

SEIRV

This example is taken from the documentation of the R package [epidemics](#).

```
# load epidemics
library(epidemics)
library(socialmixr)
```

Attaching package: 'socialmixr'

The following object is masked from 'package:utils':

`cite`

```
library(ggplot2)
library(data.table)
```

```
# load contact and population data from socialmixr::polymod
polymod <- socialmixr::polymod
contact_data <- socialmixr::contact_matrix(
  polymod,
  countries = "United Kingdom",
  age.limits = c(0, 20, 40),
  symmetric = TRUE
)
```

Using POLYMOD social contact data. To cite this in a publication, use the 'cite' function

Removing participants that have contacts without age information. To change this behaviour, s

```

# prepare contact matrix
contact_matrix <- t(contact_data$matrix)

# prepare the demography vector
demography_vector <- contact_data$demography$population
names(demography_vector) <- rownames(contact_matrix)

# initial conditions: one in every 1 million is infected
initial_i <- 1e-6
initial_conditions <- c(
  S = 1 - initial_i, E = 0, I = initial_i, R = 0, V = 0
)

# build for all age groups
initial_conditions <- rbind(
  initial_conditions,
  initial_conditions,
  initial_conditions
)
rownames(initial_conditions) <- rownames(contact_matrix)

uk_population <- population(
  name = "UK",
  contact_matrix = contact_matrix,
  demography_vector = demography_vector,
  initial_conditions = initial_conditions
)

# simulate a pandemic, with an R0,
# an infectious period, and an pre-infectious period
pandemic_influenza <- infection(
  r0 = 1.5,
  preinfectious_period = 3,
  infectious_period = 7
)

pandemic_influenza

```

```

<infection>
infection name: NA

```

R0: 1.5
Infectious period: 7
Other infection parameters:
"preinfectious_period"

```
# run an epidemic model using `epidemic()`  
system.time(output <- epidemic(  
  model = "default",  
  population = uk_population,  
  infection = pandemic_influenza,  
  time_end = 600, increment = 1.0  
))
```

```
user  system elapsed  
0.009  0.001  0.011
```

```
# plot figure of epidemic curve  
ggplot(  
  output[compartment %in% c("exposed", "infectious")],  
  aes(  
    x = time,  
    y = value,  
    col = demography_group,  
    linetype = compartment  
  )  
) +  
  geom_line() +  
  scale_y_continuous(  
    labels = scales::comma  
  ) +  
  scale_colour_brewer(  
    palette = "Dark2",  
    name = "Age group"  
  ) +  
  expand_limits(  
    y = c(0, 500e3)  
  ) +  
  coord_cartesian(  
    expand = FALSE  
  ) +
```

```

theme_classic() +
theme(
  legend.position = "top"
) +
labs(
  x = "Simulation time (days)",
  linetype = "Compartment",
  y = "Individuals"
)

```

