

Package ‘swash’

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Type Package

Title Swash-Backwash Model for the Single Epidemic Wave

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Description The Swash-Backwash Model for the Single Epidemic Wave was developed by Cliff and Haggett (2006) <[doi:10.1007/s10109-006-0027-8](https://doi.org/10.1007/s10109-006-0027-8)> to model the velocity of spread of infectious diseases across space. This package enables the calculation of the Swash-Backwash Model for user-supplied panel data on regional infections. The package also provides additional functions for bootstrap confidence intervals and data management.

License GPL (>= 2)

Imports methods

NeedsCompilation no

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swash-package	<i>Implementation of the Swash-Backwash Model for the Single Epidemic Wave and additional functions in R</i>
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Description

Swash-Backwash Model for the single epidemic wave (Cliff and Haggett 2006) with additional functions for bootstrap confidence intervals and data management

Details

The Swash-Backwash Model 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). 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()` 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 package also contains additional helper functions.

Author(s)

Thomas Wieland

References*Swash-Backwash Model:*

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 (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

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Basics of epidemiological modeling:

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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

Spatio-temporal analysis and modeling of infectious diseases:

Bourdin S, Jeanne L, Nadou F, Noiret G (2021) Does lockdown work? A spatial analysis of the spread and concentration of Covid-19 in Italy. *Regional Studies*, 55, 1182–1193. doi:10.1080/00343404.2021.1887471

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.8b55f4bad99ac5c5db3663e916803261

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 (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

```
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 (
    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
```

Description

Methods for function confint

Methods

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

COVID19Cases_geoRegion

FOPH 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). Note that the reporting date equals the date of SARS-CoV-2 testing.

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.

Source

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

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
```

Description

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

Usage

```
hist_ci(x, lower, upper, col_bars = "grey", col_ci = "red", ...)
```

Arguments

<code>x</code>	A numeric vector
<code>lower</code>	Lower confidence interval (numeric)
<code>upper</code>	Upper confidence interval (numeric)
<code>col_bars</code>	Color of bars in histogram
<code>col_ci</code>	Color of lines for confidence interval
<code>...</code>	Additional arguments passed to <code>barplot()</code>

Details

Helper function for `plot(sbm_ci)`

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,
  lower = quantile(numeric_vector, probs = 0.025),
  upper = quantile(numeric_vector, probs = 0.975)
)
```

is_balanced	<i>Test whether Panel Data is Balanced</i>
-------------	--

Description

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

Usage

```
is_balanced(  
  data,  
  col_cases,  
  col_date,  
  col_region,  
  balance = FALSE,  
  fill_missing = 0  
)
```

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)
balance	Currently not used
fill_missing	Currently not used

Details

The Swash-Backwash Model for 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, but can also be used separately.

Value

List with two entries:

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

Author(s)

Thomas Wieland

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

```

plot-methods

Methods for Function plot

Description

Methods for function plot

Methods

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

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-methods

Methods for Function print

Description

Methods for function print

Methods

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

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

 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`.

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

`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

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

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
`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

Examples

```
showClass("sbm_ci")
```

show-methods	<i>Methods for Function show</i>
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Description

Methods for function show

Methods

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

summary-methods	<i>Methods for Function summary</i>
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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)

swash	<i>Swash-Backwash Model for the Single Epidemic Wave</i>
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Description

Analysis of regional infection/surveillance data using the Swash-Backwash Model for the single epidemic wave by Cliff and Haggett (2006)

Usage

```
swash(data, col_cases, col_date, col_region)
```

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)

Details

The function performs the analysis of the input panel data using the Swash-Backwash Model. The output is an object of class "sbm". The results can be viewed using `summary(sbm)`.

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`

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 (  
  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
```

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