

Package: lookout (via r-universe)

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Type Package

Title Leave One Out Kernel Density Estimates for Outlier Detection

Version 0.1.5

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Description Outlier detection using leave-one-out kernel density estimates and extreme value theory. The bandwidth for kernel density estimates is computed using persistent homology, a technique in topological data analysis. Using peak-over-threshold method, a generalized Pareto distribution is fitted to the log of leave-one-out kde values to identify outliers.

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Encoding UTF-8

LazyData true

RoxygenNote 7.3.1

Imports TDAstats, evd, RANN, ggplot2, tidyr

Suggests knitr, rmarkdown

URL <https://sevvandi.github.io/lookout/>

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

RemoteUrl <https://github.com/sevvandi/lookout>

RemoteRef HEAD

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autoplot.lookoutliers *Plots outliers identified by lookout algorithm.*

Description

Scatterplot of two columns from the data set with outliers highlighted.

Usage

```
## S3 method for class 'lookoutliers'  
autoplot(object, columns = 1:2, ...)
```

Arguments

object	The output of the function 'lookout'.
columns	Which columns of the original data to plot (specified as either numbers or strings)
...	Other arguments currently ignored.

Value

A ggplot object.

Examples

```
X <- rbind(  
  data.frame(x = rnorm(500),  
            y = rnorm(500)),  
  data.frame(x = rnorm(5, mean = 10, sd = 0.2),  
            y = rnorm(5, mean = 10, sd = 0.2))  
)  
lo <- lookout(X)  
autoplot(lo)
```

autoplot.persistingoutliers

Plots outlier persistence for a range of significance levels.

Description

This function plots outlier persistence for a range of significance levels using the algorithm lookout, an outlier detection method that uses leave-one-out kernel density estimates and generalized Pareto distributions to find outliers.

Usage

```
## S3 method for class 'persistingoutliers'
autoplot(object, alpha = object$alpha, ...)
```

Arguments

object	The output of the function 'persisting_outliers'.
alpha	The significance levels to plot.
...	Other arguments currently ignored.

Value

A ggplot object.

Examples

```
X <- rbind(
  data.frame(
    x = rnorm(500),
    y = rnorm(500)
  ),
  data.frame(
    x = rnorm(5, mean = 10, sd = 0.2),
    y = rnorm(5, mean = 10, sd = 0.2)
  )
)
plot(X, pch = 19)
outliers <- persisting_outliers(X, unitize = FALSE)
autoplot(outliers)
```

find_tda_bw

Identifies bandwidth for outlier detection.

Description

This function identifies the bandwidth that is used in the kernel density estimate computation. The function uses topological data analysis (TDA) to find the badnwidth.

Usage

```
find_tda_bw(X, fast)
```

Arguments

X	The input data in a dataframe, matrix or tibble format.
fast	If set to TRUE, makes the computation faster by sub-setting the data for the bandwidth calculation.

Value

The bandwidth

Examples

```
X <- rbind(
  data.frame(x = rnorm(500),
            y = rnorm(500)),
  data.frame(x = rnorm(5, mean = 10, sd = 0.2),
            y = rnorm(5, mean = 10, sd = 0.2))
)
find_tda_bw(X, fast = TRUE)
```

lookout

Identifies outliers using the algorithm lookout.

Description

This function identifies outliers using the algorithm lookout, an outlier detection method that uses leave-one-out kernel density estimates and generalized Pareto distributions to find outliers.

Usage

```
lookout(X, alpha = 0.05, unitize = TRUE, bw = NULL, gpd = NULL, fast = TRUE)
```

Arguments

X	The input data in a dataframe, matrix or tibble format.
alpha	The level of significance. Default is 0.05.
unitize	An option to normalize the data. Default is TRUE, which normalizes each column to $[0, 1]$.
bw	Bandwidth parameter. Default is NULL as the bandwidth is found using Persistent Homology.
gpd	Generalized Pareto distribution parameters. If 'NULL' (the default), these are estimated from the data.
fast	If set to TRUE, makes the computation faster by sub-setting the data for the bandwidth calculation.

Value

A list with the following components:

outliers	The set of outliers.
outlier_probability	The GPD probability of the data.

outlier_scores The outlier scores of the data.
bandwidth The bandwidth selected using persistent homology.
kde The kernel density estimate values.
lookde The leave-one-out kde values.
gpd The fitted GPD parameters.

Examples

```
X <- rbind(  
  data.frame(x = rnorm(500),  
            y = rnorm(500)),  
  data.frame(x = rnorm(5, mean = 10, sd = 0.2),  
            y = rnorm(5, mean = 10, sd = 0.2))  
)  
lo <- lookout(X)  
lo  
autoplot(lo)
```

lookout_ts	<i>Identifies outliers in univariate time series using the algorithm lookout.</i>
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Description

This is the time series implementation of lookout.

Usage

```
lookout_ts(x, alpha = 0.05)
```

Arguments

x The input univariate time series.
alpha The level of significance. Default is 0.05.

Value

A lookout object.

See Also

[lookout](#)

Examples

```

set.seed(1)
x <- arima.sim(list(order = c(1,1,0), ar = 0.8), n = 200)
x[50] <- x[50] + 10
plot(x)
lo <- lookout_ts(x)
lo

```

`persisting_outliers` *Computes outlier persistence for a range of significance values.*

Description

This function computes outlier persistence for a range of significance values, using the algorithm `lookout`, an outlier detection method that uses leave-one-out kernel density estimates and generalized Pareto distributions to find outliers.

Usage

```

persisting_outliers(
  X,
  alpha = seq(0.01, 0.1, by = 0.01),
  st_qq = 0.9,
  unitize = TRUE,
  num_steps = 20
)

```

Arguments

<code>X</code>	The input data in a matrix, data.frame, or tibble format. All columns should be numeric.
<code>alpha</code>	Grid of significance levels.
<code>st_qq</code>	The starting quantile for death radii sequence. This will be used to compute the starting bandwidth value.
<code>unitize</code>	An option to normalize the data. Default is TRUE, which normalizes each column to $[\emptyset, 1]$.
<code>num_steps</code>	The length of the bandwidth sequence.

Value

A list with the following components:

<code>out</code>	A 3D array of $N \times \text{num_steps} \times \text{num_alpha}$ where N denotes the number of observations, <code>num_steps</code> denote the length of the bandwidth sequence and <code>num_alpha</code> denotes the number of significance levels. This is a binary array and the entries are set to 1 if that observation is an outlier for that particular bandwidth and significance level.
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<code>bw</code>	The set of bandwidth values.
<code>gpdparas</code>	The GPD parameters used.
<code>lookoutbw</code>	The bandwidth chosen by the algorithm lookout using persistent homology.

Examples

```
X <- rbind(
  data.frame(x = rnorm(500),
            y = rnorm(500)),
  data.frame(x = rnorm(5, mean = 10, sd = 0.2),
            y = rnorm(5, mean = 10, sd = 0.2))
)
plot(X, pch = 19)
outliers <- persisting_outliers(X, unitize = FALSE)
outliers
autoplot(outliers)
```

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