SEIRV

This example is taken from the documentation of the R package [epidemics](https://github.com/epiverse-trace/epidemics/blob/main/vignettes/epidemics.Rmd).

# 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, set the 'missing.contact.age' option

# 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"  
 )

