

# Modelling Club

## Model Code

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### SEIR with Vaccination

Remember for setting up compartmental models, there are several steps. First we load the `deSolve` package, which we use to solve equations in the model.

```
library(deSolve)
```

We want a model that includes the option to vaccinate the population. We assume it takes time to vaccinate, so there will be a vaccination rate  $\nu$  to show how many susceptible people are vaccinated per day. We assume the protection from the vaccine is imperfect, so some vaccinated people will still get infected. Protection levels from the vaccine are given by a vaccine efficacy. This efficacy can be obtained from different manufacturers based on the results of clinical vaccine trials. We can assume the efficacy will be lower in real-life circumstances (i.e. vaccine effectiveness  $VE$ ).

We need to set up the compartments and equations for the model inside a function, which we call `seir.vac`. An SEIR model with vaccination has compartments  $S$ ,  $V$ ,  $E$ ,  $I$ ,  $R$  and parameters  $\beta$ ,  $\nu$ ,  $VE$ ,  $\sigma$ , and  $\gamma$ .

```
seir.vac <- function (t, x, params) { # the function needs three arguments
  S <- x[1] # create local variable S
  V <- x[2] # create local variable V
  E <- x[3] # create local variable E
  I <- x[4] # create local variable I
  R <- x[5] # create local variable R
  with( # code is simpler using "with"
    as.list(params), # with takes variables as a list
    { # the system of rate equations
      dS <- -beta*S*I - nu*S # nu*S is people getting vaccinated
      dV <- nu*S - beta*(1-VE)*V*I # (1-VE) is unprotected vaccinated
      dE <- beta*S*I + beta*(1-VE)*V*I - sigma*E
      dI <- sigma*E - gamma*I
      dR <- gamma*I
      dx <- c(dS,dV, dE,dI,dR) # combine results into vector dx
      list(dx) # return result as a list
    }
  )
}
```

As with our previous compartmental models, we set up the initial conditions for the compartments in `xstart` (the proportion of people in each compartment), the values of the model parameters  $\beta$ ,  $\nu$ ,  $VE$ ,  $\sigma$ , and  $\gamma$  in

params, and the amount of time to run the model in times. Parameter  $VE$  should be a proportion, and  $\nu$  is also a proportion. Think of how many people could be vaccinated in a day, and divide that number by the total in the population to get this number. We start with the example of 100 vaccinations per day and 80% vaccine effectiveness.

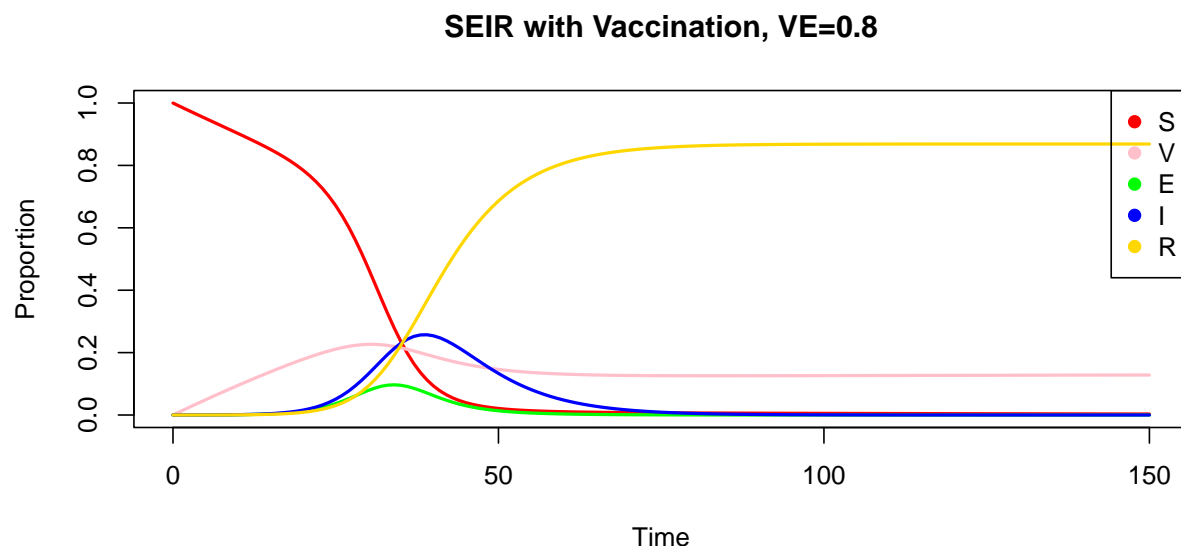
```
xstart <- c(S=9999/10000, V=0, E=0, I=1/10000, R=0) # initial conditions
times <- seq(0, 150, by=1) # 150 days
params <- c(beta=0.7, nu=0.01, VE=0.80, sigma=1/2, gamma=1/7) # parameters
```

We run the model with the numbers we've set, using the function `lsoda()` to solve the equations.

```
out <- as.data.frame(lsoda(xstart, times, seir.vac, params))
```

The output is the proportion of people in each compartment at each time step (each day). We can plot this:

```
plot(NA, NA, xlab="Time", ylab="Proportion", main=paste0("SEIR with Vaccination, VE=", params[3]),
     ylim=c(0,1), xlim=c(0, max(times)))
lines(out$time, out$S, col="red", lwd=2)
lines(out$time, out$V, col="pink", lwd=2)
lines(out$time, out$E, col="green", lwd=2)
lines(out$time, out$I, col="blue", lwd=2)
lines(out$time, out$R, col="gold", lwd=2)
legend("topright", pch=19, c("S", "V", "E", "I", "R"), col=c("red", "pink", "green", "blue", "gold"))
```



We can find the total proportion that were infected:

```
# proportion who were infected are those who recovered
max(out$R)
```

```
[1] 0.868611
```

If you change the values for  $VE$ , you can compare how it impacts the total proportion who were infected. This can also be compared to a scenario without vaccination (i.e. set  $\nu$  to zero).