

Package ‘solitude’

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Type Package

Title An Implementation of Isolation Forest

Version 1.1.3

Description Isolation forest is anomaly detection method introduced by the paper Isolation based Anomaly Detection (Liu, Ting and Zhou <[doi:10.1145/2133360.2133363](https://doi.org/10.1145/2133360.2133363)>).

URL <https://github.com/talegari/solitude>

BugReports <https://github.com/talegari/solitude/issues>

Imports ranger (>= 0.11.0), data.table (>= 1.11.4), igraph (>= 1.2.2),
future.apply (>= 0.2.0), R6 (>= 2.4.0), lgr (>= 0.3.4),

Depends R (>= 3.5.0),

Suggests tidyverse, uwot, mlbench, rsample

License GPL-3

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NeedsCompilation no

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isolationForest

Fit an Isolation Forest

Description

'solitude' class implements the isolation forest method introduced by paper Isolation based Anomaly Detection (Liu, Ting and Zhou <doi:10.1145/2133360.2133363>). The extremely randomized trees (extratrees) required to build the isolation forest is grown using [ranger](#) function from **ranger** package.

Design

`$new()` initiates a new 'solitude' object. The possible arguments are:

- `sample_size`: (positive integer, default = 256) Number of observations in the dataset to used to build a tree in the forest
- `num_trees`: (positive integer, default = 100) Number of trees to be built in the forest
- `replace`: (boolean, default = FALSE) Whether the sample of observations should be chosen with replacement when `sample_size` is less than the number of observations in the dataset
- `seed`: (positive integer, default = 101) Random seed for the forest
- `nproc`: (NULL or a positive integer, default: NULL, means use all resources) Number of parallel threads to be used by `ranger`
- `respect_unordered_factors`: (string, default: "partition") See `respect.unordered.factors` argument in [ranger](#)
- `max_depth`: (positive number, default: `ceiling(log2(sample_size))`) See `max.depth` argument in [ranger](#)

`$fit()` fits a isolation forest for the given dataframe or sparse matrix, computes depths of terminal nodes of each tree and stores the anomaly scores and average depth values in `$scores` object as a `data.table`

`$predict()` returns anomaly scores for a new data as a `data.table`

Details

- Parallelization: [ranger](#) is parallelized and by default uses all the resources. This is supported when `nproc` is set to NULL. The process of obtaining depths of terminal nodes (which is excuted with `$fit()` is called) may be parallelized separately by setting up a **future** backend.

Methods

Public methods:

- [isolationForest\\$new\(\)](#)
- [isolationForest\\$fit\(\)](#)
- [isolationForest\\$predict\(\)](#)
- [isolationForest\\$clone\(\)](#)

Method new():*Usage:*

```
isolationForest$new(  
  sample_size = 256,  
  num_trees = 100,  
  replace = FALSE,  
  seed = 101,  
  nproc = NULL,  
  respect_unordered_factors = NULL,  
  max_depth = ceiling(log2(sample_size))  
)
```

Method fit():*Usage:*

```
isolationForest$fit(dataset)
```

Method predict():*Usage:*

```
isolationForest$predict(data)
```

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

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

Arguments:

deep Whether to make a deep clone.

Examples

```
## Not run:  
library("solitude")  
library("tidyverse")  
library("mlbench")  
  
data(PimaIndiansDiabetes)  
PimaIndiansDiabetes = as_tibble(PimaIndiansDiabetes)  
PimaIndiansDiabetes  
  
splitter = PimaIndiansDiabetes %>%  
  select(-diabetes) %>%  
  rsample::initial_split(prop = 0.5)  
pima_train = rsample::training(splitter)  
pima_test = rsample::testing(splitter)  
  
iso = isolationForest$new()  
iso$fit(pima_train)  
  
scores_train = pima_train %>%  
  iso$predict() %>%  
  arrange(desc(anomaly_score))
```

```

scores_train

umap_train = pima_train %>%
  scale() %>%
  uwot::umap() %>%
  setNames(c("V1", "V2")) %>%
  as_tibble() %>%
  rowid_to_column() %>%
  left_join(scores_train, by = c("rowid" = "id"))

umap_train

umap_train %>%
  ggplot(aes(V1, V2)) +
  geom_point(aes(size = anomaly_score))

scores_test = pima_test %>%
  iso$predict() %>%
  arrange(desc(anomaly_score))

scores_test

## End(Not run)

```

is_integerish

Check for a single integer

Description

for a single integer

Usage

```
is_integerish(x)
```

Arguments

x input

Value

TRUE or FALSE

Examples

```
## Not run: is_integerish(1)
```

solitude*An Implementation of Isolation Forest*

Description

Isolation forest is an anomaly detection method introduced by the paper Isolation based Anomaly Detection (Liu, Ting and Zhou <doi:10.1145/2133360.2133363>)

Author(s)

Srikanth Komala Sheshachala

See Also

Useful links:

- <https://github.com/talegari/solitude>
- Report bugs at <https://github.com/talegari/solitude/issues>

terminalNodesDepth*Depth of each terminal node of all trees in a ranger model*

Description

Depth of each terminal node of all trees in a ranger model is returned as a three column tibble with column names: 'id_tree', 'id_node', 'depth'. Note that root node has the node_id = 0.

Usage

```
terminalNodesDepth(model)
```

Arguments

model A ranger model

Details

This function may be parallelized using a future backend.

Value

A tibble with three columns: 'id_tree', 'id_node', 'depth'.

Examples

```
rf = ranger::ranger(Species ~ ., data = iris, num.trees = 100)
terminalNodesDepth(rf)
```

`terminalNodesDepthPerTree`*Depth of each terminal node of a single tree in a ranger model*

Description

Depth of each terminal node of a single tree in a ranger model. Note that root node has the `id_node = 0`.

Usage

```
terminalNodesDepthPerTree(treelike)
```

Arguments

<code>treelike</code>	Output of 'ranger::treeInfo'
-----------------------	------------------------------

Value

data.table with two columns: `id_node` and `depth`

Examples

```
## Not run:  
rf = ranger::ranger(Species ~ ., data = iris)  
terminalNodesDepthPerTree(ranger::treeInfo(rf, 1))  
  
## End(Not run)
```

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