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Description Within epidemic outbreaks, infections grow and decline differently between regions, and the velocity of spatial spread differs between countries. The swash library offers a set of model-based analyses for these topics. Spread velocity may be analysed with the Swash-Backwash Model of the Single Epidemic Wave by Cliff and Haggett (2006) <doi:10.1007/s10109-006-0027-8> and corresponding functions for bootstrap confidence intervals, country comparison, and visualization of results. Differences in epidemic growth between regions may be analysed using logistic growth models, exponential growth models, Hawkes processes and breakpoint analyses. Cluster and hotspot analyses can be conducted using neighborhood matrices. See Wieland (2020) <doi:10.18335/region.v7i2.324> for an application of some of the mentioned analysis methods. All functionalities are accessed by the class ``infpan'' for infections panel data defined in this package, which is built from a data.frame provided by the user.

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Imports methods

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`swash-package` *swash: Health Geography Toolbox for Model-Based Analysis of Infections Panel Data*

Description

The R library `swash` provides a toolbox for quantitative analyses in health geography with respect to the spatial spread of infectious diseases. The focus of the package is the analysis of infections panel data, for example, daily or weekly infections for T time points and N regions within a country. Examples of research questions include: How quickly does an infectious disease spread across a country? Are there differences in the spread velocity between countries? Are there regional differences in the growth rates of the infection wave? When was the peak (inflection point) of infections reached in each region? Are there significant hotspots or clusters of infections?

The target audience of this `R` package consists of researchers and practitioners in the fields of health geography, spatial epidemiology, and statistics. However, many applications are also relevant to other fields of research, such as econometrics or geoinformation science. The package bundles functions and analysis workflows developed by the author between 2020 and 2023 for the quantitative analysis of (panel) infection data during the COVID-19 pandemic. The aim was to consolidate these methods and analysis tools into a unified and coherent framework. Users simply need to import their infection panel data once; based on this, they can calculate additional indicators and run the built-in analyses successively.

In order to use all functionalities, the user should import her/his infections panel data using the function `load_infections_paneldata()`, which returns an instance of class `infpan`. The panel data is checked whether it is balanced and whether it includes missing values. From an `infpan` object, the user may utilize the following built-in analysis and visualization functions:

- *Swash-Backwash Model of the Single Epidemic Wave*, including further analysis towards bootstrap-based inference and country comparison as well as visualization
- *Growth Analysis* with *logistic* and *exponential growth models* for cumulative or new (e.g., daily, weekly) infections, including visualization
- *Hawkes process* models for new infection cases (e.g., daily, weekly), including visualization
- *Breakpoints analysis* using the *Bai-Perron algorithm* implemented in `strucchange::breakpoints`, including visualization
- Spatial statistics for the identification of clusters/hotspots, such as *Moran's I* and *Getis-Ord*, implemented in `spdep` and `sfdep`
- Calculation of further epidemic indicators from the infections panel data such as the *effective reproduction number*
- *Plots* of infection curves by region
- Map plots of infection indicators and (local) spatial statistics

`infpan` objects and objects resulting from the functions mentioned above have `summary()` and `plot()` methods. All mentioned functions may be used stand-alone as well. Every change (e.g., the calculation of a new indicator) within an object is tracked with a timestamp.

Details

Based on an `infpan` object, several indicators may be calculated from new infections values, such as incidence or effective reproduction number R_t. Infection curves may be plotted by `plot(infpan)`. It is also possible to import spatial features (`sf` spatial data frame) into an `infpan` object in order to plot maps of specified indicator at a given time point. All built-in model analyses mentioned below may be conducted based on an instance of class `infpan`, but may also be used independently.

The Swash-Backwash Model of the Single Epidemic Wave (SBM) is the spatial equivalent of the classic epidemiological SIR (Susceptible-Infected-Recovered) model. It was developed by Cliff and Haggett (2006) to model the velocity of spread of infectious diseases across space. Current applications may be found, for example, in Smallman-Raynor et al. (2022a,b). This package enables the calculation of the Swash-Backwash Model for user-supplied panel data on regional infections. The core of this is the `swash_backwash()` function, which calculates the model and creates a model object of the `sbm` class defined in this package. This class can be used to visualize results (`summary()`, `plot()`) and calculate bootstrap confidence intervals for the model estimates (`confint(sbm)`); the latter returns an object of the built-in class `sbm_ci`. Two `sbm_ci` objects for different countries may be compared with `compare_countries()`, which allows the estimation of mean differences of a user-specified model parameter (e.g., spatial reproduction number R_{OA}) between two countries. This makes it possible to check whether the spatial spread velocity of a communicable disease is significantly different in one country than in another country; the result is an object of class `countries`. To calculate the SBM model based on an `infpan` object, use the corresponding method `swash(infpan)`.

The library allows for estimating growth models based on time series of infections. Logistic and exponential growth models (see, e.g., Chowell et al. 2014, 2015, Pell et al. 2018, Wieland 2020a, 2020b) as well as Hawkes process models (see, e.g. Rizoiu et al. 2018) are provided. Logistic and exponential growth models are estimated via OLS (Ordinary Least Squares) and/or NLS (Nonlinear least squares). All model estimations include the calculation of goodness-of-fit metrics (e.g., R^2, $RMSE$, MAE, $MAPE$). Additionally, breakpoints in time series (see, e.g., Wieland 2020b) may be detected based on the *Bai-Perron algorithm* (Bai and Perron 2003) which is included in the `breakpoints` function of the `strucchange` package (Zeileis et al. 2003) accessed in the functions of this package. A model for a single time series may be estimated with the built-in functions `logistic_growth()`, `exponential_growth()`, `hawkes_growth()`, or `breaks_growth()`, respectively. These function return objects of class `loggrowth`, `expgrowth`, `hawkes`, and `breaksgrowth`, respectively, all of them defined in this package. Plotting is available via the `plot()` method. Estimating such a model based on an `infpan` object is provided by the `infpan` methods `growth()`, `growth_initial()`, `growth_hawkes()`, and `growth_breaks()`, respectively, all of them resulting in an object of class `growthmodels`.

Spatial statistics regarding autocorrelation or clustering can be calculated either based on an `infpan` object or independently of it, with the class `nbmatrix` existing for the latter. Neighboring spatial features can be identified, and descriptive statistics (e.g., sum, mean) can be calculated for the neighboring regions. Within the `nbmatrix` class, statistics such as Moran's I and Getis-Ord may be calculated. The methods `moran()`, `getisord()`, and `gstar()` are available for this purpose. The `swash` package internally uses the packages `spdep` (Bivand and Wong 2018) and `sfdep` (Parry and Locke 2024).

The library also includes various auxiliary statistical functions that are integrated into the main functions and methods but can also be used standalone. For example, `metrics()` and `binary_metrics()` calculate goodness-of-fit metrics for observed and predicted values for continuous and binary outcome variables, respectively. The `plot_coef_ci()` function allows regression model results (estimates and confidence intervals) to be visualized in an appealing way. The package includes example data from the COVID-19 pandemic.

Author(s)

Thomas Wieland

References

Bivand RS, Wong DWS (2018) Comparing implementations of global and local indicators of spatial association. *TEST* 27, 716–748. doi:10.1007/s117490180599x

Chowell G, Simonsen L, Viboud C, Yang K (2014) Is West Africa Approaching a Catastrophic Phase or is the 2014 Ebola Epidemic Slowing Down? Different Models Yield Different Answers for Liberia. *PLoS currents 6*. doi:10.1371/currents.outbreaks.b4690859d91684da963dc40e00f3da81

Chowell G, Viboud C, Hyman JM, Simonsen L (2015) The Western Africa ebola virus disease epidemic exhibits both global exponential and local polynomial growth rates. *PLOS Currents Outbreaks*, ecurrents.outbreaks.8b55f4bad99ac5c5db3663e916803261. doi:10.1371/currents.outbreaks.8b55f4bad99ac5c5db36

Cliff AD, Haggett P (2006) A swash-backwash model of the single epidemic wave. *Journal of Geographical Systems* 8(3), 227-252. doi:10.1007/s1010900600278

Li, MY (2018) An Introduction to Mathematical Modeling of Infectious Diseases. doi:10.1007/9783319721224

Nishiura H, Chowell G (2009) The effective reproduction number as a prelude to statistical estimation of time-dependent epidemic trends. In Chowell G, Hyman JM, Bettencourt LMA (eds.) Mathematical and statistical estimation approaches in epidemiology, 103–121. doi:10.1007/97890-48123131_5

Parry J, Locke D (2024) sfdep: Spatial Dependence for Simple Features. R package version 0.2.5. doi:10.32614/CRAN.package.sfdep

Pell B, Kuang Y, Viboud C, Chowell G (2018) Using phenomenological models for forecasting the 2015 ebola challenge. *Epidemics* 22, 62–70. doi:10.1016/j.epidem.2016.11.002

Rizoiu MA, Mishra S, Kong Q, Carman M, Xie L. (2018) SIR-Hawkes: Linking Epidemic Models and Hawkes Processes to Model Diffusions in Finite Populations. In: *Proceedings of the 2018 World Wide Web Conference. WWW'18*. Republic and Canton of Geneva, CHE: International World Wide Web Conferences Steering Committee, p. 419–428. doi:10.1145/3178876.3186108

Rotejanaprasert C, Chinpong K, Lawson AB, Chienwichai P, Maude RJ (2024) Evaluation and comparison of spatial cluster detection methods for improved decision making of disease surveillance: a case study of national dengue surveillance in Thailand. *BMC Medical Research Methodology* 24, 14. doi:10.1186/s12874023021359

Smallman-Raynor MR, Cliff AD, Stickler PJ (2022a) Meningococcal Meningitis and Coal Mining in Provincial England: Geographical Perspectives on a Major Epidemic, 1929–33. *Geographical Analysis* 54, 197–216. doi:10.1111/gean.12272

Smallman-Raynor MR, Cliff AD, The COVID-19 Genomics UK (COG-UK) Consortium (2022b) Spatial growth rate of emerging SARS-CoV-2 lineages in England, September 2020–December 2021. *Epidemiology and Infection* 150, e145. doi:10.1017/S0950268822001285.

Viboud C, Bjørnstad ON, Smith DL, Simonsen L, Miller MA, Grenfell BT (2006) Synchrony, Waves, and Spatial Hierarchies in the Spread of Influenza. *Science* 312, 447-451. doi:10.1126/science.1125237

Wieland T (2020a) Flatten the Curve! Modeling SARS-CoV-2/COVID-19 Growth in Germany at the County Level. *REGION* 7(2), 43–83. doi:10.18335/region.v7i2.324

Wieland T (2020b) A phenomenological approach to assessing the effectiveness of COVID-19 related nonpharmaceutical interventions in Germany. *Safety Science* 131, 104924. doi:10.1016/j.ssci.2020.104924

Wieland T (2022) Spatial patterns of excess mortality in the first year of the COVID-19 pandemic in Germany. *European Journal of Geography* 13(4), 18-33. doi:10.48088/ejg.t.wie.13.4.018.033

Wieland T (2025) Assessing the effectiveness of non-pharmaceutical interventions in the SARS-CoV-2 pandemic: results of a natural experiment regarding Baden-Württemberg (Germany) and Switzerland in the second infection wave. *Journal of Public Health* 33(11), 2497-2511. doi:10.1007/s1038902402218x

Zeileis C, Kleiber W, Krämer K, Hornik K (2003) Testing and dating of structural changes in practice. *Computational Statistics & Data Analysis* 44(1-2), 109-123. doi:10.1016/S01679473(03)00030-6

Examples

```
data(COVID19Cases_geoRegion)
# Get SWISS COVID19 cases at NUTS 3 level

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[!COVID19Cases_geoRegion$geoRegion %in% c("CH", "CHFL"),]
# Exclude CH = Switzerland total and CHFL = Switzerland and Liechtenstein total

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[COVID19Cases_geoRegion$datum <= "2020-05-31",]
# Extract first COVID-19 wave

infpan_CH <- load_infections_paneldata(
    data = COVID19Cases_geoRegion,
    col_cases = "entries",
    col_date = "datum",
    col_region = "geoRegion",
    other_cols = c(
      "Population" = "pop"
        ),
    verbose = TRUE
  )
# Import as infections panel data set (class infpan)

is(infpan_CH)
# "infpan"

plot(
  infpan_CH,
  plot_rollmean = TRUE
  )
# Plot cases

infpan_CH <- calculate_Rt(
  infpan_CH,
  verbose = TRUE
  )
# Calculate effective reproduction number

summary(infpan_CH)
```

```
# Summary of infpan object

timestamps(infpan_CH)
# Time stamps of infpan object

CH_covidwave1 <-
  swash(
    infpan_CH,
    verbose = TRUE
    )
# Swash-Backwash Model for Swiss COVID19 cases
# Spatial aggregate: NUTS 3 (cantons)

summary(CH_covidwave1)
# Summary of Swash-Backwash Model
```

`add_geodata` *Adding Geodata to Infpan Object*

Description

Assigns geodata (`sf` object) to an `infpan` object.

Usage

```
add_geodata(
    object,
    sf_geodata,
    unit_col,
    verbose = FALSE
  )
```

Arguments

`object`	object of class `infpan`
`sf_geodata`	`sf` object containing features (polygons) representing the study area (e.g., counties)
`unit_col`	Unique ID column of the regions in the `sf` object
`verbose`	`bool` argument which indicates whether progress messages are displayed

Details

Adds geodata (`sf` object) to the `infpan` object. Included geodata is mandatory for plotting indicators via `plot_map`.

Value

Input `infpan` object including geodata

Author(s)

Thomas Wieland

References

Wieland T (2020) Flatten the Curve! Modeling SARS-CoV-2/COVID-19 Growth in Germany at the County Level. *REGION* 7(2), 43–83. doi:10.18335/region.v7i2.324

See Also

infpan-class, load_infections_paneldata, calculate_incidence, calculate_cum, calculate_rollmean, calculate_rollsum, calculate_Rt

Examples

```
data(COVID19Cases_geoRegion)
# Get SWISS COVID19 cases at NUTS 3 level

data(K4kant20260101gf_ch2007Poly)
# Cantonal boundaries of Switzerland

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[!COVID19Cases_geoRegion$geoRegion %in% c("CH", "CHFL"),]
# Exclude CH = Switzerland total and CHFL = Switzerland and Liechtenstein total

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[COVID19Cases_geoRegion$datum <= "2020-05-31",]
# Extract first COVID-19 wave

infpan_CH <- load_infections_paneldata(
    data = COVID19Cases_geoRegion,
    col_cases = "entries",
    col_date = "datum",
    col_region = "geoRegion",
    other_cols = c("Population" = "pop"),
    verbose = TRUE
  )
# Import as infections panel data set (class infpan)

infpan_CH <- calculate_incidence(
  infpan_CH,
  col_name = "incidence",
  verbose = TRUE
)
# Calculate incidence of cases as "incidence"

infpan_CH <- add_geodata(
  infpan_CH,
  K4kant20260101gf_ch2007Poly,
  unit_col = "cant_abbrev"
)
# Adding geodata (sf) to infpan object
```

```
summary(infpan_CH)
# Summary of infpan object

timestamps(infpan_CH)
# Time stamps of infpan object

plot_map(
  infpan_CH,
  attribute = "Incidence",
  main = "COVID-19 Incidence 2020-05-31",
  breaks = c(0, 0.05, 0.1, 0.2, 1),
  verbose = TRUE
)
# Simple map of incidence for the most current date (timepoint=NULL)
```

`add_geodata-methods` *Methods for Function* `add_geodata`

Description

Methods for function `add_geodata`

Methods

`signature( object = "infpan", sf_geodata, unit_col, verbose = FALSE)` Adds geodata (`sf` object) to the `infpan` object.

Author(s)

Thomas Wieland

`as_balanced` *Correction of Non-balanced Panel Dataset with Regional Infection Data*

Description

This function corrects non-balanced input panel data by replacing missing entries with a user-given constant (e.g., 0).

Usage

```
as_balanced(
  data,
  col_cases,
  col_date,
  col_region,
  fill_missing = NA,
  drop_duplicates = TRUE,
  verbose = FALSE
  )
```

Arguments

`data`	`data.frame` with regional infection data
`col_cases`	Column containing the cases (numeric)
`col_date`	Column containing the time points (e.g., days)
`col_region`	Column containing the unique identifier of the regions (e.g., name, NUTS 3 code)
`fill_missing`	Constant to fill missing values (default and recommended: 0)
`drop_duplicates`	`bool` argument which indicates whether duplicated region/time combinations are removed
`verbose`	`bool` argument which indicates whether progress messages are displayed

Details

The Swash-Backwash Model of the Single Epidemic Wave does not necessarily require balanced panel data in order for the calculations to be carried out. However, for a correct estimation it is implicitly assumed that the input data is balanced. The function corrects non-balanced panel data. It is executed automatically within the `swash_backwash()` function and `swash()` method, respectively, but can also be used separately.

Value

Corrected input dataset (`data.frame`)

Author(s)

Thomas Wieland

See Also

`is_balanced`

Examples

```
data(COVID19Cases_geoRegion)
# Get SWISS COVID19 cases at NUTS 3 level

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[!COVID19Cases_geoRegion$geoRegion %in% c("CH", "CHFL"),]
# Exclude CH = Switzerland total and CHFL = Switzerland and Liechtenstein total

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[COVID19Cases_geoRegion$datum <= "2020-05-31",]
# Extract first COVID-19 wave

COVID19Cases_geoRegion_balanced <-
  is_balanced(
  data = COVID19Cases_geoRegion,
  col_cases = "entries",
  col_date = "datum",
  col_region = "geoRegion"
)
# Test whether "COVID19Cases_geoRegion" is balanced panel data

COVID19Cases_geoRegion_balanced$data_balanced
# Balanced? TRUE or FALSE

if (COVID19Cases_geoRegion_balanced$data_balanced == FALSE) {
  COVID19Cases_geoRegion <-
    as_balanced(
    COVID19Cases_geoRegion,
    col_cases = "entries",
    col_date = "datum",
    col_region = "geoRegion"
  )
}
# Correction of dataset "COVID19Cases_geoRegion"
# not necessary as parameter balance of is_balanced is set TRUE by default
```

---

binary_metrics *Fit metrics of observed and expected binary variables*

Description

Calculation of fit metrics for binary variables (Sensitivity, specificity, accuracy)

Usage

```
binary_metrics(
  observed,
  expected,
  no_information_rate = "negative",
```

```
  na.rm = TRUE
  )
```

Arguments

observed	Numeric vector: Y observed
expected	Numeric vector: Y expected
no_information_rate	character argument which indicates whether the no-information rate is calculated based on negatives or positives
na.rm	bool argument which indicates whether NA values should be skipped before computation.

Details

The function computes model performance metrics for binary outcomes. Observed and expected data must be stated by the user. The function returns sensitivity, specificity, accuracy, and no-information rate.

Value

list with two entries:

fit_metrics:	list with fit metrics (sens, spec, ...)
observed_expected:	data.frame with observed, expected and hit (1/0)

Author(s)

Thomas Wieland

References

Altman DG, Bland JM (1994) Diagnostic tests. 1: Sensitivity and specificity. *British Medical Journal* 308, 1552. doi:10.1136/bmj.308.6943.1552.

Boehmke B, Greenwell B (2020) Hands-On Machine Learning with R (1 ed.). Taylor & Francis, New York, NY.

See Also

metrics, binary_metrics_glm

Examples

```
obs <- c(1,1,0,0,0,0,1,0,1)
exp <- c(0,1,0,0,0,0,1,0,0)

binary_metrics(
  obs,
  exp
)
```

`binary_metrics_glm` *Fit metrics for binary logit model*

Description

Calculation of fit metrics for binary variables (Sensitivity, specificity, accuracy) out of binary logit models (`glm` object)

Usage

```
binary_metrics_glm(
  logit_model,
  threshold = 0.5
  )
```

Arguments

`logit_model`	`glm` object with binary logit model
`threshold`	Threshold for distinction of probability with respect to TRUE or FALSE

Details

The function computes model performance metrics for binary outcomes. A binary logit model (glm) must be stated by the user. The function returns sensitivity, specificity, accuracy, and no-information rate.

Value

`list` with two entries:

`fit_metrics:`	`list` with fit metrics (`sens`, `spec`, ...)
`observed_expected:`	`data.frame` with observed, expected and hit (1/0)

Author(s)

Thomas Wieland

References

Altman DG, Bland JM (1994) Diagnostic tests. 1: Sensitivity and specificity. *British Medical Journal* 308, 1552. doi:10.1136/bmj.308.6943.1552.

Boehmke B, Greenwell B (2020) Hands-On Machine Learning with R (1 ed.). Taylor & Francis, New York, NY.

See Also

`metrics`, `binary_metrics`

Examples

```
dep <- c(1,1,0,0,0,0,1,0,1, 1)
x <- c(2,3,1,1,0,1,3,2,1,3)

testmodel <-
  glm(
    dep~x,
    family=binomial()
  )

summary(testmodel)

binary_metrics_glm(testmodel)
```

---

breaks_growth *Time Series Model with Breakpoints*

Description

Estimation of breakpoints in linear regression models from infections cases over time

Usage

```
breaks_growth(
  y,
  t = NULL,
  ln = FALSE,
  impute_missing_values = FALSE,
  add_constant = 1,
  alpha = 0.05,
  ...,
  verbose = FALSE
  )
```

Arguments

y	numeric vector with (new or cumulative) infections data over time
t	vector of class numeric or Date with time points or dates
ln	bool argument which indicates whether dependent variable should be transformed by natural logarithm
impute_missing_values	bool argument which indicates whether missing values have to be imputed via linear imputation
add_constant	Numeric constant to be added to y if zero values occur
alpha	Significance level α for 1-α*100 confidence intervals
...	Other parameters passed to strucchange::breakpoints (see the corresponding documentation)
verbose	bool argument which indicates whether progress messages are displayed

Details

This function allows detecting breakpoints in a linear regression time series model. The user must specify the dependent variable (e.g, daily infections) and the time variable (time counter or date values). The estimation is performed using OLS. The function internally uses the function `breakpoints` from the `strucchange` package (Zeileis et al. 2003), where breakpoints are identified using the Bai-Perron algorithm (Bai & Perron 2003). See Wieland (2020) for an empirical application on COVID-19 cases.

Value

object of class `breaksgrowth-class`

Author(s)

Thomas Wieland

References

Bai J, Perron P (2003) Computation and analysis of multiple structural change models. *Journal of Applied Econometrics* 18(1), 1-22. doi:10.1002/jae.659

Wieland T (2020) A phenomenological approach to assessing the effectiveness of COVID-19 related nonpharmaceutical interventions in Germany. *Safety Science* 131, 104924. doi:10.1016/j.ssci.2020.104924

Zeileis C, Kleiber W, Krämer K, Hornik K (2003) Testing and dating of structural changes in practice. *Computational Statistics & Data Analysis* 44(1-2), 109-123. doi:10.1016/S01679473(03)00030-6

See Also

`exponential_growth`, `logistic_growth`, `hawkes_growth`

Examples

```
data(Infections)
# Confirmed SARS-CoV-2 cases in Germany

breakpoints_infections <- breaks_growth(
  y = Infections$infections_daily,
  t = Infections$day,
  ln = TRUE,
  verbose = TRUE
)
# Breakpoints for time series of infections

summary(breakpoints_infections)
# Summary of breakpoints

plot(breakpoints_infections)
# Plot breakpoints
```

`breaksgrowth-class` *Class* `"breaksgrowth"`

Description

The class `"breaksgrowth"` contains the results of the breaks_growth() function. Use `summary(breaksgrowth)` for results summary.

Objects from the Class

Objects can be created by the function `breaks_growth`.

Slots

`GrowthModel_OLS`**:** Object of class `list` Results of the OLS fit (predicted, parameters)

`t`**:** Object of class `numeric` Input time points data

`y`**:** Object of class `numeric` Input infections data

`config`**:** Object of class `list` Model fit configurations

Methods

summary `signature(object = "breaksgrowth")`: Prints a summary of `breaksgrowth` objects

plot `signature(x = "breaksgrowth")`: Plots the results of the breakpoint analysis

print `signature(x = "breaksgrowth")`: Prints an `breaksgrowth` object; use `summary(breaksgrowth)` for results

Author(s)

Thomas Wieland

References

Bai J, Perron P (2003) Computation and analysis of multiple structural change models. *Journal of Applied Econometrics* 18(1), 1-22. doi:10.1002/jae.659

Wieland T (2020) A phenomenological approach to assessing the effectiveness of COVID-19 related nonpharmaceutical interventions in Germany. *Safety Science* 131, 104924. doi:10.1016/j.ssci.2020.104924

Zeileis C, Kleiber W, Krämer K, Hornik, K (2003) Testing and dating of structural changes in practice. *Computational Statistics & Data Analysis* 44(1-2), 109-123. doi:10.1016/S01679473(03)00030-6

Examples

```
showClass("breaksgrowth")
```

C19dNUTSdata *Regional cumulative COVID-19 deaths*

Description

Cumulative COVID-19 deaths absolute and per 100,000 pop at NUTS3 level for 31 EU/EFTA countries

Usage

```
data("C19dNUTSdata")
```

Format

A data frame with 1,143 observations (each one represents a spatial NUTS unit).

`NUTS_ID` NUTS ID of the spatial unit

`CNTR_CODE` Country code (= NUTS 0 ID) of the given spatial unit

`NUTS_Level` NUTS level of the given spatial unit (0 = national, 1, 2, 3)

`NUTS2_ID` NUTS 2 ID of the spatial unit

`NUTS1_ID` NUTS 1 ID of the spatial unit

`NUTS_Name` Latin name of the spatial unit

`C19deaths` Cumulative COVID-19 deaths [persons]

`pop2020` Population in 2020 [persons]

`C19deaths_per100000` Cumulative COVID-19 deaths [per 100,000]

`annotation` Annotation)

Details

Note: This data was originally released in the author's package C19dNUTS in 2022 (https://cran.r-project.org/package=C19dNUTS). Some of the URLs referred to here were moved or deleted.

The dataset contains cumulative COVID-19 deaths at the regional level (mostly NUTS 3, N=1,143) for 31 EU/EFTA countries (AT, BE, BG, CH, CY, CZ, DE, DK, EE, EL, ES, FI, FR, HR, HU, IE, IS, IT, LT, LU, LV, MT, NL, NO, PL, PT, RO, SE, SI, SK, UK). The `C19deaths` variable contains the absolute number of COVID-19 related deaths, and the variable `C19deaths_per100000` equals the death numbers relative to the population (per 100,000).

Unless otherwise noted, data includes all reported COVID-19 related deaths since the beginning of the COVID-19 pandemic through June 2022. Please refer to the source section below for the exact date on which each raw dataset was retrieved. The spatial level is the current NUTS 2021 classification of the European Union (see 'https://ec.europa.eu/eurostat/web/nuts/background'), with one slight modification (see "Technical details" below). The variable `NUTS_Level` documents the spatial level for which the numbers apply (mostly `NUTS_Level` = 3 for NUTS3).

Technical details:

This dataset contains cumulative numbers and no time series, as many countries only publish cumulative data on COVID-19 deaths. In cases where countries only publish COVID-19 deaths in the form of daily data, the numbers were summed up over the entire period under consideration at the respective spatial level.

The definition of a COVID-19 death may vary between countries. The respective definition can usually be found on the website of the national health authority. In some countries, data is reported based on different definitions. For example, Lithuania uses three different definitions, namely a) based on the main cause of death in the death certificate, b) based on a mention in the death certificate and c) died within 28 days of a positive SARS-CoV-2 test (https://open-data-sets-ls-osp-sdg.hub.arcgis.com/datasets/ba35de03e111430f88a86f7d1f351de6_0/about). In England, for example, a distinction is made between the deceased who tested positive and those who died from COVID-19 based on the death certificate (https://coronavirus.data.gov.uk/details/deaths). In these cases, the definition used has always been the equivalent of the total number of COVID-19 deaths as reported by the national figures from Johns Hopkins University (https://coronavirus.jhu.edu/data/cumulative-cases).

In some cases, countries publish regional COVID-19 data directly at NUTS3 level (e.g., Germany) or NUTS2 level (e.g., Italy). In most cases, the regional level had to be linked manually using the name of the region (e.g., Bulgaria, Norway, Switzerland). Some countries even publish the relevant data on a smaller scale, i.e. below NUTS3 (e.g., Austria, Netherlands, Poland, England). In these cases, where a reference table (subnational spatial unit <-> NUTS3) was available, the lower level was linked to the NUTS3 level (e.g., England). If no reference table but geodata (shapefiles) for the lower spatial level was available (e.g., Austria, Netherlands, Poland), the lower level was linked to the NUTS3 level via a spatial join (Polygon centroids; in cases where the centroid was outside the polygon, it was placed inside the polygon manually). In these cases, the numbers were then summed up at NUTS3 level.

The spatial reference used here is the current EU NUTS Shapefile (https://ec.europa.eu/eurostat/web/gisco/geodata/reference-data/administrative-units-statistical-units/nuts; accessed 2022-06-23). The dataset can be linked directly to this shapefile, where the unique id field to which the link can be made is the column `NUTS_ID`. However, there is one exception: To ensure data compatibility, the UK NUTS3 regions UKM61 and UKM63 were aggregated into one region (UKM61).

The data reflects 1,309,326 COVID-19 related deaths in the 31 countries in the investigated time period. The variable `C19deaths_per100000` is non-normally distributed (Shapiro-Wilk test: $W = 0.92284$, $p < 0.01$). The natural log of `C19deaths_per100000` is spatially autocorrelated (Moran's I with queen contiguous spatial weighting: $I = 0.65228$, $p < 0.01$).

Data limitations:

It can be assumed that there are differences between countries and possibly also over time in the definition of a COVID-19 death (see "Technical details" above). Please check the definition on the website of the respective national health authority.

Data on COVID-19 deaths are incomplete for the following EU/EFTA countries: Bulgaria, France, Poland. In Bulgaria, regional COVID-19 deaths were only published for the years 2020 and 2021 (36,142 COVID-19 related deaths in total), i.e. the cases for 2022 are missing. France only publishes the COVID-19 patients which died in a hospital at the regional level, which equals 120,630 COVID-19 related deaths over the period under consideration (as of 2022-06-30). The total number of COVID-19 related deaths in France for the same time is equal to 149,533, which means that there is a lack of 28,903 COVID-19 fatalities (19.3 %, e.g., people which died in nursing homes). Polish deaths are missing COVID-19 deaths from the first pandemic wave. Therefore only the COVID-19

fatalities from the date 2020-11-24 are included, which equals 102,449 deaths. In the previous period, 13,780 COVID-19 deaths were reported, which are not included in the data set, i.e. 11.9% of the deaths are missing.

Of the 31 EU/EFTA countries included, regional data are only available for 24 countries. The following countries have not published sub-national data for COVID-19 deaths: Cyprus, Finland, Iceland, Hungary, Estonia, Latvia, Malta. The values for Finland, Hungary, Estonia and Latvia refer to the national level (NUTS 0), which is indicated by the variable `NUTS_Level` = 0. In the cases of Cyprus, Malta and Iceland (which are rather small countries), the NUTS 0 level also corresponds to the NUTS 2 level, which is why they are marked here in the dataset with `NUTS_Level` = 2. It is comparatively difficult to compare the data with Belgium because COVID-19 death figures are only published there at NUTS 1 level (3 regions; `NUTS_Level` = 1).

Some countries report separately persons who died of/with COVID-19 who live outside the country or cannot be assigned to a region (e.g., Greece, Norway). These cases are shown separately in the dataset, but cannot be related to population numbers and cannot be linked to the NUTS shapefile.

Norway does not provide COVID-19 data for the NUTS3 regions NO0B1 and NO0B2.

In the UK, each country (England, Wales, Scotland, and Northern Ireland) is independently responsible for publishing COVID-19 data. Therefore the data are not all available at the same spatial aggregation level (e.g. England: NUTS 3, Wales: NUTS 2).

Source

Raw data of COVID-19 deaths:

Note: Some of the URLs have been moved or deleted.

AT: https://covid19-dashboard.ages.at/data/CovidFaelle_Timeline_GKZ.csv (accessed 2022-06-23)

BE: https://epistat.sciensano.be/Data/COVID19BE_MORT.csv (accessed 2022-06-21)

BG: https://www.nsi.bg/sites/default/files/files/data/table/COVID_2020_2021_EN.xls (accessed 2022-06-29)

CH: https://www.covid19.admin.ch/api/data/20220621-t6j901v4/downloads/sources-csv.zip (accessed 2022-06-21)

CY: https://covid19.who.int/region/euro/country/cy (accessed 2022-06-30)

CZ: https://onemocneni-aktualne.mzcr.cz/api/v2/covid-19/umrti.csv (accessed 2022-06-24)

DE: https://npgeo-corona-npgeo-de.hub.arcgis.com/datasets/917fc37a709542548cc3be077a786c17_0/about (accessed 2022-06-23)

DK: https://files.ssi.dk/covid19/overvagning/dashboard/overvaagningsdata-dashboard-covid19-28062022 (accessed 2022-06-29), folder: "Regionalt_DB", file: "07_antal_doede_pr_dag_pr_region"

EE: https://www.terviseamet.ee/en/coronavirus/coronavirus-dataset (accessed 2022-07-11)

EL: https://github.com/Sandbird/covid19-Greece (accessed 2022-07-02), file "regions"

ES: https://cnecovid.isciii.es/covid19/resources/casos_hosp_uci_def_sexo_edad_provres.csv (accessed 2022-06-28)

FI: https://covid19.who.int/region/euro/country/fi (accessed 2022-07-01)

FR: https://www.data.gouv.fr/fr/datasets/synthese-des-indicateurs-de-suivi-de-lepidemie-covid-19/ (accessed 2022-07-01), file "table-indicateurs-open-data-dep-2022-06-30-19h00"

HR: https://www.koronavirus.hr/zupanije/139 (accessed 2022-06-28)

HU: https://covid19.who.int/region/euro/country/hu (accessed 2022-07-02)

IE: https://epi-covid-19-hpscireland.hub.arcgis.com/ (accessed 2022-06-29)

IS: https://www.covid.is/data (accessed 2022-06-27)

IT: https://github.com/pcm-dpc/COVID-19/tree/master/dati-regioni (accessed 2022-06-24), file "dpc-covid19-ita-regioni-latest_raw"

LV: https://covid19.gov.lv/en/node/16387 (accessed 2022-07-27)

LT: https://open-data-ls-osp-sdg.hub.arcgis.com/datasets/ba35de03e111430f88a86f7d1f351de6_0/explore (accessed 2022-06-27)

LU: https://covid19.public.lu/fr/graph.html (accessed 2022-06-27)

MT: https://covid19.who.int/table (accessed 2022-07-01)

NL: https://data.rivm.nl/covid-19/COVID-19_aantallen_gemeente_per_dag.csv (accessed 2022-06-27)

NO: https://www.fhi.no/contentassets/8a971e7b0a3c4a06bdbf381ab52e6157/vedlegg/2022/ukerapport-uke-20-16.05—22.05.22.pdf (accessed 2022-07-07)

PL: https://www.gov.pl/web/koronawirus/wykaz-zarazen-koronawirusem-sars-cov-2 (accessed 2022-06-23)

PT: https://github.com/dssg-pt/covid19pt-data/blob/master/data.csv (accessed 2022-06-29)

RO: https://covid19.geo-spatial.org/?map=decese (accessed 2022-07-01)

SE: https://experience.arcgis.com/experience/19fc7e3f61ec4e86af178fe2275029c5 (accessed 2022-06-23)

SI: https://www.nijz.si/sites/www.nijz.si/files/uploaded/tedenski_prikaz_umrli20220627.xlsx (accessed 2022-06-28)

SK: https://github.com/Institut-Zdravotnych-Analyz/covid19-data (accessed 2022-06-28), folder "Deaths", file "OpenData_Slovakia_Covid_Deaths_AgeGroup_District"

UK - England: https://coronavirus.data.gov.uk/details/deaths (accessed 2022-06-24), file "ltla_2022_06_23_cumDeaths60Da

UK - Northern Ireland: https://www.nisra.gov.uk/system/files/statistics/Weekly_Deaths%20-%20w%20e%2017th%20June%202022.XLSX (accessed 2022-07-01)

UK - Scotland: https://www.nrscotland.gov.uk/files//statistics/covid19/covid-deaths-22-data-week-25.xlsx (data for 2021-2022) and https://www.nrscotland.gov.uk/files//statistics/covid19/covid-deaths-20-data-final.xlsx (data for 2022) (accessed 2022-07-01)

UK - Wales: https://public.tableau.com/app/profile/public.health.wales.health.protection/viz/COVID-19Rapidmortalitydata/Summary (accessed 2022-07-04)

Population data:

https://ec.europa.eu/eurostat/databrowser/view/DEMO_R_PJANGRP3/default/table?lang=en&category=reg.reg_dem.reg_dempoar (accessed 2022-06-22)

Examples

```
data(C19dNUTSdata)

# Summary:
```

```
summary(C19dNUTSdata)

# Check for normal distribution:
hist(C19dNUTSdata$C19deaths_per100000)
shapiro.test(C19dNUTSdata$C19deaths_per100000)

# no. of regions for each country:
table(C19dNUTSdata$CNTR_CODE)
# only for countries with data on at least NUTS 2 level:
table(C19dNUTSdata[C19dNUTSdata$NUTS_Level > 1,]$CNTR_CODE)
```

`calculate_cum` *Cumulative Infection Numbers*

Description

Calculation of the cumulative values of infection numbers for infections panel data.

Usage

```
calculate_cum(
  object,
  col_name = NULL,
  overwrite = FALSE,
  verbose = FALSE
  )
```

Arguments

`object`	object of class `infpan`
`col_name`	`character` value specifying the column name of the computed cumulative values
`overwrite`	`bool` argument which indicates whether the column should be overwritten if already existing
`verbose`	`bool` argument which indicates whether progress messages are displayed

Details

Calculates the cumulative values of the infections panel data for all time points for each region. If `col_name` is `NULL`, the column is defined as "<Column name of cases>_cum". Set `overwrite` to TRUE, if an existing column should be overwritten. The method uses the function `cumsum` from the `base` package (see the corresponding documentation).

Value

`infpan` object including column with cumulative values in the infections panel data

Author(s)

Thomas Wieland

References

Wieland T (2020) Flatten the Curve! Modeling SARS-CoV-2/COVID-19 Growth in Germany at the County Level. *REGION* 7(2), 43–83. doi:10.18335/region.v7i2.324

Wieland T (2020) A phenomenological approach to assessing the effectiveness of COVID-19 related nonpharmaceutical interventions in Germany. *Safety Science* 131, 104924. doi:10.1016/j.ssci.2020.104924

See Also

infpan-class, load_infections_paneldata, calculate_Rt, calculate_incidence, calculate_rollmean

Examples

```
data(COVID19Cases_geoRegion)
# Get SWISS COVID19 cases at NUTS 3 level

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[!COVID19Cases_geoRegion$geoRegion %in% c("CH", "CHFL"),]
# Exclude CH = Switzerland total and CHFL = Switzerland and Liechtenstein total

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[COVID19Cases_geoRegion$datum <= "2020-05-31",]
# Extract first COVID-19 wave

infpan_CH <- load_infections_paneldata(
    data = COVID19Cases_geoRegion,
    col_cases = "entries",
    col_date = "datum",
    col_region = "geoRegion",
    other_cols = c("Population" = "pop"),
    verbose = TRUE
  )
# Import as infections panel data set (class infpan)

infpan_CH <- calculate_cum(
  infpan_CH,
  col_name = "cumulatives",
  verbose = TRUE
)
# Calculate rolling mean of cases as "cumulatives"

summary(infpan_CH)
# Summary of infpan object
```

calculate_cum-methods *Methods for Function* calculate_cum

Description

Methods for function calculate_cum

Methods

signature(object = "infpan", col_name = NULL, overwrite = FALSE, verbose = FALSE) Calculates the cumulative values of the infections panel data for all time points for each region. If col_name is NULL, the column is defined as "<Column name of cases>_cum". The method uses the function cumsum from the base package (see the corresponding documentation).

Author(s)

Thomas Wieland

calculate_incidence *Incidence from Infection Numbers*

Description

Calculation of the incidence from infection numbers and population for infections panel data.

Usage

```
calculate_incidence(
  object,
  use_column = NULL,
  col_name = NULL,
  pop_factor = 100000,
  overwrite = FALSE,
  verbose = FALSE
  )
```

Arguments

object	object of class infpan
use_column	character value specifying which column should be used for incidence calculation
col_name	character value specifying the column name of the computed incidence
pop_factor	numeric value specifying the factor with which the incidence should be multiplied (e.g., cases/pop*100000)
overwrite	bool argument which indicates whether the column should be overwritten if already existing
verbose	bool argument which indicates whether progress messages are displayed

Details

Calculates the incidence of the infections panel data for all time points for each region. Use `use_column` to specify which column should be used for the calculation of incidence. The following values are permitted: "Cases" (default, new infection cases), "Cum. cases" (cumulative cases), "Roll. mean" (rolling mean of cases), or "Roll. sum" (rolling sum of cases). If the specified column does not exist in the infections panel data of the `infpan` object, the function raises an error. If in the `infpan` object, no "Population" column is defined, incidence calculation is not possible. If `col_name` is `NULL`, the column is defined as "<Column name of cases>_inc". Set `overwrite` to TRUE, if an existing column should be overwritten.

Value

`infpan` object including column with incidence values in the infections panel data

Author(s)

Thomas Wieland

References

an der Heiden M, Hamouda O (2020) Schätzung der aktuellen Entwicklung der SARS-CoV-2-Epidemie in Deutschland - Nowcasting. *Epidemiologisches Bulletin* 17, 10-15. doi:10.25646/6692

Wieland T (2020) Flatten the Curve! Modeling SARS-CoV-2/COVID-19 Growth in Germany at the County Level. *REGION* 7(2), 43–83. doi:10.18335/region.v7i2.324

See Also

`infpan-class`, `load_infections_paneldata`, `calculate_Rt`, `calculate_cum`, `calculate_rollmean`

Examples

```
data(COVID19Cases_geoRegion)
# Get SWISS COVID19 cases at NUTS 3 level

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[!COVID19Cases_geoRegion$geoRegion %in% c("CH", "CHFL"),]
# Exclude CH = Switzerland total and CHFL = Switzerland and Liechtenstein total

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[COVID19Cases_geoRegion$datum <= "2020-05-31",]
# Extract first COVID-19 wave

infpan_CH <- load_infections_paneldata(
    data = COVID19Cases_geoRegion,
    col_cases = "entries",
    col_date = "datum",
    col_region = "geoRegion",
    other_cols = c("Population" = "pop"),
    verbose = TRUE
  )
```

```
# Import as infections panel data set (class infpan)

infpan_CH <- calculate_incidence(
  infpan_CH,
  col_name = "incidence",
  verbose = TRUE
)
# Calculate incidence of cases as "incidence"

summary(infpan_CH)
# Summary of infpan object
```

`calculate_incidence-methods` *Methods for Function* `calculate_incidence`

Description

Methods for function `calculate_incidence`

Methods

`signature( object, use_column = "Cases", col_name = NULL, pop_factor = 100000, overwrite = FALSE, verbose =`

Calculates the incidence of the infections panel data for all time points for each region. Use `use_column` to specify which column should be used for the calculation of incidence. The following values are permitted: "Cases" (default, new infection cases), "Cum. cases" (cumulative cases), "Roll. mean" (rolling mean of cases), or "Roll. sum" (rolling sum of cases). If the specified column does not exist in the infections panel data of the `infpan` object, the function raises an error. If in the `infpan` object, no "Population" column is defined, incidence calculation is not possible. If `col_name` is `NULL`, the column is defined as "<Column name of cases>_inc". Set `overwrite` to TRUE, if an existing column should be overwritten.

Author(s)

Thomas Wieland

`calculate_rollmean` *Rolling Means of Infection Numbers*

Description

Calculation of the rolling means of infection numbers for infections panel data.

Usage

```
calculate_rollmean(
  object,
  k = 7,
  align = "center",
  fill = NA,
  col_name = NULL,
  overwrite = FALSE,
  verbose = FALSE
  )
```

Arguments

object	object of class infpan
k	integer width of the rolling window (default: 7)
align	character specifying whether the rolling mean should be left- or right-aligned or centered (default) compared to the rolling window (default: center)
fill	numeric value or NA for the filling value at the left/within/right end of the data range
col_name	character value specifying the column name of the computed rolling means
overwrite	bool argument which indicates whether the column should be overwritten if already existing
verbose	bool argument which indicates whether progress messages are displayed

Details

Calculates the rolling mean of the infections panel data for all time points for each region. Set the rolling window by the parameter k (default: 7). Set the fill value for the observations left/within/right to the data range with parameter fill (default: NA). Parameter align defines whether the index of the result should be left- or right-aligned or centered (default). If col_name is NULL, the column is defined as "<Column name of cases>_rm". Set overwrite to TRUE, if an existing column should be overwritten. The method uses the function rollmean from the zoo package (see the corresponding documentation).

Value

infpan object including column with rolling means in the infections panel data

Author(s)

Thomas Wieland

References

Wieland T (2025) Assessing the effectiveness of non-pharmaceutical interventions in the SARS-CoV-2 pandemic: results of a natural experiment regarding Baden-Württemberg (Germany) and Switzerland in the second infection wave. *Journal of Public Health* 33(11), 2497-2511. doi:10.1007/s1038902402218x

See Also

infpan-class, load_infections_paneldata, calculate_rollsum, calculate_Rt, calculate_cum, calculate_incidence

Examples

```
data(COVID19Cases_geoRegion)
# Get SWISS COVID19 cases at NUTS 3 level

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[!COVID19Cases_geoRegion$geoRegion %in% c("CH", "CHFL"),]
# Exclude CH = Switzerland total and CHFL = Switzerland and Liechtenstein total

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[COVID19Cases_geoRegion$datum <= "2020-05-31",]
# Extract first COVID-19 wave

infpan_CH <- load_infections_paneldata(
    data = COVID19Cases_geoRegion,
    col_cases = "entries",
    col_date = "datum",
    col_region = "geoRegion",
    other_cols = c("Population" = "pop"),
    verbose = TRUE
  )
# Import as infections panel data set (class infpan)

infpan_CH <- calculate_rollmean(
  infpan_CH,
  col_name = "RollingMean",
  verbose = TRUE
)
# Calculate rolling mean of cases as "RollingMean"

summary(infpan_CH)
# Summary of infpan object
```

---

calculate_rollmean-methods

Methods for Function calculate_rollmean

Description

Methods for function calculate_rollmean

Methods

signature(object = "infpan", k = 7, align = "center", fill = NA, col_name = NULL, verbose = FALSE)

Calculates the rolling mean of the infections panel data for all time points for each region. Set

the rolling window by the parameter k (default: 7). Set the fill value for the observations left/within/right to the data range with parameter fill (default: NA). Parameter align defines whether the index of the result should be left- or right-aligned or centered (default). If col_name is NULL, the column is defined as "<Column name of cases>_rm". The method uses the function rollmean from the zoo package (see the corresponding documentation).

Author(s)

Thomas Wieland

`calculate_rollsum` *Rolling Sums of Infection Numbers*

Description

Calculation of the rolling sums of infection numbers for infections panel data.

Usage

```
calculate_rollsum(
  object,
  k = 7,
  align = "center",
  fill = NA,
  col_name = NULL,
  overwrite = FALSE,
  verbose = FALSE
  )
```

Arguments

object	object of class infpan
k	integer width of the rolling window (default: 7)
align	character specifying whether the rolling mean should be left- or right-aligned or centered (default) compared to the rolling window (default: center)
fill	numeric value or NA for the filling value at the left/within/right end of the data range
col_name	character value specifying the column name of the computed rolling sums
overwrite	bool argument which indicates whether the column should be overwritten if already existing
verbose	bool argument which indicates whether progress messages are displayed

Details

Calculates the rolling sum of the infections panel data for all time points for each region. Set the rolling window by the parameter k (default: 7). Set the fill value for the observations left/within/right to the data range with parameter `fill` (default: NA). Parameter `align` defines whether the index of the result should be left- or right-aligned or centered (default). If `col_name` is `NULL`, the column is defined as "<Column name of cases>_rs". Set `overwrite` to TRUE, if an existing column should be overwritten. The method uses the function `rollsum` from the `zoo` package (see the corresponding documentation).

Value

`infpan` object including column with rolling sums in the infections panel data

Author(s)

Thomas Wieland

References

Wieland T (2025) Assessing the effectiveness of non-pharmaceutical interventions in the SARS-CoV-2 pandemic: results of a natural experiment regarding Baden-Württemberg (Germany) and Switzerland in the second infection wave. *Journal of Public Health* 33(11), 2497-2511. doi:10.1007/s1038902402218x

See Also

`infpan-class`, `load_infections_paneldata`, `calculate_rollmean`, `calculate_Rt`, `calculate_cum`, `calculate_incidence`

Examples

```
data(COVID19Cases_geoRegion)
# Get SWISS COVID19 cases at NUTS 3 level

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[!COVID19Cases_geoRegion$geoRegion %in% c("CH", "CHFL"),]
# Exclude CH = Switzerland total and CHFL = Switzerland and Liechtenstein total

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[COVID19Cases_geoRegion$datum <= "2020-05-31",]
# Extract first COVID-19 wave

infpan_CH <- load_infections_paneldata(
    data = COVID19Cases_geoRegion,
    col_cases = "entries",
    col_date = "datum",
    col_region = "geoRegion",
    other_cols = c("Population" = "pop"),
    verbose = TRUE
  )
# Import as infections panel data set (class infpan)
```

```
infpan_CH <- calculate_rollsum(
  infpan_CH,
  col_name = "RollingMSum",
  verbose = TRUE
)
# Calculate rolling sum of cases as "RollingSum"

summary(infpan_CH)
# Summary of infpan object
```

`calculate_rollsum-methods` *Methods for Function* `calculate_rollsum`

Description

Methods for function `calculate_rollsum`

Methods

`signature( object = "infpan", k = 7, align = "center", fill = NA, col_name = NULL, verbose = FALSE)`
: Calculates the rolling sum of the infections panel data for all time points for each region. Set the rolling window by the parameter `k` (default: 7). Set the fill value for the observations left/within/right to the data range with parameter `fill` (default: NA). Parameter `align` defines whether the index of the result should be left- or right-aligned or centered (default). If `col_name` is `NULL`, the column is defined as "<Column name of cases>_rs". The method uses the function `rollsum` from the `zoo` package (see the corresponding documentation).

Author(s)

Thomas Wieland

`calculate_Rt` *Effective Reproduction Number*

Description

Calculation of the effective reproduction number for infections panel data.

Usage

```
calculate_Rt(
  object,
  GP = 4,
  correction = FALSE,
  col_name = NULL,
  overwrite = FALSE,
  verbose = FALSE
  )
```

Arguments

object	object of class infpan
GP	Generation period, in time units (typically days)
correction	Correction of values equal to zero? (Recommended)
col_name	character value specifying the column name of the computed rolling means
overwrite	bool argument which indicates whether the column should be overwritten if already existing
verbose	bool argument which indicates whether progress messages are displayed

Details

Calculates the effective reproduction number R_t for all time points for each region in the infections panel data. Set the generation period by the parameter GP (default: 4). If correction is TRUE, values equal to zero are increased by one. The method uses the built-in function R_t().

Value

infpan object including R_t column in the infections panel data

Author(s)

Thomas Wieland

References

an der Heiden M, Hamouda O (2020) Schätzung der aktuellen Entwicklung der SARS-CoV-2-Epidemie in Deutschland - Nowcasting. *Epidemiologisches Bulletin* 17, 10-15. doi:10.25646/6692

Bonifazi G, Lista L, Menasce D, Mezzetto M, Pedrini D, Spighi R, Zoccoli A (2021) A simplified estimate of the effective reproduction number Rt using its relation with the doubling time and application to Italian COVID-19 data. *The European Physical Journal Plus* 136, 386. doi:10.1140/epjp/s13360021013396

Wieland T (2020) A phenomenological approach to assessing the effectiveness of COVID-19 related nonpharmaceutical interventions in Germany. *Safety Science* 131, 104924. doi:10.1016/j.ssci.2020.104924

Wieland T (2025) Assessing the effectiveness of non-pharmaceutical interventions in the SARS-CoV-2 pandemic: results of a natural experiment regarding Baden-Württemberg (Germany) and

Switzerland in the second infection wave. *Journal of Public Health* 33(11), 2497-2511. doi:10.1007/s1038902402218x

See Also

infpan-class, load_infections_paneldata, calculate_incidence, calculate_cum, calculate_rollmean

Examples

```
data(COVID19Cases_geoRegion)
# Get SWISS COVID19 cases at NUTS 3 level

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[!COVID19Cases_geoRegion$geoRegion %in% c("CH", "CHFL"),]
# Exclude CH = Switzerland total and CHFL = Switzerland and Liechtenstein total

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[COVID19Cases_geoRegion$datum <= "2020-05-31",]
# Extract first COVID-19 wave

infpan_CH <- load_infections_paneldata(
    data = COVID19Cases_geoRegion,
    col_cases = "entries",
    col_date = "datum",
    col_region = "geoRegion",
    other_cols = c("Population" = "pop"),
    verbose = TRUE
  )
# Import as infections panel data set (class infpan)

infpan_CH <- calculate_Rt(
  infpan_CH,
  verbose = TRUE
  )
# Calculate effective reproduction number

summary(infpan_CH)
# Summary of infpan object
```

---

calculate_Rt-methods *Methods for Function* calculate_Rt

Description

Methods for function calculate_Rt

Methods

signature(object = "infpan", GP = 4, correction = FALSE, col_name = NULL, verbose = FALSE)
: Calculates the effective reproduction number R_t for all time points for each region in the infections panel data. Set the generation period by the parameter GP (default: 4). If correction is TRUE, values equal to zero are increased by one. Set overwrite to TRUE, if an existing column should be overwritten. The method uses the built-in function R_t().

Author(s)

Thomas Wieland

---

compare_countries *Two-country Comparison of Swash-Backwash Model Parameters*

Description

This function enables bootstrap estimates for the mean difference of Swash-Backwash Model parameters of two countries to be compared.

Usage

```
compare_countries(
  sbm1,
  sbm2,
  country_names = c("Country 1", "Country 2"),
  indicator = "R_0A",
  iterations = 20,
  samples_ratio = 0.8,
  alpha = 0.05,
  replace = TRUE
  )
```

Arguments

sbm1	A sbm object for country 1
sbm2	A sbm object for country 2
country_names	list with user-given country names (two entries)
indicator	character, indicator to be analyzed ("S_A", "I_A", "R_A", "t_LE", "t_LE", or "R_0A" (default and recommended: "R_0A"))
iterations	Number of iterations for resampling (default: 100)
samples_ratio	Proportion of regions included in each sample (default: 0.8)
alpha	Significance level α for 1-α*100 confidence intervals (default: 0.05)
replace	Resampling with replacement (TRUE or FALSE, default: TRUE = bootstrap resampling)

Details

The combination of the Swash-Backwash Model and bootstrap resampling allows the estimation of mean differences of a user-specified model parameter (e.g., spatial reproduction number R_{OA}) between two countries. This makes it possible to check whether the spatial spread velocity of a communicable disease is significantly different in one country than in another country. Since the initial data in the Swash-Backwash Model should be balanced, *entity-based bootstrap sampling* is carried out in the `compare_countries()` function. This means that not, for example, 80% of all observations are included in each sample at a sample ratio equal to p = 0.8, but rather all observations for 80% of the regions. For both countries, B bootstrap samples (default: 100) are drawn for which the Swash-Backwash Model is calculated. Based on the distribution of indicators, confidence intervals are calculated at the user-specified significance level α. The `compare_countries()` function calculates the differences of the user's desired indicator between the two samples, D, and also calculates α confidence intervals for this.

Value

object of class `countries`, see `countries-class`

Author(s)

Thomas Wieland

References

Cliff AD, Haggett P (2006) A swash-backwash model of the single epidemic wave. *Journal of Geographical Systems* 8(3), 227-252. doi:10.1007/s1010900600278

Efron B, Tibshirani RJ (1993) An Introduction to the Bootstrap.

Ramachandran KM, Tsokos CP (2021) Mathematical Statistics with Applications in R (Third Edition). Ch. 13.3.1 (Bootstrap confidence intervals). doi:10.1016/B9780128178157.000130

Smallman-Raynor MR, Cliff AD, Stickler PJ (2022) Meningococcal Meningitis and Coal Mining in Provincial England: Geographical Perspectives on a Major Epidemic, 1929–33. *Geographical Analysis* 54, 197–216. doi:10.1111/gean.12272

Smallman-Raynor MR, Cliff AD, The COVID-19 Genomics UK (COG-UK) Consortium (2022) Spatial growth rate of emerging SARS-CoV-2 lineages in England, September 2020–December 2021. *Epidemiology and Infection* 150, e145. doi:10.1017/S0950268822001285.

See Also

`swash`, `countries-class`

Examples

```
data(COVID19Cases_geoRegion)
# Get Swiss COVID19 cases at NUTS 3 level

data(Oesterreich_Faelle)
# Get Austrian COVID19 cases at NUTS 3 level
# (first wave, same final date as in Swiss data: 2020-05-31)
```

```
COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[!COVID19Cases_geoRegion$geoRegion %in% c("CH", "CHFL"),]
# Exclude CH = Switzerland total and CHFL = Switzerland and Liechtenstein total

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[COVID19Cases_geoRegion$datum <= "2020-05-31",]
# Extract first COVID-19 wave

CH_covidwave1 <-
  swash_backwash(
    data = COVID19Cases_geoRegion,
    col_cases = "entries",
    col_date = "datum",
    col_region = "geoRegion"
    )
# Swash-Backwash Model for Swiss COVID19 cases
# Spatial aggregate: NUTS 3 (cantons)

AT_covidwave1 <-
  swash_backwash(
    data = Oesterreich_Faelle,
    col_cases = "Faelle",
    col_date = "Datum",
    col_region = "NUTS3"
  )
# Swash-Backwash Model for Austrian COVID19 cases
# Spatial aggregate: NUTS 3

AT_vs_CH <-
  compare_countries(
    CH_covidwave1,
    AT_covidwave1,
    country_names = c("Switzerland", "Austria"))
# Country comparison Switzerland vs. Austria
# default config: 20 iterations, alpha = 0.05, sample ratio = 80%,
# indicator: R_0A

summary(AT_vs_CH)
# Summary of country comparison

plot(AT_vs_CH)
# Plot of country comparison
```

`confint-methods` *Methods for Function* `confint`

Description

Methods for function `confint`

Methods

`signature(object = "sbm", iterations = 100, samples_ratio = 0.8, alpha = 0.05, replace = TRUE)`
: Creates bootstrap confidence intervals for `sbm` objects. The argument `iterations` indicates the number of bootstrap samples which are drawn. Since the initial data in the Swash-Backwash Model should be balanced, *entity-based bootstrap sampling* is carried out. This means that not, for example, 80% of all observations are included in each sample at a sample ratio equal to $p = 0.8$ (`samples_ratio = 0.8`), but rather all observations for 80% of the regions. The significance level for the confidence intervals α is set by the argument `alpha` (default: 0.05, which corresponds to a 95% confidence level).

Author(s)

Thomas Wieland

References

Cliff AD, Haggett P (2006) A swash-backwash model of the single epidemic wave. *Journal of Geographical Systems* 8(3), 227-252. doi:10.1007/s1010900600278

Efron B, Tibshirani RJ (1993) An Introduction to the Bootstrap.

Ramachandran KM, Tsokos CP (2021) Mathematical Statistics with Applications in R (Third Edition). Ch. 13.3.1 (Bootstrap confidence intervals). doi:10.1016/B9780128178157.000130

Smallman-Raynor MR, Cliff AD, Stickler PJ (2022) Meningococcal Meningitis and Coal Mining in Provincial England: Geographical Perspectives on a Major Epidemic, 1929–33. *Geographical Analysis* 54, 197–216. doi:10.1111/gean.12272

Smallman-Raynor MR, Cliff AD, The COVID-19 Genomics UK (COG-UK) Consortium (2022) Spatial growth rate of emerging SARS-CoV-2 lineages in England, September 2020–December 2021. *Epidemiology and Infection* 150, e145. doi:10.1017/S0950268822001285.

See Also

`sbm_ci-class`

`countries-class` *Class* `"countries"`

Description

The class `countries` contains the results of a two-country comparison analysis using the Swash-Backwash Model, including two `sbm_ci` objects for each country. Use `summary(countries)` and `plot(countries)` for results summary and plotting, respectively.

Objects from the Class

Objects can be created by the function `compare_countries(sbm1, sbm2)`.

Slots

`sbm_ci1`: Object of class `"sbm_ci"` Results of `"confint(sbm1)"` for country 1

`sbm_ci2`: Object of class `"sbm_ci"` Results of `"confint(sbm2)"` for country 2

`D`: Object of class `"numeric"` Results: Difference D between the samples with respect to the chosen indicator

`D_ci`: Object of class `"numeric"` Results: α confidence intervals of D

`config`: Object of class `"list"` Configuration details for bootstrap sampling

`country_names`: Object of class `"character"` User-stated country names

`indicator`: Object of class `"character"` User-stated indicator to be tested

Methods

plot `signature(x = "countries")`: Plots the results of a two-country comparison with the Swash-Backwash Model

show `signature(object = "countries")`: Prints an `countries` object; use `summary(countries)` for results

print `signature(x = "countries")`: Prints an `countries` object; use `summary(countries)` for results

summary `signature(object = "countries")`: Prints a summary of a `countries` object (results of the two-country comparison)

Author(s)

Thomas Wieland

Examples

```
showClass("countries")
```

COVID19Cases_geoRegion

Switzerland Daily COVID-19 cases by region

Description

A dataset containing COVID-19 cases by region (NUTS 3 = cantons) and time periods (days) for Switzerland (Source: Federal Office of Public Health FOPH).

Usage

```
data(COVID19Cases_geoRegion)
```

Format

A data.frame with multiple columns:

geoRegion (character) Region for which the data was collected.
datum (Date) Date of record.
entries (integer) Number of reported cases on this date.
sumTotal (integer) Cumulative case numbers.
timeframe_14d (logical) Indicates whether the time period covers the last 14 days.
timeframe_all (logical) Indicates whether the time period covers all previous data.
offset_last7d (integer) Offset of the last 7 days.
sumTotal_last7d (integer) Cumulative case numbers of the last 7 days.
offset_last14d (integer) Offset of the last 14 days.
sumTotal_last14d (integer) Cumulative case numbers of the last 14 days.
offset_last28d (integer) Offset of the last 28 days.
sumTotal_last28d (integer) Cumulative case numbers of the last 28 days.
sum7d (numeric) Sum of the last 7 days.
sum14d (numeric) Sum of the last 14 days.
mean7d (numeric) Average of the last 7 days.
mean14d (numeric) Average of the last 14 days.
entries_diff_last_age (integer) Difference from the last age group.
pop (integer) Population of the region.
inz_entries (numeric) Incidence of the entries.
inzsumTotal (numeric) Incidence of cumulative cases.
inzmean7d (numeric) Incidence of the 7-day average.
inzmean14d (numeric) Incidence of the 14-day average.
inzsumTotal_last7d (numeric) Incidence of cumulative cases in the last 7 days.
inzsumTotal_last14d (numeric) Incidence of cumulative cases in the last 14 days.
inzsumTotal_last28d (numeric) Incidence of cumulative cases in the last 28 days.
inzsum7d (numeric) Incidence of the last 7 days.
inzsum14d (numeric) Incidence of the last 14 days.
sumdelta7d (numeric) Difference in sums of the last 7 days.
inzdelta7d (numeric) Difference in incidence of the last 7 days.
type (character) Type of recorded data (e.g., COVID-19 cases).
type_variant (character) Variant of the data type.
version (character) Version of the data collection.
datum_unit (character) Unit of date specification (e.g., day).
entries_letzter_stand (integer) Last known count of entries.
entries_neu_gemeldet (integer) Newly reported entries.
entries_diff_last (integer) Difference in last entries.

Details

The data is included as it was published by the Swiss Federal Office of Public Health (Bundesamt fuer Gesundheit, BAG). Note that the reporting date equals the date of SARS-CoV-2 testing.

Source

Federal Office of Public Health - FOPH (2023) COVID-19 Dashboard Source Data. https://www.covid19.admin.ch/api/data/documentation (retrieved 2023-06-28)

References

Wieland T (2025) Assessing the effectiveness of non-pharmaceutical interventions in the SARS-CoV-2 pandemic: results of a natural experiment regarding Baden-Württemberg (Germany) and Switzerland in the second infection wave. *Journal of Public Health* 33(11), 2497-2511. doi:10.1007/s1038902402218x

Examples

```
data(COVID19Cases_geoRegion)
# Get SWISS COVID19 cases at NUTS 3 level

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[!COVID19Cases_geoRegion$geoRegion %in% c("CH", "CHFL"),]
# Exclude CH = Switzerland total and CHFL = Switzerland and Liechtenstein total

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[COVID19Cases_geoRegion$datum <= "2020-05-31",]
# Extract first COVID-19 wave

COVID19Cases_geoRegion_balanced <-
  is_balanced(
  data = COVID19Cases_geoRegion,
  col_cases = "entries",
  col_date = "datum",
  col_region = "geoRegion"
)
# Test whether "COVID19Cases_geoRegion" is balanced panel data

COVID19Cases_geoRegion_balanced$data_balanced
# Balanced? TRUE or FALSE
```

---

did_fatalities_splm_coef

Results from a Difference-in-Differences Model

Description

Example data frame with results from a difference-in-differences model

Usage

```
data(did_fatalities_splm_coef)
```

Format

A `data.frame` with multiple columns:

Var Coefficient name

Estimate Coef. estimate

Std_Error_Bonferroni Coef. standard error

t_value_Bonferroni Coef. t value

Pr_t_Bonferroni Coef. p value

CI_lower_Bonferroni Coef. lower confidence interval

CI_upper_Bonferroni Coef. upper confidence interval

Details

Data frame with results from a difference-in-differences model (SPLM model), example data

Source

Wieland T (2025) Assessing the effectiveness of non-pharmaceutical interventions in the SARS-CoV-2 pandemic: results of a natural experiment regarding Baden-Württemberg (Germany) and Switzerland in the second infection wave. *Journal of Public Health* 33(11), 2497-2511. doi:10.1007/s1038902402218x

Examples

```
data(did_fatalities_splm_coef)
# Results of a difference-in-differences model

plot_coef_ci(
  point_estimates = did_fatalities_splm_coef$Estimate,
  confint_lower = did_fatalities_splm_coef$CI_lower_Bonferroni,
  confint_upper = did_fatalities_splm_coef$CI_upper_Bonferroni,
  coef_names = did_fatalities_splm_coef$Var,
  skipvars = c(
    "Alpha_share",
    "lambda",
    "rho",
    "log(D_Infections_daily_7dsum_per100000_lag2weeks)",
    "vacc_cum_per100000_lag2weeks"
    ),
  lwd = 13,
  pch = 19,
  auto_color = TRUE
)
# Plot with point estimates and confidence intervals
```

`expgrowth-class` *Class* `"expgrowth"`

Description

The class `"expgrowth"` contains the results of the exponential_growth() function. Use `summary(expgrowth)` for results summary.

Objects from the Class

Objects can be created by the function `exponential_growth`.

Slots

`GrowthModel_OLS`**:** Object of class `list` Results of the OLS fit (predicted, parameters)

`GrowthModel_NLS`**:** Object of class `list` Results of the NLS fit (predicted, parameters)

`t`**:** Object of class `numeric` Input time points data

`y`**:** Object of class `numeric` Input infections data

`config`**:** Object of class `list` Model fit configurations

Methods

summary `signature(object = "expgrowth")`: Prints a summary of `expgrowth` objects

plot `signature(x = "expgrowth")`: Plots the results of the exponential growth model (observed, predicted)

print `signature(x = "expgrowth")`: Prints an `expgrowth` object; use `summary(expgrowth)` for results

Author(s)

Thomas Wieland

References

Bonifazi G, Lista L, Menasce D, Mezzetto M, Pedrini D, Spighi R, Zoccoli A (2021) A simplified estimate of the effective reproduction number Rt using its relation with the doubling time and application to Italian COVID-19 data. *The European Physical Journal Plus* 136, 386. doi:10.1140/epjp/s13360021013396

Chowell G, Viboud C, Hyman JM, Simonsen L (2015) The Western Africa ebola virus disease epidemic exhibits both global exponential and local polynomial growth rates. *PLOS Currents Outbreaks*, ecurrents.outbreaks.8b55f4bad99ac5c5db3663e916803261. doi:10.1371/currents.outbreaks.8b55f4bad99ac5c5db36

Pell B, Kuang Y, Viboud C, Chowell G (2018) Using phenomenological models for forecasting the 2015 ebola challenge. *Epidemics* 22, 62–70. doi:10.1016/j.epidem.2016.11.002

Wieland T (2020) A phenomenological approach to assessing the effectiveness of COVID-19 related nonpharmaceutical interventions in Germany. *Safety Science* 131, 104924. doi:10.1016/j.ssci.2020.104924

Examples

```
showClass("expgrowth")
```

`exponential_growth` *Exponential Growth Model for Epidemic Data*

Description

Estimation of exponential growth models from daily infections data

Usage

```
exponential_growth(
  y,
  t = NULL,
  GI = 4,
  nls = TRUE,
  nls_start = list(a = 1, b = 0.1),
  impute_missing_values = FALSE,
  add_constant = 1,
  verbose = FALSE
  )
```

Arguments

`y`	`numeric vector` with cumulative infections data over time
`t`	`vector` of class `numeric` or `Date` with time points or dates
`GI`	Generation interval for computing R_0
`nls`	Nonlinear estimation? `TRUE` or `FALSE`
`nls_start`	A `list` with start values for the two parameters to be estimated
`impute_missing_values`	`bool` argument which indicates whether missing values have to be imputed via linear imputation
`add_constant`	Numeric constant to be added to y if zero values occur (only relevant for OLS estimation)
`verbose`	`bool` argument which indicates whether progress messages are displayed

Details

This function allows the estimation of an exponential growth model. This model is designed for the analysis of the *initial* phase of an epidemic spread. The user must specify the dependent variable (e.g., daily infections) and the time variable (time counter or date values). The estimation is performed using a linearized model as an OLS estimator, and, if `nls=TRUE`, also by NLS. The results are the exponential growth rate r, basic reproduction number R_0, and the doubling rate. See Rawlings et al. (1998) for the basics of intrinsically linear models such as the logistic or exponential growth model. See Wieland (2020) for the documentation of the fitting procedure applied in this function.

Value

object of class expgrowth-class

Author(s)

Thomas Wieland

References

Bonifazi G, Lista L, Menasce D, Mezzetto M, Pedrini D, Spighi R, Zoccoli A (2021) A simplified estimate of the effective reproduction number Rt using its relation with the doubling time and application to Italian COVID-19 data. *The European Physical Journal Plus* 136, 386. doi:10.1140/epjp/s13360021013396

Chowell G, Viboud C, Hyman JM, Simonsen L (2015) The Western Africa ebola virus disease epidemic exhibits both global exponential and local polynomial growth rates. *PLOS Currents Outbreaks*, ecurrents.outbreaks.8b55f4bad99ac5c5db3663e916803261. doi:10.1371/currents.outbreaks.8b55f4bad99ac5c5db36

Pell B, Kuang Y, Viboud C, Chowell G (2018) Using phenomenological models for forecasting the 2015 ebola challenge. *Epidemics 22*, 62–70. doi:10.1016/j.epidem.2016.11.002

Rawlings JO, Pantula SG, Dickey DA (1998) Applied Regression Analysis: A Research Tool. Second Edition. New York: Springer. doi:10.1007/b98890

Wieland T (2020) A phenomenological approach to assessing the effectiveness of COVID-19 related nonpharmaceutical interventions in Germany. *Safety Science* 131, 104924. doi:10.1016/j.ssci.2020.104924

See Also

growth_initial, logistic_growth

Examples

```
data(COVID19Cases_geoRegion)
# Get SWISS COVID19 cases at NUTS 3 level

COVID19Cases_ZH <-
  COVID19Cases_geoRegion[
  (COVID19Cases_geoRegion$geoRegion == "ZH")
  & (COVID19Cases_geoRegion$sumTotal > 0)
  ,]
# COVID cases for Zurich

expgrowth_ZH <- exponential_growth(
  y = COVID19Cases_ZH$entries[1:28],
  t = COVID19Cases_ZH$datum[1:28]
)
# Exponential growth model for the first 4 weeks

summary(expgrowth_ZH)
# Summary of exponential growth model
```

```
plot(expgrowth_ZH)
# Plot of exponential growth model

expgrowth_ZH@GrowthModel_OLS$fit_metrics
expgrowth_ZH@GrowthModel_OLS$fit_metrics
# Fit metrics for OLS and NLS models
```

`getisord` *Calculate Global Getis-Ord statistic*

Description

Calculating the Global Getis-Ord statistic for hotspot analysis from an `nbmatrix` object

Usage

```
getisord(
  object,
  alternative = "greater",
  verbose = FALSE
  )
```

Arguments

`object`	Object of class `nbmatrix`
`alternative`	a character string specifying the alternative hypothesis, must be one of "greater" (default), "less" or "two.sided"; passed to `spdep::globalG.test`
`verbose`	`bool` argument which indicates whether progress messages are displayed

Details

The Global Getis-Ord statistic (Getis & Ord 1992) is a statistical measure of spatial association that assesses the spatial concentration of high or low values. Its calculation requires a spatial weights matrix that defines the spatial relationships between observations and assigns weights to neighboring observations (e.g., binary weights based on contiguity). A typical application is, for example, investigating whether high or low incidence of infectious diseases is spatially clustered, that is, whether areas with high (or low) incidence tend to be surrounded by neighboring areas that also exhibit high (or low) incidence. This function internally uses `spdep::globalG.test` for calculation (see the corresponding documentation). The results are written in the `nbmatrix` instance and displayed in the summary.

Value

object of class `nbmatrix-class`

Author(s)

Thomas Wieland

References

Cliff AD, Ord JK (1981) Spatial Processes: Models & Applications. https://archive.org/details/spatialprocesses0000clif

GeoDa Center (2026) GeoDa. An Introduction to Spatial Data Science. https://geodacenter.github.io/

Getis A, Ord JK (1992). The analysis of spatial association by use of distance statistics. *Geographical Analysis* 24 (3), 189–206. doi:10.1111/j.15384632.1992.tb00261.x

Ord JK, Getis A (1995) Local Spatial Autocorrelation Statistics: Distributional Issues and an Application. *Geographical Analysis* 27, 286-306. doi:10.1111/j.15384632.1995.tb00912.x

See Also

nbmatrix, nbstat, moran, gstar

Examples

```
data(RKI_Corona_counties)
# German counties (Source: Robert Koch Institute)

Corona_nbmat <-
  nbmatrix (
    RKI_Corona_counties,
    ID_col="AGS",
    verbose = TRUE
  )
# Creating neighborhood matrix

Corona_nbstat2 <- nbstat(
  Corona_nbmat,
  link_data = RKI_Corona_counties,
  ID_col = "AGS",
  data_col = "cases_per_",
  func = NULL,
  verbose = TRUE
)
# New nbmatrix instance
# Defining "cases_per_" (COVID-19 cases per 100,000 inhabitants) as analysis column

Corona_SpatialStatistics <- getisord(
  Corona_nbstat2,
  verbose = TRUE
)
# Calculating Global Getis-Ord statistic

summary(Corona_SpatialStatistics)
# Summary of nbmatrix object
```

getisord-methods *Methods for Function* getisord

Description

Methods for function getisord

Methods

signature(object = "nbmatrix", alternative = "greater", verbose = FALSE) Calculates the Global Getis-Ord statistic for the neighborhood matrix for a specified data column to be analyzed. The parameters randomization and alternative are passed to spdep::globalG.test, which is internally used for the calculation.

Author(s)

Thomas Wieland

growth *Logistic Growth Models for Regional Infections*

Description

Estimates N logistic growth models for N regions.

Usage

```
growth(
  object,
  S_iterations = 10,
  S_start_est_method = "bisect",
  seq_by = 10,
  nls = TRUE,
  add_constant = 1,
  overwrite = FALSE,
  verbose = FALSE
  )
```

Arguments

object	object of class infpan
S_iterations	Number of iterations for saturation value search
S_start_est_method	Method for saturation value search, either "bisect" or "trial_and_error"
seq_by	No. of segments for the "trial_and_error" estimation of the saturation value

nls	Nonlinear estimation? TRUE or FALSE
add_constant	Numeric constant to be added to y if zero values occur (only relevant for OLS estimation)
overwrite	bool argument which indicates whether the column containing cumulative cases should be overwritten if already existing
verbose	bool argument which indicates whether progress messages are displayed

Details

The function estimates logistic growth models for regional infections based on a infpan object. See logistic_growth for further details.

Value

object of class growthmodels-class

Author(s)

Thomas Wieland

References

Chowell G, Simonsen L, Viboud C, Yang K (2014) Is West Africa Approaching a Catastrophic Phase or is the 2014 Ebola Epidemic Slowing Down? Different Models Yield Different Answers for Liberia. *PLoS currents 6*. doi:10.1371/currents.outbreaks.b4690859d91684da963dc40e00f3da81

Pell B, Kuang Y, Viboud C, Chowell G (2018) Using phenomenological models for forecasting the 2015 ebola challenge. *Epidemics 22*, 62–70. doi:10.1016/j.epidem.2016.11.002

Wieland T (2020) Flatten the Curve! Modeling SARS-CoV-2/COVID-19 Growth in Germany at the County Level. *REGION* 7(2), 43–83. doi:10.18335/region.v7i2.324

See Also

logistic_growth, exponential_growth

Examples

```
data(COVID19Cases_geoRegion)
# Get SWISS COVID19 cases at NUTS 3 level

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[!COVID19Cases_geoRegion$geoRegion %in% c("CH", "CHFL"),]
# Exclude CH = Switzerland total and CHFL = Switzerland and Liechtenstein total

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[COVID19Cases_geoRegion$datum <= "2020-05-31",]
# Extract first COVID-19 wave

infpan_CH <- load_infections_paneldata(
    data = COVID19Cases_geoRegion,
```

```
    col_cases = "entries",
    col_date = "datum",
    col_region = "geoRegion",
    other_cols = c("Population" = "pop"),
    verbose = TRUE
  )
# Import as infections panel data set (class infpan)

CH_covidwave1_growth <-
  growth(infpan_CH)
summary(CH_covidwave1_growth)
# Logistic growth models for infpan object infpan_CH
```

`growth-methods` *Methods for Function* `growth`

Description

Methods for function `growth`

Methods

`signature(object = "infpan", S_iterations = 10, S_start_est_method = "bisect", seq_by = 10, nls = TRUE, add`

Estimation of N logistic growth models for N regions. Both OLS and NLS estimation are conducted by default (set `nls = FALSE` to skip NLS estimation). Parameters `S_iterations`, `S_start_est_method`, and `seq_by` are used to control the saturation value estimation (see `logistic_growth`).

Author(s)

Thomas Wieland

`growth_breaks` *Time Series Model with Breakpoints for Regional Infections*

Description

Conducts N breakpoints analyses for infection time series in N regions.

Usage

```
growth_breaks(
  object,
  ln = FALSE,
  add_constant = 1,
  alpha = 0.05,
  verbose = FALSE
  )
```

Arguments

object	object of class infpan
ln	bool argument which indicates whether the dependent variable should be transformed by natural logarithm
add_constant	Numeric constant to be added to y if zero values occur
alpha	Significance level α for 1-α*100 confidence intervals
verbose	bool argument which indicates whether progress messages are displayed

Details

The method detects breakpoints in regional infections time series based on an infpan object. The function internally uses the function breakpoints from the strucchange package (Zeileis et al. 2003), where breakpoints are identified using the Bai-Perron algorithm (Bai & Perron 2003). See breaks_growth for further details of the estimation.

Value

object of class growthmodels-class

Author(s)

Thomas Wieland

References

Bai J, Perron P (2003) Computation and analysis of multiple structural change models. *Journal of Applied Econometrics* 18(1), 1-22. doi:10.1002/jae.659

Wieland T (2020) A phenomenological approach to assessing the effectiveness of COVID-19 related nonpharmaceutical interventions in Germany. *Safety Science* 131, 104924. doi:10.1016/j.ssci.2020.104924

Zeileis C, Kleiber W, Krämer K, Hornik, K (2003) Testing and dating of structural changes in practice. *Computational Statistics & Data Analysis* 44(1-2), 109-123. doi:10.1016/S01679473(03)00030-6

Examples

```
data(COVID19Cases_geoRegion)
# Get SWISS COVID19 cases at NUTS 3 level

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[!COVID19Cases_geoRegion$geoRegion %in% c("CH", "CHFL"),]
# Exclude CH = Switzerland total and CHFL = Switzerland and Liechtenstein total

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[COVID19Cases_geoRegion$datum <= "2020-05-31",]
# Extract first COVID-19 wave

infpan_CH <- load_infections_paneldata(
```

```
    data = COVID19Cases_geoRegion,
    col_cases = "entries",
    col_date = "datum",
    col_region = "geoRegion",
    other_cols = c("Population" = "pop"),
    verbose = TRUE
  )
# Import as infections panel data set (class infpan)

CH_covidwave1_breaks <-
  growth_breaks(infpan_CH)
summary(CH_covidwave1_breaks)
# Breakpoints for infpan object infpan_CH
```

---

growth_breaks-methods *Methods for Function* growth_breaks

Description

Methods for function `growth_breaks`

Methods

`signature(object = "infpan", ln = FALSE, add_constant = 1, alpha = 0.05, verbose = FALSE)`
: Estimation of N breakpoint analyses for infections panel data for N regions. For details, see `breaks_growth`.

Author(s)

Thomas Wieland

---

growth_hawkes *Hawkes Process models for Regional Infections*

Description

Estimates N Hawkes process models for N regions.

Usage

```
growth_hawkes(
  object,
  optim_method = "L-BFGS-B",
  verbose = FALSE
  )
```

Arguments

object	object of class infpan
optim_method	character value for the optimization method. Passed to argument method in stats function optim()
verbose	bool argument which indicates whether progress messages are displayed

Details

The function estimates Hawkes process models for regional infections based on an infpan object. See hawkes_growth for further details of the estimation.

Value

object of class growthmodels-class

Author(s)

Thomas Wieland

References

Rizoiu MA, Mishra S, Kong Q, Carman M, Xie L. (2018) SIR-Hawkes: Linking Epidemic Models and Hawkes Processes to Model Diffusions in Finite Populations. In: *Proceedings of the 2018 World Wide Web Conference. WWW'18*. Republic and Canton of Geneva, CHE: International World Wide Web Conferences Steering Committee, p. 419–428. doi:10.1145/3178876.3186108

Examples

```
data(COVID19Cases_geoRegion)
# Get SWISS COVID19 cases at NUTS 3 level

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[!COVID19Cases_geoRegion$geoRegion %in% c("CH", "CHFL"),]
# Exclude CH = Switzerland total and CHFL = Switzerland and Liechtenstein total

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[COVID19Cases_geoRegion$datum <= "2020-05-31",]
# Extract first COVID-19 wave

infpan_CH <- load_infections_paneldata(
    data = COVID19Cases_geoRegion,
    col_cases = "entries",
    col_date = "datum",
    col_region = "geoRegion",
    other_cols = c("Population" = "pop"),
    verbose = TRUE
  )
# Import as infections panel data set (class infpan)

CH_covidwave1_Hawkes <-
```

```
  growth_hawkes(infpan_CH)
summary(CH_covidwave1_Hawkes)
# Hawkes process models for infpan object infpan_CH
```

`growth_hawkes-methods` *Methods for Function* `growth_hawkes`

Description

Methods for function `growth_hawkes`

Methods

`signature(object = "infpan", optim_method = "L-BFGS-B", verbose = FALSE)` Estimation of N Hawkes process models for N regions. Set argument `optim_method` for using the optimization method from `stats::optim`.

Author(s)

Thomas Wieland

`growth_initial` *Exponential Growth Models for Regional Infections*

Description

Estimates N exponential growth models for a given time period in N regions.

Usage

```
growth_initial(
  object,
  time_units = 10,
  GI = 4,
  nls = TRUE,
  nls_start = list(a = 1, b = 0.1),
  add_constant = 1,
  verbose = FALSE
  )
```

Arguments

object	object of class infpan
time_units	numeric value for the analysis time (time units from start)
GI	Generation interval for computing R_0
nls	Nonlinear estimation? TRUE or FALSE
nls_start	A list with start values for the two parameters to be estimated
add_constant	Numeric constant to be added to y if zero values occur (only relevant for OLS estimation)
verbose	bool argument which indicates whether progress messages are displayed

Details

The method estimates exponential growth models for regional infections based on an infpan object. This model is designed for the analysis of the *initial* phase of an epidemic spread. The user must state how many time units (from start) are included. See exponential_growth for further details of the estimation.

Value

object of class growthmodels-class

Author(s)

Thomas Wieland

References

Bonifazi G, Lista L, Menasce D, Mezzetto M, Pedrini D, Spighi R, Zoccoli A (2021) A simplified estimate of the effective reproduction number Rt using its relation with the doubling time and application to Italian COVID-19 data. *The European Physical Journal Plus* 136, 386. doi:10.1140/epjp/s13360021013396

Chowell G, Viboud C, Hyman JM, Simonsen L (2015) The Western Africa ebola virus disease epidemic exhibits both global exponential and local polynomial growth rates. *PLOS Currents Outbreaks*, ecurrents.outbreaks.8b55f4bad99ac5c5db3663e916803261. doi:10.1371/currents.outbreaks.8b55f4bad99ac5c5db36

Pell B, Kuang Y, Viboud C, Chowell G (2018) Using phenomenological models for forecasting the 2015 ebola challenge. *Epidemics 22*, 62–70. doi:10.1016/j.epidem.2016.11.002

Rawlings JO, Pantula SG, Dickey DA (1998) Applied Regression Analysis: A Research Tool. Second Edition. New York: Springer. doi:10.1007/b98890

Wieland T (2020) A phenomenological approach to assessing the effectiveness of COVID-19 related nonpharmaceutical interventions in Germany. *Safety Science* 131, 104924. doi:10.1016/j.ssci.2020.104924

Examples

```
data(COVID19Cases_geoRegion)
# Get SWISS COVID19 cases at NUTS 3 level

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[!COVID19Cases_geoRegion$geoRegion %in% c("CH", "CHFL"),]
# Exclude CH = Switzerland total and CHFL = Switzerland and Liechtenstein total

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[COVID19Cases_geoRegion$datum <= "2020-05-31",]
# Extract first COVID-19 wave

infpan_CH <- load_infections_paneldata(
    data = COVID19Cases_geoRegion,
    col_cases = "entries",
    col_date = "datum",
    col_region = "geoRegion",
    other_cols = c("Population" = "pop"),
    verbose = TRUE
  )
# Import as infections panel data set (class infpan)

CH_covidwave1_initialgrowth_3weeks <-
  growth_initial(
    infpan_CH,
    time_units = 21
  )
summary(CH_covidwave1_initialgrowth_3weeks)
# Exponential models for infpan object CH_covidwave1
# initial growth in the first 3 weeks
```

---

growth_initial-methods

Methods for Function growth_initial

Description

Methods for function growth_initial

Methods

signature(object = "infpan", time_units = 10, GI = 4, nls = TRUE, nls_start = list(a = 1, b = 0.1), add_const

Estimation of N exponential growth models for the initial phase of an epidemic spread for N regions. Set argument GI for the calculation of the basic reproduction number, and control OLS/NLS estimation with arguments nls, nls_start, and add_constant (see exponential_growth).

Author(s)

Thomas Wieland

`growthmodels-class` *Class* `"growthmodels"`

Description

The class `"growthmodels"` contains the results of growth model analyses and the related input data as well as additional information. The `swash` package includes the following model analyses under the heading "growth models": Exponential growth models, logistic growth models, Hawkes Process models, and time series models with breakpoints. Use `summary(growthmodels)` for results summary. See the corresponding stand-alone functions for details: exponential_growth, logistic_growth, hawkes_growth, breaks_growth.

Objects from the Class

Objects can be created by the methods `growth_initial`, `growth`, `growth_breaks`, or `growth_hawkes`.

Slots

`results`**:** Object of class `"data.frame"` Model results as a table with coefficients, fit metrics, etc.

`growth_models`**:** Object of class `"list"` containing all models

`model_type`**:** Object of class `"character"` describing the type of model

`results_cols`**:** Object of class `"character"` Vector with column names containing results

`results_cols_names`**:** Object of class `"character"` Vector with descriptions of the column names

`data_statistics`**:** Object of class `"numeric"` Diagnostics of input data

`time_format`**:** Object of class `"character"` Format of time points in time column

`timestamp`**:** Object of class `"list"` Time stamps of any update of the instance

Methods

print `signature(x = "growthmodels")`: Prints a `growthmodels` object; use `summary(growthmodels)` for results

show `signature(object = "growthmodels")`: Prints a `growthmodels` object; use `summary(growthmodels)` for results

summary `signature(object = "growthmodels")`: Prints a summary of `growthmodels` objects (model results)

Author(s)

Thomas Wieland

References

Bai J, Perron P (2003) Computation and analysis of multiple structural change models. *Journal of Applied Econometrics* 18(1), 1-22. doi:10.1002/jae.659

Bonifazi G et al. (2021) A simplified estimate of the effective reproduction number Rt using its relation with the doubling time and application to Italian COVID-19 data. *The European Physical Journal Plus* 136, 386. doi:10.1140/epjp/s13360021013396

Chowell G, Simonsen L, Viboud C, Yang K (2014) Is West Africa Approaching a Catastrophic Phase or is the 2014 Ebola Epidemic Slowing Down? Different Models Yield Different Answers for Liberia. *PLoS currents* 6. doi:10.1371/currents.outbreaks.b4690859d91684da963dc40e00f3da81

Chowell G, Viboud C, Hyman JM, Simonsen L (2015) The Western Africa ebola virus disease epidemic exhibits both global exponential and local polynomial growth rates. *PLOS Currents Outbreaks*, ecurrents.outbreaks.8b55f4bad99ac5c5db3663e916803261. doi:10.1371/currents.outbreaks.8b55f4bad99ac5c5db36

Pell B, Kuang Y, Viboud C, Chowell G (2018) Using phenomenological models for forecasting the 2015 ebola challenge. *Epidemics 22*, 62–70. doi:10.1016/j.epidem.2016.11.002

Rizoiu MA, Mishra S, Kong Q, Carman M, Xie L. (2018) SIR-Hawkes: Linking Epidemic Models and Hawkes Processes to Model Diffusions in Finite Populations. In: *Proceedings of the 2018 World Wide Web Conference. WWW'18*. Republic and Canton of Geneva, CHE: International World Wide Web Conferences Steering Committee, p. 419–428. doi:10.1145/3178876.3186108

Wieland T (2020) A phenomenological approach to assessing the effectiveness of COVID-19 related nonpharmaceutical interventions in Germany. *Safety Science* 131, 104924. doi:10.1016/j.ssci.2020.104924

Wieland T (2020) Flatten the Curve! Modeling SARS-CoV-2/COVID-19 Growth in Germany at the County Level. *REGION* 7(2), 43–83. doi:10.18335/region.v7i2.324

Zeileis C, Kleiber W, Krämer K, Hornik, K (2003) Testing and dating of structural changes in practice. *Computational Statistics & Data Analysis* 44(1-2), 109-123. doi:10.1016/S01679473(03)00030-6

Examples

```
showClass("growthmodels")
```

`gstar` *Calculate Local Getis-Ord Gi* statistic*

Description

Calculating the Local Getis-Ord Gi* for detecting significant hotspots from an `nbmatrix` object

Usage

```
gstar(
  object,
  alternative = "greater",
  nsim = 999,
  verbose = FALSE
  )
```

Arguments

`object`	Object of class `nbmatrix`
`alternative`	a character string specifying the alternative hypothesis, must be one of "greater" (default), "less" or "two.sided"; passed to `sfdep::local_gstar_perm`
`nsim`	`numeric` value with number of simulations to run; passed to `sfdep::local_gstar_perm`
`verbose`	`bool` argument which indicates whether progress messages are displayed

Details

Unlike the global Getis-Ord statistic, the Getis-Ord G_i^* statistic (Getis & Ord 1992) is calculated for each region in the study. Based on the calculated z-scores and their p-values, the analysis identifies where regions with high or low values tend to form spatial clusters. A typical application is, for example, investigating whether high or low incidence of infectious diseases is spatially clustered, that is, identifying hotspots and/or coldspots. This function internally uses `sfdep::local_gstar_perm.test` for calculation (see the corresponding documentation). The results are written in the `nbmatrix` instance and displayed in the summary.

Value

object of class `nbmatrix-class`

Author(s)

Thomas Wieland

References

Cliff AD, Ord JK (1981) Spatial Processes: Models & Applications. https://archive.org/details/spatialprocesses0000clif

GeoDa Center (2026) GeoDa. An Introduction to Spatial Data Science. https://geodacenter.github.io/

Getis A, Ord JK (1992). The analysis of spatial association by use of distance statistics. *Geographical Analysis* 24 (3), 189–206. doi:10.1111/j.15384632.1992.tb00261.x

Ord JK, Getis A (1995) Local Spatial Autocorrelation Statistics: Distributional Issues and an Application. *Geographical Analysis* 27, 286-306. doi:10.1111/j.15384632.1995.tb00912.x

See Also

`nbmatrix`, `getisord`, `nbstat`, `moran`

Examples

```
data(RKI_Corona_counties)
# German counties (Source: Robert Koch Institute)

Corona_nbmat <-
  nbmatrix (
    RKI_Corona_counties,
```

```
    ID_col="AGS",
    verbose = TRUE
  )
# Creating neighborhood matrix

Corona_nbstat2 <- nbstat(
  Corona_nbmat,
  link_data = RKI_Corona_counties,
  ID_col = "AGS",
  data_col = "cases_per_",
  func = NULL,
  verbose = TRUE
  )
# New nbmatrix instance
# Defining "cases_per_" (COVID-19 cases per 100,000 inhabitants) as analysis column

Corona_SpatialStatistics <- gstar(
  Corona_nbstat2,
  verbose = TRUE
  )
# Calculating Local Getis-Ord Gi*

summary(Corona_SpatialStatistics)
# Summary of nbmatrix object
```

`gstar-methods` *Methods for Function* `gstar`

Description

Methods for function `gstar`

Methods

`signature( object = "nbmatrix", alternative = "greater", nsim = 999, verbose = FALSE)`
: Calculates the Local Getis-Ord Gi* statistic for the neighborhood matrix for a specified data column to be analyzed. The parameters `alternative` and `nsim` are passed to `sfdep::local_gstar_perm`, which is internally used for the calculation.

Author(s)

Thomas Wieland

hawkes-class *Class* "hawkes"

Description

The class "hawkes" contains the results of the hawkes_growth() function. Use summary(hawkes) for results summary.

Objects from the Class

Objects can be created by the function hawkes_growth.

Slots

t: Object of class numeric Input time points data

y: Object of class numeric Input infections data

mu: Object of class numeric Estimated μ parameter (background rate)

alpha: Object of class numeric Estimated α parameter (excitation parameter)

beta: Object of class numeric Estimated β parameter (decay)

br: Object of class numeric Estimated breaking ratio (α/β)

y_pred: Object of class numeric Predicted values of y

fit_metrics: Object of class list Fit metrics for model, output from built-in function fit_metrics

config: Object of class list Model fit configurations

Methods

summary signature(object = "hawkes"): Prints a summary of hawkes objects

print signature(x = "hawkes"): Prints an hawkes object; use summary(hawkes) for results

plot signature(x = "hawkes"): Plots the results of the Hawkes model (observed, predicted)

Author(s)

Thomas Wieland

References

Rizoiu MA, Mishra S, Kong Q, Carman M, Xie L. (2018) SIR-Hawkes: Linking Epidemic Models and Hawkes Processes to Model Diffusions in Finite Populations. In: *Proceedings of the 2018 World Wide Web Conference. WWW'18*. Republic and Canton of Geneva, CHE: International World Wide Web Conferences Steering Committee, p. 419–428. doi:10.1145/3178876.3186108

Examples

```
showClass("hawkes")
```

hawkes_growth *Hawkes Process Model for Epidemic Data*

Description

Estimation of Hawkes Process models from new infections data

Usage

```
hawkes_growth(
  y,
  t = NULL,
  optim_method = "L-BFGS-B",
  impute_missing_values = FALSE,
  verbose = FALSE
  )
```

Arguments

y	`numeric vector` with new infection cases (e.g., daily, weekly) data over time (e.g., daily infections)
t	`vector` of class `numeric` or `Date` with time points or dates
optim_method	`character` specifying the optimization algorithm, passed to `stats::optim`
impute_missing_values	`bool` argument which indicates whether missing values have to be imputed via linear imputation
verbose	`bool` argument which indicates whether progress messages are displayed

Details

This function allows the estimation of a Hawkes Process model, with the time decay being expressed as exponential function, which results in three estimated parameters: μ (background rate), α (excitation parameter), and β (decay). The user must specify the dependent variable (new infections). The estimation is performed using nonlinear estimation via `stats::optim`. See the corresponding documentation for available optimization methods (default: "L-BFGS-B").

Value

object of class `hawkes-class`

Author(s)

Thomas Wieland

References

Rizoiu MA, Mishra S, Kong Q, Carman M, Xie L. (2018) SIR-Hawkes: Linking Epidemic Models and Hawkes Processes to Model Diffusions in Finite Populations. In: *Proceedings of the 2018 World Wide Web Conference. WWW'18*. Republic and Canton of Geneva, CHE: International World Wide Web Conferences Steering Committee, p. 419–428. doi:10.1145/3178876.3186108

See Also

logistic_growth, exponential_growth, breaks_growth

Examples

```
data(Infections)
# Confirmed SARS-CoV-2 cases in Germany

hawkes_BS <- hawkes_growth(
  y = Infections$infections_daily
)
# Hawkes Process model

summary(hawkes_BS)
# Summary of Hawkes model estimates

plot(hawkes_BS)
# Plot of Hawkes Process model
```

---

hist_ci *Creating Histograms with Confidence Intervals*

Description

Plot of a histogram of a given vector `x` and the related confidence intervals (`lower`, `upper`).

Usage

```
hist_ci(
  x,
  alpha = 0.05,
  col_bars = "grey",
  col_ci = "red",
  ...
  )
```

Arguments

`x`	A numeric vector
`alpha`	Significance level α for 1-α*100 confidence intervals
`col_bars`	Color of bars in histogram

`col_ci`	Color of lines for confidence interval
`...`	Additional arguments passed to `barplot()`

Details

Helper function for `plot(sbm_ci)`, but may be used separately.

Value

Histogram plot, no returned value

Author(s)

Thomas Wieland

Examples

```
numeric_vector <- c(1,9,5,6,3,10,20,6,9,14,3,5,8,6,11)
# any numeric vector

hist_ci(numeric_vector)
```

Infections *Infections*

Description

Daily SARS-CoV-2 infection in Germany spring 2020

Usage

```
data(Infections)
```

Format

A data.frame with multiple columns:

infectedtest_CW2 Calendar week 2020 of conducted test

infection_date Estimated date of infection

infections_daily Daily infections

infections_daily_lwr Daily infections lower confidence interval

infections_daily_upr Daily infections upper confidence interval

infections_cum Cumulative infections

infections_cum_lwr Cumulative infections lower confidence interval

infections_cum_upr Cumulative infections upper confidence interval

R4 Estimated effective reproduction number R_t with generation interval = 4

R4_lwr Estimated effective reproduction number R_t with generation interval = 4 lower confidence interval

R4_upr Estimated effective reproduction number R_t with generation interval = 4 upper confidence interval

R7 Estimated effective reproduction number R_t with generation interval = 7

R7_lwr Estimated effective reproduction number R_t with generation interval = 7 lower confidence interval

R7_upr Estimated effective reproduction number R_t with generation interval = 7 upper confidence interval

onsets_of_symptoms Daily onsets of symptoms

onsets_of_symptoms_lwr Daily onsets of symptoms lower confidence interval

onsets_of_symptoms_upr Daily onsets of symptoms upper confidence interval

reported_cases Daily reported cases

day Time counter (day)

ln_inf_cum Nat. log. of cumulative infections

ln_inf_daily Nat. log. of daily infections

ln_R4 Nat. log. of estimated effective reproduction number R_t with generation interval = 4

ln_R7 Nat. log. of estimated effective reproduction number R_t with generation interval = 7

infection_date_CW Calendar week of infection data (numeric)

infection_date_CW2 Calendar week of infection data (categorical)

infectedtest_CW Calendar week of conducted test

conducted_tests No. of conducted tests

negative_tests No. of negative tests

positive_tests No. of positive tests

positive_tests_share Share of positive tests (average per day)

conducted_tests_index No. of conducted tests (average per day), index (CW 14 = 100)

conducted_tests_dailyaverage No. of conducted tests, average per day

positive_tests_dailyaverage Positive tests, average per day

infections_daily_testweighted Daily infections weighted by test volume

ln_inf_daily_tw Nat. log. of daily infections weighted by test volume

Details

Example data with daily SARS-CoV-2 infections in Germany. See Wieland (2020) for data sources and method of backdating infections.

Source

Wieland T (2020) A phenomenological approach to assessing the effectiveness of COVID-19 related nonpharmaceutical interventions in Germany. *Safety Science* 131, 104924. doi:10.1016/j.ssci.2020.104924

Examples

```
data(Infections)
```

infpan-class *Class* "infpan"

Description

The class "infpan" contains infections panel data for N regions and T time points as well as additional information. Use summary(infpan) and plot(infpan) for results summary and plotting, respectively.

Objects from the Class

Objects can be created by importing infections panel data using the function load_infections_paneldata.

Slots

input_data: Object of class "data.frame" Model result: Input infections panel data

data_statistics: Object of class "numeric" Data statistics (N regions, T time points, test whether data is balanced, etc.)

index_col_names: Object of class "character" Column names of regions and time points

cases_col_name: Object of class "character" Column name of new infection cases

other_cols: Object of class "character" Names of other relevant columns derived from new cases data, e.g. effective reproduction number R_t

time_format: Object of class "character" Format of time points in time column

time_unit: Object of class "character" Time unit, default: "days"

geodata: Object of class "sf" Geodata (sf object) of regions

timestamp: Object of class "list" Time stamps of any update of the instance

Methods

plot signature(x = "infpan"): Plots case data by region for N regions and T time points

calculate_Rt signature(x = "infpan"): Calculates the effective reproduction number R_t from infpan objects. Returns updated infpan instance.

calculate_cum signature(x = "infpan"): Calculates cumulative cases from infpan objects. Returns updated infpan instance.

calculate_rollmean signature(x = "infpan"): Calculates rolling means of cases from infpan objects. Returns updated infpan instance.

calculate_rollsum signature(x = "infpan"): Calculates rolling sums of cases from infpan objects. Returns updated infpan instance.

calculate_incidence signature(x = "infpan"): Calculates incidences of cases from infpan objects. Returns updated infpan instance.

print signature(x = "infpan"): Prints an infpan object; use summary(infpan) for results

show signature(object = "infpan"): Shows an infpan object; use summary(infpan) for results

summary `signature(object = "infpan")`: Prints a summary of `infpan` objects

swash `signature(object = "infpan")`: Performs a Swash-Backwash Model analysis from `infpan` objects. Returns `sbm` instance.

growth `signature(object = "infpan")`: Estimates logistic growth models from `infpan` objects. Returns `growthmodels` instance.

growth_initial `signature(object = "infpan")`: Estimates exponential growth models from `infpan` objects for a given time period. Returns `growthmodels` instance.

growth_hawkes `signature(object = "infpan")`: Estimates Hawkes process models from `infpan` objects. Returns `growthmodels` instance.

growth_breaks `signature(object = "infpan")`: Estimates breakpoints in linear regression models from `infpan` objects. Returns `growthmodels` instance.

add_geodata `signature(object = "infpan")`: Adds geodata (`sf` object) to the `infpan` object.

plot_map `signature(object = "infpan")`: Plots a map from an `infpan` object which displays the attribute specified.

spatial_statistic `signature(object = "infpan")`: Calculates a spatial statistic from a specified attribute in an `infpan` object. Returns `nbmatrix` instance.

Author(s)

Thomas Wieland

References

Wieland T (2020) Flatten the Curve! Modeling SARS-CoV-2/COVID-19 Growth in Germany at the County Level. *REGION* 7(2), 43–83. doi:10.18335/region.v7i2.324

Wieland T (2025) Assessing the effectiveness of non-pharmaceutical interventions in the SARS-CoV-2 pandemic: results of a natural experiment regarding Baden-Württemberg (Germany) and Switzerland in the second infection wave. *Journal of Public Health* 33(11), 2497-2511. doi:10.1007/s1038902402218x

Examples

```
showClass("infpan")
```

`is_balanced` *Test whether Panel Dataset with Regional Infection Data is Balanced*

Description

The function tests whether the input panel data with regional infections is balanced.

Usage

```
is_balanced(
  data,
  col_cases,
  col_date,
  col_region,
  as_balanced = TRUE,
  fill_missing = NA,
  drop_duplicates = TRUE,
  verbose = FALSE
  )
```

Arguments

data	data.frame with regional infection data
col_cases	Column containing the cases (numeric)
col_date	Column containing the time points (e.g., days)
col_region	Column containing the unique identifier of the regions (e.g., name, NUTS 3 code)
as_balanced	bool argument which indicates whether non-balanced panel data shall be balanced (default: TRUE)
fill_missing	Constant to fill missing values (default and recommended: 0)
drop_duplicates	bool argument which indicates whether duplicated region/time combinations are removed
verbose	bool argument which indicates whether progress messages are displayed

Details

The Swash-Backwash Model of the Single Epidemic Wave does not necessarily require balanced panel data in order for the calculations to be carried out. However, for a correct estimation it is implicitly assumed that the input data is balanced. The function tests whether the panel data is balanced. It is executed automatically within the swash() function (using automatic correction with as_balanced = TRUE) and during the import of infections panel data via load_infections_paneldata(), but can also be used separately.

Value

List with two entries:

data_balanced	Result of test (TRUE or FALSE)
data	Input dataset (data.frame)

Author(s)

Thomas Wieland

See Also

as_balanced

Examples

```
data(COVID19Cases_geoRegion)
# Get SWISS COVID19 cases at NUTS 3 level

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[!COVID19Cases_geoRegion$geoRegion %in% c("CH", "CHFL"),]
# Exclude CH = Switzerland total and CHFL = Switzerland and Liechtenstein total

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[COVID19Cases_geoRegion$datum <= "2020-05-31",]
# Extract first COVID-19 wave

COVID19Cases_geoRegion_balanced <-
  is_balanced(
  data = COVID19Cases_geoRegion,
  col_cases = "entries",
  col_date = "datum",
  col_region = "geoRegion"
)
# Test whether "COVID19Cases_geoRegion" is balanced panel data

COVID19Cases_geoRegion_balanced$data_balanced
# Balanced? TRUE or FALSE

if (COVID19Cases_geoRegion_balanced$data_balanced == FALSE) {
  COVID19Cases_geoRegion <-
    as_balanced(
    COVID19Cases_geoRegion,
    col_cases = "entries",
    col_date = "datum",
    col_region = "geoRegion"
  )
}
# Correction of dataset "COVID19Cases_geoRegion"
# not necessary as parameter balance of is_balanced is set TRUE by default
```

K4kant20260101gf_ch2007Poly

Swiss Canton Boundaries

Description

Geodata (sf) of Swiss canton boundaries

Usage

```
data("K4kant20260101gf_ch2007Poly")
```

Format

A data frame with 26 observations (each one represents a Swiss canton).

`id` Swiss canton ID

`name` Swiss canton name

`geometry` Geometry

`cant_abbrev` Swiss canton abbreviation

Details

The data is included as published by the Federal Statistical Office of Switzerland (BfS) but extended by the Geometry column and the canton abbreviation.

Source

Bundesamt fuer Statistik (2026). Kartengeometrien ThemaKart - Set 2026. https://dam-api.bfs.admin.ch/hub/api/dam/assets/36390072/thumbnail?width=1980&height=1080 (accessed 2026-08-30)

Examples

```
data(COVID19Cases_geoRegion)
# Get SWISS COVID19 cases at NUTS 3 level

data(K4kant20260101gf_ch2007Poly)
# Cantonal boundaries of Switzerland

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[!COVID19Cases_geoRegion$geoRegion %in% c("CH", "CHFL"),]
# Exclude CH = Switzerland total and CHFL = Switzerland and Liechtenstein total

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[COVID19Cases_geoRegion$datum <= "2020-05-31",]
# Extract first COVID-19 wave

infpan_CH <- load_infections_paneldata(
    data = COVID19Cases_geoRegion,
    col_cases = "entries",
    col_date = "datum",
    col_region = "geoRegion",
    other_cols = c("Population" = "pop"),
    verbose = TRUE
  )
# Import as infections panel data set (class infpan)

infpan_CH <- calculate_incidence(
```

```
  infpan_CH,
  col_name = "incidence",
  verbose = TRUE
)
# Calculate incidence of cases as "incidence"

infpan_CH <- add_geodata(
  infpan_CH,
  K4kant20260101gf_ch2007Poly,
  unit_col = "cant_abbrev"
)
# Adding geodata (sf) to infpan object

summary(infpan_CH)
# Summary of infpan object

timestamps(infpan_CH)
# Time stamps of infpan object

plot_map(
  infpan_CH,
  attribute = "Incidence",
  main = "COVID-19 Incidence 2020-05-31",
  breaks = c(0, 0.05, 0.1, 0.2, 1),
  verbose = TRUE
)
# Simple map of incidence for the most current date (timepoint=NULL)
```

`load_infections_paneldata` *Import of infections panel data*

Description

Loading infections panel data (data.frame) and creating an object of class infpan

Usage

```
load_infections_paneldata(
  data,
  col_cases,
  col_date,
  col_region,
  other_cols = NULL,
  time_format = "%Y-%m-%d",
  time_unit = "days",
  verbose = FALSE
  )
```

Arguments

data	data.frame with regional infection data
col_cases	character, Column containing the cases (numeric)
col_date	character, Column containing the time points (e.g., days)
col_region	character, Column containing the unique identifier of the regions (e.g., name, NUTS 3 code)
other_cols	list, Further columns in the input data
time_format	character, Time format of the values in col_date
time_unit	character, Time unit of the values in col_date, e.g., "days"
verbose	bool argument which indicates whether progress messages are displayed

Details

The function imports user-given infections panel data. The input data is checked in several ways (e.g., whether data is balanced or not). Other relevant columns from the input data may be defined in the character vector other_cols: "R_t" (Effective reproduction number), "Cum. cases" (Cumulative cases), "Incidence" Incidence (per xxx pop), "Population" (Population size of the region), "Roll. mean" (Rolling mean of cases), and "Roll. sum" (Rolling sum of cases).

The output is an object of class infpan. The results can be viewed using summary(infpan). From an instance of class infpan, all built-in analyses for infections panel data may be conducted, e.g., the Swash-Backwash Model (swash(infpan)) or logistic growth models (growth(infpan)).

Value

object of class infpan-class

Author(s)

Thomas Wieland

References

Wieland T (2020) Flatten the Curve! Modeling SARS-CoV-2/COVID-19 Growth in Germany at the County Level. *REGION* 7(2), 43–83. doi:10.18335/region.v7i2.324

Wieland T (2025) Assessing the effectiveness of non-pharmaceutical interventions in the SARS-CoV-2 pandemic: results of a natural experiment regarding Baden-Württemberg (Germany) and Switzerland in the second infection wave. *Journal of Public Health* 33(11), 2497-2511. doi:10.1007/s1038902402218x

See Also

infpan-class

Examples

```
data(COVID19Cases_geoRegion)
# Get SWISS COVID19 cases at NUTS 3 level

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[!COVID19Cases_geoRegion$geoRegion %in% c("CH", "CHFL"),]
# Exclude CH = Switzerland total and CHFL = Switzerland and Liechtenstein total

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[COVID19Cases_geoRegion$datum <= "2020-05-31",]
# Extract first COVID-19 wave

infpan_CH <- load_infections_paneldata(
    data = COVID19Cases_geoRegion,
    col_cases = "entries",
    col_date = "datum",
    col_region = "geoRegion",
    other_cols = c("Population" = "pop"),
    verbose = TRUE
  )
# Import as infections panel data set (class infpan)

CH_covidwave1 <-
  swash(
    infpan_CH,
    verbose = TRUE
    )
# Swash-Backwash Model for Swiss COVID19 cases
# Spatial aggregate: NUTS 3 (cantons)

summary(CH_covidwave1)
# Summary of Swash-Backwash Model
```

---

loggrowth-class *Class* "loggrowth"

Description

The class "loggrowth" contains the results of the logistic_growth() function. Use summary(loggrowth) and plot(loggrowth) for results summary and plotting, respectively.

Objects from the Class

Objects can be created by the function logistic_growth.

Slots

LinModel: Object of class list Results of the OLS helper model

`GrowthModel_OLS`: Object of class `list` Results of the OLS fit (predicted, parameters, first derivative)

`GrowthModel_NLS`: Object of class `list` Results of the NLS fit (predicted, parameters, first derivative)

`t`: Object of class `numeric` Input time points data

`y`: Object of class `numeric` Input infections data

`config`: Object of class `list` Model fit configurations

Methods

plot `signature(x = "loggrowth")`: Plots the results of the logistic growth model (observed, predicted, first derivative)

summary `signature(object = "loggrowth")`: Prints a summary of `loggrowth` objects

print `signature(x = "loggrowth")`: Prints an `loggrowth` object; use `summary(loggrowth)` for results

Author(s)

Thomas Wieland

References

Chowell G, Simonsen L, Viboud C, Yang K (2014) Is West Africa Approaching a Catastrophic Phase or is the 2014 Ebola Epidemic Slowing Down? Different Models Yield Different Answers for Liberia. *PLoS currents 6*. doi:10.1371/currents.outbreaks.b4690859d91684da963dc40e00f3da81

Pell B, Kuang Y, Viboud C, Chowell G (2018) Using phenomenological models for forecasting the 2015 ebola challenge. *Epidemics 22*, 62–70. doi:10.1016/j.epidem.2016.11.002

Wieland T (2020) Flatten the Curve! Modeling SARS-CoV-2/COVID-19 Growth in Germany at the County Level. *REGION* 7(2), 43–83. doi:10.18335/region.v7i2.324

Examples

```
showClass("loggrowth")
```

---

logistic_growth *Logistic Growth Model for Epidemic Data*

Description

Estimation of logistic growth models from cumulative infections data, linearized OLS and/or NLS

Usage

```
logistic_growth(
  y,
  t,
  S = NULL,
  S_start = NULL,
  S_end = NULL,
  S_iterations = 10,
  S_start_est_method = "bisect",
  seq_by = 10,
  plot_trial_and_error = TRUE,
  nls = TRUE,
  impute_missing_values = FALSE,
  add_constant = 1,
  verbose = FALSE
  )
```

Arguments

y	numeric vector with cumulative infections data over time
t	vector of class numeric or Date with time points or dates
S	Saturation value for the model
S_start	Start value of the saturation value for estimation
S_end	End value of the saturation value for estimation
S_iterations	Number of iterations for saturation value search
S_start_est_method	Method for saturation value search, either "bisect" or "trial_and_error"
seq_by	No of segments for the "trial_and_error" estimation of the saturation value
plot_trial_and_error	bool argument which indicates whether tried values are plotted if S_start_est_method = "trial_and_error"
nls	Nonlinear estimation? TRUE or FALSE
impute_missing_values	bool argument which indicates whether missing values have to be imputed via linear imputation
add_constant	Numeric constant to be added to y if zero values occur (only relevant for OLS estimation)
verbose	bool argument which indicates whether progress messages are displayed

Details

This function allows the estimation of a logistic growth model. The user must specify the dependent variable (cumulative infections) and the time variable (time counter or date values). The estimation is performed using a linearized model with an OLS estimator and nonlinear least squares. For the former, the saturation value can either be specified by the user or found using a search algorithm.

The parameters from the OLS fit are used as starting values for the NLS estimation. See Rawlings et al. (1998) for the basics of intrinsically linear models such as the logistic or exponential growth model. See Wieland (2020) for the documentation of the fitting procedure applied in this function.

Value

object of class loggrowth-class

Author(s)

Thomas Wieland

References

Chowell G, Simonsen L, Viboud C, Yang K (2014) Is West Africa Approaching a Catastrophic Phase or is the 2014 Ebola Epidemic Slowing Down? Different Models Yield Different Answers for Liberia. *PLoS currents* 6. doi:10.1371/currents.outbreaks.b4690859d91684da963dc40e00f3da81

Pell B, Kuang Y, Viboud C, Chowell G (2018) Using phenomenological models for forecasting the 2015 ebola challenge. *Epidemics* 22, 62-70. doi:10.1016/j.epidem.2016.11.002

Rawlings JO, Pantula SG, Dickey DA (1998) Applied Regression Analysis: A Research Tool. Second Edition. New York: Springer. doi:10.1007/b98890

Wieland T (2020) Flatten the Curve! Modeling SARS-CoV-2/COVID-19 Growth in Germany at the County Level. *REGION* 7(2), 43–83. doi:10.18335/region.v7i2.324

See Also

loggrowth-class, growth, exponential_growth

Examples

```
data(COVID19Cases_geoRegion)
# Get SWISS COVID19 cases at NUTS 3 level

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[!COVID19Cases_geoRegion$geoRegion %in% c("CH", "CHFL"),]
# Exclude CH = Switzerland total and CHFL = Switzerland and Liechtenstein total

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[COVID19Cases_geoRegion$datum <= "2020-05-31",]
# Extract first COVID-19 wave

COVID19Cases_BS <-
  COVID19Cases_geoRegion[(COVID19Cases_geoRegion$geoRegion == "ZH")
                         & (COVID19Cases_geoRegion$sumTotal > 0),]
# COVID cases for Zurich

loggrowth_BS <- logistic_growth (
  y = as.numeric(COVID19Cases_BS$sumTotal),
  t = COVID19Cases_BS$datum,
  S = 5557,
```

```
  S_start = NULL,
  S_end = NULL,
  S_iterations = 10,
  S_start_est_method = "bisect",
  seq_by = 10,
  nls = TRUE
)
# Logistic growth model with stated saturation value

summary(loggrowth_BS)
# Summary of logistic growth model

plot(loggrowth_BS)
# Plot of logistic growth model
```

`metrics` *Fit metrics of observed and expected numeric variables*

Description

Calculation of fit metrics for observed and expected numeric variables (e.g. R^2, $RMSE$, MAE, $MAPE$).

Usage

```
metrics(
  observed,
  expected,
  plot = TRUE,
  plot.main = "Observed vs. expected",
  xlab = "Observed",
  ylab = "Expected",
  point.col = "blue",
  point.pch = 19,
  line.col = "red",
  plot_residuals.main = "Residuals",
  legend.cex = 0.7,
  na.rm = TRUE
)
```

Arguments

`observed`	Numeric vector of observed values.
`expected`	Numeric vector of expected or predicted values.
`plot`	Logical. If `TRUE`, diagnostic plots for observed vs. expected values and relative residual distributions are created.
`plot.main`	Character string. Title of the observed vs. expected plot.

`xlab`	Character string. Label of the x-axis.
`ylab`	Character string. Label of the y-axis.
`point.col`	Color of points in the observed vs. expected plot.
`point.pch`	Plotting character used for points.
`line.col`	Color of the identity line ($y = x$).
`plot_residuals.main`	Character string. Title of the residuals bar plot.
`legend.cex`	Numeric. Character expansion factor for legends.
`na.rm`	`bool` argument which indicates whether NA values should be skipped before computation; passed to `mean` and `sum`.

Details

The function computes several goodness-of-fit metrics comparing observed and expected numeric values. In addition to classical error measures such as mean squared error (MSE), root mean squared error (RMSE), mean absolute error (MAE), and mean absolute percentage error (MAPE), the coefficient of determination (R^2) is calculated.

If `plot = TRUE`, the function produces:

- a scatter plot of observed versus expected values including the identity line,
- a bar plot of relative residual frequencies.

Value

A `list` with two elements:

`fit_metrics`	A `list` containing the computed fit metrics: `SQR`, `SAR`, `SQT`, `R2`, `MSE`, `RMSE`, `MAE`, and `MAPE`.
`observed_expected`	A `data.frame` containing observed values, expected values, residuals, and derived residual measures.

Author(s)

Thomas Wieland

References

Boehmke B, Greenwell B (2020). *Hands-On Machine Learning with R* (1st ed.). Taylor & Francis, New York, NY.

See Also

`binary_metrics`

Examples

```
obs <- c(10, 12, 15, 18, 20)
exp <- c(11, 13, 14, 17, 21)

metrics(
  observed = obs,
  expected = exp
)
```

`moran` *Calculate Global Moran's I statistic*

Description

Calculating the Global Moran's I statistic for spatial autocorrelation from an `nbmatrix` object

Usage

```
moran(
  object,
  randomization = TRUE,
  alternative = "greater",
  verbose = FALSE
  )
```

Arguments

`object`	Object of class `nbmatrix`
`randomization`	`bool` argument that indicates which test is conducted (under randomization or normality); passed to `spdep::moran.test`
`alternative`	a character string specifying the alternative hypothesis, must be one of greater (default), less or two.sided; passed to `spdep::moran.test`
`verbose`	`bool` argument which indicates whether progress messages are displayed

Details

Moran's I (Moran 1950) is a statistical measure of spatial autocorrelation. Its calculation requires a spatial weights matrix that defines the spatial relationships between observations and assigns weights to neighboring observations (e.g., binary weights based on contiguity). A typical application is, for example, investigating whether spatial autocorrelation exists in the incidence of infectious diseases, that is, whether areas with high (or low) incidence are surrounded by neighboring areas that also exhibit high (or low) incidence (Wieland 2020, 2022). This function internally uses `spdep::moran.test` for calculation (see the corresponding documentation). The results are written in the `nbmatrix` instance and displayed in the summary.

Value

object of class `nbmatrix-class`

Author(s)

Thomas Wieland

References

Cliff AD, Ord JK (1981) Spatial Processes: Models & Applications. https://archive.org/details/spatialprocesses0000clif

GeoDa Center (2026) GeoDa. An Introduction to Spatial Data Science. https://geodacenter.github.io/

Moran PAP (1950) Notes on Continuous Stochastic Phenomena. *Biometrika* 37(1/2) 17–23. doi:10.2307/2332142

Wieland T (2020) Flatten the Curve! Modeling SARS-CoV-2/COVID-19 Growth in Germany at the County Level. *REGION* 7(2), 43–83. doi:10.18335/region.v7i2.324

Wieland T (2022) Spatial patterns of excess mortality in the first year of the COVID-19 pandemic in Germany. *European Journal of Geography* 13(4), 18-33. doi:10.48088/ejg.t.wie.13.4.018.033

See Also

nbmatrix, nbstat, getisord, gstar

Examples

```
data(RKI_Corona_counties)
# German counties (Source: Robert Koch Institute)

Corona_nbmat <-
  nbmatrix (
    RKI_Corona_counties,
    ID_col="AGS",
    verbose = TRUE
  )
# Creating neighborhood matrix

Corona_nbstat2 <- nbstat(
  Corona_nbmat,
  link_data = RKI_Corona_counties,
  ID_col = "AGS",
  data_col = "cases_per_",
  func = NULL,
  verbose = TRUE
)
# New nbmatrix instance
# Defining "cases_per_" (COVID-19 cases per 100,000 inhabitants) as analysis column

Corona_SpatialStatistics <- moran(
  Corona_nbstat2,
  verbose = TRUE
  )
# Calculating Global Moran's I
```

```
summary(Corona_SpatialStatistics)
# Summary of nbmatrix object
```

---

moran-methods *Methods for Function* moran

Description

Methods for function moran

Methods

signature(object = "nbmatrix", randomization = TRUE, alternative = "greater", verbose = FALSE)
: Calculates the Global Moran's I statistic for the neighborhood matrix for a specified data column to be analyzed. The parameters randomization and alternative are passed to spdep::moran.test, which is internally used for the calculation.

Author(s)

Thomas Wieland

---

nbmatrix *Construct Neighbourhood Matrix from Polygons*

Description

Building a neighbourhood matrix based on regions (polygons) with contiguous boundaries

Usage

```
nbmatrix(
  polygon_sf,
  ID_col,
  row.names = NULL,
  snap = NULL,
  queen = TRUE,
  weights_style = "W",
  weights_zeropolicy = NULL,
  verbose = FALSE
  )
```

Arguments

polygon_sf	sf object with polygons
ID_col	Column of polygon_sf with unique ID of each polygon
row.names	row.names for the sf object, passed to spdep::poly2nb
snap	Snapping distance, passed to spdep::poly2nb
queen	If TRUE, a single shared boundary point meets the contiguity condition; passed to spdep::poly2nb
weights_style	weights_style can take values "W", "B", "C", "U", "minmax" and "S"; passed to the style argument of spdep::nb2listw
weights_zeropolicy	if FALSE stop with error for any empty neighbour sets, if TRUE permit the weights list to be formed with zero-length weights vectors; passed to the zero.policy argument of spdep::nb2listw
verbose	bool argument which indicates whether progress messages are displayed

Details

The function is based on spdep::poly2nb, which creates neighbours lists, and spdep::nb2listw, which computes spatial weights for neighbours lists. Please consult the corresponding documentation for a more detailed description of the parameters. The input is a sf object (spatial data frame) and the results (contained in a {nbmatrix-class} object) include 1) a nb list (poly2nb result), 2) a listw object (spatial weights), 3) a data.frame with a linear neighbor matrix, 4) a data.frame with the number of neighbors, and other elements (statistics etc.)

Value

object of class nbmatrix-class

Author(s)

Thomas Wieland

References

Cliff AD, Ord JK (1981) Spatial Processes: Models & Applications. https://archive.org/details/spatialprocesses0000clif

GeoDa Center (2026) GeoDa. An Introduction to Spatial Data Science. https://geodacenter.github.io/

Wieland T (2020) Flatten the Curve! Modeling SARS-CoV-2/COVID-19 Growth in Germany at the County Level. *REGION* 7(2), 43–83. doi:10.18335/region.v7i2.324

Wieland T (2022) Spatial patterns of excess mortality in the first year of the COVID-19 pandemic in Germany. *European Journal of Geography* 13(4), 18-33. doi:10.48088/ejg.t.wie.13.4.018.033

See Also

nbstat, moran, getisord, gstar

Examples

```
data(RKI_Corona_counties)
# German counties (Source: Robert Koch Institute)

Corona_nbmat <-
  nbmatrix (
    RKI_Corona_counties,
    ID_col="AGS",
    verbose = TRUE
  )
# Creating neighborhood matrix

Corona_nbstat <- nbstat(
  Corona_nbmat,
  link_data = RKI_Corona_counties,
  ID_col = "AGS",
  data_col = "EWZ",
  func = "sum",
  verbose = TRUE
  )
# Sum of population (EWZ) of neighboring counties

plot(
  Corona_nbstat,
  main = "No. of inhabitants"
)
# Plot simple map of "EWZ"
```

---

nbmatrix-class *Class* "nbmatrix"

Description

The class "nbmatrix" contains the results of a neighborhood matrix analysis, built by the nbmatrix function and the "nbmatrix" methods. Use summary(nbmatrix) and plot(nbmatrix) for results summary and plotting, respectively.

Objects from the Class

Objects may be created by the function nbmatrix.

Slots

nb Object of class "nb": Neighborhood matrix list generated by spdep::poly2nb

nbmat Object of class "data.frame": Linear neighborhood matrix calculated from the nb list

weights Object of class "listw": Spatial weights generated by spdep::nb2listw

nbcount Object of class "data.frame": Table with the number of neighbors

`regions_col_name` Object of class `"character"`: Column name which represents the unique ID of the polygon features

`geodata` Object of class `"sf"`: Original geodata (`sf` object) with unique ID and `"geometry"` columns

`N` Object of class `"numeric"`: No. of features (total, with valid unique ID, with valid geometry)

`N_neighbors` Object of class `"numeric"`: Total and average no. of neighbors

`polygon_data` Object of class `"sf"`: Geodata (`sf` object containing the geometries and the analysis column)

`nbmat_data` Object of class `"data.frame"`: Neighborhood matrix data

`nbmat_data_aggregate` Object of class `"data.frame"`: Aggregated neighborhood matrix data

`func` Object of class `"character"`: Function used for the calculation of the neighborhood statistic

`moran` Object of class `"list"`: Results of the Global Moran's I calculation (estimate, expected value, etc.)

`getisord` Object of class `"list"`: Results of the Global Getis-Ord calculation (estimate, expected value, etc.)

`gstar` Object of class `"list"`: Results of the Local Gi* calculation (`data.frame` with estimates and expected values etc., analysis configuration)

`data_col` Object of class `"character"`: Column name which represents the analysis data for nbstat, Moran's I, etc.

`config` Object of class `"list"`: Configuration details with respect to zero policy of the neighborhood matrix etc.

`timestamp` Object of class `"list"`: Time stamps of any update of the instance

Methods

nbstat `signature(object = "nbmatrix")`: Calculates a specified statistic for the neighboring regions.

moran `signature(object = "nbmatrix")`: Calculates the Global Moran's I statistic for the neighborhood matrix

getisord `signature(object = "nbmatrix")`: Calculates the Global Getis-Ord statistic for the neighborhood matrix

gstar `signature(object = "nbmatrix")`: Calculates the Local Getis-Ord Gi* statistic for the neighborhood matrix

plot `signature(x = "nbmatrix")`: Plots the results of the calculation (Neighborhood statistic or Local Getis-Ord Gi*)

print `signature(x = "nbmatrix")`: Prints an `nbmatrix` object; use `summary(nbmatrix)` for results

show `signature(object = "nbmatrix")`: Prints an `nbmatrix` object; use `summary(nbmatrix)` for results

summary `signature(object = "nbmatrix")`: Prints a summary of `nbmatrix` objects (results of the spatial statistics calculation)

Author(s)

Thomas Wieland

References

Cliff AD, Ord JK (1981) Spatial Processes: Models & Applications. https://archive.org/details/spatialprocesses0000clif

GeoDa Center (2026) GeoDa. An Introduction to Spatial Data Science. https://geodacenter.github.io/

Wieland T (2020) Flatten the Curve! Modeling SARS-CoV-2/COVID-19 Growth in Germany at the County Level. *REGION* 7(2), 43–83. doi:10.18335/region.v7i2.324

Wieland T (2022) Spatial patterns of excess mortality in the first year of the COVID-19 pandemic in Germany. *European Journal of Geography* 13(4), 18-33. doi:10.48088/ejg.t.wie.13.4.018.033

See Also

nbstat, moran, getisord, gstar, nbmatrix

Examples

```
showClass("nbmatrix")
```

---

nbstat *Calculate Neighbourhood Statistics from Polygons*

Description

Calculating descriptive neighbourhood statistics based on regions (polygons) with contiguous boundaries from an object of class nbmatrix

Usage

```
nbstat(
  object,
  link_data,
  ID_col,
  data_col,
  func = "sum",
  verbose = FALSE
  )
```

Arguments

object	nbmatrix object
link_data	data.frame to merge with
ID_col	Column with unique ID of each polygon feature in the link_data data.frame
data_col	Column with regarded numeric values in data.frame
func	Descriptive statistic (FUN) to be computed for data_col of the neighbouring regions
verbose	bool argument which indicates whether progress messages are displayed

Details

Calculates a specified statistic (e.g., mean or sum) for the neighboring regions within a nbmatrix object. The user must specify a (spatial) data frame with the parameter link_data. The results are saved in the nbmatrix object. If func is set to NULL, nbstat is used to specify the data column used for further analyses (e.g., moran()).

Value

object of class nbmatrix-class

Author(s)

Thomas Wieland

References

Cliff AD, Ord JK (1981) Spatial Processes: Models & Applications. https://archive.org/details/spatialprocesses0000clif

GeoDa Center (2026) GeoDa. An Introduction to Spatial Data Science. https://geodacenter.github.io/

Wieland T (2020) Flatten the Curve! Modeling SARS-CoV-2/COVID-19 Growth in Germany at the County Level. *REGION* 7(2), 43–83. doi:10.18335/region.v7i2.324

Wieland T (2022) Spatial patterns of excess mortality in the first year of the COVID-19 pandemic in Germany. *European Journal of Geography* 13(4), 18-33. doi:10.48088/ejg.t.wie.13.4.018.033

See Also

nbmatrix, moran, getisord, gstar

Examples

```
data(RKI_Corona_counties)
# German counties (Source: Robert Koch Institute)

Corona_nbmat <-
  nbmatrix (
    RKI_Corona_counties,
```

```
    ID_col="AGS",
    verbose = TRUE
  )
# Creating neighborhood matrix

Corona_nbstat <- nbstat(
  Corona_nbmat,
  link_data = RKI_Corona_counties,
  ID_col = "AGS",
  data_col = "EWZ",
  func = "sum",
  verbose = TRUE
  )
# Sum of population (EWZ) of neighboring counties

plot(
  Corona_nbstat,
  main = "No. of inhabitants"
  )
# Plot simple map of "EWZ"
```

---

nbstat-methods *Methods for Function* nbstat

Description

Methods for function nbstat

Methods

signature(object = "nbmatrix", link_data, ID_col, data_col, func = "sum", verbose = FALSE)
: Calculates a specified statistic (e.g., mean or sum) for the neighboring regions within a nbmatrix object. The user must specify a (spatial) data frame with the parameter link_data. The results are saved in the nbmatrix object. If func is set to NULL, nbstat is used to specify the data column used for further analyses (e.g., moran()).

Author(s)

Thomas Wieland

`Oesterreich_Faelle` *Austria Daily COVID-19 cases by region 2020-02-26 to 2020-05-31*

Description

A dataset containing COVID-19 cases by region (NUTS 3) and time periods (days) for Austria (Source: BMSGPK).

Usage

```
data(Oesterreich_Faelle)
```

Format

A data.frame with multiple columns:

NUTS3 (character) Region for which the data was collected.

Datum (Date) Date of record.

Faelle (integer) Number of reported cases on this date.

Details

The data was originally published by BMSGPK at a smaller spatial scale level (political districts, "Politische Bezirke"). The data was linked to a corresponding shapefile from Statistik Austria (2022), joined to the NUTS3 level via a spatial join, and summed over the Austrian NUTS3 regions. The spatial join is based on polygon centroids of the political districts level; in cases where the centroid was outside the polygon, it was placed inside the polygon manually.

Source

BMSGPK, Oesterreichisches COVID-19 Open Data Informationsportal (2022) COVID-19: Zeitliche Darstellung von Daten zu Covid19-Faellen je Bezirk. https://www.data.gv.at/katalog/dataset/4b71eb3d-7d55-4967-b80d-91a3f220b60c (retrieved 2022-06-23)

Statistik Austria (2022) Politische Bezirke. https://www.data.gv.at/katalog/dataset/stat_gliederung-osterreichs-in-politische-bezirke131e2 (retrieved 2022-06-27, URL does not exist anymore)

Wieland T (2022) C19dNUTS: Dataset of Regional COVID-19 Deaths per 100,000 Pop (NUTS). R package v1.0.1. doi:10.32614/CRAN.package.C19dNUTS

Examples

```
data(Oesterreich_Faelle)
# Get Austrian COVID19 cases at NUTS 3 level
# (first wave, same final date as in Swiss data: 2020-05-31)

AT_covidwave1 <-
  swash_backwash(
    data = Oesterreich_Faelle,
```

```
    col_cases = "Faelle",
    col_date = "Datum",
    col_region = "NUTS3"
  )
# Swash-Backwash Model for Austrian COVID19 cases
# Spatial aggregate: NUTS 3

summary(AT_covidwave1)
# Summary of model results
```

---

plot-methods *Methods for Function* plot

Description

Methods for function plot for different S4 classes: infpan, sbm, sbm_ci, nbmatrix, loggrowth, expgrowth, hawkes, and breaksgrowth.

Methods

signature(x = "infpan") plot.infpan(x, y, ...): Plots regional infections against time

Arguments:

- x: An object of class infpan including infections panel data.
- y: Optional argument for additional customization, such as plot style or axis labels.
- ...: Additional graphical parameters that can be passed to control plot appearance.

Details: This method is used to visualize case data by region for N regions and T time points.

signature(x = "sbm") plot.sbm(x, y = NULL, col_edges = "blue", xlab_edges = "Time", ylab_edges = "Regions", main_edges = "Edges", col_SIR = c("blue", "red", "green"), lty_SIR = c("solid", "solid", "solid"), lwd_SIR = c(1,1,1), xlab_SIR = "Time", ylab_SIR = "Regions", main_SIR = "SIR integrals", col_cases = "red", lty_cases = "solid", lwd_cases = 1, xlab_cases = "Time", ylab_cases = "Infections", main_cases = "Daily infections", xlab_cum = "Cases", ylab_cum = "Regions", main_cum = "Cumulative infections per region", horiz_cum = TRUE, separate_plots = FALSE):

Plots the results of the Swash-Backwash Model. This generates four plots:

- Edges over time.
- SIR integrals.
- All-over infections.
- Total infections per time unit.

Arguments:

- x: An object of class sbm representing the results of the Swash-Backwash Model.
- y: Optional argument for additional customization, such as plot style or axis labels.
- ...: Additional graphical parameters that can be passed to control plot appearance.

Details: This method is used to visualize the output of the Swash-Backwash Model, providing insight into the dynamics of the modeled epidemic.

`signature(x = "sbm_ci") plot.sbm_ci(x, y, ...)`: Plots the results of bootstrap confidence intervals for the Swash-Backwash Model. This generates a single figure with six subplots:

- S_A (susceptible population),
- I_A (infected population),
- R_A (recovered population),
- t_{FE} (final epidemic time),
- t_{LE} (last epidemic time),
- R_{0A} (basic reproduction number).

Arguments:

- `x`: An object of class `sbm_ci` containing the bootstrap confidence intervals for the Swash-Backwash Model.
- `y`: Optional argument for additional customization, such as plot style or axis labels.
- `...`: Additional graphical parameters for fine-tuning the plots.

Details: This method is used to visualize the bootstrap confidence intervals for various parameters of the Swash-Backwash Model.

`signature(x = "countries") plot.countries(x, y = NULL, col_bars = "grey", col_ci = "red")`: Plots the results of the between-countries analysis via Swash-Backwash Model. This generates four plots:

- Indicator for country 1
- Indicator for country 2
- Boxplots of the distribution of the indicator in country 1 and 2
- Distribution of the difference between the indicators of country 1 and 2

Arguments:

- `x`: An object of class `countries` representing the results of the Swash-Backwash Model country analysis.
- `y`: Not relevant
- `col_bars`: Color of bars
- `col_ci`: Color of confidence intervals

Details: This method is used to visualize the output of the Swash-Backwash Model, providing insight into the dynamics of the modeled epidemic.

`signature(x = "loggrowth") plot.loggrowth(x, y, ...)`: Plots the results of the logistic growth model, including:

- Observed values
- Predicted values
- First derivative

Arguments:

- `x`: An object of class `loggrowth` containing the data for the logistic growth model.
- `y`: Optional argument for additional customization of the plot (e.g., color, labels).
- `...`: Additional arguments for graphical parameters.

Details: This method is useful for visualizing the observed and predicted growth patterns in an epidemic or similar phenomena modeled by logistic growth.

`signature(x = "expgrowth") plot.expgrowth(x, y, ...)`: Plots the results of the exponentai growth model, including:

- Observed values
- Predicted values

Arguments:

- `x`: An object of class `expgrowth` containing the data for the exponential growth model.
- `y`: Optional argument for additional customization of the plot (e.g., color, labels).
- `...`: Additional arguments for graphical parameters.

Details: This method is useful for visualizing the observed and predicted growth patterns in the initial phase of an epidemic or similar phenomena modeled by exponential growth.

`signature(x = "hawkes") plot.hawkes(x, y, ...)`: Plots the results of the Hawkes process model, including:

- Observed values
- Predicted values

Arguments:

- `x`: An object of class `hawkes` containing the data for the Hawkes model.
- `y`: Optional argument for additional customization of the plot (e.g., color, labels).
- `...`: Additional arguments for graphical parameters.

Details: This method is useful for visualizing the observed and predicted growth patterns of an epidemic or similar phenomena modeled as Hawkes processes.

`signature(x = "breaksgrowth") plot.breaksgrowth(x, y, ...)`: Plots the results of a breakpoint analysis, including:

- Time series data
- Breakpoints

Arguments:

- `x`: An object of class `breaksgrowth` containing the data for the breakspoints model.
- `y`: Optional argument for additional customization of the plot (e.g., color, labels).
- `...`: Additional arguments for graphical parameters.

Details: This method is useful for visualizing the derived breakpoints.

`signature(x = "nbmatrix") plot.nbmatrix(x, y, ...)`: Plots the results of a neighborhood matrix/spatial statistics analysis, including:

- Spatial features (polygons)
- Specified indicator

Arguments:

- `x`: An object of class `nbmatrix` containing the data.
- `y`: Optional argument for additional customization of the plot (e.g., color, labels).
- `statistic`: Statistic to be plotted.
- `attribute`: Attribute to be plotted.
- `verbose`: Attribute to be plotted.
- `...`: `bool` argument which indicates whether progress messages are displayed.

Details: This method is useful for visualizing the derived breakpoints.

Author(s)

Thomas Wieland

`plot_coef_ci` *Plot Point Estimates With Confidence Intervals*

Description

Plotting point estimates with confidence intervals from regression results

Usage

```
plot_coef_ci(
  point_estimates,
  confint_lower,
  confint_upper,
  coef_names,
  p = NULL,
  estimate_colors = NULL,
  confint_colors = NULL,
  auto_color = FALSE,
  alpha = 0.05,
  set_estimate_colors = c("red", "grey", "green"),
  set_confint_colors = c("#ffcccb", "lightgray", "#CCFFCC"),
  skipvars = NULL,
  plot.xlab = "Independent variables",
  plot.main = "Point estimates with CI",
  axis.at = seq(-30, 40, by = 5),
  pch = 15,
  cex = 2,
  lwd = 5,
  y.cex = 0.8
  )
```

Arguments

`point_estimates`	`numeric` vector containing point estimates
`confint_lower`	`numeric` vector containing lower confidence intervals
`confint_upper`	`numeric` vector containing upper confidence intervals
`coef_names`	`character` vector containing coefficient names
`p`	`numeric` vector containing p values of the coefficients (optional)
`estimate_colors`	vector containing colors for the point estimates (optional)
`confint_colors`	vector containing colors for the confidence intervals (optional)

auto_color	bool value which indicates whether the colors are found automatically based on coef and CI values
alpha	Significance level α for 1-α*100 confidence intervals
set_estimate_colors	Colors for point estimates (significant negative, not significant, significant positive)
set_confint_colors	Colors for confidence intervals (significant negative, not significant, significant positive)
skipvars	List with coefficients to be dropped
plot.xlab	Label of x axis
plot.main	Plot title
axis.at	Position of y axis
pch	Point type
cex	Point size
lwd	Line width (confidence intervals)
y.cex	Font size of y axis

Details

The function checks whether the input vectors have the same length. If auto_color is TRUE, the colors from set_estimate_colors and set_confint_colors are used, and the significance level is determined based on the coefficient and confidence interval values (all three below 0 = significant negative, all three above 0 = significant positive).

Value

Coefficients plot, no returned value

Author(s)

Thomas Wieland

References

Wieland T (2025) Assessing the effectiveness of non-pharmaceutical interventions in the SARS-CoV-2 pandemic: results of a natural experiment regarding Baden-Württemberg (Germany) and Switzerland in the second infection wave. *Journal of Public Health* 33(11), 2497-2511. doi:10.1007/s1038902402218x

Examples

```
data(did_fatalities_splm_coef)
# Results of a difference-in-differences model

plot_coef_ci(
  point_estimates = did_fatalities_splm_coef$Estimate,
```

```
  confint_lower = did_fatalities_splm_coef$CI_lower_Bonferroni,
  confint_upper = did_fatalities_splm_coef$CI_upper_Bonferroni,
  coef_names = did_fatalities_splm_coef$Var,
  skipvars = c(
    "Alpha_share",
    "lambda",
    "rho",
    "log(D_Infections_daily_7dsum_per100000_lag2weeks)",
    "vacc_cum_per100000_lag2weeks"
    ),
  lwd = 13,
  pch = 19,
  auto_color = TRUE
)
# Plot with point estimates and confidence intervals
```

`plot_map` *Map Plot of Specified Indicator*

Description

Plot of a map showing a speficied indicator (such as incidence) from an `infpan` object.

Usage

```
plot_map(
    object,
    attribute = "Cases",
    timepoint = NULL,
    verbose = FALSE,
    ...
  )
```

Arguments

`object`	object of class `infpan`
`attribute`	Attribute to be plotted, must be defined in `infpan` object (e.g., "Cases", "Incidence")
`timepoint`	Time point for which the attribute is to be plotted
`verbose`	`bool` argument which indicates whether progress messages are displayed
`...`	Further graphic arguments passed to `sf::plot`, e.g. breaks, colors

Details

Plots a map from an `infpan` object which displays the attribute specified with the `attribute` parameter at the timepoint specified with `timepoint`. To adjust the layout of the map, use the `...` parameters which are passed to the `plot` S3 method for the `sf` class (see the corresponding documentation). Map plot requires geodata to be specified in the `infpan` object (Use `add_geodata` to

assign your sf object). Permitted attributes are: "Cases", "R_t" (Effective reproduction number), "Cum. cases" (Cumulative cases), "Incidence" Incidence (per xxx pop), "Population" (Population size of the region), "Roll. mean" (Rolling mean of cases), and "Roll. sum" (Rolling sum of cases).

Value

Input infpan object (unchanged), plot

Author(s)

Thomas Wieland

References

Wieland T (2020) Flatten the Curve! Modeling SARS-CoV-2/COVID-19 Growth in Germany at the County Level. *REGION* 7(2), 43–83. doi:10.18335/region.v7i2.324

See Also

infpan-class, load_infections_paneldata, calculate_incidence, calculate_cum, calculate_rollmean, calculate_rollsum, calculate_Rt

Examples

```
data(COVID19Cases_geoRegion)
# Get SWISS COVID19 cases at NUTS 3 level

data(K4kant20260101gf_ch2007Poly)
# Cantonal boundaries of Switzerland

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[!COVID19Cases_geoRegion$geoRegion %in% c("CH", "CHFL"),]
# Exclude CH = Switzerland total and CHFL = Switzerland and Liechtenstein total

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[COVID19Cases_geoRegion$datum <= "2020-05-31",]
# Extract first COVID-19 wave

infpan_CH <- load_infections_paneldata(
    data = COVID19Cases_geoRegion,
    col_cases = "entries",
    col_date = "datum",
    col_region = "geoRegion",
    other_cols = c("Population" = "pop"),
    verbose = TRUE
  )
# Import as infections panel data set (class infpan)

infpan_CH <- calculate_incidence(
  infpan_CH,
  col_name = "incidence",
  verbose = TRUE
```

```
)
# Calculate incidence of cases as "incidence"

infpan_CH <- add_geodata(
  infpan_CH,
  K4kant20260101gf_ch2007Poly,
  unit_col = "cant_abbrev"
)
# Adding geodata (sf) to infpan object

summary(infpan_CH)
# Summary of infpan object

timestamps(infpan_CH)
# Time stamps of infpan object

plot_map(
  infpan_CH,
  attribute = "Incidence",
  main = "COVID-19 Incidence 2020-05-31",
  breaks = c(0, 0.05, 0.1, 0.2, 1),
  verbose = TRUE
)
# Simple map of incidence for the most current date (timepoint=NULL)
```

`plot_map-methods` *Methods for Function* `plot_map`

Description

Methods for function `plot_map`

Methods

`signature( object = "infpan", attribute = "Cases", timepoint = NULL, verbose = FALSE, ...)`
: Plots a map from an `infpan` object which displays the attribute specified with the `attribute` parameter at the timepoint specified with `timepoint`. To adjust the layout of the map, use the `...` parameters which are passed to the `plot` S3 method for the `sf` class (see the corresponding documentation).

Author(s)

Thomas Wieland

print-methods *Methods for Function* print

Description

Methods for function print

Methods

signature(object = "infpan") Prints an infpan object; use summary(infpan) for results

signature(x = "sbm") Prints a sbm object; use summary(sbm) for results

signature(x = "sbm_ci") Prints a sbm_ci object; use summary(sbm_ci) for results

signature(object = "countries") Prints an countries object; use summary(countries) for results

signature(x = "loggrowth") Prints a loggrowth object; use summary(loggrowth) for results

signature(x = "expgrowth") Prints an expgrowth object; use summary(expgrowth) for results

signature(x = "hawkes") Prints a hawkes object; use summary(hawkes) for results

signature(x = "breaksgrowth") Prints a breaksgrowth object; use summary(breaksgrowth) for results

quantile_ci *Computing Quantiles for a given Numeric Vector*

Description

Computes quantiles for a given vector x and the related confidence intervals (lower, upper).

Usage

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

Arguments

x	A numeric vector
alpha	Significance level α for 1-α*100 confidence intervals

Details

Helper function for plot(sbm_ci), but may be used separately.

Value

A numeric vector with lower and upper quantile

Author(s)

Thomas Wieland

Examples

```
numeric_vector <- c(1,9,5,6,3,10,20,6,9,14,3,5,8,6,11)
# any numeric vector

quantile_ci(numeric_vector)
```

R_t *Effective Reproduction Number for Epidemic Data*

Description

Calculation of the effective reproduction number for infection/surveillance data

Usage

```
R_t(
  infections,
  GP = 4,
  correction = FALSE
  )
```

Arguments

infections	numeric vector with infection data
GP	Generation period, in time units (typically days)
correction	Correction of values equal to zero? (Recommended)

Details

The function calculates the effective reproduction number, R_t, of an infections time series. Set the generation period by the parameter GP (default: 4). If correction is TRUE, values equal to zero are increased by one.

Value

list with two entries:

R_t:	Object of class "numeric" R_t values
infections_data:	Object of class "data.frame" Dataset with infections data and R_t

Author(s)

Thomas Wieland

References

an der Heiden M, Hamouda O (2020) Schätzung der aktuellen Entwicklung der SARS-CoV-2-Epidemie in Deutschland - Nowcasting. *Epidemiologisches Bulletin* 17, 10-15. doi:10.25646/6692

Bonifazi G, Lista L, Menasce D, Mezzetto M, Pedrini D, Spighi R, Zoccoli A (2021) A simplified estimate of the effective reproduction number Rt using its relation with the doubling time and application to Italian COVID-19 data. *The European Physical Journal Plus* 136, 386. doi:10.1140/epjp/s13360021013396

Wieland T (2020) A phenomenological approach to assessing the effectiveness of COVID-19 related nonpharmaceutical interventions in Germany. *Safety Science* 131, 104924. doi:10.1016/j.ssci.2020.104924

See Also

logistic_growth, exponential_growth

Examples

```
data(COVID19Cases_geoRegion)
# Get SWISS COVID19 cases at NUTS 3 level

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[!COVID19Cases_geoRegion$geoRegion %in% c("CH", "CHFL"),]
# Exclude CH = Switzerland total and CHFL = Switzerland and Liechtenstein total

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[COVID19Cases_geoRegion$datum <= "2020-05-31",]
# Extract first COVID-19 wave

COVID19Cases_BS <-
  COVID19Cases_geoRegion[(COVID19Cases_geoRegion$geoRegion == "ZH")
                         & (COVID19Cases_geoRegion$sumTotal > 0),]
# COVID cases for Zurich

Rt_BS <- R_t(infections = COVID19Cases_BS$entries)
# Effective reproduction number

Rt_BS
```

RKI_Corona_counties *German Counties with COVID-19 Cases*

Description

A dataset containing German counties (NUTS 3) with COVID-19 cases (Source: Robert Koch Institute).

Usage

```
data(RKI_Corona_counties)
```

Format

A data.frame with multiple columns:

OBJECTID unknown/not necessary

ADE unknown/not necessary

GF unknown/not necessary

BSG unknown/not necessary

RS (character) County code 1

AGS (character) County code 2

SDV_RS (character) County code 3

GEN (character) County name

BEZ (character) County type

IBZ unknown/not necessary

BEM unknown/not necessary

NBD unknown/not necessary

SN_L unknown/not necessary

SN_R unknown/not necessary

SN_K unknown/not necessary

SN_V1 unknown/not necessary

SN_V2 unknown/not necessary

SN_G unknown/not necessary

FK_S3 unknown/not necessary

NUTS (character) NUTS 3 code

RS_0 unknown/not necessary

AGS_0 unknown/not necessary

WSK unknown/not necessary

EWZ (numeric) Population

KFL (numeric) Area in sq. km

DEBKG_ID unknown/not necessary

Shape__Are unknown/not necessary

Shape__Len unknown/not necessary

death_rate

cases (numeric) COVID-19 cases

deaths (numeric) COVID-19 associated deaths

cases_per_ (numeric) COVID-19 cases per 100,000 inhabitants

cases_pe_1 unknown/not necessary

BL (character) Federal state

BL_ID (integer) Federal state ID

county (character) County name

last_updat Date of last update

geometry Geometry

Details

The data is included as it was published by the Robert Koch Institute (Robert Koch-Institut, RKI) but extended by the geometry column (Original data: shapefile).

Source

RKI (2020) RKI Corona Landkreise. Robert Koch-Institut (RKI), dl-de/by-2-0. Attribution: Robert Koch-Institut, Bundesamt für Kartographie und Geodäsie. https://npgeo-corona-npgeo-de.hub.arcgis.com/datasets/917fc37a7095 (retrieved 2020-03-30)

Examples

```
data(RKI_Corona_counties)
# German counties (Source: Robert Koch Institute)

Corona_nbmat <-
  nbmatrix (
    RKI_Corona_counties,
    ID_col="AGS",
    verbose = TRUE
  )
# Creating neighborhood matrix

Corona_nbstat <- nbstat(
  Corona_nbmat,
  link_data = RKI_Corona_counties,
  ID_col = "AGS",
  data_col = "EWZ",
  func = "sum",
  verbose = TRUE
  )
# Sum of population (EWZ) of neighboring counties

plot(
  Corona_nbstat,
  main = "No. of inhabitants"
)
# Plot simple map of "EWZ"
```

sbm-class *Class* "sbm"

Description

The class "sbm" contains the results of the Swash-Backwash Model and the related input data as well as additional information. Use summary(sbm) and plot(sbm) for results summary and plotting, respectively.

Objects from the Class

Objects can be created by the function swash_backwash and the infpan method swash, respectively.

Slots

R_0A: Object of class "numeric" Model result: spatial reproduction number R_{0A}

integrals: Object of class "numeric" Model result: integrals S_A, I_A, and R_A

velocity: Object of class "numeric" Model result: velocity measures t_{FE} and t_{LE}

occ_regions: Object of class "data.frame" Model result: Occurrence at regional level

SIR_regions: Object of class "data.frame" Model result: Susceptible, infected and recovered regions over time

cases_by_date: Object of class "data.frame" Total cases by date

cases_by_region: Object of class "data.frame" Cumulative cases by region

input_data: Object of class "data.frame" Input data

data_statistics: Object of class "numeric" Diagnostics of input data

col_names: Object of class "character" Original column names in input data

timestamp: Object of class "list" Time stamps of any update of the instance

Methods

confint signature(object = "sbm"): Creates bootstrap confidence intervals for sbm objects.

plot signature(x = "sbm"): Plots the results of the Swash-Backwash Model; two plots: edges over time, total infections per time unit

print signature(x = "sbm"): Prints an sbm object; use summary(sbm) for results

show signature(object = "sbm"): Prints an sbm object; use summary(sbm) for results

summary signature(object = "sbm"): Prints a summary of sbm objects (results of the Swash-Backwash Model)

Author(s)

Thomas Wieland

References

Cliff AD, Haggett P (2006) A swash-backwash model of the single epidemic wave. *Journal of Geographical Systems* 8(3), 227-252. doi:10.1007/s1010900600278

Smallman-Raynor MR, Cliff AD, Stickler PJ (2022) Meningococcal Meningitis and Coal Mining in Provincial England: Geographical Perspectives on a Major Epidemic, 1929–33. *Geographical Analysis* 54, 197–216. doi:10.1111/gean.12272

Smallman-Raynor MR, Cliff AD, The COVID-19 Genomics UK (COG-UK) Consortium (2022) Spatial growth rate of emerging SARS-CoV-2 lineages in England, September 2020–December 2021. *Epidemiology and Infection* 150, e145. doi:10.1017/S0950268822001285.

Examples

```
showClass("sbm")
```

`sbm_ci-class` *Class* `"sbm_ci"`

Description

The class `"sbm_ci"` contains the results of the Swash-Backwash Model, confidence intervals for the model estimates, and the related input data as well as additional information. Use `summary(sbm_ci)` and `plot(sbm_ci)` for results summary and plotting, respectively.

Objects from the Class

Objects can be created by the function `confint(sbm)`.

Slots

`R_0A`: Object of class `"numeric"` Model result: spatial reproduction number R_{0A}

`integrals`: Object of class `"numeric"` Model result: integrals S_A, I_A, and R_A

`velocity`: Object of class `"numeric"` Model result: velocity measures t_{FE} and t_{LE}

`occ_regions`: Object of class `"data.frame"` Model result: Occurrence at regional level

`cases_by_date`: Object of class `"data.frame"` Total cases by date

`cases_by_region`: Object of class `"data.frame"` Cumulative cases by region

`input_data`: Object of class `"data.frame"` Input data

`data_statistics`: Object of class `"numeric"` Diagnostics of input data

`col_names`: Object of class `"character"` Column names in input data

`integrals_ci`: Object of class `"list"` Confidence intervals for integrals S_A, I_A, and R_A

`velocity_ci`: Object of class `"list"` Confidence intervals for velocity measures t_{FE} and t_{LE}

`R_0A_ci`: Object of class `"numeric"` Confidence intervals for spatial reproduction number R_{0A}

`iterations`: Object of class `"data.frame"` Results of bootstrap sampling iterations

`ci`: Object of class `"numeric"` Lower and upper confidence intervals based on user input

`config`: Object of class `"list"` Configuration details for bootstrap sampling

Methods

plot `signature(x = "sbm_ci")`: Plots the results of bootstrap confidence intervals for the Swash-Backwash Model; one figure with six plots: S_A, I_A, R_A, t_{FE}, t_{LE}, and R_{0A}

print `signature(x = "sbm_ci")`: Prints an `sbm_ci` object; use `summary(sbm_ci)` for results

show `signature(object = "sbm_ci")`: Prints an `sbm_ci` object; use `summary(sbm_ci)` for results

summary `signature(object = "sbm_ci")`: Prints a summary of `sbm_ci` objects (bootstrap confidence intervals for Swash-Backwash Model estimates)

Author(s)

Thomas Wieland

References

Cliff AD, Haggett P (2006) A swash-backwash model of the single epidemic wave. *Journal of Geographical Systems* 8(3), 227-252. doi:10.1007/s1010900600278

Efron B, Tibshirani RJ (1993) An Introduction to the Bootstrap.

Ramachandran KM, Tsokos CP (2021) Mathematical Statistics with Applications in R (Third Edition). Ch. 13.3.1 (Bootstrap confidence intervals). doi:10.1016/B9780128178157.000130

Smallman-Raynor MR, Cliff AD, Stickler PJ (2022) Meningococcal Meningitis and Coal Mining in Provincial England: Geographical Perspectives on a Major Epidemic, 1929–33. *Geographical Analysis* 54, 197–216. doi:10.1111/gean.12272

Smallman-Raynor MR, Cliff AD, The COVID-19 Genomics UK (COG-UK) Consortium (2022) Spatial growth rate of emerging SARS-CoV-2 lineages in England, September 2020–December 2021. *Epidemiology and Infection* 150, e145. doi:10.1017/S0950268822001285.

Examples

```
showClass("sbm_ci")
```

`show-methods` *Methods for Function* `show`

Description

Methods for function `show`

Methods

`signature(object = "infpan")` Prints an `infpan` object; use `summary(infpan)` for results

`signature(object = "sbm")` Prints an `sbm` object; use `summary(sbm)` for results

`signature(object = "sbm_ci")` Prints an `sbm_ci` object; use `summary(sbm_ci)` for results

`signature(object = "countries")` Prints an `countries` object; use `summary(countries)` for results

`signature(object = "loggrowth")` Prints an `loggrowth` object; use `summary(loggrowth)` for results

`signature(object = "expgrowth")` Prints an `expgrowth` object; use `summary(expgrowth)` for results

`spatial_statistic` *Calculating Spatial Statistics*

Description

Calculation of a specified spatial statistic for the data from an infpan object.

Usage

```
spatial_statistic(
    object,
    attribute = "Cases",
    timepoint = NULL,
    statistic = "nbstat",
    func = NULL,
    row.names = NULL,
    snap = NULL,
    queen = TRUE,
    weights_style = "W",
    weights_zeropolicy = NULL,
    verbose = FALSE,
    ...
  )
```

Arguments

`object`	object of class `infpan`
`attribute`	Attribute for which the statistic is calculated, must be defined in `infpan` object (e.g., "Cases", "Incidence")
`timepoint`	Time point for which the statistic is calculated
`statistic`	Statistic to be computed
`func`	If `statistic == "nbstat"`: Descriptive statistic (`FUN`) to be computed for `data_col` of the neighbouring regions
`row.names`	row.names for the `sf` object, passed to `spdep::poly2nb`
`snap`	Snapping distance, passed to `spdep::poly2nb`
`queen`	If TRUE, a single shared boundary point meets the contiguity condition; passed to `spdep::poly2nb`

weights_style	weights_style can take values "W", "B", "C", "U", "minmax" and "S"; passed to the style argument of spdep::nb2listw
weights_zeropolicy	if FALSE stop with error for any empty neighbour sets, if TRUE permit the weights list to be formed with zero-length weights vectors; passed to the zero.policy argument of spdep::nb2listw
verbose	bool argument which indicates whether progress messages are displayed
...	Further arguments passed to the spatial statistics functions (see details)

Details

The user must choose a specific time point using the timepoint argument. If no time point is stated, the most current time point is chosen automatically.

The ... arguments are passed to the specific spatial statistics function which depends on what is specified by argument statistic. See moran, getisord, gstar.

Value

nbmatrix object including the spatial statistic to be calculated

Author(s)

Thomas Wieland

References

Cliff AD, Ord JK (1981) Spatial Processes: Models & Applications. https://archive.org/details/spatialprocesses0000clif

GeoDa Center (2026) GeoDa. An Introduction to Spatial Data Science. https://geodacenter.github.io/

Wieland T (2020) Flatten the Curve! Modeling SARS-CoV-2/COVID-19 Growth in Germany at the County Level. *REGION* 7(2), 43–83. doi:10.18335/region.v7i2.324

Wieland T (2022) Spatial patterns of excess mortality in the first year of the COVID-19 pandemic in Germany. *European Journal of Geography* 13(4), 18-33. doi:10.48088/ejg.t.wie.13.4.018.033

See Also

infpan-class, nbstat, nbmatrix, moran, getisord, gstar

Examples

```
data(COVID19Cases_geoRegion)
# Get SWISS COVID19 cases at NUTS 3 level

data(K4kant20260101gf_ch2007Poly)
# Cantonal boundaries of Switzerland

COVID19Cases_geoRegion <-
```

```
  COVID19Cases_geoRegion[!COVID19Cases_geoRegion$geoRegion %in% c("CH", "CHFL"),]
# Exclude CH = Switzerland total and CHFL = Switzerland and Liechtenstein total

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[COVID19Cases_geoRegion$datum <= "2020-05-31",]
# Extract first COVID-19 wave

infpan_CH <- load_infections_paneldata(
  data = COVID19Cases_geoRegion,
  col_cases = "entries",
  col_date = "datum",
  col_region = "geoRegion",
  other_cols = c(
    "Population" = "pop"
  ),
  verbose = TRUE
)
# Import as infections panel data set (class infpan)

infpan_CH <- add_geodata(
  infpan_CH,
  K4kant20260101gf_ch2007Poly,
  unit_col = "cant_abbrev"
)
# Adding geodata (sf) to infpan object

summary(infpan_CH)
# Summary of infpan object

timestamps(infpan_CH)
# Time stamps of infpan object

moran_incidence <-
  spatial_statistic(
    infpan_CH,
    statistic = "moran",
    randomization = FALSE
  )
# Calculating Moran's I test under normality
# Result = nbmatrix object
```

`spatial_statistic-methods`

Methods for Function `spatial_statistic`

Description

Methods for function `spatial_statistic`

Methods

signature(object = "infpan", attribute = "Cases", timepoint = NULL, statistic = "nbstat", func = NULL, row
: Calculation of a specified spatial statistic for the data from an infpan object. The user must choose a specific time point using the timepoint argument. If no time point is stated, the most current time point is chosen automatically.

Author(s)

Thomas Wieland

---

summary-methods *Methods for Function* summary

Description

Methods for function summary

Methods

signature(object = "sbm") Prints a summary of sbm objects (results of the Swash-Backwash Model)

signature(object = "sbm_ci") Prints a summary of sbm_ci objects (bootstrap confidence intervals for Swash-Backwash Model estimates)

signature(object = "countries") Prints a summary of a countries object built with the function compare_countries

signature(object = "loggrowth") Prints a summary of a loggrowth object built with the function logistic_growth

signature(object = "expgrowth") Prints a summary of a expgrowth object built with the function exponential_growth

signature(object = "hawkes") Prints a summary of a hawkes object built with the function hawkes_growth

signature(object = "breaksgrowth") Prints a summary of a breaksgrowth object built with the function breaks_growth

swash *Swash-Backwash Model of the Single Epidemic Wave*

Description

Analysis of regional infection/surveillance data stored in `infpan` object using the Swash-Backwash Model of the Single Epidemic Wave by Cliff and Haggett (2006).

Usage

```
swash(
  object,
  verbose = FALSE
  )
```

Arguments

`object`	object of class `infpan`
`verbose`	`bool` argument which indicates whether progress messages are displayed

Details

The method performs the analysis of the input panel data with N regions and T time points using the Swash-Backwash Model based on an `infpan` object. The output is an object of class `sbm`. The results can be viewed using `summary(sbm)`. The built-in function `swash_backwash` is used for the analysis. See `swash_backwash` for further details.

Value

object of class `sbm-class`

Author(s)

Thomas Wieland

References

Cliff AD, Haggett P (2006) A swash-backwash model of the single epidemic wave. *Journal of Geographical Systems* 8(3), 227-252. doi:10.1007/s1010900600278

Smallman-Raynor MR, Cliff AD, Stickler PJ (2022) Meningococcal Meningitis and Coal Mining in Provincial England: Geographical Perspectives on a Major Epidemic, 1929–33. *Geographical Analysis* 54, 197–216. doi:10.1111/gean.12272

Smallman-Raynor MR, Cliff AD, The COVID-19 Genomics UK (COG-UK) Consortium (2022) Spatial growth rate of emerging SARS-CoV-2 lineages in England, September 2020–December 2021. *Epidemiology and Infection* 150, e145. doi:10.1017/S0950268822001285.

See Also

sbm-class, swash_backwash

Examples

```
data(COVID19Cases_geoRegion)
# Get SWISS COVID19 cases at NUTS 3 level

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[!COVID19Cases_geoRegion$geoRegion %in% c("CH", "CHFL"),]
# Exclude CH = Switzerland total and CHFL = Switzerland and Liechtenstein total

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[COVID19Cases_geoRegion$datum <= "2020-05-31",]
# Extract first COVID-19 wave

infpan_CH <- load_infections_paneldata(
    data = COVID19Cases_geoRegion,
    col_cases = "entries",
    col_date = "datum",
    col_region = "geoRegion",
    other_cols = c("Population" = "pop"),
    verbose = TRUE
  )
# Import as infections panel data set (class infpan)

CH_covidwave1 <-
  swash(
    infpan_CH,
    verbose = TRUE
    )
# Swash-Backwash Model for Swiss COVID19 cases
# Spatial aggregate: NUTS 3 (cantons)

summary(CH_covidwave1)
# Summary of Swash-Backwash Model
```

---

swash-methods *Methods for Function* swash

Description

Methods for function swash

Methods

`signature( object = "infpan", verbose = FALSE)` Performs the analysis of the input panel data with N regions and T time points using the Swash-Backwash Model based on an `infpan` object. The output is an object of class `"sbm"`. The results can be viewed using `summary(sbm)`. See swash_backwash for further details of the model analysis.

Author(s)

Thomas Wieland

`swash_backwash` *Swash-Backwash Model of the Single Epidemic Wave*

Description

Analysis of regional infection/surveillance data using the Swash-Backwash Model of the Single Epidemic Wave by Cliff and Haggett (2006).

Usage

```
swash_backwash(
  infpan = NULL,
  data = NULL,
  col_cases = NULL,
  col_date = NULL,
  col_region = NULL,
  time_format = "%Y-%m-%d",
  verbose = FALSE
  )
```

Arguments

`infpan`	`infpan` object containing regional infection data
`data`	`data.frame` with regional infection data
`col_cases`	Column containing the cases (numeric)
`col_date`	Column containing the time points (e.g., days)
`col_region`	Column containing the unique identifier of the regions (e.g., name, NUTS 3 code)
`time_format`	`character`, Time format of the values in `col_date`
`verbose`	`bool` argument which indicates whether progress messages are displayed

Details

The function performs the analysis of the input panel data with N regions and T time points using the Swash-Backwash Model. The user must state panel data with daily infections.

The Swash-Backwash Model (SBM) for the Single Epidemic Wave is the spatial equivalent of the classic epidemiological SIR (Susceptible-Infected-Recovered) model. It was developed by Cliff and Haggett (2006) to model the velocity of spread of infectious diseases across space. Current applications can be found, for example, in Smallman-Raynor et al. (2022a,b). The function `swash_backwash()` enables the calculation of the Swash-Backwash Model for user-supplied panel data on regional infections. It calculates the model and creates a model object of the `sbm` class defined in this package. This class can be used to visualize results (`summary()`, `plot()`) and calculate

bootstrap confidence intervals for the model estimates (`confint(sbm)`); the latter returns an object of class `sbm_ci` as defined in this package. Two `sbm_ci` objects for different countries may be compared with `compare_countries()`, which allows the estimation of mean differences of a user-specified model parameter (e.g., spatial reproduction number R_{OA}) between two countries. This makes it possible to check whether the spatial spread velocity of a communicable disease is significantly different in one country than in another country; the result is an object of class `countries`.

To calculate the SBM model based on an `infpan` object, use the corresponding method `swash(infpan)`.

Value

object of class `sbm-class`

Author(s)

Thomas Wieland

References

Cliff AD, Haggett P (2006) A swash-backwash model of the single epidemic wave. *Journal of Geographical Systems* 8(3), 227-252. doi:10.1007/s1010900600278

Smallman-Raynor MR, Cliff AD, Stickler PJ (2022) Meningococcal Meningitis and Coal Mining in Provincial England: Geographical Perspectives on a Major Epidemic, 1929–33. *Geographical Analysis* 54, 197–216. doi:10.1111/gean.12272

Smallman-Raynor MR, Cliff AD, The COVID-19 Genomics UK (COG-UK) Consortium (2022) Spatial growth rate of emerging SARS-CoV-2 lineages in England, September 2020–December 2021. *Epidemiology and Infection* 150, e145. doi:10.1017/S0950268822001285.

See Also

`sbm-class`, `swash`

Examples

```
data(COVID19Cases_geoRegion)
# Get SWISS COVID19 cases at NUTS 3 level

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[!COVID19Cases_geoRegion$geoRegion %in% c("CH", "CHFL"),]
# Exclude CH = Switzerland total and CHFL = Switzerland and Liechtenstein total

COVID19Cases_geoRegion <-
  COVID19Cases_geoRegion[COVID19Cases_geoRegion$datum <= "2020-05-31",]
# Extract first COVID-19 wave

CH_covidwave1 <-
  swash_backwash(
    data = COVID19Cases_geoRegion,
    col_cases = "entries",
    col_date = "datum",
    col_region = "geoRegion"
```

```
    )
# Swash-Backwash Model for Swiss COVID19 cases
# Spatial aggregate: NUTS 3 (cantons)

summary(CH_covidwave1)
# Summary of Swash-Backwash Model

plot(CH_covidwave1)
# Plot of Swash-Backwash Model edges and total epidemic curve
```

`timestamps` *Show timestamps*

Description

Print timestamps stored in an object.

Usage

```
timestamps(object)
```

Arguments

`object`	An object with a `timestamp` slot.

Value

Prints formatted timestamps to the console.

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