method** sample(): Sample features from their marginal distribution.

*Usage:*

```
MarginalSampler$sample(feature, row_ids = NULL)
```

*Arguments:*

feature (character()) Feature name(s) to sample.

row\_ids (integer() | NULL) Row IDs from task to use.

*Returns:* Modified copy with sampled feature(s).

**Method** sample\_newdata(): Sample from external data.

*Usage:*

```
MarginalSampler$sample_newdata(feature, newdata)
```

*Arguments:*

feature (character()) Feature(s) to sample.

newdata (data.table) External data to use.

*Returns:* Modified copy with sampled feature(s).

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

*Usage:*

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

*Arguments:*

deep Whether to make a deep clone.

---

op-null-default

*Default value for NULL*

---

**Description**

A backport of %||% available in R versions from 4.4.0.

**Usage**

```
x %||% y
```

**Arguments**

`x, y`                    If `x` is NULL or length 0, will return `y`; otherwise returns `x`.

**Examples**

```
1 %||% 2
NULL %||% 2
```

---

PerturbationImportance

*Perturbation Feature Importance Base Class*

---

**Description**

Abstract base class for perturbation-based importance methods PFI, CFI, and RFI

**Super class**

`xplainfi::FeatureImportanceMethod` -> PerturbationImportance

**Public fields**

`sampler` (`FeatureSampler`) Sampler object for feature perturbation

**Methods****Public methods:**

- `PerturbationImportance$new()`
- `PerturbationImportance$importance()`
- `PerturbationImportance$clone()`

**Method** `new()`: Creates a new instance of the PerturbationImportance class

*Usage:*

```
PerturbationImportance$new(
  task,
  learner,
  measure = NULL,
  resampling = NULL,
  features = NULL,
  groups = NULL,
  sampler = NULL,
  relation = "difference",
  n_repeats = 1L,
  batch_size = NULL
)
```

*Arguments:*

task, learner, measure, resampling, features, groups Passed to [FeatureImportanceMethod](#).  
 sampler ([FeatureSampler](#)) Sampler to use for feature perturbation.  
 relation (character(1): "difference") How to relate perturbed and baseline scores. Can also be "ratio".  
 n\_repeats (integer(1): 1L) Number of permutation/conditional sampling iterations. Can be overridden in \$compute().  
 batch\_size (integer(1) | NULL: NULL) Maximum number of rows to predict at once. When NULL, predicts all test\_size \* n\_repeats rows in one call. Use smaller values to reduce memory usage at the cost of more prediction calls. Can be overridden in \$compute().

**Method** importance(): Get aggregated importance scores. Extends the base \$importance() method to support the additional "cpi" ci\_method.

*Usage:*

```
PerturbationImportance$importance(
  relation = NULL,
  standardize = FALSE,
  ci_method = c("none", "raw", "nadeau_bengio", "quantile", "cpi"),
  conf_level = 0.95,
  test = c("t", "wilcoxon", "fisher", "binomial"),
  B = 1999,
  ...
)
```

*Arguments:*

relation (character(1)) How to relate perturbed scores to originals ("difference" or "ratio"). If NULL, uses stored parameter value.  
 standardize (logical(1): FALSE) If TRUE, importances are standardized by the highest score so all scores fall in [-1, 1].  
 ci\_method (character(1): "none") Variance estimation method. In addition to base methods ("none", "raw", "nadeau\_bengio", "quantile"), perturbation methods support "cpi" (Conditional Predictive Impact). CPI is specifically designed for [CFI](#) with knockoff samplers and uses one-sided hypothesis tests.  
 conf\_level (numeric(1): 0.95) Confidence level for confidence intervals when ci\_method != "none".  
 test (character(1): "t") Test to use for CPI. One of "t", "wilcoxon", "fisher", or "binomial". Only used when ci\_method = "cpi".  
 B (integer(1): 1999) Number of replications for Fisher test. Only used when ci\_method = "cpi" and test = "fisher".  
 ... Additional arguments passed to the base method.

*Returns:* ([data.table](#)) Aggregated importance scores.

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

*Usage:*

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

*Arguments:*

deep Whether to make a deep clone.

## Description

Implementation of Permutation Feature Importance (PFI) using modular sampling approach. PFI measures the importance of a feature by calculating the increase in model error when the feature's values are randomly permuted, breaking the relationship between the feature and the target variable.

## Details

Permutation Feature Importance was originally introduced by Breiman (2001) as part of the Random Forest algorithm. The method works by:

1. Computing baseline model performance on the original dataset
2. For each feature, randomly permuting its values while keeping other features unchanged
3. Computing model performance on the permuted dataset
4. Calculating importance as the difference (or ratio) between permuted and original performance

## Super classes

`xplainfi::FeatureImportanceMethod` -> `xplainfi::PerturbationImportance` -> PFI

## Methods

### Public methods:

- `PFI$new()`
- `PFI$compute()`
- `PFI$clone()`

**Method** `new()`: Creates a new instance of the PFI class

*Usage:*

```
PFI$new(
  task,
  learner,
  measure = NULL,
  resampling = NULL,
  features = NULL,
  groups = NULL,
  relation = "difference",
  n_repeats = 1L,
  batch_size = NULL
)
```

*Arguments:*

task, learner, measure, resampling, features, groups, relation, n\_repeats, batch\_size  
 Passed to [PerturbationImportance](#)

**Method** compute(): Compute PFI scores

*Usage:*

```
PFI$compute(
  n_repeats = NULL,
  batch_size = NULL,
  store_models = TRUE,
  store_backends = TRUE
)
```

*Arguments:*

n\_repeats (integer(1); NULL) Number of permutation iterations. If NULL, uses stored value.  
 batch\_size (integer(1) | NULL: NULL) Maximum number of rows to predict at once. If NULL, uses stored value.  
 store\_models, store\_backends (logical(1): TRUE) Whether to store fitted models / data backends, passed to [mlr3::resample](#) internally for the initial fit of the learner. This may be required for certain measures and is recommended to leave enabled unless really necessary.

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

*Usage:*

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

*Arguments:*

deep Whether to make a deep clone.

## References

Breiman L (2001). “Random Forests.” *Machine Learning*, **45**(1), 5–32. doi:10.1023/A:1010933404324.  
 Fisher A, Rudin C, Dominici F (2019). “All Models Are Wrong, but Many Are Useful: Learning a Variable’s Importance by Studying an Entire Class of Prediction Models Simultaneously.” *Journal of Machine Learning Research*, **20**, 177. <https://pmc.ncbi.nlm.nih.gov/articles/PMC8323609/>.  
 Strobl C, Boulesteix A, Kneib T, Augustin T, Zeileis A (2008). “Conditional Variable Importance for Random Forests.” *BMC Bioinformatics*, **9**(1), 307. doi:10.1186/147121059307.

## Examples

```
library(mlr3)
library(mlr3learners)

task <- sim_dgp_correlated(n = 500)

pfi <- PFI$new(
  task = task,
  learner = lrn("regr.ranger", num.trees = 10),
  measure = msr("regr.mse")
)
pfi$compute()
pfi$importance()
```

RFI

*Relative Feature Importance***Description**

RFI generalizes CFI and PFI with arbitrary conditioning sets and samplers.

**Super classes**

`xplainfi::FeatureImportanceMethod` -> `xplainfi::PerturbationImportance` -> RFI

**Methods****Public methods:**

- `RFI$new()`
- `RFI$compute()`
- `RFI$clone()`

**Method** `new()`: Creates a new instance of the RFI class

*Usage:*

```
RFI$new(
  task,
  learner,
  measure = NULL,
  resampling = NULL,
  features = NULL,
  groups = NULL,
  conditioning_set = NULL,
  relation = "difference",
  n_repeats = 1L,
  batch_size = NULL,
  sampler = NULL
)
```

*Arguments:*

`task`, `learner`, `measure`, `resampling`, `features`, `groups`, `relation`, `n_repeats`, `batch_size`  
Passed to `PerturbationImportance`.

`conditioning_set` (`character()`) Set of features to condition on. Can be overridden in `$compute()`. Default (`character(0)`) is equivalent to PFI. In CFI, this would be set to all features except that of interest.

`sampler` (`ConditionalSampler`) Optional custom sampler. Defaults to `ConditionalARFSampler`.

**Method** `compute()`: Compute RFI scores

*Usage:*



```
RFI$compute(
  conditioning_set = NULL,
  n_repeats = NULL,
  batch_size = NULL,
  store_models = TRUE,
  store_backends = TRUE
)
```

*Arguments:*

`conditioning_set` (`character()`) Set of features to condition on. If `NULL`, uses the stored parameter value.

`n_repeats` (`integer(1)`) Number of permutation iterations. If `NULL`, uses stored value.

`batch_size` (`integer(1) | NULL: NULL`) Maximum number of rows to predict at once. If `NULL`, uses stored value.

`store_models`, `store_backends` (`logical(1): TRUE`) Whether to store fitted models / data backends, passed to `mlr3::resample` internally for the initial fit of the learner. This may be required for certain measures and is recommended to leave enabled unless really necessary.

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

*Usage:*

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

*Arguments:*

`deep` Whether to make a deep clone.

## References

König G, Molnar C, Bischl B, Grosse-Wentrup M (2021). “Relative Feature Importance.” In *2020 25th International Conference on Pattern Recognition (ICPR)*, 9318–9325. doi:10.1109/ICPR48806.2021.9413090.

## Examples

```
library(mlr3)
task = tgen("friedman1")$generate(n = 200)
rfi = RFI$new(
  task = task,
  learner = lrn("regr.ranger", num.trees = 50),
  measure = msr("regr.mse"),
  conditioning_set = c("important1")
)
rfi$compute()
rfi$importance()
```

SAGE

*Shapley Additive Global Importance (SAGE) Base Class***Description**

Base class for SAGE (Shapley Additive Global Importance) feature importance based on Shapley values with marginalization. This is an abstract class - use [MarginalSAGE](#) or [ConditionalSAGE](#).

**Details**

SAGE uses Shapley values to fairly distribute the total prediction performance among all features. Unlike perturbation-based methods, SAGE marginalizes features by integrating over their distribution. This is approximated by averaging predictions over a reference dataset.

**Standard Error Calculation:** The standard errors (SE) reported in `$convergence_history` reflect the uncertainty in Shapley value estimation across different random permutations within a single resampling iteration. These SEs quantify the Monte Carlo sampling error for a fixed trained model and are only valid for inference about the importance of features for that specific model. They do not capture broader uncertainty from model variability across different train/test splits or resampling iterations.

**Super class**

`xplainfi::FeatureImportanceMethod` -> SAGE

**Public fields**

`n_permutations` (`integer(1)`) Number of permutations to sample.

`convergence_history` (`data.table`) History of SAGE values during computation.

`converged` (`logical(1)`) Whether convergence was detected.

`n_permutations_used` (`integer(1)`) Actual number of permutations used.

**Methods****Public methods:**

- `SAGE$new()`
- `SAGE$compute()`
- `SAGE$plot_convergence()`
- `SAGE$clone()`

**Method** `new()`: Creates a new instance of the SAGE class.

*Usage:*

```
SAGE$new(
  task,
  learner,
  measure = NULL,
```

```

    resampling = NULL,
    features = NULL,
    n_permutations = 10L,
    batch_size = 5000L,
    n_samples = 100L,
    early_stopping = TRUE,
    se_threshold = 0.01,
    min_permutations = 10L,
    check_interval = 1L
  )

```

*Arguments:*

`task`, `learner`, `measure`, `resampling`, `features` Passed to `FeatureImportanceMethod`.

`n_permutations` (`integer(1)`: 10L) Number of permutations to sample for SAGE value estimation. The total number of evaluated coalitions is 1 (empty) + `n_permutations` \* `n_features`.

`batch_size` (`integer(1)`: 5000L) Maximum number of observations to process in a single prediction call.

`n_samples` (`integer(1)`: 100L) Number of samples to use for marginalizing out-of-coalition features. For [MarginalSAGE](#), this is the number of marginal data samples ("background data" in other implementations). For [ConditionalSAGE](#), this is the number of conditional samples per test instance retrieved from sampler.

`early_stopping` (`logical(1)`: TRUE) Whether to enable early stopping based on convergence detection.

`se_threshold` (`numeric(1)`: 0.01) Convergence threshold for relative standard error. Convergence is detected when the maximum relative SE across all features falls below this threshold. Relative SE is calculated as SE divided by the range of importance values (max - min), making it scale-invariant across different loss metrics. Default of 0.01 means convergence when relative SE is below 1% of the importance range.

`min_permutations` (`integer(1)`: 10L) Minimum permutations before checking for convergence. Convergence is judged based on the standard errors of the estimated SAGE values, which requires a sufficiently large number of samples (i.e., evaluated coalitions).

`check_interval` (`integer(1)`: 1L) Check convergence every N permutations.

**Method** `compute()`: Compute SAGE values.

*Usage:*

```

SAGE$compute(
  store_backends = TRUE,
  batch_size = NULL,
  early_stopping = NULL,
  se_threshold = NULL,
  min_permutations = NULL,
  check_interval = NULL
)

```

*Arguments:*

`store_backends` (`logical(1)`) Whether to store data backends.

`batch_size` (`integer(1)`: 5000L) Maximum number of observations to process in a single prediction call.

early\_stopping (logical(1): TRUE) Whether to check for convergence and stop early.  
 se\_threshold (numeric(1): 0.01) Convergence threshold for relative standard error. SE is normalized by the range of importance values (max - min) to make convergence detection scale-invariant. Default 0.01 means convergence when relative SE < 1%.  
 min\_permutations (integer(1): 10L) Minimum permutations before checking convergence.  
 check\_interval (integer(1): 1L) Check convergence every N permutations.

**Method** plot\_convergence(): Plot convergence history of SAGE values.

*Usage:*

```
SAGE$plot_convergence(features = NULL)
```

*Arguments:*

features (character | NULL) Features to plot. If NULL, plots all features.

*Returns:* A [ggplot2](#) object

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

*Usage:*

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

*Arguments:*

deep Whether to make a deep clone.

## References

Covert I, Lundberg S, Lee S (2020). “Understanding Global Feature Contributions With Additive Importance Measures.” In *Advances in Neural Information Processing Systems*, volume 33, 17212–17223. <https://proceedings.neurips.cc/paper/2020/hash/c7bf0b7c1a86d5eb3be2c722cf2cf746-Abstract.html>.

## See Also

[MarginalSAGE](#) [ConditionalSAGE](#)

---

sim\_dgp\_ewald

*Simulate data as in Ewald et al. (2024)*

---

## Description

Reproduces the data generating process from Ewald et al. (2024) for benchmarking feature importance methods. Includes correlated features and interaction effects.

## Usage

```
sim_dgp_ewald(n = 500)
```

## Arguments

n (integer(1)) Number of samples to create.

## Details

### Mathematical Model:

$$\begin{aligned}X_1, X_3, X_5 &\sim \text{Uniform}(0, 1) \\X_2 &= X_1 + \varepsilon_2, \quad \varepsilon_2 \sim N(0, 0.001) \\X_4 &= X_3 + \varepsilon_4, \quad \varepsilon_4 \sim N(0, 0.1) \\Y &= X_4 + X_5 + X_4 \cdot X_5 + \varepsilon, \quad \varepsilon \sim N(0, 0.1)\end{aligned}$$

### Feature Properties:

- X1, X3, X5: Independent uniform(0,1) distributions
- X2: Nearly perfect copy of X1 (correlation approximately 0.99)
- X4: Noisy copy of X3 (correlation approximately 0.67)
- Y depends on X4, X5, and their interaction

## Value

A regression task (`mlr3::TaskRegr`) with `data.table` backend.

## References

Ewald F, Bothmann L, Wright M, Bischl B, Casalicchio G, König G (2024). “A Guide to Feature Importance Methods for Scientific Inference.” In Longo L, Lapuschkin S, Seifert C (eds.), *Explainable Artificial Intelligence*, 440–464. ISBN 978-3-031-63797-1, doi:10.1007/9783031637971\_22.

## See Also

Other simulation: [sim\\_dgp\\_scenarios](#)

## Examples

```
sim_dgp_ewald(100)
```

---

sim\_dgp\_scenarios

*Simulation DGPs for Feature Importance Method Comparison*

---

## Description

These data generating processes (DGPs) are designed to illustrate specific strengths and weaknesses of different feature importance methods like PFI, CFI, and RFI. Each DGP focuses on one primary challenge to make the differences between methods clear.

**Usage**

```

sim_dgp_correlated(n = 500L, r = 0.9)

sim_dgp_mediated(n = 500L)

sim_dgp_confounded(n = 500L, hidden = TRUE)

sim_dgp_interactions(n = 500L)

sim_dgp_independent(n = 500L)

```

**Arguments**

**n** (integer(1): 500L) Number of observations to generate.

**r** (numeric(1): 0.9) Correlation between x1 and x2. Must be between -1 and 1.

**hidden** (logical(1): TRUE) Whether to hide the confounder from the returned task. If FALSE, the confounder is included as a feature, allowing direct adjustment. If TRUE (default), only the proxy is available, simulating unmeasured confounding.

**Details**

**Correlated Features DGP:** This DGP creates highly correlated predictors where PFI will show artificially low importance due to redundancy, while CFI will correctly identify each feature's conditional contribution.

**Mathematical Model:**

$$(X_1, X_2)^T \sim \text{MVN}(0, \Sigma)$$

where  $\Sigma$  is a  $2 \times 2$  covariance matrix with 1 on the diagonal and correlation  $r$  on the off-diagonal.

$$X_3 \sim N(0, 1), \quad X_4 \sim N(0, 1)$$

$$Y = 2 \cdot X_1 + X_3 + \varepsilon$$

where  $\varepsilon \sim N(0, 0.2^2)$ .

**Feature Properties:**

- x1: Standard normal from MVN, direct causal effect on y ( $\beta = 2.0$ )
- x2: Correlated with x1 (correlation =  $r$ ), NO causal effect on y ( $\beta = 0$ )
- x3: Independent standard normal, direct causal effect on y ( $\beta = 1.0$ )
- x4: Independent standard normal, no effect on y ( $\beta = 0$ )

**Expected Behavior:**

- **Marginal methods** (PFI, Marginal SAGE): Will falsely assign importance to x2 due to correlation with x1
- **Conditional methods** (CFI, Conditional SAGE): Should correctly assign near-zero importance to x2
- **Key insight:** x2 is a "spurious predictor" - correlated with causal feature but not causal itself

**Mediated Effects DGP:** This DGP demonstrates the difference between total and direct causal effects. Some features affect the outcome only through mediators.

**Mathematical Model:**

$$\begin{aligned} \text{exposure} &\sim N(0, 1), & \text{direct} &\sim N(0, 1) \\ \text{mediator} &= 0.8 \cdot \text{exposure} + 0.6 \cdot \text{direct} + \varepsilon_m \\ Y &= 1.5 \cdot \text{mediator} + 0.5 \cdot \text{direct} + \varepsilon \end{aligned}$$

where  $\varepsilon_m \sim N(0, 0.3^2)$  and  $\varepsilon \sim N(0, 0.2^2)$ .

**Feature Properties:**

- exposure: Has no direct effect on y, only through mediator (total effect = 1.2)
- mediator: Mediates the effect of exposure on y
- direct: Has both direct effect on y and effect on mediator
- noise: No causal relationship to y

**Causal Structure:** exposure -> mediator -> y <- direct -> mediator

**Expected Behavior:**

- **PFI:** Shows total effects (exposure appears important)
- **CFI:** Shows direct effects (exposure appears less important when conditioning on mediator)
- **RFI with mediator:** Should show direct effects similar to CFI

**Confounding DGP:** This DGP includes a confounder that affects both a feature and the outcome. Uses simple coefficients for easy interpretation.

**Mathematical Model:**

$$\begin{aligned} H &\sim N(0, 1) \\ X_1 &= H + \varepsilon_1 \\ \text{proxy} &= H + \varepsilon_p, & \text{independent} &\sim N(0, 1) \\ Y &= H + X_1 + \text{independent} + \varepsilon \end{aligned}$$

where all  $\varepsilon \sim N(0, 0.5^2)$  independently.

**Model Structure:**

- Confounder  $H \sim N(0,1)$  (potentially unobserved)
- $x_1 = H + \text{noise}$  (affected by confounder)
- $\text{proxy} = H + \text{noise}$  (noisy measurement of confounder)
- $\text{independent} \sim N(0,1)$  (truly independent)
- $y = H + x_1 + \text{independent} + \text{noise}$

**Expected Behavior:**

- **PFI:** Will show inflated importance for  $x_1$  due to confounding
- **CFI:** Should partially account for confounding through conditional sampling
- **RFI conditioning on proxy:** Should reduce confounding bias by conditioning on proxy

**Interaction Effects DGP:** This DGP demonstrates a pure interaction effect where features have no main effects.

**Mathematical Model:**

$$Y = 2 \cdot X_1 \cdot X_2 + X_3 + \varepsilon$$

where  $X_j \sim N(0, 1)$  independently and  $\varepsilon \sim N(0, 0.5^2)$ .

**Feature Properties:**

- x1, x2: Independent features with ONLY interaction effect (no main effects)
- x3: Independent feature with main effect only
- noise1, noise2: No causal effects

**Expected Behavior:**

- **PFI:** Should assign near-zero importance to x1 and x2 (no marginal effect)
- **CFI:** Should capture the interaction and assign high importance to x1 and x2
- **Ground truth:** x1 and x2 are important ONLY through their interaction

**Independent Features DGP:** This is a baseline scenario where all features are independent and their effects are additive. All importance methods should give similar results.

**Mathematical Model:**

$$Y = 2.0 \cdot X_1 + 1.0 \cdot X_2 + 0.5 \cdot X_3 + \varepsilon$$

where  $X_j \sim N(0, 1)$  independently and  $\varepsilon \sim N(0, 0.2^2)$ .

**Feature Properties:**

- important1-3: Independent features with different effect sizes
- unimportant1-2: Independent noise features with no effect

**Expected Behavior:**

- **All methods:** Should rank features consistently by their true effect sizes
- **Ground truth:** important1 > important2 > important3 > unimportant1,2 (approximately 0)

## Value

A regression task ([mlr3::TaskRegr](#)) with [data.table](#) backend.

## Functions

- `sim_dgp_correlated()`: Correlated features demonstrating PFI's limitations
- `sim_dgp_mediated()`: Mediated effects showing direct vs total importance
- `sim_dgp_confounded()`: Confounding scenario for conditional sampling
- `sim_dgp_interactions()`: Interaction effects between features
- `sim_dgp_independent()`: Independent features baseline scenario



## References

Ewald F, Bothmann L, Wright M, Bischl B, Casalicchio G, König G (2024). “A Guide to Feature Importance Methods for Scientific Inference.” In Longo L, Lapuschkin S, Seifert C (eds.), *Explainable Artificial Intelligence*, 440–464. ISBN 978-3-031-63797-1, [doi:10.1007/9783031637971\\_22](https://doi.org/10.1007/9783031637971_22).

## See Also

Other simulation: `sim_dgp_ewald()`

Other simulation: `sim_dgp_ewald()`

Other simulation: `sim_dgp_ewald()`

Other simulation: `sim_dgp_ewald()`

Other simulation: `sim_dgp_ewald()`

## Examples

```
task = sim_dgp_correlated(200)
task$data()

# With different correlation
task_high_cor = sim_dgp_correlated(200, r = 0.95)
cor(task_high_cor$data()$x1, task_high_cor$data()$x2)
task = sim_dgp_mediated(200)
task$data()

# Hidden confounder scenario (traditional)
task_hidden = sim_dgp_confounded(200, hidden = TRUE)
task_hidden$feature_names # proxy available but not confounder

# Observable confounder scenario
task_observed = sim_dgp_confounded(200, hidden = FALSE)
task_observed$feature_names # both confounder and proxy available
task = sim_dgp_interactions(200)
task$data()
task = sim_dgp_independent(200)
task$data()
```

---

wvim\_design\_matrix      *Create Feature Selection Design Matrix*

---

## Description

Creates a logical design matrix for leave-in or leave-out feature evaluation. Used internally with `mlr3fselect` to evaluate feature subsets.

**Usage**

```
wvim_design_matrix(
  all_features,
  feature_names = all_features,
  direction = c("leave-out", "leave-in")
)
```

**Arguments**

**all\_features** (character()) All available feature names from the task.

**feature\_names** (character() | list of character()) Features or feature groups to evaluate. Can be a vector for individual features or a named list for grouped features. Defaults to `all_features` if unspecified.

**direction** (character(1)) Either "leave-in" or "leave-out" (default). Controls which features are selected in the design matrix. "leave-out" sets features of interest to FALSE, and "leave-in" analogously sets them to TRUE.

**Value**

data.table with logical columns for each feature in `all_features` and `length(feature_names)` rows, one for each entry in `feature_names`

**Examples**

```
task = mlr3::tsk("mtcars")

# Individual features
feature_names = task$feature_names[1:3]
wvim_design_matrix(task$feature_names, feature_names, "leave-in")
wvim_design_matrix(task$feature_names, feature_names, "leave-out")

# Feature groups
feature_groups = list(
  A = task$feature_names[1:2],
  B = task$feature_names[3:5]
)
wvim_design_matrix(task$feature_names, feature_groups, "leave-out")
```

---

xplain\_opt

*xplainfi Package Options*


---

**Description**

Get or set package-level options for `xplainfi`.

**Usage**

```
xplain_opt(...)
```

**Arguments**

... Option names to retrieve (as character strings) or options to set (as named arguments).

- To **get** an option: `xplain_opt("verbose")` returns the current value
- To **set** an option: `xplain_opt(verbose = FALSE)` sets the value
- To **get all** options: `xplain_opt()` returns a named list of all options

**Details**

Options can be set in three ways (in order of precedence):

1. Using `xplain_opt(option_name = value)` (recommended)
2. Using `options("xplain.option_name" = value)`
3. Using environment variables `XPLAIN_OPTION_NAME=value`

**Available Options:**

Option	Default	Description
<code>verbose</code>	<code>TRUE</code>	Show informational messages (e.g., when using default measure or resampling)
<code>progress</code>	<code>FALSE</code>	Show progress bars during computation
<code>sequential</code>	<code>FALSE</code>	Force sequential execution (disable parallelization)
<code>debug</code>	<code>FALSE</code>	Enable debug output for development and troubleshooting

**Value**

- When **getting** a single option: the option value (logical)
- When **getting** multiple options: a named list of option values
- When **setting** options: the previous values (invisibly)

**Examples**

```
# Get current value of an option
xplain_opt("verbose")

# Get all options
xplain_opt()

# Set an option (returns previous value invisibly)
old <- xplain_opt(verbose = FALSE)
xplain_opt("verbose") # Now FALSE

# Restore previous value
xplain_opt(verbose = old$verbose)
```

```
# Temporary option change with withr
if (requireNamespace("withr", quietly = TRUE)) {
  withr::with_options(
    list("xplain.verbose" = FALSE),
    {
      # Code here runs with verbose = FALSE
      xplain_opt("verbose")
    }
  )
}
```

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