

# Package ‘multigroup.vaccine’

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**Type** Package

**Title** Analyze Outbreak Models of Multi-Group Populations with Vaccination

**Version** 0.1.1

**Description** Model infectious disease dynamics in populations

with multiple subgroups having different vaccination rates, transmission characteristics, and contact patterns. Calculate final and intermediate outbreak sizes, form age-structured contact models with automatic fetching of U.S. census data, and explore vaccination scenarios with an interactive 'shiny' dashboard for a model with two subgroups, as described in Nguyen et al. (2024) <[doi:10.1016/j.jval.2024.03.039](https://doi.org/10.1016/j.jval.2024.03.039)> and Duong et al. (2026) <[doi:10.1093/ofid/ofaf695.217](https://doi.org/10.1093/ofid/ofaf695.217)>.

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aggregateByAgeGroups *Aggregate population counts into age groups*

---

## Description

Aggregate per-age population counts into coarser age groups defined by the (sorted) lower bounds in `age_groups`. When `length(age_groups) == 1`, all ages  $\geq$  that value are aggregated into a single open-ended group ("Xplus"). When `length(age_groups) > 1`, groups are formed as `age_groups[i]` to `age_groups[i+1] - 1` for  $i = 1:(n-1)$  and `age_groups[n]` and above for the final group. Human-readable labels are produced: "under1" for the 0–0 group, "ageX" for single-year groups, "XtoY" for ranges, and "Xplus" for the final open group. When `verbose = TRUE`, the function prints aggregation summaries to the console for each group using `cat()`.

## Usage

```
aggregateByAgeGroups(ages, pops, age_groups, verbose = FALSE)
```

## Arguments

ages	Numeric vector of ages (typically integers) corresponding to the entries in pops.
pops	Numeric vector of population counts for each age; must be the same length as ages. Note: NA values in pops will propagate into group sums because <code>na.rm = TRUE</code> is not used; clean or impute missing values beforehand if required.
age_groups	Numeric vector of lower bounds for desired age groups. Must be sorted in ascending order. If length is 1, the single value defines an "Xplus" group (ages $\geq$ X). For length $> 1$ , contiguous non-overlapping groups are created as described above.
verbose	Logical, if TRUE prints aggregation messages for each group. Default is FALSE.

## Details

- Group boundaries are inclusive at both ends for finite ranges (i.e. ages satisfying  $\text{lower} \leq \text{age} \leq \text{upper}$ ). For the last group the upper bound is infinite.
- If no ages fall into a group the aggregated count for that group is 0 (because `sum(numeric(0)) == 0`).
- When `verbose = TRUE`, the function writes progress messages to the console with `cat()` for each aggregated group (useful for debugging / logging). By default (`verbose = FALSE`), the function is silent.

## Value

A named list with components:

**pops** Numeric vector of aggregated population counts, one element per group.

**labels** Character vector of labels for each group (e.g. "under1", "age5", "0to4", "65plus").

**age\_ranges** List of numeric vectors of length 2 giving the inclusive lower and upper bounds for each group; the upper bound for the final group is `Inf`.

## Examples

```
# Multiple groups example
ages <- 0:100
pops <- rep(100, length(ages))
aggregateByAgeGroups(ages, pops, c(0, 5, 18, 65))

# Single open-ended group (65plus)
aggregateByAgeGroups(ages, pops, 65)
```

---

**contactMatrixAgeSchool**

*Calculate a contact matrix for age groups and schools*

---

**Description**

Calculate a contact matrix for age groups and schools

**Usage**

```
contactMatrixAgeSchool(
  agelims,
  agepops,
  schoolagegroups,
  schoolpops,
  schportion
)
```

**Arguments**

agelims	minimum age in years for each age group
agepops	population size of each age group
schoolagegroups	index of the age group covered by each school
schoolpops	population size of each school
schportion	portion of within-age-group contacts that are exclusively within school

**Value**

a square matrix with the contact rate of each group (row) with members of each other group (column)

**Examples**

```
contactMatrixAgeSchool(agelims = c(0, 5, 18), agepops = c(500, 1300, 8200),
  schoolagegroups = c(2, 2), schoolpops = c(600, 700), schportion = 0.7)
```

---

contactMatrixPolymod *Calculate a contact matrix for age groups based on Polymod contact survey data*

---

## Description

Calculate a contact matrix for age groups based on Polymod contact survey data

## Usage

```
contactMatrixPolymod(agelims, agepops = NULL)
```

## Arguments

agelims	minimum age in years for each age group. The maximum valid age limit is 90, as the socialmixr contact_matrix function supports ages up to 90. Age limits greater than 90 will be replaced with 90 and a warning will be issued.
agepops	population size of each group, defaulting to demography of Polymod survey population. If provided, must match the length of the age groups defined by agelims (after any adjustments for exceeding the 90-year limit).

## Details

The socialmixr contact\_matrix function supports age limits up to 90. Any age limits above 90 will be adjusted to 90 with a warning, and the corresponding populations will be aggregated into a single "90+" group.

## Value

A symmetric contact matrix with row and column names indicating the age groups.

## Examples

```
#Default population distribution uses population data from POLYMOD survey locations:  
contactMatrixPolymod(agelims = c(0, 5, 18))  
#Specifying the age distribution will lead to an adjusted version:  
contactMatrixPolymod(agelims = c(0, 5, 18), agepops = c(500, 1300, 8200))
```

---

contactMatrixPropPref	<i>Calculate group contact matrix with proportional mixing and preferential mixing within group</i>
-----------------------	---

---

## Description

Calculate group contact matrix with proportional mixing and preferential mixing within group

## Usage

```
contactMatrixPropPref(popsize, contactrate, ingroup)
```

## Arguments

popsize	population size of each group
contactrate	overall contact rate of each group
ingroup	fraction of each group's contacts that are exclusively in-group

## Value

a square matrix with the contact rate of each group (row) with members of each other group (column)

## Examples

```
contactMatrixPropPref(popsize = c(100, 150, 200), contactrate = c(1.1, 1, 0.9),
ingroup = c(0.2, 0.25, 0.22))
```

---

finalsize	<i>Calculate final outbreak size or distribution of a multigroup transmission model for a given basic reproduction number, contact/transmission assumptions, and initial conditions</i>
-----------	---

---

## Description

Calculate final outbreak size or distribution of a multigroup transmission model for a given basic reproduction number, contact/transmission assumptions, and initial conditions

**Usage**

```
finalsize(
  popsize,
  R0,
  contactmatrix,
  relsusc,
  reltransm,
  initR,
  initI,
  initV,
  method = "ODE",
  nsims = 1
)
```

**Arguments**

popsize	the population size of each group
R0	the basic reproduction number
contactmatrix	matrix of group-to-group contact rates
relsusc	relative susceptibility to infection per contact of each group
reltransm	relative transmissibility per contact of each group
initR	initial number of each group already infected and removed (included in size result)
initI	initial number of each group infectious
initV	initial number of each group vaccinated
method	the method of final size calculation or simulation to use
nsims	the number of simulations to run for stochastic methods

**Value**

a vector (nsims = 1) or matrix (nsims > 1) with the final number infected from each group (column) in each simulation (row)

**Examples**

```
popsize <- c(800, 200)
R0 <- 2
contactmatrix <- contactMatrixPropPref(popsize = popsize, contactrate = c(1, 1),
 ingroup = c(0.2, 0.2))
relsusc <- c(1, 1)
reltransm <- c(1, 1)
initR <- c(0, 0)
initI <- c(1, 0)
initV <- 0.2 * popsize
# Default method "ODE" numerical solves ordinary differential equations until infectious count
# is close to 0
finalsize(popsize, R0, contactmatrix, relsusc, reltransm, initR, initI, initV)
```

```
finalsize(popsize, R0, contactmatrix, relsusc, reltransm, initR, initI, initV,
method = "analytic")
finalsize(popsize, R0, contactmatrix, relsusc, reltransm, initR, initI, initV,
method = "stochastic", nsims = 10)
# All "escaped" outbreaks set to deterministic final size:
finalsize(popsize, R0, contactmatrix, relsusc, reltransm, initR, initI, initV,
method = "hybrid", nsims = 10)
```

---

getCensusData*Get Census Population Data by Age and County*

---

**Description**

Downloads and processes U.S. Census Bureau population estimates for a specified state and county, organized by age groups. Supports single-year age data with optional sex disaggregation.

**Usage**

```
getCensusData(
  state_fips,
  county_name,
  year = 2024,
  age_groups = NULL,
  by_sex = FALSE,
  csv_path = NULL,
  cache_dir = NULL,
  verbose = FALSE
)
```

**Arguments**

state_fips	Two-digit FIPS code for the state (e.g., "49" for Utah)
county_name	Name of the county (e.g., "Salt Lake County")
year	Census estimate year: 2020-2024 for July 1 estimates, or 2020.1 for April 1, 2020 base
age_groups	Vector of age limits for grouping (e.g., c(0, 5, 18, 65)). Default NULL returns single-year ages 0-85+
by_sex	Logical, if TRUE returns separate male/female groups
csv_path	Optional path to a previously downloaded census CSV file. If provided, data will be read from this file instead of downloading. Use cache_dir for automatic caching.
cache_dir	Optional directory path for caching downloaded census files. If provided, the function will check for an existing cached file and use it, or download and save a new one. Default is NULL (no caching). Use "." for current directory or specify a custom path like "~/census_cache"
verbose	Logical, if TRUE prints messages about data loading and age aggregation. Default is FALSE.

**Value**

A list containing:

county	County name
state	State name
year	Census year
total_pop	Total population
age_pops	Vector of populations by age group
age_labels	Labels for each age group
sex_labels	If <code>by_sex=TRUE</code> , labels indicating sex
data	Full filtered data frame

**Examples**

```
# Use the included example data (recommended for package examples)
slc_data <- get CensusData(
  state_fips = "49",
  county_name = "Salt Lake County",
  year = 2024,
  csv_path = getCensusDataPath()
)

# Get age groups without sex disaggregation
slc_grouped <- get CensusData(
  state_fips = "49",
  county_name = "Salt Lake County",
  year = 2024,
  age_groups = c(0, 5, 18, 65),
  csv_path = getCensusDataPath()
)

# Get age groups by sex
slc_by_sex <- get CensusData(
  state_fips = "49",
  county_name = "Salt Lake County",
  year = 2024,
  age_groups = c(0, 5, 18, 65),
  by_sex = TRUE,
  csv_path = getCensusDataPath()
)

# Download from web (requires internet)
slc_web <- get CensusData(
  state_fips = "49",
  county_name = "Salt Lake County",
  year = 2024
)
```

```
# Use caching to avoid repeated downloads
slc_cached <- getCensusData(
  state_fips = "49",
  county_name = "Salt Lake County",
  year = 2024,
  cache_dir = "~/census_cache"
)
```

---

getCensusDataPath	<i>Get path to example census data file</i>
-------------------	---

---

## Description

Returns the path to the example Utah census data CSV file included with the package. This is useful for examples, testing, and when internet access is not available.

## Usage

```
getCensusDataPath()
```

## Value

Character string with the path to the example census CSV file for Utah (FIPS 49)

## Examples

```
# Get path to example Utah census file
utah_csv <- getCensusDataPath()

# Use it with getCensusData

slc_data <- getCensusData(
  state_fips = "49",
  county_name = "Salt Lake County",
  year = 2024,
  csv_path = getCensusDataPath()
)
```

---

<code>getCityData</code>	<i>Get City Population Data by Age</i>
--------------------------	--

---

### Description

Reads and processes population data for specific cities from ACS 5-year estimates, organized by age groups. The ACS data provides 5-year age groupings (0-4, 5-9, etc.) which can be disaggregated into single-year ages or aggregated into custom age groups.

### Usage

```
getCityData(
  city_name,
  csv_path,
  age_groups = c(0, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85),
  verbose = FALSE
)
```

### Arguments

<code>city_name</code>	Name of the city (e.g., "Hildale city, Utah")
<code>csv_path</code>	Path to the city population CSV file
<code>age_groups</code>	Vector of age limits for grouping. If NULL, returns single-year ages (disaggregated from 5-year ACS groups). Default uses 5-year intervals: c(0,5,10,...,85)
<code>verbose</code>	Logical, if TRUE prints messages about age aggregation. Default is FALSE.

### Value

A list containing:

<code>city</code>	City name
<code>year</code>	Data year
<code>total_pop</code>	Total population
<code>age_pops</code>	Vector of populations by age group
<code>age_labels</code>	Labels for each age group
<code>data</code>	Full data frame

### Examples

```
# Load Hildale data with default 5-year age groups
hildale_data <- getCityData(
  city_name = "Hildale city, Utah",
  csv_path = system.file("extdata", "hildale_ut_2023.csv", package = "multigroup.vaccine")
)

# Load with single-year ages (disaggregated)
```

```

hildale_single <- getCityData(
  city_name = "Hildale city, Utah",
  csv_path = system.file("extdata", "hildale_ut_2023.csv", package = "multigroup.vaccine"),
  age_groups = NULL
)

# Load with custom age groups
hildale_custom <- getCityData(
  city_name = "Hildale city, Utah",
  csv_path = system.file("extdata", "hildale_ut_2023.csv", package = "multigroup.vaccine"),
  age_groups = c(0, 18, 65)
)

```

---

**getFinalSizeAnalytic** *Calculate final size of outbreak: the total number of infections in each group, by solving the analytic final size equation*

---

## Description

Calculate final size of outbreak: the total number of infections in each group, by solving the analytic final size equation

## Usage

```
getFinalSizeAnalytic(transmrates, recoveryrate, popsize, initR, initI, initV)
```

## Arguments

transmrates	matrix of group-to-group (column-to-row) transmission rates
recoveryrate	inverse of mean infectious period
popsize	the population size of each group
initR	initial number of each group already infected and removed (included in final size)
initI	initial number of each group infectious
initV	initial number of each group vaccinated

## Value

vector of final sizes (number of infected over whole outbreak) for each group

## Examples

```
getFinalSizeAnalytic(transmrates = matrix(0.2, 2, 2), recoveryrate = 0.3,
popsize = c(100, 150), initR = c(0, 0), initI = c(0, 1), initV = c(10, 10))
```

---

getFinalSizeDist	<i>Estimate the distribution of final outbreak sizes by group using stochastic simulations of multi-group model</i>
------------------	---

---

### Description

Estimate the distribution of final outbreak sizes by group using stochastic simulations of multi-group model

### Usage

```
getFinalSizeDist(n, transmrates, recoveryrate, popsize, initR, initI, initV)
```

### Arguments

n	the number of simulations to run
transmrates	matrix of group-to-group (column-to-row) transmission rates
recoveryrate	inverse of mean infectious period
popsize	the population size of each group
initR	initial number of each group already infected and removed (included in size result)
initI	initial number of each group infectious
initV	initial number of each group vaccinated

### Value

a matrix with the final number infected from each group (column) in each simulation (row)

### Examples

```
getFinalSizeDist(n = 10, transmrates = matrix(0.2, 2 ,2), recoveryrate = 0.3,
popsize = c(100, 150), initR = c(0, 0), initI = c(0, 1), initV = c(10, 10))
```

---

getFinalSizeDistEscape	<i>Estimate the distribution of final outbreak sizes by group using a hybrid model: stochastic simulations for smaller-sized outbreaks and deterministic ordinary differential equation model for "escaped" outbreaks</i>
------------------------	---

---

### Description

Estimate the distribution of final outbreak sizes by group using a hybrid model: stochastic simulations for smaller-sized outbreaks and deterministic ordinary differential equation model for "escaped" outbreaks

**Usage**

```
getFinalSizeDistEscape(
  n,
  transmrates,
  recoveryrate,
  popsize,
  initR,
  initI,
  initV
)
```

**Arguments**

n	the number of simulations to run
transmrates	matrix of group-to-group (column-to-row) transmission rates
recoveryrate	inverse of mean infectious period
popsize	the population size of each group
initR	initial number of each group already infected and removed (included in size result)
initI	initial number of each group infectious
initV	initial number of each group vaccinated

**Value**

a matrix with the final number infected from each group (column) in each simulation (row)

**Examples**

```
getFinalSizeDistEscape(n = 10, transmrates = matrix(0.2, 2, 2), recoveryrate = 0.3,
popsize = c(100, 150), initR = c(0, 0), initI = c(0, 1), initV = c(10, 10))
```

---

getFinalSizeODE	<i>Calculate outbreak final size, the total number of infections in each group, by numerically solving the multi-group ordinary differential equation</i>
-----------------	---

---

**Description**

Calculate outbreak final size, the total number of infections in each group, by numerically solving the multi-group ordinary differential equation

**Usage**

```
getFinalSizeODE(transmrates, recoveryrate, popsize, initR, initI, initV)
```

**Arguments**

transmrates	matrix of group-to-group (column-to-row) transmission rates
recoveryrate	inverse of mean infectious period
popsize	the population size of each group
initR	initial number of each group already infected and removed (included in final size)
initI	initial number of each group infectious
initV	initial number of each group vaccinated

**Value**

vector of final sizes (number of infected over whole outbreak) for each group

**Examples**

```
getFinalSizeODE(transmrates = matrix(0.2, 2, 2), recoveryrate = 0.3,
popsize = c(100, 150), initR = c(0, 0), initI = c(0, 1), initV = c(10, 10))
```

getSizeAtTime	<i>Calculate outbreak size at a given time</i>
---------------	--

**Description**

Calculate outbreak size at a given time

**Usage**

```
getSizeAtTime(time, transmrates, recoveryrate, popsize, initR, initI, initV)
```

**Arguments**

time	the time at which to calculate the outbreak size
transmrates	matrix of group-to-group (column-to-row) transmission rates
recoveryrate	inverse of mean infectious period
popsize	the population size of each group
initR	initial number of each group already infected and removed (included in size result)
initI	initial number of each group infectious
initV	initial number of each group vaccinated

**Value**

a list with totalSize (total cumulative infections) and activeSize (total currently infected) in each group at the specified time

**Examples**

```
getSizeAtTime(time = 30, transmrates = matrix(0.2, 2, 2), recoveryrate = 0.3,
popsize = c(100, 150), initR = c(0, 0), initI = c(0, 1), initV = c(10, 10))
```

getStateFIPS

*Get state FIPS code by state name***Description**

Get state FIPS code by state name

**Usage**

```
getStateFIPS(state_name)
```

**Arguments**

state_name	State name (e.g., "Utah")
------------	---------------------------

**Value**

Two-digit FIPS code as character

**Examples**

```
getStateFIPS("Utah") # Returns "49"
```

listCounties

*List available counties for a state***Description**

List available counties for a state

**Usage**

```
listCounties(
  state_fips,
  year = 2024,
  csv_path = NULL,
  cache_dir = NULL,
  verbose = FALSE
)
```

**Arguments**

state_fips	Two-digit FIPS code for the state
year	Census year (2020-2024), default 2024
csv_path	Optional path to a previously downloaded census CSV file
cache_dir	Optional directory path for caching downloaded census files
verbose	Logical, if TRUE prints messages about data loading. Default is FALSE.

**Value**

Character vector of county names

**Examples**

```
# Use the included example data
utah_counties <- listCounties(
  state_fips = "49",
  year = 2024,
  csv_path = getCensusDataPath()
)

# Download from web (requires internet)
utah_counties_web <- listCounties(state_fips = "49", year = 2024)

# With caching
utah_counties_cached <- listCounties(state_fips = "49", cache_dir = "~/census_cache")
```

**odeSIR**

*Ordinary differential equation function for multi-group susceptible-infectious-removed (SIR) model used as "func" argument passed to the ode() function from deSolve package*

**Description**

Ordinary differential equation function for multi-group susceptible-infectious-removed (SIR) model used as "func" argument passed to the ode() function from deSolve package

**Usage**

```
odeSIR(time, state, par)
```

**Arguments**

time	vector of times at which the function will be evaluated
state	vector of number of individuals in each group at each state: S states followed by I states followed by R states
par	vector of parameter values: group-to-group transmission rate matrix elements (row-wise) followed by recovery rate

**Value**

a list of three vectors of derivatives dS, dI, and dR for each group, evaluated at the given state values

**Examples**

```
# Intended only for use as the func argument to the ode() function from the deSolve package:
y0 <- c(S1 = 79999, S2 = 20000, I1 = 1, I2 = 0, R1 = 0, R2 = 0)
parms <- c(beta11 = 1.6e-6, beta21 = 1.5e-6, beta12 = 1.4e-6, beta22 = 8.7e-6, recoveryrate = 1/7)
times <- seq(0, 350, len = 10)
deSolve::ode(y0, times, odeSIR, parms)
```

---

run\_my\_app

*Runs the shiny app*

---

**Description**

Runs the shiny app

**Usage**

run\_my\_app(...)

**Arguments**

... Further arguments passed to [shiny::shinyAppDir\(\)](#).

**Details**

The app featured in this package is the one presented in the shiny demo: <https://shiny.posit.co/r/getstarted/shiny-basics/lesson1/index.html>.

**Value**

Starts the execution of the app, printing the port on the console.

**Examples**

```
# To be executed interactively only
if (interactive()) {
  run_my_app()
}
```

---

transmissionRates	<i>Calculate transmission rate matrix for multi-group model with specified R0</i>
-------------------	---

---

## Description

Calculate transmission rate matrix for multi-group model with specified R0

## Usage

```
transmissionRates(R0, meaninf, reltransm)
```

## Arguments

R0	overall basic reproduction number
meaninf	mean duration of infectious period
reltransm	matrix with relative transmission rates, from column-group to row-group

## Value

a matrix of transmission rates to (row) and from (column) each group, in same time units as meaninf

## Examples

```
transmissionRates(R0 = 15, meaninf = 7,
                  reltransm = rbind(c(1, 0.5, 0.9), c(0.3, 1.9, 1), c(0.3, 0.6, 2.8)))
```

---

vaxrepnum	<i>Calculate reproduction number for a multigroup model with a given state of vaccination and immunity</i>
-----------	--

---

## Description

Calculate reproduction number for a multigroup model with a given state of vaccination and immunity

## Usage

```
vaxrepnum(meaninf, popsize, trmat, initR, initV, vaxeff)
```

**Arguments**

meaninf	mean infectious period with same time units as trmat
popsize	the population size of each group
trmat	matrix of group-to-group (column-to-row) transmission rates
initR	initial number of each group already infected and immune
initV	initial number of each group vaccinated
vaxeff	effectiveness (0 to 1) of vaccine in producing immunity to infection

**Value**

the reproduction number

**Examples**

```
meaninf <- 7
popsize <- c(200, 800)
initR <- c(0, 0)
initV <- c(0, 0)
vaxeff <- 1
trmat <- matrix(c(0.63, 0.31, 0.19, 1.2), 2, 2)
vaxreppnum(meaninf, popsize, trmat, initR, initV, vaxeff)
vaxreppnum(meaninf, popsize, trmat, initR, initV = c(160, 750), vaxeff)
```

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