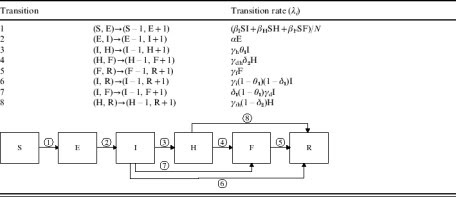
Consider a population of size N, and assume that S is the number of susceptible, E the number of exposed, I the number of infectious, and R for the number recovered (or immune) individuals, \displaystyle{\begin{aligned}{\frac {dS}{dt}}&=-\beta {\frac {I}{N}}S\\[8pt]{\frac {dE}{dt}}&=\beta {\frac {I}{N}}S-aE\\[8pt]{\frac {dI}{dt}}&=aE-b I\\[8pt]{\frac {dR}{dt}}&=b I\end{aligned}}Between S and I, the transition rate is \beta I, where \beta is the average number of contacts per person per time, multiplied by the probability of disease transmission in a contact between a susceptible and an infectious subject. Between I and R, the transition rate is b (simply the rate of recovered or dead, that is, number of recovered or dead during a period of time divided by the total number of infected on that same period of time). And finally, the incubation period is a random variable with exponential distribution with parameter a, so that the average incubation period is a^{-1}.

Probably more interesting, [Understanding the dynamics of ebola epidemics](https://doi.org/10.1017/S0950268806007217) suggested a more complex model, with susceptible people S, exposed E, Infectious, but either in community I, or in hospitals H, some people who died F and finally those who either recover or are buried and therefore are no longer susceptible R.



Thus, the following dynamic model is considered\displaystyle{\begin{aligned}{\frac {dS}{dt}}&=-(\beta\_II+\beta\_HH+\beta\_FF)\frac{S}{N}\\[8pt]\frac {dE}{dt}&=(\beta\_II+\beta\_HH+\beta\_FF)\frac{S}{N}-\alpha E\\[8pt]\frac {dI}{dt}&=\alpha E+\theta\gamma\_H I-(1-\theta)(1-\delta)\gamma\_RI-(1-\theta)\delta\gamma\_FI\\[8pt]\frac {dH}{dt}&=\theta\gamma\_HI-\delta\lambda\_FH-(1-\delta)\lambda\_RH\\[8pt]\frac {dF}{dt}&=(1-\theta)(1-\delta)\gamma\_RI+\delta\lambda\_FH-\nu F\\[8pt]\frac {dR}{dt}&=(1-\theta)(1-\delta)\gamma\_RI+(1-\delta)\lambda\_FH+\nu F\end{aligned}}In that model, parameters are \alpha^{-1} is the (average) incubation period (7 days), \gamma\_H^{-1} the onset to hospitalization (5 days), \gamma\_F^{-1} the onset to death (9 days), \gamma\_R^{-1} the onset to “recovery” (10 days), \lambda\_F^{-1} the hospitalisation to death (4 days) while \lambda\_R^{-1} is the hospitalisation to recovery (5 days), \eta^{-1} is the death to burial (2 days). Here, numbers are from [Understanding the dynamics of ebola epidemics](https://doi.org/10.1017/S0950268806007217) (in the context of ebola). The other parameters are \beta\_I the transmission rate in community (0.588), \beta\_H the transmission rate in hospital (0.794) and \beta\_F the transmission rate at funeral (7.653). Thus

|  |  |
| --- | --- |
| 1  2  3  4  5  6 | epsilon = 0.001  Z = **c**(S = 1-epsilon, E = epsilon, **I**=0,H=0,**F**=0,R=0)  p=**c**(alpha=1/7\*7, theta=0.81, delta=0.81, betai=0.588,  betah=0.794, blambdaf=7.653,N=1, gammah=1/5\*7,  gammaf=1/9.6\*7, gammar=1/10\*7, lambdaf=1/4.6\*7,  lambdar=1/5\*7, nu=1/2\*7) |

If \boldsymbol{Z}=(S,E,I,H,F,R), if we write \frac{\partial \boldsymbol{Z}}{\partial t} = SEIHFR(\boldsymbol{Z})where SEIHFR is

|  |  |
| --- | --- |
| 1  2  3  4  5  6  7  8  9  10  11  12  13  14  15 | SEIHFR = **function**(**t**,Z,p){  S=Z[1]; E=Z[2]; **I**=Z[3]; H=Z[4]; **F**=Z[5]; R=Z[6]  alpha=p["alpha"]; theta=p["theta"]; delta=p["delta"]  betai=p["betai"]; betah=p["betah"]; gammah=p["gammah"]  gammaf=p["gammaf"]; gammar=p["gammar"]; lambdaf=p["lambdaf"]  lambdar=p["lambdar"]; nu=p["nu"]; blambdaf=p["blambdaf"]  N=S+E+**I**+H+**F**+R  dS=-(betai\***I**+betah\*H+blambdaf\***F**)\*S/N  dE=(betai\***I**+betah\*H+blambdaf\***F**)\*S/N-alpha\*E  dI=alpha\*E-theta\*gammah\*I-(1-theta)\*(1-delta)\*gammar\*I-(1-theta)\*delta\*gammaf\***I**  dH=theta\*gammah\*I-delta\*lambdaf\*H-(1-delta)\*lambdaf\*H  dF=(1-theta)\*(1-delta)\*gammar\***I**+delta\*lambdaf\*H-nu\***F**  dR=(1-theta)\*(1-delta)\*gammar\***I**+(1-delta)\*lambdar\*H+nu\***F**  dZ=**c**(dS,dE,dI,dH,dF,dR)  **list**(dZ)} |

We can solve it, or at least study the dynamics from some starting values

|  |  |
| --- | --- |
| 1  2  3 | **library**(deSolve)  times = **seq**(0, 50, **by** = .1)  resol = ode(y=Z, times=times, func=SEIHFR, parms=p) |

For instance, the proportion of people infected is the following

|  |  |
| --- | --- |
| 1  2 | **plot**(resol[,"time"],resol[,"I"],type="l",xlab="time",ylab="",**col**="red")  **lines**(resol[,"time"],resol[,"H"],**col**="blue") |

