Package 'outbreaks'

October 14, 2022

Title A Collection of Disease Outbreak Data

Version 1.9.0

Description Empirical or simulated disease outbreak data, provided either as
RData or as text files.

Depends R (>= 3.0.0)

License GPL (>= 2)

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

Suggests testthat, covr, ape, incidence

URL https://github.com/reconhub/outbreaks

BugReports https://github.com/reconhub/outbreaks/issues

NeedsCompilation no

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Repository CRAN

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R topics documented:

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covid19_england_nhscalls_2020

Potential COVID19 cases reported through NHS pathways

Description

This dataset contains daily numbers of reports on potential COVID-19 cases reported in England through the NHS 111 calls, 999 calls, and 111-online systems. The present dataset was last updated on 21 September 2020. See example for a command line allowing to download the latest version.

Usage

```
covid19_england_nhscalls_2020
```

Format

A 'data.frame' containing:

site_type the system through which data were reported: 111/999 calls, or 111-online

date the data of reporting

sex the gender of the patient

age the age of the patient, in years

ccg_code NHS code for the Clinical Commissioning Groups (CCGs) (finer geographic unit)

ccg_name name of the Clinical Commissioning Groups (CCGs) (smaller spatial unit)

count number of potential COVID-19 cases reported

postcode the postcode of the CCG

nhs_region the NHS region (larger geographic unit)

day the date as the number of days since the first reporting day

weekday the day of the week, broken down into: weekend, Monday, and the rest of the week; this is used for modelling reporting effects

Author(s)

National Health Services (NHS) for England. Additional data and cleaning by Quentin Leclerc.

Source

Data is available at https://digital.nhs.uk/dashboards/nhs-pathways; this precise dataset adds some cleaning and additional informaion (on NHS regions) and is taken from Quentin Leclerc's github repository: https://github.com/qleclerc/nhs_pathways_report

Examples

```
## Not run:
# These commands will download the latest version of the data:
library(tidyverse)

# download data
pathways <- tempfile()
url <- paste0("https://github.com/qleclerc/nhs_pathways_report/",
              "raw/master/data/rds/pathways_latest.rds")
download.file(url, pathways)
pathways <- readRDS(pathways)
head(pathways)


## End(Not run)
```

---

dengue_fais_2011 *Dengue on the island of Fais, Micronesia, 2011*

Description

These data describe incidence of clincal cases of Dengue on the island of Fais, Micronesia.

Usage

```
dengue_fais_2011
```

Format

A data frame with 57 rows and 3 columns

onset_date Date

nr Days after starting date

value Number of cases

The data on Dengue incidence reported by Funk et al. (2016) cover the period from 2011-09-15 to 2012-02-14, over which time a total of 157 clinical cases were reported among 294 residents. The first reported case is thought to be the index case. The population of Fais is concentrated in a single population centre, and is thought to have been immunologically naive at the time of infection.

Author(s)

Data from Funk et al. (2016), provided by Sebastian Funk (github.com/sbnfunk). Transfer to R and documentation by Finlay Campbell (<finlaycampbell93@gmail.com>).

Source

Funk et al. (2016)

References

S. Funk, et al. 2016. Comparative Analysis of Dengue and Zika Outbreaks Reveals Differences by Setting and Virus. PLOS Neglected Tropical Diseases, 10(12), e0005173. http://doi.org/10.1371/journal.pntd.0005173

Examples

```
## show first few weeks of Dengue incidence
head(dengue_fais_2011)
```

---

dengue_yap_2011   *Dengue on the Yap Main Islands, Micronesia, 2011*

Description

These data describe incidence of clincal cases of Dengue on the Yap Main Islands, Micronesia.

Usage

```
dengue_yap_2011
```

Format

A data frame with 185 rows and 3 columns

onset_date Date

nr Days after starting date

value Number of cases

The data on Dengue incidence reported by Funk et al. (2016) cover the period from 2011-07-07 to 2012-04-12, over which time a total of 978 cases were reported among 7391 residents. Suspected Dengue cases were identified by the Yap Department of Health, using the WHO (2009) case definition. A small proportion of cases (9 time series for the Yap Main Islands. Dengue virus serotype 2 was confirmed by reverse transcriptase polymerase chain reaction by the CDC Dengue Branch, Puerto Rico.

Author(s)

Data from Funk et al. (2016), provided by Sebastian Funk (github.com/sbnfunk). Transfer to R and documentation by Finlay Campbell (<finlaycampbell93@gmail.com>).

Source

Funk et al. (2016)

References

S. Funk, et al. 2016. Comparative Analysis of Dengue and Zika Outbreaks Reveals Differences by Setting and Virus. PLOS Neglected Tropical Diseases, 10(12), e0005173. http://doi.org/10.1371/journal.pntd.0005173

Examples

```
## show first few weeks of Dengue incidence
head(dengue_yap_2011)
```

---

ebola_kikwit_1995　　　　　*Ebola in Kikwit, Democratic Republic of the Congo, 1995*

Description

These data comprise of new cases of Ebola haemorrhagic fever in Kikwit, Democratic Republic of the Congo.

Usage

```
ebola_kikwit_1995
```

Format

A data frame with 192 rows and 4 columns

date Date

onset Number of new cases

deaths Number of deaths per day

reporting Whether data were reported on a daily basis

The data on daily cases reported by Khan et al. (1999) cover the period 1995-03-01 to 1995-07-16, over which time there were 291 cases and 236 deaths. The first case became ill on 1995-01-06, which is taken as the first timepoint in this version of the data. Over the entire period, there were 316 cases i.e. the onset times are not reported for 24 individuals, and the recovery times for the individuals who did not die are not reported.

Author(s)

Data from Khan et al. (1999), provided by T.J. McKinley. Transfer to R and documentation by Simon Frost (<sdwfrost@gmail.com>).

Source

Khan et al. (1999)

References

A.S. Khan, et al. 1999. The reemergence of Ebola hemorrhagic fever, Democratic Republic of the Congo, 1995. J Infect Dis 179:S76-S86.

Examples

```
## show first few cases
head(ebola_kikwit_1995)
```

---

ebola_sierraleone_2014

Ebola in Sierra Leone, 2014

Description

These data consist of confirmed and suspected cases of Ebola haemorrhagic fever in Sierra Leone from 2014 to 2015.

Usage

```
ebola_sierraleone_2014
```

Format

A data frame with 11,903 rows and 8 columns

id Case ID

age Age

sex Sex

status Case definition (confirmed or suspected)

date_of_onset Date of symptom onset

date_of_sample Date of sample testing

district District

chiefdom Chiefdom

The linelist data reported by Fang et al. (2016) cover the period 2014-05-18 to 2015-09-13, over which time there were 8538 confirmed cases and 3545 suspected cases.

Author(s)

Data from Fang et al. (2016) Transfer to R and documentation by Finlay Campbell (<finlaycampbell93@gmail.com>).

Source

Fang et al. (2016)

References

L. Fang, et al. 2016. Ebola virus disease in Sierra Leone. Proceedings of the National Academy of Sciences, 113 (16) 4488-4493; DOI: 10.1073/pnas.1518587113

Examples

```
## show first few cases
head(ebola_sierraleone_2014)
```

---

ebola_sim   *Simulated Ebola outbreak*

Description

This simulated outbreak of Ebola Virus Disease matches some key properties of the West African Ebola outbreak of 2014-2015. Specifically, care was taken to use realistic delays (incubation period, serial interval, time to hospitalisation, etc.) and reproduction number (see references).

Usage

```
ebola_sim
```

```
ebola_sim_clean
```

Format

An object of class list of length 2.

An object of class list of length 2.

Details

This dataset is used for teaching purposes during Imperial College's short course on infectious disease modelling. The exercise aims to simulate the response to an Ebola outbreak taking place in a single large city, and evaluate the impact of an intervention (increased bed capacity).

Note that to ensure realism, some errors have been introduced in this dataset. These can be identified as negative incubation periods (delay from infection to onset of symptoms). See example for a simple way to identify these cases. The dataset ebola_sim_clean is the same dataset, only dates of infection and onset have been set to 'NA'.

Author(s)

Data simulated by Pierre Nouvellet (<p.nouvellet@imperial.ac.uk>). Transfer to R and documentation by Thibaut Jombart (<thibautjombart@gmail.com>).

References

WHO Ebola Response Team. 2014. Ebola virus disease in West Africa–the first 9 months of the epidemic and forward projections. The New England journal of medicine 371:1481–1495.

WHO Ebola Response Team, J. Agua-Agum, A. Ariyarajah, B. Aylward, I. M. Blake, R. Brennan, A. Cori, C. A. Donnelly, I. Dorigatti, C. Dye, T. Eckmanns, N. M. Ferguson, P. Formenty, C. Fraser, E. Garcia, T. Garske, W. Hinsley, D. Holmes, S. Hugonnet, S. Iyengar, T. Jombart, R. Krishnan, S. Meijers, H. L. Mills, Y. Mohamed, G. Nedjati-Gilani, E. Newton, P. Nouvellet, L. Pelletier, D. Perkins, S. Riley, M. Sagrado, J. Schnitzler, D. Schumacher, A. Shah, M. D. Van Kerkhove, O. Varsaneux, and N. Wijekoon Kannangarage. 2015. West African Ebola epidemic after one year–slowing but not yet under control. The New England journal of medicine 372:584–587.

Examples

```
## identify mistakes in data entry (negative incubation period)
mistakes <- which(ebola_sim$linelist$date_of_onset <= ebola_sim$linelist$date_of_infection)
mistakes
ebola_sim$linelist[mistakes, ]

## check that ebola_sim_clean is identical after removing mistakes
identical(ebola_sim_clean$linelist, ebola_sim$linelist[-mistakes, ])
```

fluH7N9_china_2013	*Influenza A H7N9 in China, 2013*

Description

These data comprise of 136 cases of influenza A H7N9 in China, analysed by Kucharski et al. (2014).

Usage

```
fluH7N9_china_2013
```

Format

A data frame with 136 rows and 8 columns

Author(s)

Data collated by Adam Kucharski et al. from ProMed, WHO, FluTrackers, news reports and research articles. Transfer to R and documentation by Simon Frost (<sdwfrost@gmail.com>).

Source

https://datadryad.org/stash/dataset/doi:10.5061/dryad.2g43n

References

A. Kucharski, H. Mills, A. Pinsent, C. Fraser, M. Van Kerkhove, C. A. Donnelly, and S. Riley. 2014. Distinguishing between reservoir exposure and human-to-human transmission for emerging pathogens using case onset data. PLOS Currents Outbreaks. Mar 7, edition 1. doi: 10.1371/currents.outbreaks.e1473d9bfc99d080ca242139a06c455f.

A. Kucharski, H. Mills, A. Pinsent, C. Fraser, M. Van Kerkhove, C. A. Donnelly, and S. Riley. 2014. Data from: Distinguishing between reservoir exposure and human-to-human transmission for emerging pathogens using case onset data. Dryad Digital Repository. http://dx.doi.org/10.5061/dryad.2g43n.

Examples

```
## show first few cases
head(fluH7N9_china_2013)
```

---

influenza_england_1978_school

Influenza in a boarding school in England, 1978

Description

These data comprise of a time series of influenza cases in a boarding school in England. The original data were available only in a figure with some additional data in the main text; hence, the exact numbers vary depending on the source. These data are from Chapter 9 of De Vries et al. (1996).

Usage

```
influenza_england_1978_school
```

Format

A data frame with 14 rows and 3 columns

date Date

in_bed Number in bed

convalescent Number convalescing

Details

The index case was infected by 1978-01-10, and had febrile illness from 1978-01-15 to 1978-01-18. 512 boys out of 763 became ill.

Author(s)

Data from De Vries et al. (2006), from the original Anonymous (1978) figure. Transfer to R and documentation by Simon Frost (<sdwfrost@gmail.com>).

Source

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1603269/pdf/brmedj00115-0064.pdf>

References

Anonymous. 1978. Influenza in a boarding school. British Medical Journal 1:578.

G. De Vries, T. Hillen, M. Lewis, J. Mueller, and B. Schoenfisch. 2006. A Course in Mathematical Biology: Quantitative Modeling with Mathematical and Computational Methods. Society for Industrial and Applied Mathematics.

Examples

```
## show first few cases
head(influenza_england_1978_school)
```

---

measles_hagelloch_1861

Measles in Hagelloch, Germany, 1861

Description

These data comprise of 188 cases of measles among children in the German city of Hagelloch, 1861. The data were originally collected by Dr. Albert Pfeilsticker (1863) and augmented and re-analysed by Dr. Heike Oesterle (1992).

Usage

measles_hagelloch_1861

Format

A data frame with 188 rows and 12 columns

case_ID Case ID number

infector Number of patient who is the putative source of infection

date_of_prodrome Date of onset of prodromal symptoms

date_of_rash Date of onset of rash

date_of_death Date of death (NA implies recovered)

age Age in years (fractions ignored)

gender Gender of the individual (factor: f, m)

family_ID Family ID number

class School class (factor: 0, preschool; 1, 1st class; 2, 2nd class)

complications Complications (factor: no, yes)

x_loc x coordinate of house (in metres). Scaling in metres is obtained by multiplying the original coordinates by 2.5 (see details in Neal and Roberts (2004))

y_loc y coordinate of house (in metres). See x_loc above.

Author(s)

This version of the data was formatted from hagelloch.df in the surveillance package, which in turn was provided by Niels Becker via Peter Neal. Formatting to fit in with the other datasets in the outbreaks package by Simon Frost (<sdwfrost@gmail.com>).

Source

Pfeilsticker (1863) and Oesterle (1992).

References

Pfeilsticker, A. 1863. Beiträge zur Pathologie der Masern mit besonderer Berücksichtigung der statistischen Verhältnisse, M.D. Thesis, Eberhard-Karls-Universität Tübingen. Available as `http://www.archive.org/details/beitrgezurpatho00pfeigoog`.

Oesterle, H. 1992. Statistische Reanalyse einer Masernepidemie 1861 in Hagelloch, M.D. Thesis, Eberhard-Karls-Universitäat Tübingen.

Neal, P. J. and Roberts, G. O. 2004. Statistical inference and model selection for the 1861 Hagelloch measles epidemic, Biostatistics 5(2):249-261.

Höhle M. 2007. surveillance: An R package for the monitoring of infectious diseases. Computational Statistics, 22:571-582.

Meyer, S., Held, L., & Höhle, M. 2017. Spatio-Temporal Analysis of Epidemic Phenomena Using the R Package surveillance. Journal of Statistical Software, 77(11), 1 - 55.

Examples

```
## show first few cases
head(measles_hagelloch_1861)
```

---

mers_korea_2015	*Middle East respiratory syndrome in South Korea, 2015*

Description

These datasets correspond to the initial information collected by the Epidemic Intelligence group at European Centre for Disease Prevention and Control (ECDC) during the first weeks of the outbreak of Middle East respiratory syndrome (MERS-CoV) outbreak (South Korea) in 2015. The data were used to follow the daily evolution of this outbreak using public information available.

Usage

```
mers_korea_2015
```

Format

A list of two dataframes:

`$linelist`: A dataframe of MERS-CoV cases and their attributes

- id: Unique identifier
- age: Age
- age_class: Age using 10-year groups
- sex: Sex
- place_infect: Probable region of infection
- reporting_ctry: Country reporting the case

- loc_hosp: Local hospital name where the case was hospitalized
- dt_onset: Date of onset of symptoms
- dt_report: Date of reporting
- week_report: Week number of date of reporting
- dt_start_exp: Date of first probable exposure to another MERS Co-V case
- dt_end_exp: Date of last probable exposure to another MERS Co-V case
- dt_diag: Date of MERS Co-V diagnosis
- outcome: Outcome (alive or dead)
- dt_death: Date of death

$contacts: A dataframe describing the relationship between MERS Co-V cases

- from: Unique identifier of the probably source patient
- to: Unique identifier of the secondary case
- exposure: Probable place of exposure
- diff_dt_onset: Time in days between two successive cases

Details

This dataset is meant for teaching purposes; it represents neither the final outbreak investigation results nor a consolidated and complete description of the transmission chain.

Author(s)

Data collected by the European Centre for Disease Prevention and Control (Epidemic Intelligence and Response section, contact: Bertrand Sudre (< bertrand.sudre@ecdc.europa.eu>) and Kaja Kaasik Aaslav(<Kaja.KaasikAaslav@ecdc.europa.eu>). Transfer to R and documentation by Bertrand Sudre (< bertrand.sudre@ecdc.europa.eu>).

References

More information on the intial stage of the outbreak in the following reference: Penttinen PM, Kaasik-Aaslav K, Friaux A, Donachie A, Sudre B, Amato-Gauci AJ, Memish ZA, Coulombier D. Taking stock of the first 133 MERS coronavirus cases globally–Is the epidemic changing? Euro Surveill. 2013 Sep 26;18(39). pii: 20596. PubMed PMID: 24094061.

Examples

```
## show the line list describing MERS Co-V cases and their attributes
head(mers_korea_2015$linelist)

## show the relationships between MERS Co-V cases
head(mers_korea_2015$contacts)
```

---

nipah_malaysia   *Nipah in Malaysia and Sinagapore, 1997-1999*

Description

These data describe incidence of human cases of Nipah virus encephalitis in Malaysia and Singapore from January 1997 through April 1999.

Usage

```
nipah_malaysia
```

Format

A data frame with 49 rows and 5 columns

date Onset date (weekly)

perak Number of cases (Perak State, Malaysia)

negeri_sembilan Number of cases (Negeri Sembilan State, Malaysia)

selangor Number of cases (Selangor State, Malaysia)

singapore Number of cases (Singapore)

Nipah virus is a paramyxovirus that occurs in flying fox (fruit bat) populations throughout Asia. The data provided are from the first known emergence of Nipah virus into humans. During this outbreak, the virus was transmitted from bats to pigs, where it circulated in commercial pig farms, infecting mostly farm and abbatoir workers. The outbreak started in Perak State, later spreading to Negeri Sembilan and Seleangor through sale of infected pigs. There were also 11 cases reported among abbatoir workers in Singapor. The data, as published in Pulliam _et al_. (2011), include all 257 clinical cases recorded in humans from 1997-01-11 to 1999-04-14, when the outbreak ended following large-scale depopulation of pig farms. Human cases represent zoonotic infections, with little or no human-to-human transmission. Thus, the epidemic curve reflects transmission and spatial spread within pigs.

Author(s)

Data from Funk et al. (2016), provided by Juliet Pulliam (github.com/jrcpulliam).

Source

Pulliam et al. (2011)

References

J.R.C. Pulliam, et al. 2011. Agricultural intensification, priming for persistence and the emergence of Nipah virus: a lethal bat-borne zoonosis. _Journal of the Royal Society Interface_, 9(66), 20110223. https://doi.org/10.1098/rsif.2011.0223

Examples

```
## show first few weeks of Dengue incidence
head(nipah_malaysia)

## convert data to incidence object and plot epicurve using the incidence package
library(incidence)
cases <- subset(nipah_malaysia, select = c("perak", "negeri_sembilan", "selangor",
 "singapore"))
i <- as.incidence(cases, dates = nipah_malaysia$date, interval = 7L)
plot(i)
```

---

norovirus_derbyshire_2001_school

Norovirus in a primary school in Derbyshire, England, 2001

Description

These data describe an outbreak of norovirus in the summer of 2001 in a primary school and nursery in Derbyshire, England.

Usage

```
norovirus_derbyshire_2001_school
```

Format

A data frame with 492 rows and 5 columns

class School class of the child

day_absent First day of absence from school

start_illness First day of illness

end_illness Last day of illnes

day_vomiting Day of vomiting in school

The data on norovirus cases were analysed by O'Neill and Marks (2005). As described in the paper, out of a total of 492 children in the school, 186 were absent from school with gastrointestinal symptoms. The school was cleaned on days 13 and 14, and on days 20 and 21, both of which were weekends, and the school was shut on days 18 and 19. Following the second cleaning, there were no further absences, although three children reported symptoms on day 22, the last day of the outbreak.

Author(s)

Data from O'Neill and Marks (2005), provided by Philip O'Neill. Transfer to R and documentation by Simon Frost (<sdwfrost@gmail.com> and Finlay Campbell (<finlaycampbell93@gmail.com>)).

Source

O'Neill and Marks (2005)

References

O'Neill, P. D., & Marks, P. J. (2005). Bayesian model choice and infection route modelling in an outbreak of Norovirus. Statistics in Medicine, 24(13), 2011–24.

Examples

```
## show first few cases
head(norovirus_derbyshire_2001_school)
```

---

rabies_car_2003   *Dog Rabies in Central African Republic, 2003-2012*

Description

These data document a dog rabies epidemic from 2003 to 2012 in Bangui, Central African Republic, and its surroundings. Data comprise dates and locations of the cases, as well as viral sequences of the pathogen for most cases.

Usage

```
rabies_car_2003
```

Format

A list comprising a data.frame ($linelist) and a DNAbin matrix ($dna). $linelist contains the following variables:

- $index: numeric identifier of the case
- $date: date of case reporting
- $latitude: the latitude of the collection point
- $longitude: the longitude of the collection point
- $has_dna: a logical indicating of the case has a matching pathogen sequence in $dna

$dna is a DNAbin matrix whose labels are to be matched against $linelist$index.

Author(s)

Data from Transfer to R and documentation by Thibaut Jombart.

Source

The data were provided by the Institut Pasteur de Bangui, Bangui, République Centrafricaine, and the Institut Pasteur, Unit Lyssavirus Dynamics and Host Adaptation, WHO Collaborating Centre for Reference and Research on Rabies, Paris, France.

References

Cori et al. (submitted) A graph-based evidence synthesis approach to detecting outbreak clusters: an application to dog rabies.

Examples

```
if (require(incidence) && require(ape)) {
  i <- incidence(rabies_car_2003$linelist$date, 28L)
  plot(i)

  tre <- nj(dist.dna(rabies_car_2003$dna))
  plot(tre, main = "Neighbour-Joining tree")

}
```

---

sarscov2_who_2019	*SARS-CoV-2 World Health Organization Situation Reports 2019 Outbreak (COVID-19)*

Description

These data are transcribed from the WHO Situation Reports on the COVID-19 outbreak (SARS-CoV-2). Data was not available for all variables in all reports. For full details, see the original Situation Reports as published by WHO. Data were manually transcribed and errors are possible.

Usage

```
sarscov2_who_2019
```

Format

A data frame where each row represents a new Situation Report

Author(s)

Data from World Health Organization (WHO), published as Sitation Reports. Transfer to R and documentation by Eric Brown.

Source

World Health Organization (2020)

References

World Health Organization. 2020. <https://www.who.int/emergencies/diseases/novel-coronavirus-2019/situation-reports>

Examples

```
## show global cases
sarscov2_who_2019$cases_global
```

---

sars_canada_2003   *Severe Acute Respiratory Syndrome in Canada, 2003*

Description

These data comprise of new cases of SARS in Canada in 2003. These data are from Chapter 9 of De Vries et al. (1996).

Usage

```
sars_canada_2003
```

Format

A data frame with 110 rows and 5 columns

date Date

cases_travel New cases attributed to travel

cases_household New cases attributed to household transmission

cases_healthcare New cases in a healthcare setting

cases_other Other new cases

Author(s)

Data from De Vries et al. (2006), based on original data from Health Canada. Transfer to R and documentation by Simon Frost (<sdwfrost@gmail.com>).

Source

De Vries et al. (2006)

References

G. De Vries, T. Hillen, M. Lewis, J. Mueller, and B. Schoenfisch. 2006. A Course in Mathematical Biology: Quantitative Modeling with Mathematical and Computational Methods. Society for Industrial and Applied Mathematics.

Examples

```
## show first few cases
head(sars_canada_2003)
```

```
smallpox_abakaliki_1967
```
Smallpox in Abakaliki, Nigeria, 1967

Description

These data comprise of 32 cases of smallpox in Abakaliki, Nigeria in 1967, first described by Thompson and Foege (1968), which occurred predominantly in a religious group that refused medical interventions.

Usage

```
smallpox_abakaliki_1967
```

Format

A data frame with 32 rows and 8 columns

case_ID Case identification number

date_of_onset Date of onset of symptoms

age Age in years

gender Gender: female (f) or male (m) (factor)

vaccinated Previously vaccinated: no (n) or yes (y) (factor)

vaccscar Vaccination scar present: no (n) or yes (y) (factor)

ftc Member of the Faith Tabernacle: no (n) or yes (y) (factor)

compound Compound number (factor)

Author(s)

Data from Thompson and Foege (1968). Transfer to R and documentation by Simon Frost (<sdwfrost@gmail.com>).

Source

http://apps.who.int/iris/bitstream/10665/67462/1/WHO_SE_68.3.pdf

References

D. Thompson and W. Foege. 1968. Faith Tabernacle smallpox epidemic. Abakaliki, Nigeria. World Health Organization, 3:1–9

Examples

```
## show first few cases
head(smallpox_abakaliki_1967)
```

---

s_enteritidis_pt59   *Salmonella Enteritidis PT59 outbreak*

Description

This dataset covers a food-borne outbreak of Salmonella Enteritidis PT59 investigated by Public Health England. The data includes a distribution network, and genetic clusters of bacteria isolated in contaminated patients. The data is anonymised: identifiers of the food distribution network have been hashed. The object s_enteritidis_pt59 is a list containing:

Usage

```
s_enteritidis_pt59
```

Format

An object of class list of length 2.

Details

- $graph: a data.frame containing with two columns from and to specifying (directed) edges of the food distribution network, alongside reported cases (terminal branches, or 'tips').

- $cluster: a factor indicating the genetic cluster of named tips.

Author(s)

Thomas Inns <Thomas.Inns@phe.gov.uk>, Philip Ashton, Tim Dallman, Roberto Vivancos. Hashing and port to R by Thibaut Jombart.

Source

Multi-agency Salmonella Enteritidis PT59 Outbreak Control Team, chaired by Public Health England

---

varicella_sim_berlin   *Simulated Varicella outbreak*

Description

Simulated Varicella outbreak

Usage

```
varicella_sim_berlin
```

Format

A data frame with 500 rows and 13 columns

sex The gender of the simulated persons

ethnicity Simulated ethnical origin

firstname First names of the simulated persons

lastname Last names of the simulated persons

age Age of the simulated persons

center1 Name of the first center where the simulated persons stay

arrival1 Date of arrival at the first center

leave1 Date of departure at the first center

center2 Name of the second center where the simulated persons stay

arrival2 Date of arrival at the second center

leave2 Date of departure at the second center

onset Date of onset of the disease

disease Name of the disease

Background

This dataset is useful to compute incidence rates.

This dataset simulates an outbreak of varicella in german centers for foreigners. It is loosely based on the situation in 2015, when the numbers of foreigners seeking asylum exeded the available places in the center for foreigners. Varicella was the most frequent disease in these centers at that time. comparable with kindergartens and other shelters.

Description of infectious diseases in people seeking asylum in Germany in 2017 of Robert Koch-Institute, Berlin, Germany: https://www.rki.de/DE/Content/Gesundheitsmonitoring/Gesundheitsberichterstattung/GesundAZ

The dataset was created by the package outbreakcreator https://github.com/jakobschumacher/outbreakcreator/.

Author(s)

Data simulated by Jakob Schumacher (<jakob.schumacher@web.de>).

Examples

```
head(varicella_sim_berlin)
```

---

zika_girardot_2015   *Zika in Girardot, Colombia, 2015*

Description

These data describe the daily incidence of Zika virus disease in Girardot, Colombia.

Usage

```
zika_girardot_2015
```

Format

A data frame with 93 rows and 2 columns

date Date

cases Daily incidence

The data on Zika virus disease incidence reported by Rojas et al. (2016) cover the period from October 2015 to January 2016, over which time a total of 1936 cases were reported to health authorities of Girardot (population of 102,225). Suspected cases were confirmed by reverse transcription-polymerase chain reaction (RT-PCR) in the serum of acute cases within five days of symptom onset.

Author(s)

Data from Rojas et al. (2016), provided by Diana P. Rojas (<dprojas@epi.ufl.edu>). Transfer to R and documentation by Finlay Campbell (<finlaycampbell93@gmail.com>).

Source

Rojas et al. (2016)

References

Rojas, D. P., Dean, N. E., Yang, Y., Kenah, E., Quintero, J., Tomasi, S., ... Eyrolle-Guignot, D. (2016). The epidemiology and transmissibility of Zika virus in Girardot and San Andres island, Colombia, September 2015 to January 2016. Eurosurveillance, 21(28), 30283. https://doi.org/10.2807/1560-7917.ES.2016.21.28.30283

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Examples

```
## show first few days of Zika incidence
head(zika_girardot_2015)
```

---

zika_sanandres_2015   *Zika in San Andres, Colombia, 2015*

Description

These data describe the daily incidence of Zika virus disease in San Andres, Colombia.

Usage

```
zika_sanandres_2015
```

Format

A data frame with 101 rows and 2 columns

date Date

cases Daily incidence

The data on Zika virus disease incidence reported by Rojas et al. (2016) cover the period from September 2015 to January 2016, over which time a total of 928 cases were reported to health authorities of San Andres (population of 54,513). Suspected cases were confirmed by reverse transcription-polymerase chain reaction (RT-PCR) in the serum of acute cases within five days of symptom onset.

Author(s)

Data from Rojas et al. (2016), provided by Diana P. Rojas (<dprojas@epi.ufl.edu>). Transfer to R and documentation by Finlay Campbell (<finlaycampbell93@gmail.com>).

Source

Rojas et al. (2016)

References

Rojas, D. P., Dean, N. E., Yang, Y., Kenah, E., Quintero, J., Tomasi, S., ... Eyrolle-Guignot, D. (2016). The epidemiology and transmissibility of Zika virus in Girardot and San Andres island, Colombia, September 2015 to January 2016. Eurosurveillance, 21(28), 30283. http://doi.org/10.2807/1560-7917.ES.2016.21.28.30283

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Examples

```
## show first few days of Zika incidence
head(zika_sanandres_2015)
```

---

zika_yap_2007   *Zika on the Yap Main Islands, Micronesia, 2007*

Description

These data describe weekly incidence of probable and confirmed cases of Zika virus on the Yap
Main Islands, Micronesia.

Usage

```
zika_yap_2007
```

Format

A data frame with 29 rows and 3 columns

onset_date Date

nr Days after starting date

value Number of cases per week

The data on weekly cases reported by Funk et al. (2016) cover the period from 2007-02-18 to 2007-
09-02, over which time there were a total of 108 cases classified as probable (59) or confirmed (49)
in a population of 7391. Cases were identified by a combination of prospective and retrospective
surveillance at all health centres on Yap.

Author(s)

Data from Funk et al. (2016), provided by Sebastian Funk (github.com/sbnfunk). Transfer to R and
documentation by Finlay Campbell (<finlaycampbell93@gmail.com>).

Source

Funk et al. (2016)

References

S. Funk, et al. 2016. Comparative Analysis of Dengue and Zika Outbreaks Reveals Differences by
Setting and Virus. PLOS Neglected Tropical Diseases, 10(12), e0005173. http://doi.org/10.1371/journal.pntd.0005173

Examples

```
## show first few weeks of Zika incidence
head(zika_yap_2007)
```

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