R programs for calculating state probabilities following exposure so SARS-CoV-2

Alun Thomas
Division of Epidemiology
Department of Internal Medicine
University of Utah

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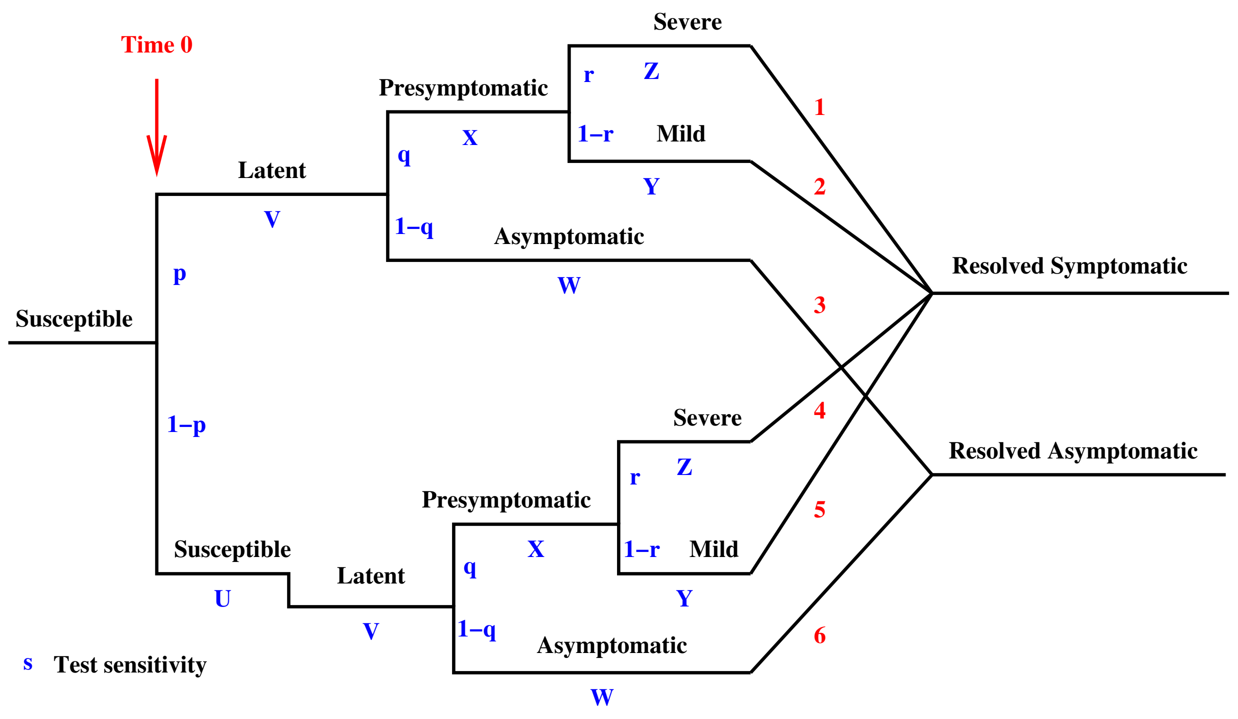
Figure 1: Model for the course of infection. Letters representing the random variables specifying the time in each state and branching probabilities are shown in blue. The red numbers enumerate the possible paths.



Preliminaries

Load required libraries, and declare some mnemonics for disease state indices and Gamma random variables corresponding to those shown in figure 1.

```
library(coga,quietly=TRUE)

.Sus = 1
.Lat = 2
.Asy = 3
.Pre = 4
.Mld = 5
.Svr = 6
.ResS = 7
.ResA = 8
.NStates = .ResA

.U = 1
.V = 2
.W = 3
.X = 4
.Y = 5
.Z = 6

stateNames = c("Sus","Lat","Asy","Pre","Mld","Svr","ResS","ResA")

stateCols = c("green","yellow","pink","orange","magenta","red","cyan","cyan")
```

Model functions

`deltaParams()`

A function to make a data structure holding parameters to model the Delta SARS-CoV-2 variant.

```
deltaParams = function()
{
        msus = 1000

        list (  Psymp = 0.5,
                Psevere = 0.1,
                Msus = msus,
                Vsus = msus^2,
                Mlat = 5.1,
                Vlat = 7.5,
                Masy = 7,
                Vasy = 7.5,
                Mpre = 3,
                Vpre = 1.0,
                Mmld = 5,
                Vmld = 45.5,
                Msev = 11,
                Vsev = 45.5
        )
}
```

`omicronParams()`

A function to make a data structure holding parameters to model the Omicron SARS-CoV-2 variant.

```
omicronParams = function()
{
        ommod = 0.6
        ommod2 = 0.9
        msus = 1000

        list( Psymp = 0.5,
                Psevere = 0.1,
                Msus = msus,
                Vsus = msus^2,
                Mlat = 5.1 * ommod,
                Vlat = 7.5 * ommod^2,
                Masy = 7 * ommod2,
                Vasy = 7.5 * ommod2^2,
                Mpre = 3 * ommod2,
                Vpre = 1.0 * ommod2^2,
                Mmld = 5 * ommod2,
                Vmld = 45.5 * ommod2^2,
                Msev = 11 * ommod2,
                Vsev = 45.5 * ommod2^2,
                ommod = ommod,
                ommod2 = ommod2
        )
}
```

`makeModel()`

A function to convert a SARS-CoV-2 model specified by means and variances into a collection of Gamma shape and rate parameters, with associated path splitting probabilities.

```
makeModel = function(Q)
{
# Order must match definitions above
        means = c(Q$Msus,Q$Mlat,Q$Masy,Q$Mpre,Q$Mmld,Q$Msev)
        vars  = c(Q$Vsus,Q$Vlat,Q$Vasy,Q$Vpre,Q$Vmld,Q$Vsev)
        list(q=Q$Psymp, r=Q$Psevere, shape=means^2/vars, rate=means/vars)
}
```

Exact computation of state probabilities

`FF()`

A function calling `pcoga()` to calculate the cumulative distribution function of a sum selected Gamma random variables.

```
FF = function(x,P,use)
{
        pcoga(x,P$shape[use],P$rate[use])
}
```

`StateProbs()`

A function to calculate the state probabilities for a vector of times `x`, using model `M`, with probability `p` that a transmission occurred at time 0.

```
StateProbs = function(x,p,M)
{
        S1 = matrix(0,nrow=.NStates,ncol=length(x))
        S1[.Sus,] = 0
        fv = FF(x,M,c(.V))
        S1[.Lat,] = 1-fv
        fvw = FF(x,M,c(.V,.W))
        S1[.Asy,] = (1-M$q)*(fv-fvw)
        fvx = FF(x,M,c(.V,.X))
        S1[.Pre,] = M$q*(fv-fvx)
        fvxy = FF(x,M,c(.V,.X,.Y))
        S1[.Mld,] = M$q*(1-M$r)*(fvx-fvxy)
        fvxz = FF(x,M,c(.V,.X,.Z))
        S1[.Svr,] = M$q*M$r*(fvx-fvxz)
        S1[.ResS,] = M$q*(M$r*fvxz + (1-M$r)*fvxy)
        S1[.ResA,] = (1-M$q)*fvw
        S0 = matrix(0,nrow=.NStates,ncol=length(x))
        fu = FF(x,M,c(.U))
        S0[.Sus,] = 1-fu
        fuv = FF(x,M,c(.U,.V))
        S0[.Lat,] = fu-fuv
        fuvw = FF(x,M,c(.U,.V,.W))
        S0[.Asy,] = (1-M$q)*(fuv-fuvw)
        fuvx = FF(x,M,c(.U,.V,.X))
        S0[.Pre,] = M$q * (fuv - fuvx)
        fuvxy = FF(x,M,c(.U,.V,.X,.Y))
        S0[.Mld,] = M$q*(1-M$r) * (fuvx - fuvxy)
        fuvxz = FF(x,M,c(.U,.V,.X,.Z))
        S0[.Svr,] = M$q*M$r * (fuvx - fuvxz)
        S0[.ResS,] = M$q* ( M$r*fuvxz + (1-M$r) * fuvxy)
        S0[.ResA,] = (1-M$q) * fuvw

        p * S1 + (1-p) * S0
}
```

Computation of state probabilties by simulation

`rCovid()`

A function to simulate the infection states at times `x` using model `M`, infected with probability `p` at time 0.

```
rCovid = function(x,p,M)
{
        G = rgamma(length(M$shape),M$shape,M$rate)

        sus = G[.U]
        if (runif(1) < p)
                sus = 0

        if (runif(1) < M$q)
        {
                s = rep(.ResS,length(x))
                if (runif(1) < M$r)
                {
                        s[x < sus + G[.V] + G[.X] + G[.Z]] = .Svr
                }
                else
                {
                        s[x < sus + G[.V] + G[.X] + G[.Y]] = .Mld
                }
                s[x < sus + G[.V] + G[.X]] = .Pre
        }
        else
        {
                s = rep(.ResA,length(x))
                s[x < sus + G[.V] + G[.W]] = .Asy
        }

        s[x < sus + G[.V]] = .Lat
        s[x < sus] = .Sus

        s
}
```

`asStateMatrix()`

A function to convert the vector of infections states into a 0/1 matrix of state probabilities.

```
asStateMatrix = function(y)
{
        s = matrix(0,nrow=.NStates,ncol=length(y))
        #for (j in 1:ncol(s))
        # s[y[j],j] = s[y[j],j]+1
        for (i in 1:nrow(s))
                s[i,y==i] = s[i,y==i]+1
        s
}
```

`SimStateProbs()`

A function to caluclate the state probabilities for a vector of times `x`, using the parameters in the model `M`, with probability `p` that a transmission occurred at time 0, based on `sims` individual state simulations.

```
SimStateProbs = function(x,p,M,sims=10000)
{
        s = matrix(0,nrow=.NStates,ncol=length(x))
        for (i in 1:sims)
                s = s+asStateMatrix(rCovid(x,p,M))
        s/sims
}
```

Conditioning events

Vectors and functions specifying vectors that give the probabilities of events given the underlying states. Used to calculate, by Bayes rule, the probabilities of the underlying states given the observed events. The events include:

- `Unconditional`: no observation.
- `NoSymptoms`: no symptoms are observed.
- `Infected`: the individual is infected.
- `PcrTest()`: a NEGATIVE PCR test with specified sensitivity and specificity is observed.
- `AntigenTest()`: a NEGATIVE antigen test with specified sensitivity and specificity is observed.

```
Unconditional = c(1,1,1,1,1,1,1,1)
NoSymptoms = c(1,1,1,1,0,0,0,1)
Infected = c(0,1,1,1,1,1,0,0)

PcrTest = function(sens,spec=1)
{
        c(spec,spec,1-sens,1-sens,1-sens,1-sens,1-sens,1-sens)
}

AntigenTest = function(sens,spec=1)
{
        c(spec,spec,1-sens,1-sens,1-sens,1-sens,spec,spec)
}
```

`ProbInfected()`

A function to calculate the probability that an individual is infected at a vector of times `x` following exposure, where the probability of transmission is `p`, the SARS-CoV-2 model is specified by the structure `M`. The probabilities are conditional given the observations specified by the vector `observation`.

```
ProbInfected = function(probs,observation)
{
        bot = observation %*% probs
        top = (Infected * observation) %*% probs
        top/bot
}
```

`ConditionalStateProbs()`

A function to calculate the conditional state probabilities for an individual at a vector of times `x` following exposure, where the probability of transmission is `p`, the SARS-CoV-2 model is specified by the structure `M`. The probabilities are conditional given the observations specified by the vector `observation`.

```
ConditionalStateProbs = function(probs,observation)
{
        y = probs
        for (j in 1:length(y[1,]))
        {
                y[,j] = y[,j]*observation
                y[,j] = y[,j]/sum(y[,j])
        }
        y
}
```

`PostProbTransmission()`

A function to calculate the posterior probability that a transmission occurred at time 0, given an observation specified by `observation`. The prior probability of transmission is specified by `p`.

```
PostProbTransmission = function(P0,P1,observation,p)
{
        q1 = observation %*% P1
        q0 = observation %*% P0
        q1 * p / (q1 * p + q0 * (1-p))
}
```

Functions to plot output

Functions to plot a pile up of state probabilities

First a function to draw a frame suitable for plotting probabilities.

```
frame = function(x,xl="Days from exposure",yl="Probability",ymax=1)
{
        plot(x,x,type="n",ylim=c(0,ymax), ylab=yl, xlab=xl)
}
```

Then a function to find the first index into a vector where the value is the maximum of the vector.

```
maximizer = function(x)
{
        (1:length(x))[x==max(x)][1]
}
```

Then a function to draw the pileup given the vector of times, the state probabilities, some colours and labels.

```
skeletonPileup = function(x,ss,stCols,stNames)
{
        frame(x,yl="Cumulative probability")
        s = apply(ss,2,cumsum)
        lns = rev(1:length(s[,1]))
        for (i in lns)
        {
                lines(x,s[i,])
                polygon(c(x,max(x),0),c(s[i,],0,0),col=stCols[i],border=NA)
        }

        for (i in lns)
        {
                zz = ss[i,]
                if (i > 1)
                        z = s[i-1,]
                else
                        z = rep(0,length(zz))

                if (max(zz) > 0)
                {
                        whj = maximizer(zz)
                        whx = x[whj]
                        whx = min(c(whx,0.90*max(x)))
                        whx = max(c(whx,0.05*max(x)))
                        why = z[whj] + zz[whj]/2
                        text(whx,why,stNames[i])
                }
        }
}
```

A function to draw a pileup of all the states.

```
pileUp = function(x,ss)
{
        skeletonPileup(x,ss,stateCols,stateNames)
}
```

A function to draw a pileup with some states combined.

```
pileup = function(x,sss,opt=2)
{
        ss = matrix(0,ncol=ncol(sss),nrow=nrow(sss)-2)

        if (opt == 2)
        {
                stCols = c("green","yellow","pink","orange","red","cyan")
                stNames = c("Sus","Lat","Asy","Pre","Sym","Res")
                ss[1:4,] = sss[1:4,]
                ss[5,] = sss[5,] + sss[6,]
                ss[6,] = sss[7,] + sss[8,]
        }

        if (opt == 1)
        {
                stCols = c("yellow","pink","orange","red","cyan","green")
                stNames = c("Lat","Asy","Pre","Sym","Res","Sus")
                ss[1:3,] = sss[2:4,]
                ss[4,] = sss[5,] + sss[6,]
                ss[5,] = sss[7,] + sss[8,]
                ss[6,] = sss[1,]
        }

        skeletonPileup(x,ss,stCols,stNames)
}
```