

# Package ‘finalsize’

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**Title** Calculate the Final Size of an Epidemic

**Version** 0.1

**Description** Calculate the final size of a susceptible-infectious-recovered epidemic in a population with demographic variation in contact patterns and susceptibility to disease, as discussed in Miller (2012) <[doi:10.1007/s11538-012-9749-6](https://doi.org/10.1007/s11538-012-9749-6)>.

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**URL** <https://epiverse-trace.github.io/finalsize/>,  
<https://github.com/epiverse-trace/finalsize>

**BugReports** <https://github.com/epiverse-trace/finalsize/issues>

**Imports** Rcpp

**LinkingTo** Rcpp, RcppEigen

**Suggests** colorspace, covr, data.table, knitr, bookdown, scales,  
socialmixr, testthat (>= 3.0.0), xml2, ggplot2, ggtext,  
rmarkdown, usethis

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**LazyData** true

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final_size	<i>Final size of an epidemic</i>
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### Description

final\_size calculates the final size of an epidemic outbreak in a population with heterogeneous mixing, and with heterogeneous susceptibility to infection such as that conferred by an immunisation programme.

### Usage

```
final_size(
  r0,
  contact_matrix,
  demography_vector,
  p_susceptibility,
  susceptibility,
  solver = c("iterative", "newton"),
  control = list()
)
```

### Arguments

r0	The basic reproductive number $R_0$ of the disease.
contact_matrix	Social contact matrix. Entry $m_{ij}$ gives average number of contacts in group $i$ reported by participants in group $j$
demography_vector	Demography vector. Entry $v_i$ gives proportion of total population in group $i$ (model will normalise if needed).
p_susceptibility	A matrix giving the probability that an individual in demography group $i$ is in risk (or susceptibility) group $j$ . Each row represents the overall distribution of individuals in demographic group $i$ across risk groups, and each row <i>must sum to 1.0</i> .
susceptibility	A matrix giving the susceptibility of individuals in demographic group $i$ and risk group $j$ .
solver	Which solver to use. Options are "iterative" (default) or "newton", for the iterative solver, or the Newton solver, respectively. Special conditions apply when using the Newton solver, see the control argument.
control	A list of named solver options, see <i>Solver options</i> .

**Value**

A data.frame of the proportion of infected individuals, within each demography group and susceptibility group combination. If the demography groups and susceptibility groups are named, these names are added to relevant columns. If the groups are not named, synthetic names are added (e.g. demo\_grp\_1, susc\_grp\_1).

**Solver options**

The control argument accepts a list of solver options, with the iterative solver taking two extra arguments than the Newton solver. This is an optional argument, and default options are used within the solver functions if an argument is missing. Arguments provided override the solver defaults.

**Common options:**

1. iterations: The number of iterations over which to solve for the final size, unless the error is below the solver tolerance. Default = 10000.
2. tolerance: The solver tolerance; solving for final size ends when the error drops below this tolerance. Defaults to set 1e-6. Larger tolerance values are likely to lead to inaccurate final size estimates.

**Iterative solver options:**

1. step\_rate: The solver step rate. Defaults to 1.9 as a value found to work well.
2. adapt\_step: Boolean, whether the solver step rate should be changed based on the solver error. Defaults to TRUE.

**Examples**

```
# load example POLYMOD data included in the package
data(polymod_uk)
r0 <- 2.0
contact_matrix <- polymod_uk$contact_matrix
demography_vector <- polymod_uk$demography_vector

# define the number of age and susceptibility groups
n_demo_grps <- length(demography_vector)
n_risk_grps <- 3

# prepare p_susceptibility and susceptibility
psusc <- matrix(
  data = 1, nrow = n_demo_grps, ncol = n_risk_grps
)
psusc <- psusc / rowSums(psusc)
# In this example, all risk groups from all age groups are fully
# susceptible
susc <- matrix(
  data = 1, nrow = n_demo_grps, ncol = n_risk_grps
)

# using default arguments for `solver` and `control`
final_size(
  r0 = r0,
```

```

    contact_matrix = contact_matrix,
    demography_vector = demography_vector,
    p_susceptibility = psusc,
    susceptibility = susc
  )

# using manually specified solver settings for the iterative solver
control <- list(
  iterations = 100,
  tolerance = 1e-3,
  step_rate = 1.9,
  adapt_step = TRUE
)

final_size(
  r0 = r0,
  contact_matrix = contact_matrix,
  demography_vector = demography_vector,
  p_susceptibility = psusc,
  susceptibility = susc,
  solver = "iterative",
  control = control
)

# manual settings for the newton solver
control <- list(
  iterations = 100,
  tolerance = 1e-3
)

final_size(
  r0 = r0,
  contact_matrix = contact_matrix,
  demography_vector = demography_vector,
  p_susceptibility = psusc,
  susceptibility = susc,
  solver = "newton",
  control = control
)

```

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polymod\_uk

*Example POLYMOD social contact data for the U.K.*

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## Description

An example of social contact and demography data for use with `finalsize`, accessed from the POLYMOD social contacts dataset using the `socialmixr` package. Data are for the United Kingdom, and age limits are set at 0, 20, and 40 years, with `symmetric = TRUE`. Code to get these data is given in `data-raw/polymod_uk.R`.

### Usage

`polymod_uk`

### Format

`polymod_uk`:

A list with two named elements:

**contact\_matrix** A contact matrix with mean contacts between age groups. This matrix is scaled by its largest real eigenvalue, and each row is scaled by the corresponding element in the `demography_vector`.

**demography\_vector** A vector with the number of individuals in each of three age groups: 0 – 20, 20 – 40, 40+.

### Source

[doi:10.1371/journal.pmed.0050074](https://doi.org/10.1371/journal.pmed.0050074); obtained using `socialmixr::polymod`. See further methods in `data-raw/polymod_uk.R`.

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