

contact_abm

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Agent-based contact model

input parameters

```
hh_total <- 3000          # total households
hh_size  <- 3             # average number of household
pop      <- hh_total*hh_size # total population

dur_infect <- 5           # infectiousness period = 5 days
gamma_rate <- 1/dur_infect # recovery rate per day
trans_hh   <- 1/dur_infect # transmission probability, household
nhh_ratio  <- 0.18        # relative risk of transmission, non-household vs household
trans_nhh  <- trans_hh*nhh_ratio # transmission probability, non-household
mask_eff   <- 0.8         # relative risk of mask wearing policy
```

output table

```
t_end <- 50                # timeframe for simulation (days)
Outp <- data.frame(
  Time      = 0:t_end,
  I         = rep(0, t_end+1),
  R         = rep(0, t_end+1),
  inc_hh    = rep(0, t_end+1),
  inc_nhh   = rep(0, t_end+1),
  rt_hh     = rep(0, t_end+1),
  rt_nhh    = rep(0, t_end+1),
  inf_hh_0  = rep(0, t_end+1),
  inf_hh_1  = rep(0, t_end+1),
  inf_hh_2  = rep(0, t_end+1)
)
```

initial state

state indicator: 0 = susceptible, 1 = infectious, 2 = recovered

```
t <- 0
Y <- matrix(0, hh_total, hh_size)
```

```

Y[1:5, 1] <- 1
Outp$I[1] <- sum(Y == 1)
Outp$R[1] <- sum(Y == 2)
Outp$inf_hh_0[1] <- table(rowSums((Y == 1)|(Y == 2)))[1]
Outp$inf_hh_1[1] <- table(rowSums((Y == 1)|(Y == 2)))[2]

```

model

```

for (t in 1:t_end){

  if (t <= t_end/2){
    ct_all = 9.14 # number of daily contacts, total
    ct_hh = 2.26 # number of daily contacts, household
    ct_nhh = ct_all - ct_hh # number of daily contacts, non-household
    beta_hh = ct_hh*trans_hh # transmission rate per day, household (density-dependent)
    beta_nhh = ct_nhh*trans_nhh/pop # transmission rate per day, non-household (frequency-dependent)

    if (t == 1) {
      print("=== transmission rates, survey wave 1 ===")
      print(paste0("household = ", sprintf("%.2e", beta_hh)))
      print(paste0("non-household = ", sprintf("%.2e", beta_nhh)))
    }

  } else {
    ct_all = 3.97
    ct_hh = 2.20
    ct_nhh = ct_all - ct_hh
    beta_hh = ct_hh*trans_hh
    beta_nhh = (ct_nhh*trans_nhh/pop)*mask_eff

    if (t == (t_end/2+1)) {
      print("=== transmission rates, survey wave 3 ===")
      print(paste0("household = ", sprintf("%.2e", beta_hh)))
      print(paste0("non-household = ", sprintf("%.2e", beta_nhh)))
    }

  }

  # Event (A): household transmission
  # -- occurs when there are both susceptible and infectious in a household
  # -- depends on (household transmission rate) * (cases in the same household)
  inc_hh <- t(apply(Y, 1, function(y) {
    rbinom(hh_size, size = 1, prob = pexp(1, beta_hh * sum(y == 1)))
  }))
  inc_hh[Y != 0] <- 0

  # Event (B): non-household transmission
  # -- depends on (non-household transmission rate) *
  # (total cases in the population excluding those in the same household)
  n_I <- sum(Y == 1)
  inc_nhh <- t(apply(Y, 1, function(y) {

```

```

    rbinom(hh_size, size = 1, prob = pexp(1, beta_nhh * (n_I - sum(y == 1))))
  ))
  inc_nhh[Y != 0] <- 0
  inc_nhh[inc_hh == 1] <- 0

  # -- alternative assumption for non-household transmission:
  #   includes contacts with own family outside household
  # inc_nhh <- matrix(rbinom(hh_total * hh_size, size = 1,
  #                           prob = pexp(1, beta_nhh * sum(Y == 1))),
  #                   hh_total, hh_size)
  # inc_nhh[Y != 0] <- 0
  # inc_nhh[inc_hh == 1] <- 0
  # -----

  # Event (C): recovery
  recov <- matrix(rbinom(hh_total, size = 1, prob = pexp(1, gamma_rate)),
                  hh_total, hh_size)

  # calculate Rt
  rt_hh <- t(apply(Y, 1, function(y) {
    rbinom(hh_size, size = 1, prob = pexp(1 / gamma_rate, beta_hh * sum(y == 1)))
  }))
  rt_hh[Y != 0] <- 0

  rt_nhh <- t(apply(Y, 1, function(y) {
    rbinom(hh_size, size = 1, prob = pexp(1 / gamma_rate, beta_nhh * (n_I - sum(y == 1))))
  }))
  rt_nhh[Y != 0] <- 0
  rt_nhh[rt_hh == 1] <- 0
  Outp$rt_hh[t+1] = sum(rt_hh)/sum(Y == 1)
  Outp$rt_nhh[t+1] = sum(rt_nhh)/sum(Y == 1)

  # number of new infections
  Outp$inc_hh[t+1] = sum(inc_hh)      # from household transmission
  Outp$inc_nhh[t+1] = sum(inc_nhh)    # from non-household transmission

  # update output
  Y[Y == 0 & (inc_hh == 1 | inc_nhh)] <- 1
  Y[Y == 1 & recov == 1] <- 2

  Outp$I[t+1] <- sum(Y == 1)
  Outp$R[t+1] <- sum(Y == 2)

  # number of households with 0, 1, 2 infected populations
  Outp$inf_hh_0[t+1] <- table(rowSums((Y == 1)|(Y == 2)))[1]
  Outp$inf_hh_1[t+1] <- table(rowSums((Y == 1)|(Y == 2)))[2]
  Outp$inf_hh_2[t+1] <- table(rowSums((Y == 1)|(Y == 2)))[3]
}

```

```

## [1] "=== transmission rates, survey wave 1 ==="
## [1] "household = 4.52e-01"

```

```
## [1] "non-household = 2.75e-05"
## [1] "=== transmission rates, survey wave 3 ==="
## [1] "household = 4.40e-01"
## [1] "non-household = 5.66e-06"
```

plots

Fig 1. Distribution of I and R

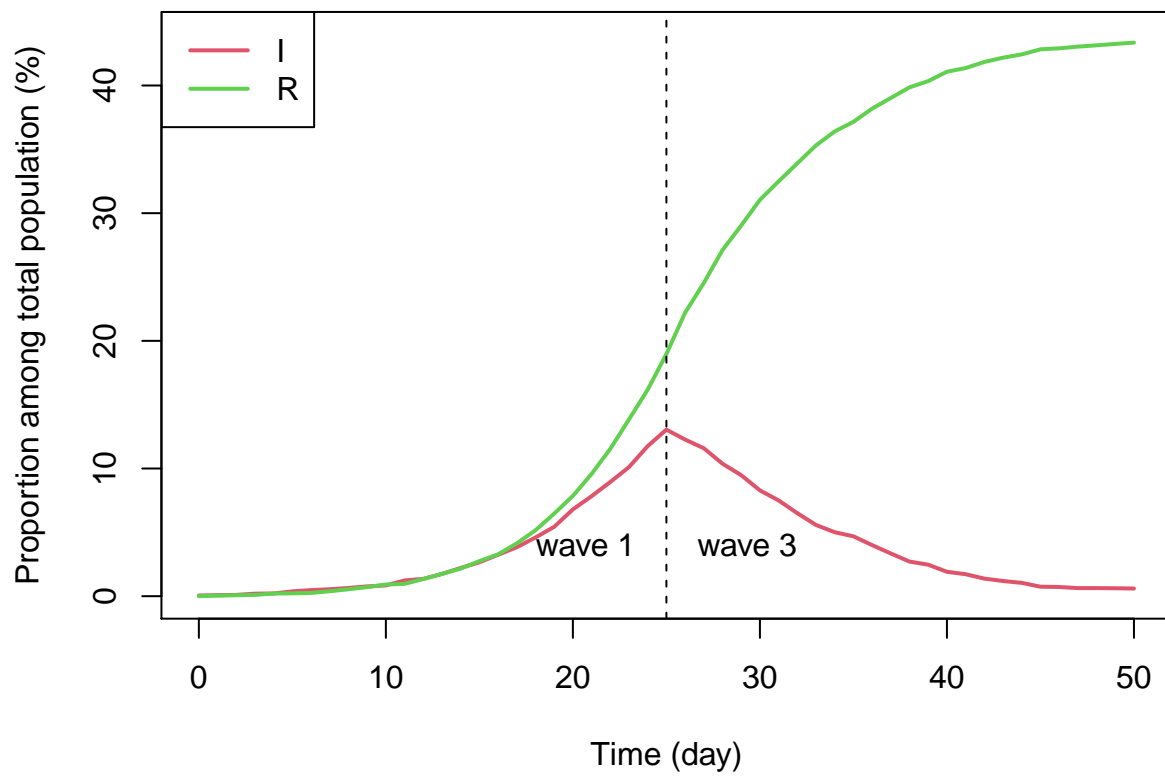


Fig 2. Household and non-household R_t

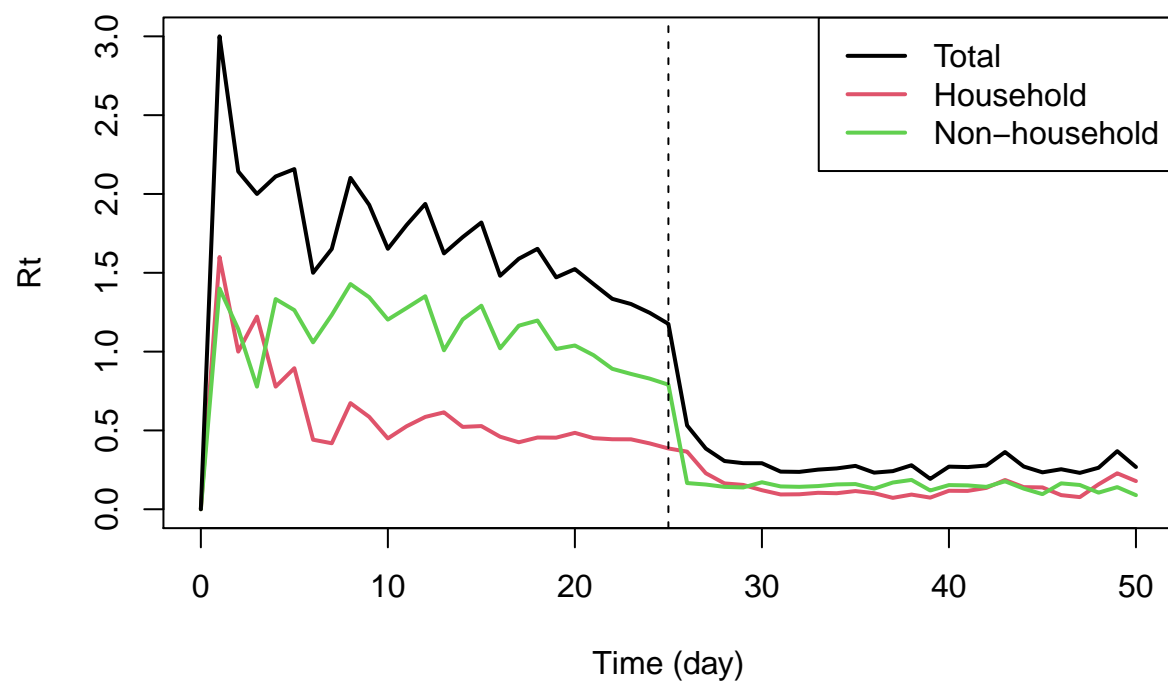


Fig 3. Household and non-household infections

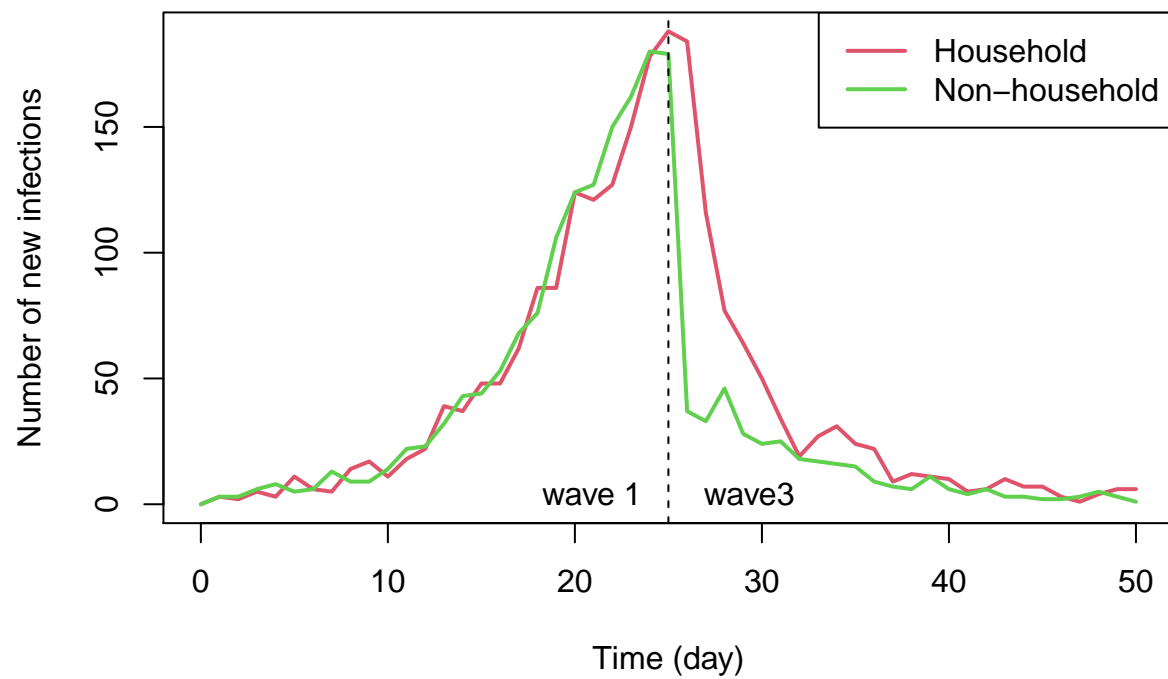


Fig 4. Number of infected within a household

