2D epidemic model

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Epidemic model

Basic definition

Use

$$\begin{aligned} S_{t+1} &= S_t + m(N - S_t) - S_t\left(1 - e^{-\beta I_t}\right) \\ I_{t+1} &= I_t + S_t\left(1 - e^{-\beta I_t}\right) - (m+\gamma) I_t \end{aligned}$$

Parameters: m, birth/death rate ($1/m$ is the average lifespan measured in units of Δt); γ, recovery rate ($1/\gamma$ is the average length of infectivity, ditto); β is the contact rate (new infections per susceptible per infective per time period); N is the population size (can be rescaled to proportion of population if we rescale β as well, unless we are dealing with a discrete-population model).

Stability of DFE (disease-free equilibrium)

As mentioned in class, it's hard to solve for the equilibrium analytically, let alone say very much about its stability.

In general, the Jacobian is

$$\begin{pmatrix} -m + e^{-\beta I^*} & -\beta S^* e^{-\beta I^*} \\ \left(1 - e^{-\beta I^*}\right) & 1 + \beta S^* e^{-\beta I^*} - (m+\gamma) \end{pmatrix}$$

At the disease-free equilibrium ($I = 0, S = N$):

$$\begin{pmatrix} 1 - m & -\beta N \\ 0 & 1 + \beta N - (m+\gamma) \end{pmatrix}$$

From this we can work out (with some effort!) that

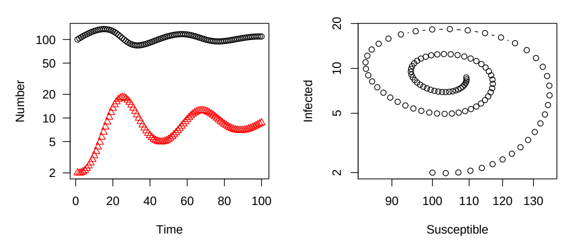
$$\begin{aligned} T &= 2 - 2m - \gamma + \beta N \\ \Delta &= (1-m)(1 + \beta N - m - \gamma) \\ &= 1 - 2m - \gamma + \beta N - m(\beta N - (m+\gamma)) \\ \Delta + 1 &= T - m(\beta N - (m+\gamma)) \end{aligned}$$

The $|T| < 1 + \Delta$ criterion is therefore violated if $\beta N/(m+\gamma) \equiv R_0 > 1$. As discussed in class, βN is the rate of infection for 1 infected individual in an otherwise susceptible population (should perhaps be $\beta(N-1)$, but not important if N large); $1/(m+\gamma)$ is the average length of infectivity, accounting both for recovery and death. (Don't know if the negative condition, $-T > 1 + \Delta$, makes sense or not ...)

$\Delta > 1$ only if $(\beta N - \frac{m}{1-m})/(m+\gamma) > 1$, which is more stringent than the case above.

Basic R implementation

```
> params0 <- c(N=1000,beta=0.005,m=0.005,gamma=0.5)
> ## define updating function with magic 'with' command
> F <- function(X,params) {
   with(c(as.list(X),as.list(params)),
        c(S=S+m*(N-S)-S*(1-exp(-beta*I)),
          I=I+S*(1-exp(-beta*I))-(m+gamma)*I))
 }
> nt <- 100
> res <- matrix(ncol=2,nrow=nt)
> colnames(res) <- c("S","I")
> res[1,] <- c(100,2)
> for (i in 2:nt) {
   res[i,] <- F(res[i-1,],params0)
 }
```



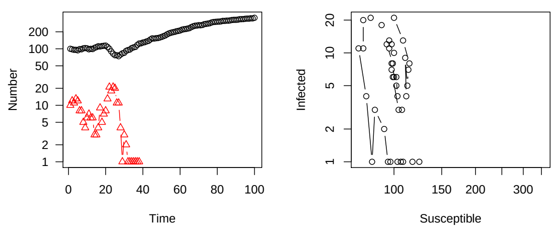
I can't prove it's generally true for all $R_0 > 1$, but in this case it looks as though the endemic (internal) equilibrium is stable (noting that we started from $\{100, 2\}$, we can see that the curve is spiralling in rather than out). (Used `matplot` and `plot` to produce these graphs.)

Demographic stochasticity: make birth a Poisson variable; death, recovery, and infection are binomial variables (we don't need to keep track of death and recovery for I separately).

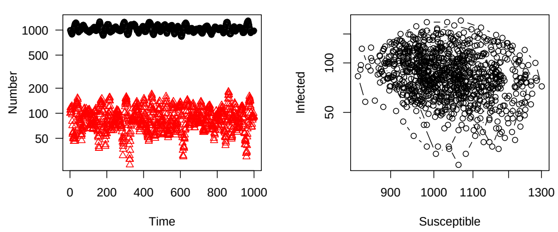
```
> F_ds <- function(X,params) {
   with(c(as.list(X),as.list(params)),
```

```
{ birth <- rpois(1,m*N)
  Sdeath <- rbinom(1,prob=m,size=S)
  Irdeath <- rbinom(1,prob=m+gamma,size=I)
  infec <- rbinom(1,prob=1-exp(-beta*I),size=S)
  c(S=S+birth-Sdeath-infec,
    I=I+infec-Irdeath)
})}
```

With default parameters and starting values $\{S = 100, I = 10\}$ the disease actually goes extinct pretty quickly:



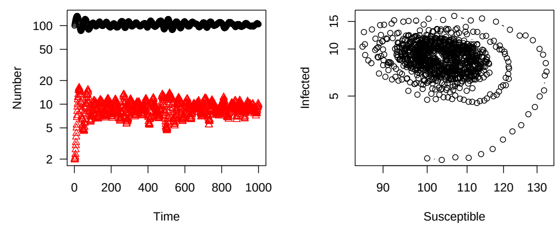
Now increase N to 10^4 and scale β down to 5×10^{-4} (i.e., maintaining the same value of R_0): run for 1000 time steps.



Alternatively, we could add variation in β. We'll make the variation log-normal: for small values of σ, σ describes the proportional variation around the mean.

```
> F_es <- function(X,params) {
   with(c(as.list(X),as.list(params)),
        {
          betaval <- rlnorm(1,meanlog=log(beta),
                            sdlog=sdbeta)
          c(S=S+m*(N-S)-S*(1-exp(-betaval*I)),
            I=I+S*(1-exp(-betaval*I))-(m+gamma)*I)
        })}
```

With $\sigma_\beta = 0.1$ (otherwise back to the original parameters):



Finally, we'll try a case with occasional catastrophes. With a small probability ($p_{\text{cat}} = 0.02$) β is much larger than (m_{cat} times) its usual value:

```
> F_cat <- function(X,params) {
   with(c(as.list(X),as.list(params)),
        {
          if (runif(1)<catprob) {
            betaval <- catmult*beta
          } else betaval <- beta
          c(S=S+m*(N-S)-S*(1-exp(-betaval*I)),
            I=I+S*(1-exp(-betaval*I))-(m+gamma)*I)
          })
 }
```

With $m_{\text{cat}} = 10$, $p_{\text{cat}} = 0.02$,