

# Package: tetragon (via r-universe)

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**Type** Package

**Title** Automatic Sequence Prediction by Expansion of the Distance Matrix

**Version** 1.3.0

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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), fastDummies (>= 1.6.3), fANCOVA (>= 0.6-1)

**URL** [https://rpubs.com/giancarlo\\_vercellino/tetragon](https://rpubs.com/giancarlo_vercellino/tetragon)

**NeedsCompilation** no

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**Repository** <https://pugian.r-universe.dev>

**RemoteUrl** <https://github.com/cran/tetragon>

**RemoteRef** HEAD

**RemoteSha** e911bff67175f16279fd5aeab1ae670f1ee2b14b

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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](http://www.ecdc.europa.eu)

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|          |                 |
|----------|-----------------|
| 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,  
  smoother = F,  
  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>smoother</code>        | Logical. Perform optimal smoothing using standard loess. Default: FALSE   |
| <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](https://rpubs.com/giancarlo_vercellino/tetragon)

**Examples**

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

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