

Package ‘tetragon’

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Type Package

Title Automatic Sequence Prediction by Expansion of the Distance Matrix

Version 1.2.0

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Description Each sequence is predicted by expanding the distance matrix. The compact set of hyper-parameters is tuned through random search.

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

Depends R (>= 4.1)

Imports purrr (>= 0.3.4), abind (>= 1.4-5), ggplot2 (>= 3.3.5), readr (>= 2.0.1), stringr (>= 1.4.0), lubridate (>= 1.7.10), narray (>= 0.4.1.1), imputeTS (>= 3.2), scales (>= 1.1.1), tictoc (>= 1.0.1), modeest (>= 2.4.0), moments (>= 0.14), greybox (>= 1.0.1), dqrng (>= 0.3.0), entropy (>= 1.3.1), Rfast (>= 2.0.6), philentropy (>= 0.5.0)

URL https://rpubs.com/giancarlo_vercellino/tetragon

NeedsCompilation no

Repository CRAN

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covid_in_europe	<i>covid_in_europe data set</i>
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Description

A data frame with with daily and cumulative cases of Covid infections and deaths in Europe since March 2021.

Usage

```
covid_in_europe
```

Format

A data frame with 5 columns and 163 rows.

Source

www.ecdc.europa.eu

tetragon	<i>tetragon</i>
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Description

Each sequence is predicted by expanding the distance matrix. The compact set of hyper-parameters is tuned via grid or random search.

Usage

```
tetragon(  
  df,  
  seq_len = NULL,  
  ci = 0.8,  
  method = NULL,  
  distr = NULL,  
  n_windows = 3,  
  n_sample = 30,  
  dates = NULL,  
  error_scale = "naive",  
  error_benchmark = "naive",  
  seed = 42  
)
```

Arguments

<code>df</code>	A data frame with time features as columns. They could be continuous variables or not.
<code>seq_len</code>	Positive integer. Time-step number of the projected sequence. Default: NULL (random selection between maximum boundaries).
<code>ci</code>	Confidence interval. Default: 0.8.
<code>method</code>	String. Distance method for calculating distance matrix among sequences. Options are: "euclidean", "manhattan", "maximum", "minkowski". Default: NULL (random selection among all possible options).
<code>distr</code>	String. Distribution used to expand the distance matrix. Options are: "norm", "logis", "t", "exp", "chisq". Default: NULL (random selection among all possible options).
<code>n_windows</code>	Positive integer. Number of validation tests to measure/sample error. Default: 3 (but a larger value is strongly suggested to really understand your accuracy).
<code>n_sample</code>	Positive integer. Number of samples for random search. Default: 30.
<code>dates</code>	Date. Vector with dates for time features.
<code>error_scale</code>	String. Scale for the scaled error metrics (only for continuous variables). Two options: "naive" (average of naive one-step absolute error for the historical series) or "deviation" (standard error of the historical series). Default: "naive".
<code>error_benchmark</code>	String. Benchmark for the relative error metrics (only for continuous variables). Two options: "naive" (sequential extension of last value) or "average" (mean value of true sequence). Default: "naive".
<code>seed</code>	Positive integer. Random seed. Default: 42.

Value

This function returns a list including:

- exploration: list of all explored models, complete with predictions, testing metrics and plots
- history: a table with the sampled models, hyper-parameters, validation errors
- best: results for the best model including:
 - predictions: min, max, q25, q50, q75, quantiles at selected ci, and a bunch of specific measures for each point fo predicted sequences
 - testing_errors: testing errors for one-step and sequence for each ts feature
 - plots: confidence interval plot for each time feature
- time_log

Author(s)

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See Also

Useful links:

- https://rpubs.com/giancarlo_vercellino/tetragon

Examples

```
tetragon(covid_in_europe[, c(2, 4)], seq_len = 40, n_sample = 2)
```

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