Initial Model

2024-03-13

LaTeX Equations (for Bevin's Model): $S_h = -\lambda_h N_{sy} + 1 - \alpha N_{sy}(\iota) + 1 - \omega_a \mu_a N_{ih} - \mu_a N_{sh}$ $S_l = -\lambda_l N_{sl} + 1 - \alpha * N_{sy} * (\iota) + 1 - \omega_a \mu_a N_{il} - \mu_a N_{sh}$ $S_y = -\lambda_y N_{sy} + 1 - \alpha N_{sy}(\iota) + 1 - \omega_y N_{sh}$

$I_h = -\lambda_h N_{sy} + 1 - \alpha * N_{sy} * (\iota) + 1 - \omega_a \mu_a * N_h - \mu_a * N_{sh}$ $I_l = -\lambda_l * N_{sl} + 1 - \alpha * N_{sy} * (\iota) + 1 - \omega_a * \mu_a * N_h - \mu_a * N_{sh}$ $I_y = -\lambda_y * N_{sy} + 1 - \alpha * N_{sy} * (\iota) + 1 - \omega_y * N_{sh}$

$R_h = \gamma * N_{ih} + 1 - \alpha * N_{ry} * (\iota) + 1 - \mu_a * N_h * N_{rh}$ $R_l = \gamma * N_{il} + 1 - \alpha * N_{ry} * (\iota) + 1 - \mu_a * N_h * N_{rl}$ $R_y = \gamma * N_{iy} + 1 - \alpha * N_{ry} * (\iota) + 1 - \mu_a * N_h * N_{ry}$

$V_h = \omega_a N_h - \mu_a N_{vh} + 1 - \omega_y * N_{sy} * \iota$ $V_h = \omega_a N_l - \mu_a N_{vl} + 1 - \omega_y * N_{sy} * \iota$

Where l = low risk group h = high risk group y = young group

```
AoN <- function(t, t0, parms) {
  with(as.list(c(t0, parms)), {
    # 1.Track the population sizes
    h.num <- s.h.num + i.h.num + r.h.num + v.h.num
    l.num <- s.l.num + i.l.num + r.l.num + v.l.num
    y.num <- s.y.num + i.y.num + r.y.num #12-15, this is planned to be removed
    num <- h.num + l.num + y.num

    # 2. Define Contact Rate for low-sexual activity based on the rate for high sexual activity. Define
      beta1 <- ce1 / h.num
      beta2 <- ce2 / num
      beta3 <- ce3 / y.num
      # we are assuming there is a higher contact rate between high-high contacts and then lower contac

#Can we make this assumption that the ce would be the same for these other ones

    # 3.Define lambda
      lambda.hh <- beta1 * i.h.num
      lambda.hl <- 0.5 * beta2 * i.l.num
      lambda.h <- lambda.hh + lambda.hl

      lambda.ll <- beta2 * i.l.num
      lambda.lh <- 0.5 * beta2 * i.h.num
      lambda.l <- lambda.ll + lambda.lh

      lambda.y <- beta3 * i.y.num


# Unsure on this (we have infection probability * contact rate times number of people infected overall?

    mu.a <- 1/lifespan
    mu.y <- 1/childspan # I have no idea how to define death rate for 12-15 year olds
    gamma <- 1/dur.inf
```

```r
    alpha <- 1/puberty_span
    # 3.Write eight differential equations

    #iota represents some parameter we need to represent the proportion of young people that become hig
    #Assume that only susceptible young persons are getting vaccinated.
    #vaccine provides 100% protection so we dont need chi
    # we will model both vaccination of children and adults

    #Susceptibles
    dSh <- (-lambda.h * s.h.num) + (1-(alpha*s.y.num*(iota))) + ((1 - (omega.a)) * (mu.a * h.num)) - (mu
    dSl <- (-lambda.l * s.l.num) + (alpha*s.y.num*(iota)) + ((1 - (omega.a)) * (mu.a * l.num)) - (mu.a *
    dSy <- (-lambda.y * s.y.num) - (alpha*s.y.num) - (mu.y * s.y.num) - (omega.y*s.y.num)

    #Infected
    dIh <- (lambda.h * s.h.num)  + (1-(alpha*i.y.num*(iota))) - (gamma * i.h.num) - (mu.a * i.h.num)
    dIl <- (lambda.l * s.l.num) + (alpha*i.y.num*(iota)) - (gamma * i.l.num) - (mu.a * i.l.num)
    dIy <- (lambda.y * s.y.num) - (alpha*i.y.num) - (gamma * i.y.num) - (mu.y * i.y.num)

    #Recovered
    dRh <- (gamma * i.h.num) + (1-(alpha*r.y.num*(iota))) - (mu.a * r.h.num)
    dRl <- (gamma * i.l.num) + (alpha*r.y.num*(iota)) - (mu.a * r.l.num)
    dRy <- (gamma * i.y.num) - (alpha*r.y.num) - (mu.y * r.y.num)

    #Vaccinated
    dVh <- (omega.a * (mu.a)*(h.num)) - (mu.a * v.h.num) + (1-(omega.y*s.y.num*iota))
    dVl <- (omega.a * (mu.a)*(l.num)) - (mu.a * v.l.num) + (omega.y*s.y.num*iota)
    # 4.Outputs
    list(c(dSh, dSl, dSy,dIh, dIl, dIy, dRh, dRl, dRy, dVh, dVl,
           si.h.flow = lambda.h * s.h.num,
           si.l.flow = lambda.l * s.l.num,
           v.h.flow = (omega.a * mu.a * h.num + (1-(omega.y * s.y.num * iota))),
           v.l.flow = (omega.a * mu.a * l.num + (omega.y * s.y.num * iota))
    ))
  })
}

param <- param.dcm(tau = 0.5, ce1 = 0.34, ce2 = 0.07, ce3 = 0.001, lifespan = (50*365), childspan = (80*
                   dur.inf = 14, omega.a = 0.25, omega.y = 0.5, chi = 0.5, iota = 0.9)

init <- init.dcm(s.h.num = 100, s.l.num = 100, s.y.num = 100, i.h.num = 1, i.l.num = 1, i.y.num = 1, r.
                 si.h.flow = 0, si.l.flow = 0, v.h.flow = 0, v.l.flow = 0)

control <- control.dcm(nsteps = (5*365), new.mod = AoN)

mod <- dcm(param, init, control)
mod
```

```
## EpiModel Simulation
## =======================
## Model class: dcm
##
## Simulation Summary
## -----------------------
```

```
## No. runs: 1
## No. time steps: 1825
##
## Model Parameters
## -----------------------
## tau = 0.5
## ce1 = 0.34
## ce2 = 0.07
## ce3 = 0.001
## lifespan = 18250
## childspan = 29200
## puberty_span = 1095
## dur.inf = 14
## omega.a = 0.25
## omega.y = 0.5
## chi = 0.5
## iota = 0.9
##
## Model Output
## -----------------------
## Variables: s.h.num s.l.num s.y.num i.h.num i.l.num i.y.num
## r.h.num r.l.num r.y.num v.h.num v.l.num si.h.flow si.l.flow
## v.h.flow v.l.flow
```

```r
#Note: Added more code similar to this below, made some modifications which you may find to be easier
# Add number infected and prevalence

mod <- mutate_epi(mod, h.num = s.h.num + i.h.num + r.h.num + v.h.num, l.num = s.l.num + i.l.num + r.l.n
mod <- mutate_epi(mod, h.prev = i.h.num / h.num, l.prev = i.l.num / l.num)


par(mfrow = c(2,2), mar = c(3,3,2,1), mgp = c(2,1,0))

plot(mod, y = "i.h.num", main = "number infected high_activity",
legend = "lim", lwd = 1)

plot(mod, y = "i.l.num", main = "number infected low_activity",
legend = "lim", lwd = 1)

plot(mod, y = "h.prev", main = "prev infected high_activity",
legend = "lim", lwd = 1, ylim = c(0, 0.5))

plot(mod, y = "l.prev", main = "prev infected low_activity",
legend = "lim", lwd = 1, ylim = c(0, 0.1))
```
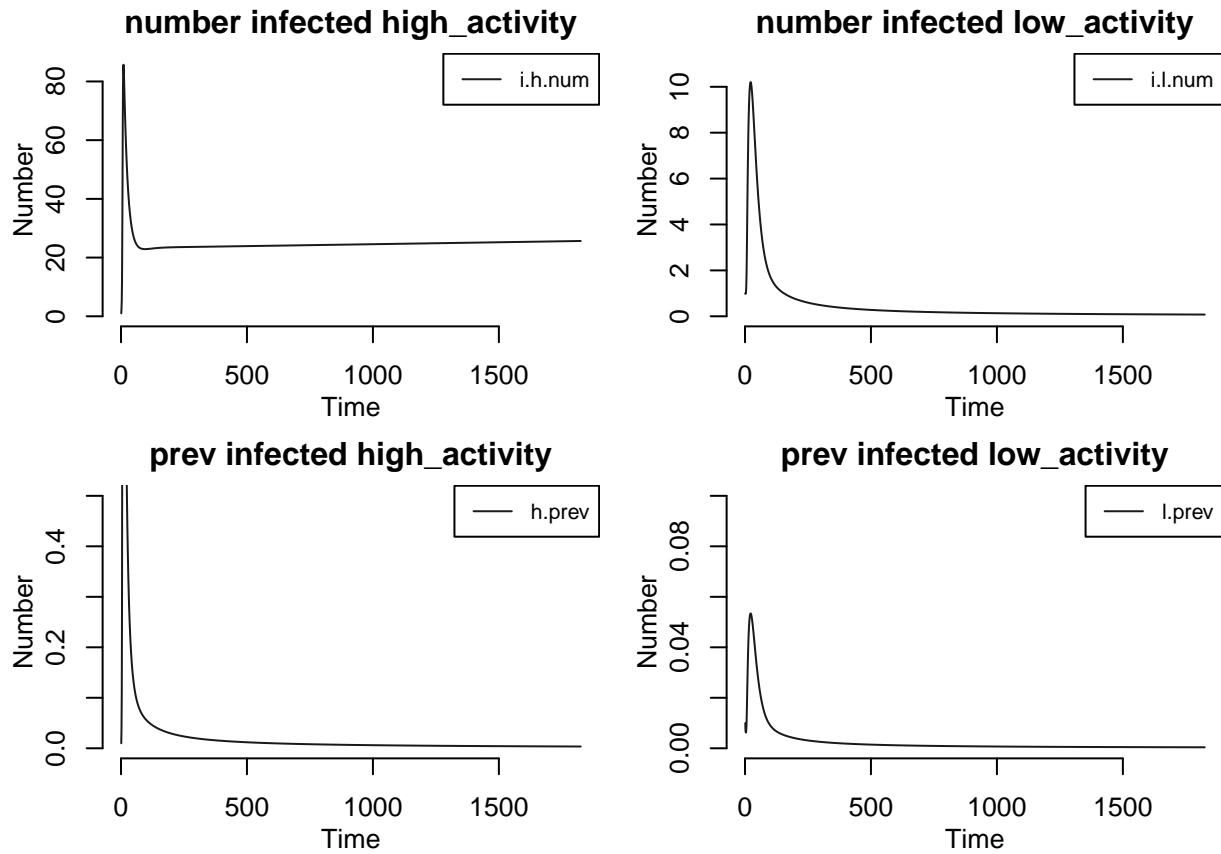
number infected high_activity

number infected low_activity

prev infected high_activity

prev infected low_activity

```r
#Graphs for S, I, R, V
H <- c("s.h.num","i.h.num","r.h.num","v.h.num")
L <- c("s.l.num","i.l.num","r.l.num","v.l.num")
Y <- c("s.y.num","i.y.num","r.y.num","v.y.num")

df_mod <- as.data.frame(mod)
colnames(mod)
```
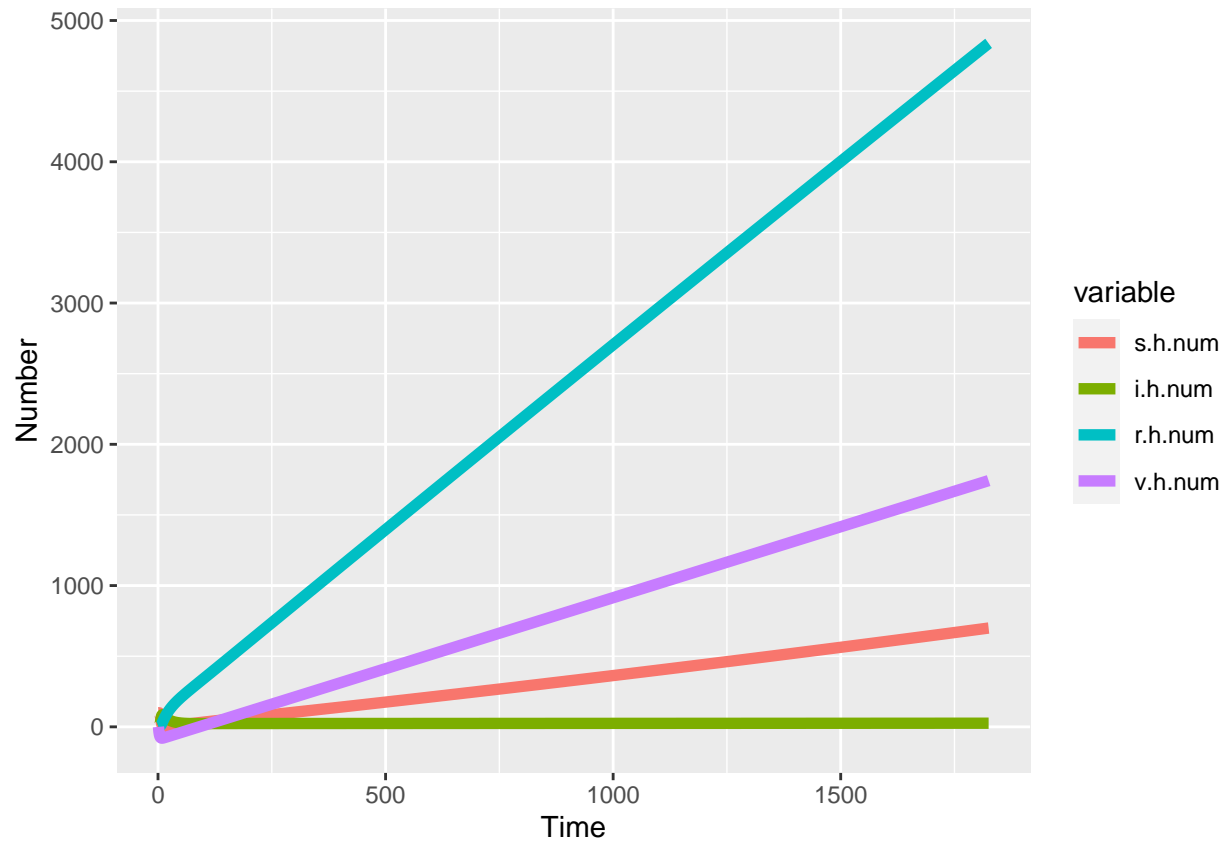
```
## NULL
```

```r
mod_long <- melt(as.data.frame(mod),"time")

mod_long_subset1 <- subset(mod_long, variable %in% H)
mod_long_subset2 <- subset(mod_long, variable %in% L)
mod_long_subset3 <- subset(mod_long, variable %in% Y)

ggplot(mod_long_subset1,aes(x=time,y=value,colour=variable,group=variable))+
  geom_line(lwd=2)+              #Add line
  xlab("Time")+ylab("Number")
```

```
ggplot(mod_long_subset2,aes(x=time,y=value,colour=variable,group=variable))+
  geom_line(lwd=2)+              #Add line
  xlab("Time")+ylab("Number")
```
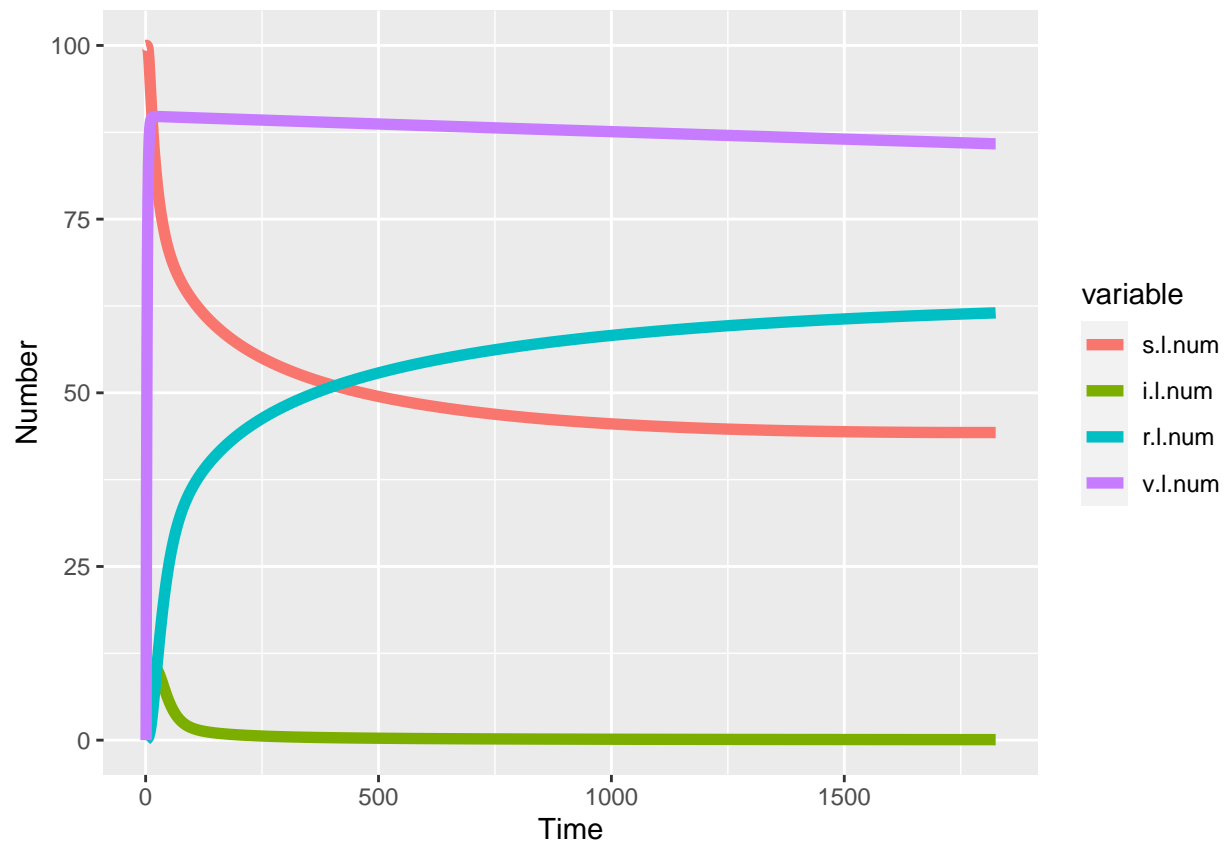
```
ggplot(mod_long_subset3,aes(x=time,y=value,colour=variable,group=variable))+
  geom_line(lwd=2)+                  #Add line
  xlab("Time")+ylab("Number")
```