

Package: nccovid (via r-universe)

August 23, 2024

Title Pull North Carolina Covid-19 Outbreak Information

Version 0.0.21

Description This package allows users to easily retrieve data that have been pulled from the North Carolina Department of Health and Human Services Covid-19 Dashboard.

License MIT + file LICENSE

BugReports <https://github.com/conedatascience/nccovid/issues>

URL <https://github.com/conedatascience/nccovid>,
<https://conedatascience.github.io/nccovid/>

Encoding UTF-8

LazyData true

RoxygenNote 7.1.2.9000

Depends R (>= 2.10)

Imports data.table, dplyr, stringr, tidyr, tigris, magrittr, ggplot2, scales

Suggests testthat (>= 3.0.0), entropy, broom, purrr

Config/testthat/edition 3

Repository <https://medewitt.r-universe.dev>

RemoteUrl <https://github.com/conedatascience/nccovid>

RemoteRef HEAD

RemoteSha eb5257a7a6d746c9832f79481fe2b35a3da8a7e8

Contents

aerosol_concentration	3
aerosol_emission	3
calculate_community_immunity	4
calculate_shannon	5
calculate_transmission_increase	6

calc_risk	6
cone_region	7
covid_mortality_data	7
decrease_cases	8
effective_ve_wane	8
epi_convolve	9
epi_finalsize	9
generate_vax_coverage_age	10
get_cdc_detail	10
get_cdc_vax	11
get_county_covid_demographics	11
get_county_tests	12
get_covid_county_plus	12
get_covid_demographics	13
get_covid_state	13
get_covid_zip	14
get_google_mobility	15
get_google_mobility2	15
get_hospitalizations	16
get_vaccinations	16
get_vaccinations_demo	17
hit	17
increase_cases	18
infection_probability	18
italy_rates	19
lambertW	19
nc_county_demos	20
nc_county_fips	20
nc_delay	21
nc_events	21
nc_fatality_estimates	22
nc_hc_coalitions	22
nc_population	23
nc_pop_age	23
nc_pop_dhhs	24
nc_svi_county	24
pull_covid_summary	25
pull_estimates	25
pull_hospitalization_demos	26
pull_vaccine_census	27
pull_wastewater	27
r2R	28
rna_content	29
triad_counties	29

aerosol_concentration *Aerosol Concentration*

Description

Estimate the aerosol concentration given environment parameters

Usage

```
aerosol_concentration(  
  room_area = 60,  
  room_height = 3,  
  emission_breathing = 0.06,  
  emission_speaking = 0.6,  
  speaking_ratio = 0.1,  
  resp_rate = 10  
)
```

Arguments

room_area	a double, meters squared
room_height	a double, meters
emission_breathing	a double, emission while breathing cm ³
emission_speaking	a double, emission while speaking cm ³
speaking_ratio	a double, between 0 and 1 for ratio between speaking and breathing
resp_rate	a double, the respiratory rate in liters per minute

aerosol_emission *Aerosol Emission per Hour*

Description

Estimate the aerosol emission rate per hours

Usage

```
aerosol_emission(  
  emission_breathing = 0.06,  
  emission_speaking = 0.6,  
  speaking_ratio = 0.1,  
  resp_rate = 10  
)
```

Arguments

emission_breathing
a double, emission while breathing cm^3

emission_speaking
a double, emission while speaking cm^3

speaking_ratio a double, between 0 and 1 for ratio between speaking and breathing

resp_rate a double, the respiratory rate in liters per minute

calculate_community_immunity

Calculating Community Immunity

Description

Considering Proportion of the Vaccinated and Those Who Were Infected

Usage

```
calculate_community_immunity(prop_infected, prop_vaccinated)
```

Arguments

prop_infected a numeric representing the proportion of the population with natural infection

prop_vaccinated
a numeric representing the proportion of the population that is vaccinated.

Source

Lopman, B. A. et al. A framework for monitoring population immunity to SARS-CoV-2. *Annals of Epidemiology* S1047279721002635 (2021) doi:10.1016/j.annepidem.2021.08.013.

Examples

```
{  
  
calculate_community_immunity(.3,.5)  
  
plot(seq(.4,.7,.1),  
calculate_community_immunity(prop_infected = seq(.4,.7,.1),  
prop_vaccinated = .5),  
ylab = "Community Immunity",  
xlab = "Proportion Infected",  
main = "Community Immunity Given 50% Vaccinated",  
adj =0)  
}
```

calculate_shannon	<i>Calculate Shannon Index for a Series</i>
-------------------	---

Description

Calculate Shannon Index for a Series

Usage

```
calculate_shannon(incidence)
```

Arguments

incidence numeric, the case incidence

Value

double, the intensity of epidemic calculated via Shannon index

Examples

```
dat <- nccovid::get_covid_state(c("Guilford", "Forsyth", "Mecklenburg", "Wake"))

library(dplyr)
library(ggplot2)

counties <- unique(dat$county)
entropy_values = dat %>%
  group_by(county) %>%
  dplyr::group_split() %>%
  lapply( function(x) calculate_shannon(incidence = x$cases_daily) ) %>%
  unlist()

entropy_values = data.frame(county = counties, intensity = entropy_values)
entropy_values %>%
  filter(county %in% nccovid::triad_counties) %>%
  ggplot(aes(reorder(county,intensity), intensity))+
  geom_point()+
  coord_flip()+
  labs(
    title = "Epidemic Intensity"
  )
)
```

calculate_transmission_increase
Transmission Increase

Description

Calculating the Transmission Increase from Factors

Usage

```
calculate_transmission_increase(R_w, rho, D = 4.7, omega = 0)
```

Arguments

R_w	a numeric, the baseline effective reproduction number
rho	a numeric, the estimated transmission advantage
D	a numeric, the generation time (average)
omega	a numeric with default of NULL indicating proportion of the population that has immunity against earlier variants

Examples

```
c(4,6) * calculate_transmission_increase(R_w = .8, .43, D = 5.2, omega = NULL)
```

```
c(4,6) * calculate_transmission_increase(R_w = .8, .43, D = 5.2, omega = .25)
```

calc_risk *Converts Infected persons, Number of Contact and Population to the associated probability of a contact*

Description

Uses a Taylor approximation for repeated Binomial trials Classically associated with the "Birthday Problem"

Usage

```
calc_risk(I, n, pop)
```

Arguments

I	integer, the number of persons infected
n	integer, the number of contacts per day
pop	integer, the total population

Details

$$P(A) = 1 - P(A)'$$

cone_region *Regions in Cone Region of Service*

Description

Regions in Cone Region of Service

Usage

cone_region

Format

a vector

covid_mortality_data *Mortality Estimates from Verity Et Al for Covid*

Description

Mortality Estimates from Verity Et Al for Covid

Usage

covid_mortality_data

Format

data frame

decrease_cases *Decrease Cases*

Description

Decreased previous observed cases back to scale

Usage

```
decrease_cases(calculated_cases, pos_rate, m = 10.83, k = 0.5)
```

Arguments

calculated_cases	
pos_rate	numeric, the calculated cases
m	numeric, the observed positivity rate
k	scaling factor
	scaling factor with default of 1/2 on range [0,1]

Source

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4809590/>

effective_ve_wane *Vaccine Effectiveness*

Description

Calculates Effective Vaccine Effectiveness as a function of parameters and time since vaccination. Includes heavyside function to accomodate the daily from injection

Usage

```
effective_ve_wane(VE = 0.8, omega = 0.1, t, theta = 0.3, t_2 = 14)
```

Arguments

VE	a numeric, the maximum vaccine efficacy
omega	a numeric, the rate parameter of wane
t	an integer, the day of interest
theta	a numeric, the general wane of the vaccine to be calibrated
t_2	an integer, the inflection of the heavyside

Examples

```
plot(0:30, effective_ve_wane(t = 0:30))
```

epi_convolve	<i>Convolution</i>
--------------	--------------------

Description

Perform a convolution given a pdf

Usage

```
epi_convolve(cases, pdf, direction = "forward")
```

Arguments

cases	numeric, the observed cases
pdf	numeric vector, the pdf of cases
direction	string, one of forward or backwards convolution

Examples

```
{
  true_cases <- rpois(100, 5)
  out <- data.frame(reported = ceiling(epi_convolve(true_cases, pdf = c(.2,.2,.3,.2,.1))),
    true_cases,
    date = 1:100
  )

  library(ggplot2)
  ggplot(out, aes(date))+
    geom_line(aes(y = true_cases))+
    geom_line(aes(y = reported), color = "blue")
}
```

epi_finalsize	<i>Final Size of An Epidemic</i>
---------------	----------------------------------

Description

Calculate the final size of an epidemic. Use the following logic:

Usage

```
epi_finalsize(r0)
```

Arguments

r0	a double, the reproduction number (can be basic or Reff)
----	--

Details

$$1 + 1/R0*W(-R0exp(-R0))$$
Examples

```
## Not run:
epi_finalsize(3.5)

plot(seq(1,3,.01), epi_finalsize(seq(1,3,.01)),xlab = "R",
ylab = "Percent Infected", type = "l")

## End(Not run)
```

```
generate_vax_coverage_age
```

Vaccine Coverage by Age

Description

Generates a graphic that shows the vaccine coverage by age band as a stacked bar chart in order to show the coverage as well as the raw number of vaccinated versus unvaccinated individuals.

Usage

```
generate_vax_coverage_age(county_use = nccovid::cone_region)
```

Arguments

```
county_use      a string vector representing the North Carolina counties to be displayed
```

```
get_cdc_detail
```

Retrieve CDC COVID-19 Spread by County

Description

Utilizes the CDC's COVID-19 Tracker to General Information About the Spread of Disease.

Usage

```
get_cdc_detail()
```

Value

a data.table with details regarding disease spread by county

Source

<<https://covid.cdc.gov/covid-data-tracker/#datatracker-home>>

 get_cdc_vax

Retrieve CDC Vaccination Rates by County

Description

Utilizes the CDC's COVID-19 Tracker to Retrieve Vaccination Rates

Usage

```
get_cdc_vax()
```

Value

a data.table with vaccination information by county by day

Source

<<https://covid.cdc.gov/covid-data-tracker/#datatracker-home>>

 get_county_covid_demographics

Get Reported Demographics by County

Description

Retrieve Latest Demographic data from NC DHHS.

Usage

```
get_county_covid_demographics(
  demographic = "age_group",
  region = NULL,
  add_population = TRUE
)
```

Arguments

demographic a string, one of age, k_12, ethnicity, gender, or race

region a string vector, could a string or vector of the counties of interest

add_population a boolean, TRUE to add the population estimates (may not be available for all demographics)

Examples

```

library(ggplot2)
library(data.table)
out <- get_county_covid_demographics(region = "Guilford", demographic = "age")

out[,per_capita:=cases/(population/100000)]
ggplot(out, aes(week_of, per_capita, colour = metric))+
  geom_line()+
  theme_bw()+
  theme(legend.position = "top")+
  labs(
    title = "SARS-CoV-2 Cases per 100k Residents",
    subtitle = "Guilford County, North Carolina",
    x = "Cases per 100k",
    y = NULL
  )

```

get_county_tests

Pull Testing Information at County Level

Description

Pulling information on tests and percent positive at the county level. Notes that these data are updated manually.

Usage

```
get_county_tests(county_select = NULL)
```

Arguments

county_select a string, the county of counties of interest

get_covid_county_plus

Append Additional Information to COVID-19 Count Information

Description

Combined NCDHHS Case and Death Counts with CDC Details

Usage

```
get_covid_county_plus(county = NULL, adjusted = TRUE)
```

Arguments

- county a string vector, representing the counties of interest. If left NULL then all counties in North Carolina will be returned
- adjusted a logical, should the adjusted cases be used (to account for reporting gaps on weekends and holidays from NCDHHS). Defaults to TRUE

Value

a data.table with combined values for all counties or specified counties

`get_covid_demographics`
Pull Covid-19 Demographics

Description

These data originate from the North Carolina DHHS Covid-19 Dashboard

Usage

```
get_covid_demographics()
```

`get_covid_state` *Retrieve Covid19 Data*

Description

This functions hits the Johns Hopkins Covid Data Repository and filters down to North Carolina Data. Alternatively, it can retrieve any state.

Usage

```
get_covid_state(  
  state = "North Carolina",  
  select_county = NULL,  
  data_source = c("cone", "hopkins"),  
  reporting_adj = FALSE  
)
```

Arguments

state	with a default of North Carolina
select_county	the county, if desired
data_source	which data source you would like to use one of "cove" or "hopkins"
reporting_adj	a boolean, default of FALSE which adjust for two known issues with North Carolina Report occurring on 2020-09-25 when all antigen tests were added and on 2020-11-13 where only 10 hours of data were reported and the remaining cases were rolled into 2020-11-14. Also corrects for reporting lapses on Thanksgiving and Christmas Eve/ Christmas Day. On 2021-02-28 the dashboard was taken down for maintenance and thus unavailable on that day. Additionally note that on 2021-03-13 NCDHHS elected to not report data on Sundays. On 2021-03-19 NCDHHS notified users that on 2021-03-26 data would be updated Monday - Friday. Updated for Good Friday in which no results were posted.

Examples

```
## Not run:  
# To get all counties  
get_covid_state()  
  
# To get a single county  
get_covid_state(select_county = "Guilford")  
  
## End(Not run)
```

`get_covid_zip`*Pull Covid Data by Zip Code*

Description

This function will pull down NC Covid Information by Zip Code

Usage

```
get_covid_zip()
```

get_google_mobility *Get Google Mobility Data*

Description

This is a helper function to automatically access Google's Mobility data for North Carolina Counties

Usage

```
get_google_mobility(counties = NULL)
```

Arguments

counties a string vector of the desired counties default of NULL returns all counties.

Source

<https://www.gstatic.com/covid19/mobility/Global_Mobility_Report.csv>

Examples

```
## Not run:
# Return All NC Counties
get_google_mobility()

# Return a Specific County
get_google_mobility("Alamance County")

## End(Not run)
```

get_google_mobility2 *Get Google Mobility (Version 2) This is a helper function to automatically access Google's Mobility data for North Carolina Counties. It's a bit faster than 'get_google_mobility' which downloads the entire csv for the world*

Description

Get Google Mobility (Version 2) This is a helper function to automatically access Google's Mobility data for North Carolina Counties. It's a bit faster than 'get_google_mobility' which downloads the entire csv for the world

Usage

```
get_google_mobility2(counties = NULL, state_in = "North Carolina")
```

Arguments

counties a string vector of the desired counties default of NULL returns all counties.
state_in a string vector representing state or states of interest

get_hospitalizations *Get Reported Hospitalisation Data*

Description

Retrieve Latest Hospitalisation data from NC DHHS. This is not an automatic Scrap so there could be some delay.

Usage

```
get_hospitalizations()
```

get_vaccinations *Pull Vaccination Rates by County*

Description

Pulled from <conedatascience/covid-data>

Usage

```
get_vaccinations(county_list = NULL, add_population = TRUE)
```

Arguments

county_list a string, the county to pull. default is all counties
add_population a boolean, default of TRUE to add a population

Examples

```
{  
  
get_vaccinations(county_list = "Guilford")  
  
}
```

get_vaccinations_demo *Pull Vaccinations by County and Demographic*

Description

Pulled from <conedatascience/covid-data>. The column `vax_n` returns vaccination counts. Population references are available for the user to calculate distribution and/or per capita rates.

Usage

```
get_vaccinations_demo(county_list = NULL, demographic = NULL, status = NULL)
```

Arguments

<code>county_list</code>	a string, the county to pull. default is all counties.
<code>demographic</code>	a string, the demographic requested. one or more of "race", "age", "ethnicity", "sex". default is all demographics
<code>status</code>	string, either 'partial' or 'full' for number of people with partially or fully vaccinated. Default of NULL returns both.

Examples

```
{
  get_vaccinations_demo(county_list = "Guilford",
                        demographic = 'race', status = 'partial')
}
```

`hit` *Calculate Herd Immunity Threshold*

Description

Calculates Basic Herd Immunity Threshold Based on the Basic Reproduction Number

Usage

```
hit(R0)
```

Arguments

<code>R0</code>	a positive double, the basic reproduction number
-----------------	--

Examples

```
# Calculate the Herd Immunity Threshold for R0 Between 1 and 9
o <- vapply(seq(1,9, .1), hit, FUN.VALUE = numeric(1))

plot(seq(1,9, .1), o, main = "HIT", type = "l",
      ylab = "Prop with Immunity", xlab = expression(R[0]))
```

increase_cases *Increase Cases*

Description

Increase case count in the presence of high testing positivity

Usage

```
increase_cases(observed_cases, pos_rate, m = 10.83, k = 0.5)
```

Arguments

observed_cases numeric, the reported cases
 pos_rate numeric, the observed positivity rate
 m scaling factor
 k scaling factor with default of 1/2 on range [0,1]

Source

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4809590/>

infection_probability *Infection Probability*

Description

Calculate Infection probability given D50 $1-10^{-(\log_{10}(.5)/D50)}$

Usage

```
infection_probability(D50 = 316)
```

Arguments

D50 a double, #RNA for 50 percent infection probability (D50)

italy_rates	<i>Italy Estimates</i>
-------------	------------------------

Description

Italy Estimates

Usage

```
italy_rates
```

Format

a data.frame

lambertW	<i>Lambert W function</i>
----------	---------------------------

Description

Computes the Lambert W function, giving efficient solutions to the equation $x \cdot \exp(x) = z$. `lambertW(z, b = 0, maxiter = 10, eps = .Machine$double.eps, min.imag = 1e-09)`

Usage

```
lambertW(z, b = 0, maxiter = 10, eps = .Machine$double.eps, min.imag = 1e-09)
```

Arguments

<code>z</code>	(complex) vector of values for which to compute the function
<code>b</code>	integer, defaults to 0. vector of branches: <code>b=0</code> specifies the principal branch, 0 and -1 are the ones that can take non-complex values
<code>maxiter</code>	maximum numbers of iterations for convergence
<code>eps</code>	convergence tolerance
<code>min.imag</code>	maximum magnitude of imaginary part to chop when returning solutions

Details

Compute the Lambert W function of z . This function satisfies $W(z) \cdot \exp(W(z)) = z$, and can thus be used to express solutions of transcendental equations involving exponentials or logarithms. The Lambert W function is also available in Mathematica (as the `ProductLog` function), and in Maple and Wolfram.

Author(s)

Nici Schraudolph <schraudo at inf.ethz.ch> (original version (c) 1998), Ben Bolker (R translation)
See <<https://stat.ethz.ch/pipermail/r-help/2003-November/042793.html>>

References

Corless, Gonnet, Hare, Jeffrey, and Knuth (1996), "On the Lambert W Function", *Advances in Computational Mathematics* 5(4):329-359

nc_county_demos	<i>NC Biological Sex Information by County</i>
-----------------	--

Description

NC Biological Sex Information by County

Usage

nc_county_demos

Format

a data.frame, with NC DHHS county level demographic metrics

Source

American Community Survey (2020 Vintage)

nc_county_fips	<i>NC Fips by County</i>
----------------	--------------------------

Description

NC Fips by County

Usage

nc_county_fips

Format

a data.frame

Source

<https://www.lib.ncsu.edu/gis/countyfips>

`nc_delay`*NCDHHS Reported Delay Distribution*

Description

Reported testing and reporting delays were fit using the EpiNow2 bootstrapped gamma fit. The reported delays were manually collected from the NCDHHS website.

Usage`nc_delay`**Format**

a list, with parameters for a gamma distribution fit to delays

Source

<https://covid19.ncdhhs.gov/dashboard/testing>

`nc_events`*Key North Carolina Events*

Description

Key North Carolina Events

Usage`nc_events`**Format**

a data.frame

Source

various and <https://www.nc.gov/covid-19/staying-ahead-curve>

nc_fatality_estimates *Mortality and Hospitalization Estimates*

Description

Mortality and Hospitalization Estimates

Usage

nc_fatality_estimates

Format

data.frame

nc_hc_coalitions *NC Hospital Preparedness Coalitions*

Description

NC Hospital Preparedness Coalitions

Usage

nc_hc_coalitions

Format

a data.frame, with NC county name and associated coalition

Source

<https://easternhpc.com/state-coalition-map/>

nc_population *North Carolina Population by County*

Description

North Carolina Population by County

Usage

nc_population

Format

a data.frame

Source

Source: North Carolina OSBM, Standard Population Estimates, Vintage 2018 and Population Projections, Vintage 2019 <<https://www.osbm.nc.gov/demog/county-estimates>>

nc_pop_age *North Carolina Population by County by Age*

Description

North Carolina Population by County by Age

Usage

nc_pop_age

Format

a data.frame

Source

ACS2020 Metrics

nc_pop_dhhs

NC Population by NCDHHS Age Band

Description

NC Population by NCDHHS Age Band

Usage

nc_pop_dhhs

Format

a data.frame

Source

2020 ACS Survey

nc_svi_county

CDC Social Vulnerability for North Carolina by County

Description

CDC Social Vulnerability for North Carolina by County

Usage

nc_svi_county

Format

a data.frame

Source

[U.S. Centers for Disease Prevention and Control (CDC) Social Vulnerability Index (SVI)](<https://svi.cdc.gov/>)

pull_covid_summary	<i>Retrieve State Summary Metrics</i>
--------------------	---------------------------------------

Description

This pulls the most up to date summary data from the state.

Usage

```
pull_covid_summary()
```

Value

a data.table with information for North Carolina

pull_estimates	<i>Pull Latest Estimates</i>
----------------	------------------------------

Description

All estimates for North Carolina and some select regions have been precalculated and available for download. These estimates are utilising the EpiNow2 package

Usage

```
pull_estimates(region = NULL, variable = "R")
```

Arguments

region	a string or string vector, the region or county of interest
variable	a string or string vector, the measure of interest

`pull_hospitalization_demos`*Pull Hospitalization Demographics*

Description

A Helper Function That Pull Hospitalizations by Demographics as Posted by NCDHHS

Usage

```
pull_hospitalization_demos()
```

Value

a data.table

Examples

```
o <- pull_hospitalization_demos()

age_only <- o[demographic=="Age"&covid_status=="Confirmed"]

age_only <- age_only[date<Sys.Date()-90]

plot(NULL,
      xlim=range(age_only$date),
      ylim=range(age_only$value), ylab="Admissions",
      xlab="Date", main = "Admissions by Age")

buckets <- unique(age_only$category)

my_cols <- c("#00A2B2", "#F1BD51", "#00205C", "#c9c9c9", "#7750A9", "#B7D866",
            "#5C5859", "#DB2B27", "#63CCFF", "#000000", "#123453")
names(my_cols) <- buckets

for(i in buckets){
  lines(age_only[category==i]$date,
        age_only[category==i]$value,
        col = my_cols[[i]])
}
```

pull_vaccine_census *Pull Vaccine Information by Census Tract*

Description

The purpose of this function is to pull data provided by NCDHHS on vaccination rates by census tract. Additionally, information on SVI and other demographics is provided

Usage

```
pull_vaccine_census(county_pull = NULL)
```

Arguments

county_pull a vector, the counties to select for the query

Value

a data.table with vaccination rates at the census tract level

pull_wastewater *Pull Wastewater Treatment Data*

Description

A helper function to pull SARS-CoV-2 Copies Detected in Wastewater

Usage

```
pull_wastewater(county_in = NULL)
```

Arguments

county_in a string vector indicating the counties served with a default of NULL returning all counties

Examples

```
raw_dat <- pull_wastewater(county_in = "Guilford")
raw_dat <- raw_dat[!is.na(sars_cov2_raw_copiesL)][,copies_log10 := log10(sars_cov2_normalized)]

par(mar = c(5, 4, 4, 4) + 0.3)
plot(copies_log10~date_new, data = raw_dat, type = "b",
     xlab = "Date", ylab = "SARS-CoV-2 RNA Copies (Log10)")
par(new = TRUE)
plot(log10(cases_new_cens_per10k)~date_new, data = raw_dat,
     type = "l", axes = FALSE, bty = "n", xlab = "", ylab = "", col = "orange")
```

```
axis(side=4, at = pretty(range(log10(raw_dat$cases_new_cens_per10k))))
mtext("Log10(New Cases per 100k)", side=4, line=3)
title("Guilford SARS-CoV-2 Detected in Wastewater vs New Cases per 100k")
```

r2R

Convert Growth Rate to Reproduction Number

Description

Convenience function to convert a growth rate (little r) to a reproduction number (R) given a particular generation time.

Usage

```
r2R(r, mu_gamma = 4.7, sd_gamma = 2.9)
```

Arguments

r	a double representing the growth rate
mu_gamma	a double representing mean of the gamma function characterizing the generation time.
sd_gamma	a double representing standard deviation of the gamma function characterizing the generation time.

Source

<https://royalsocietypublishing.org/doi/10.1098/rsif.2020.0144>

Examples

```
cases <- rpois(10,2.5)
t <- 1:10
fit <- glm(cases ~ t, family = "poisson")

r2R(coef(fit)[2])
```

rna_content	<i>RNA Content in Aerosol</i>
-------------	-------------------------------

Description

Estimate the RNA Content in an Aerosol

Usage

```
rna_content(resp_fluid = 5e+08, wet_aerosol_diameter = 5)
```

Arguments

resp_fluid a double, respiratory fluid RNA conc [/cm³]
wet_aerosol_diameter
 a double, mean wet aerosol diameter [um]

triad_counties	<i>List of Triad Counties</i>
----------------	-------------------------------

Description

List of Triad Counties

Usage

```
triad_counties
```

Format

a vector

Index

* datasets

- cone_region, 7
- covid_mortality_data, 7
- italy_rates, 19
- nc_county_demos, 20
- nc_county_fips, 20
- nc_delay, 21
- nc_events, 21
- nc_fatality_estimates, 22
- nc_hc_coalitions, 22
- nc_pop_age, 23
- nc_pop_dhhs, 24
- nc_population, 23
- nc_svi_county, 24
- triad_counties, 29

aerosol_concentration, 3

aerosol_emission, 3

calc_risk, 6

calculate_community_immunity, 4

calculate_shannon, 5

calculate_transmission_increase, 6

cone_region, 7

covid_mortality_data, 7

decrease_cases, 8

effective_ve_wane, 8

epi_convolve, 9

epi_finalsize, 9

generate_vax_coverage_age, 10

get_cdc_detail, 10

get_cdc_vax, 11

get_county_covid_demographics, 11

get_county_tests, 12

get_covid_county_plus, 12

get_covid_demographics, 13

get_covid_state, 13

get_covid_zip, 14

get_google_mobility, 15

get_google_mobility2, 15

get_hospitalizations, 16

get_vaccinations, 16

get_vaccinations_demo, 17

hit, 17

increase_cases, 18

infection_probability, 18

italy_rates, 19

lambertW, 19

nc_county_demos, 20

nc_county_fips, 20

nc_delay, 21

nc_events, 21

nc_fatality_estimates, 22

nc_hc_coalitions, 22

nc_pop_age, 23

nc_pop_dhhs, 24

nc_population, 23

nc_svi_county, 24

pull_covid_summary, 25

pull_estimates, 25

pull_hospitalization_demos, 26

pull_vaccine_census, 27

pull_wastewater, 27

r2R, 28

rna_content, 29

triad_counties, 29