

# Package: swash (via r-universe)

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**Type** Package

**Title** Swash-Backwash Model for the Single Epidemic Wave

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**Author** Thomas Wieland [aut, cre]

(<https://orcid.org/0000-0001-5168-9846>)

**Maintainer** Thomas Wieland <geowieland@googlemail.com>

**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, country comparison, visualization of results, 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

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.

*Basics of epidemiological modeling:*

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

*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.8b55f4bad99ac5c5db36

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

*Panel data:*

Greene, WH (2012) *Econometric Analysis*. Ch. 11.

Wooldridge, JM (2012) *Introductory Econometrics. A Modern Approach*. Ch. 13.

*Bootstrapping und bootstrap confidence intervals:*

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

## 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

```

---

as_balanced	<i>Correction of Non-balanced Panel Dataset with Regional Infection Data</i>
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---

## 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 = 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)
fill_missing	Constant to fill missing values (default and recommended: 0)

## 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 corrects non-balanced panel data. It is executed automatically within the `swash()` function (when using the function `is_balanced()`), but can also be used separately.

**Value**

data                    Corrected input dataset (data.frame)

**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 (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.

*Panel data:*

Greene, WH (2012) *Econometric Analysis*. Ch. 11.

Wooldridge, JM (2012) *Introductory Econometrics. A Modern Approach*. Ch. 13.

**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

```

---

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 = 100,
  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 $\alpha$ for the 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  $\alpha$ . The `compare_countries()` function calculates the differences of the user's desired indicator between the two samples,  $D$ , and also calculates  $\alpha$  confidence intervals for this.

## Value

object of class `countries`, see [countries-class](#)

## 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 (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.

*Bootstrapping und bootstrap confidence intervals:*

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

## 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 (
    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 (
    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: 100 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

```



## 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  $\alpha$  is set by the argument `alpha` (default: 0.05, which corresponds to a 95% confidence level).

## 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](https://doi.org/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](https://doi.org/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](https://doi.org/10.1017/S0950268822001285).

*Bootstrapping und bootstrap confidence intervals:*

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](https://doi.org/10.1016/B9780128178157.000130)

## 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" classes for each country. Use `summary(countries)` and `plot(countries)` for results summary and plotting, respectively.

### Objects from the Class

Objects can be created by calls of the form `new("countries", ...)`. 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(sbm1)" 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:  $\alpha$  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(sbm_ci)` 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 in ???. 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)

### 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,  
  alpha = 0.05,  
  col_bars = "grey",  
  col_ci = "red",  
  ...  
)
```

**Arguments**

<code>x</code>	A numeric vector
<code>alpha</code>	Significance level $\alpha$ for $1-\alpha*100$ confidence intervals
<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)`, 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)
```

---

is_balanced	<i>Test whether Panel Dataset with Regional Infection 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,
  as_balanced = TRUE,
  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)
as_balanced	Boolean argument which indicates whether non-balanced panel data shall be balanced (default: TRUE)
fill_missing	Constant to fill missing values (default and recommended: 0)

### 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 (using automatic correction with `as_balanced = TRUE`), 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

## 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 (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.

*Panel data:*

Greene, WH (2012) *Econometric Analysis*. Ch. 11.

Wooldridge, JM (2012) *Introductory Econometrics. A Modern Approach*. Ch. 13.

## 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

```

---

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 original 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](https://www.data.gv.at/katalog/dataset/stat_gliederung-osterreichs-in-politische-bezirke131e2) (retrieved 2022-06-27)

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](https://doi.org/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 (
    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

**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  $R_{0A}$

**Author(s)**

Thomas Wieland

---

plot\_regions

*Plots of Regional Infections Over Time*


---

**Description**

Plots regional infection curves in  $N$  plots for  $N$  regions.

**Usage**

```
plot_regions(
  object,
  col = "red",
  scale = FALSE,
  normalize_by_col = NULL,
  normalize_factor = 1
)
```

**Arguments**

object	object of class sbm
col	Color of line plot
scale	Set y axis of the plots uniformly based on the maximum value across all regions? (boolean, default: FALSE)
normalize_by_col	Normalize infection numbers by stating a column in the input data frame (e.g., regional population)
normalize_factor	Multiply density/incidence with a factor (say, 100,000 inhabitants)

**Details**

Plots regional infection curves in  $N$  plots for  $N$  regions, with the number of columns equals 4 and the number of rows is calculated based the size of  $N$ .

**Value**

Plot, only no returned value

**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

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)  
  
plot_regions(CH_covidwave1)  
# Plot of regional infections
```

---

plot\_regions-methods    *Methods for Function plot\_regions*

---

### Description

Methods for function plot\_regions

### Methods

signature(object = "sbm", col = "red", scale = FALSE, normalize\_by\_col = NULL, normalize\_factor = 1)  
Plots regional infection curves in  $N$  plots for  $N$  regions, with the number of columns equals 4 and the number of rows is calculated based the size of  $N$ . Set the color by the argument col. If scale is TRUE, the y axis of the plots is set uniformly based on the maximum value across all regions. If the input data contains a column to normalize the infection numbers (such as regional population), the user may use this data to normalize the infection numbers by setting normalize\_by\_col. If this density value should be multiplied by a factor (e.g. regional infections per 100,000 inhabitants), this can be set with the argument normalize\_by\_col (default: 1).

### Author(s)

Thomas Wieland

---

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

---

`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**

<code>x</code>	A numeric vector
<code>alpha</code>	Significance level $\alpha$ for $1-\alpha*100$ 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)
```

---

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  
`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

### 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

*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 (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.

*Bootstrapping und bootstrap confidence intervals:*

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

## Examples

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

---

show-methods

*Methods for Function show*

---

## 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>
-----------------	-------------------------------------

---

**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](#)

---

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

---

**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**

<code>data</code>	data.frame with regional infection data
<code>col_cases</code>	Column containing the cases (numeric)
<code>col_date</code>	Column containing the time points (e.g., days)
<code>col_region</code>	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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