Vacamole

This example is taken from the documentation of the R package `epidemics`.

```
library(epidemics)
library(data.table)
library(ggplot2)
library(colorspace)
library(scales)
```

Prepare population and initial conditions

Prepare population and contact data.

```
# 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, 65),
  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)
```

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

Prepare initial conditions for each age group. The Vacamole model has 11 compartments and therefore requires a matrix with 11 columns.

```r
# initial conditions
initial_i <- 1e-6

# // 0| 1| 2|3| 4|5| 6|7| 8|9|10
# // S|V1|V2|E|EV|I|IV|H|HV|D|R

# make initial conditions - order is important
initial_conditions <- c(
  S = 1 - initial_i,
  V1 = 0, V2 = 0,
  E = 0, EV = 0,
  I = initial_i, IV = 0,
  H = 0, HV = 0, D = 0, R = 0
)
initial_conditions <- rbind(
  initial_conditions,
  initial_conditions,
  initial_conditions
)

# assign rownames for clarity
rownames(initial_conditions) <- rownames(contact_matrix)
```

Prepare the time in days over which to model the epidemic, with the outbreak beginning at day zero.

```r
epidemic_days <- 300
```

Prepare a population as a `population` class object.

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

Prepare pathogen parameters

```
# make infection class for Vacamole model
# note extra arguments passed as ...
infect <- infection(
  name = "covid", r0 = 3, infectious_period = 10,
  preinfectious_period = 5,
  eta = 1 / 1000, omega = 1 / 1000,
  susc_reduction_vax = 0.5,
  hosp_reduction_vax = 0.5,
  mort_reduction_vax = 0.5
)
```

Prepare a two dose vaccination campaign

We prepare a two-dose vaccination campaign by concatenating two single dose vaccination regimes, i.e., applying the function `c()` to two `vaccination` objects.

```
# prepare a two dose vaccination regime for a single age group
# prepare the first dose
dose_1 <- vaccination(
  name = "two-dose vaccination", # name given to first dose
  nu = matrix(1e-2, nrow = 3),
  time_begin = matrix(30, nrow = 3),
  time_end = matrix(epidemic_days, nrow = 3)
)

# prepare the second dose with a 30 day interval in start date
dose_2 <- vaccination(
  name = "two-dose vaccination", # name given to first dose
  nu = matrix(1e-2, nrow = 3),
  time_begin = matrix(60, nrow = 3),
  time_end = matrix(epidemic_days, nrow = 3)
)

# use `c()` to combine the two doses
```

```r
double_vaccination <- c(dose_1, dose_2)

# print to visualise
double_vaccination
```

```
<vaccination>
Vaccination name: "two-dose vaccination"

Time begin:
     dose_1 dose_2
[1,]     30     60
[2,]     30     60
[3,]     30     60

Time end:
     dose_1 dose_2
[1,]    300    300
[2,]    300    300
[3,]    300    300

Vaccination rate:
     dose_1 dose_2
[1,]   0.01   0.01
[2,]   0.01   0.01
[3,]   0.01   0.01
```

We prepare a dummy vaccination regime of no vaccination against which to compare the two-dose vaccination campaign. This is done by using the `no_vaccination()` function and specifying the number of doses (here, 2 doses).

```r
# prepare a null vaccination regime with two doses
# use the convenience function `no_vaccination()`
no_vaccination <- no_vaccination(population = uk_population, doses = 2)
```

Model epidemic using Vacamole

First, we run the model with no vaccination.

```r
data <- epidemic(
  model_name = "vacamole",
  population = uk_population,
  infection = infect,
  vaccination = no_vaccination, # note custom no_vaccination object
  time_end = epidemic_days
)
```

Next we run the model with a two dose vaccination regime.

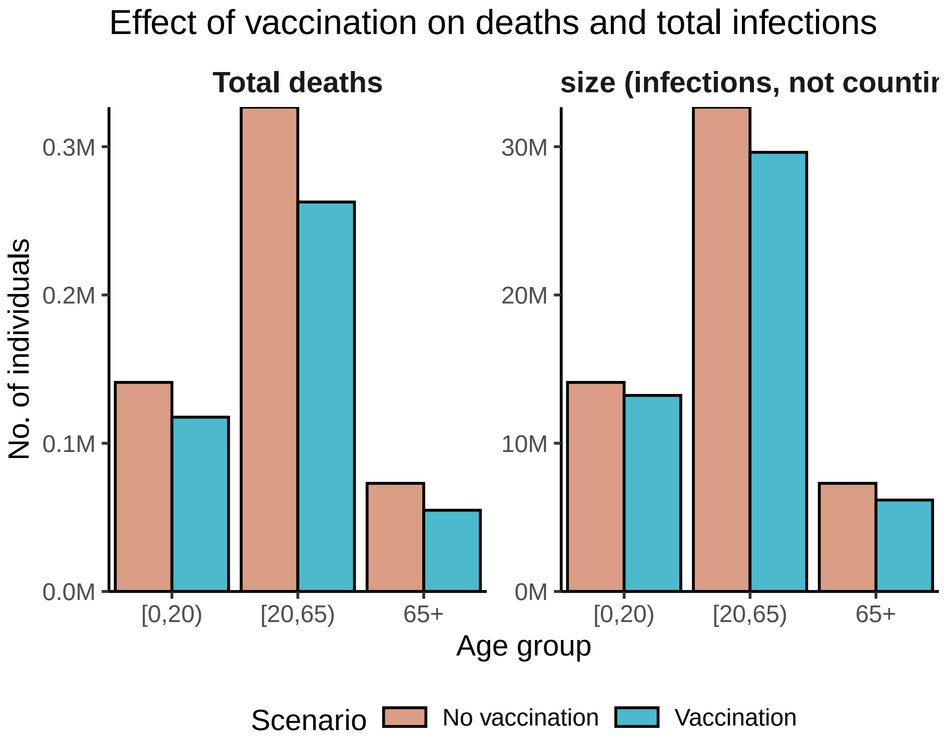
```r
data_vaccination <- epidemic(
  model_name = "vacamole",
  population = uk_population,
  infection = infect,
  vaccination = double_vaccination, # note custom object for two doses
  time_end = epidemic_days
)
```

Visualise model outcomes

First, we calculate the total number of infections resulting in recoveries and deaths over the course of the simulation; this is the epidemic's final size.

```r
# collect data from the two scenarios
data_scenarios <- list(data, data_vaccination)

# get deaths and recoveries from infection
data_scenarios <- Map(
  data_scenarios, c("no_vax", "vax"),
  f = function(df, sc) {
    df_ <- unique(df[, "demography_group"], by = "demography_group")
    # get total deaths per group
    df_$total_deaths <- df[time == max(time) & compartment == "dead", ]$value

    # get total recoveries per group using helper function `epidemic_size()`
    df_$total_recovered <- epidemic_size(df, deaths = FALSE) # do not count dead

    # add scenario information
    df_$scenario <- sc

    # return data
    df_
  }
)

# collect data
data_scenarios <- rbindlist(data_scenarios)

# transform to long format
data_scenarios <- melt(
  data_scenarios,
  id.vars = c("demography_group", "scenario")
)
```

```r
ggplot(data_scenarios) +
  geom_col(
    aes(demography_group, value, fill = scenario),
    position = "dodge",
    colour = "black"
  ) +
  facet_wrap(
    ~variable,
    scales = "free_y",
    labeller = labeller(
      variable = c(
        "total_deaths" = "Total deaths",
        "total_recovered" = "Epidemic size (infections, not counting deaths)"
      )
    )
  ) +
  scale_fill_discrete_qualitative(
    palette = "Dynamic",
    labels = c("No vaccination", "Vaccination"),
    name = "Scenario",
    na.value = "lightgrey"
  ) +
  scale_y_continuous(
    labels = label_comma(
      scale = 1e-6, suffix = "M"
    )
  ) +
  theme_classic() +
  theme(
    legend.position = "bottom",
    legend.key.height = unit(2, "mm"),
    strip.background = element_blank(),
    strip.text = element_text(
      face = "bold",
      size = 11
    )
  ) +
  expand_limits(
    x = c(0.5, length(unique(data_scenarios$demography_group)) + 0.5)
  ) +
  coord_cartesian(
    expand = FALSE
  ) +
  labs(
    x = "Age group",
    y = "No. of individuals",
    title = "Effect of vaccination on deaths and total infections"
  )
```



Finally, we can compare the peak of hospital bed occupancy in each scenario — this can be a rough indication of how much hospital capacity would be required if a pandemic of these characteristics were to occur, as well as another way to examine the effect of vaccination in reducing this requirement.

```r
# collect data from the two scenarios
data_scenarios <- list(data, data_vaccination)

peak_hospital_occupancy <- vapply(data_scenarios, function(df) {
  # get highest hospital occupancy
  # first get total hospitalisations among vaccinated and un- or part-vacc.
  df <- dcast(
    df[compartment %like% "hospitalised", ],
    time + demography_group ~ compartment,
    value.var = "value"
  )
  df[, total_hosp := hospitalised + hospitalised_vaccinated]

  # sum all age groups
  df <- df[, list(total_hosp = sum(total_hosp)), by = "time"]

  df[total_hosp == max(total_hosp), ]$total_hosp
}, FUN.VALUE = numeric(1))

# set names for comprehensibility
names(peak_hospital_occupancy) <- c("No vaccination", "Vaccination")

# show peak hospital occupancy in a readable format
format(peak_hospital_occupancy, big.mark = ",", digits = 1)
```

```
No vaccination    Vaccination
      "95,063"       "69,827"
```

This example demonstrates that implementing vaccination can substantially reduce peak hospital occupancy (by about 27%) compared to a scenario in which no vaccines are deployed.