1. The Kermack-McKendrick equation

The Kermack-McKendrick Equation is an important and simple model for a virus epidemic, which either kills its victims or renders them immune, first considered by W. O. Kermack and A. G. McKendrick in 1927.

Parameter names:

- s is the fraction of the population which is susceptible to infection.
- c is the fraction of the population which is contagious.
- r is the fraction of the population which is removed, either by recovery with immunity or by death.
- β is the transmission rate: the proportionality constant mediating transmission.
- α is the rate of decay of contagiousness: an individual has a $e^{-\alpha\tau}$ chance to still be contagious a time τ after infection; or, alternatively, an individual's level of contagiousness declines according to this exponential decay.

We assume $s + c + r = 1$, so we are supposing that the only way an individual can fail to be susceptible to the desease is either to have it or to have had it. We are thus considering only the initially susceptible population.

The three variables are often written S, I (for "infected"), and R, and this model is often called the SIR model.

Does such an epidemic eventually infect the entire population, or is it somehow self-limiting? Will it take off or sputter out? Can we relate various aspects of the course of this epidemic, such as the peak of the contagious proportion of the population and the proportion of the population which ultimately contracts the disease?

The meaning of β is that $\dot{s} = -\beta sc$.

(a) Explain this: Why should $\dot{s}$ be proportional to both s and c? Why should the proportionality constant be negative?

The meaning of α is that $\dot{c} = \beta sc - \alpha c$.

(b) Explain this: What are the two processes yielding the two terms in $\dot{c}$? Why should one of them be $-\dot{s}$?

Together we have a "system" of equations: two functions of time, and an expression of the derivative of each in terms of the values of both. This is a subject we will take up in earnest at the end of the

course, but we can already get pretty far in analyzing it. The first step is the physics-inspired idea (as in EP §1.8) of eliminating time:

(c) <u>Explain</u> why these two equations imply

$$\frac{dc}{ds} = \gamma s^{-1} - 1$$

for some constant γ. What is γ in terms of α and β? From the expression of γ in terms of the decay rate of infection α, and the transmission rate β, what would you expect small γ to mean about the equation? What would large γ mean?

(d) <u>Solve</u> this equation; you should get

$$\underline{c = \gamma \ln |s| - s + a}$$

where a is the constant of integration. <u>When c is very small, that is,</u> at the start of the epidemic, s should be near 1. This leads to $a = 1$. We choose to write the result as

(1) $$c = \gamma \ln |s| - (s - 1).$$

Once we know c in terms of s, we can substitute this back into the original equation for $\dot{s}$ to obtain

(2) $$\dot{s} = \beta s(s - 1 - \gamma \ln |s|).$$

This is a subtle variant of the logistic equation, with the advantage that one doesn't have to know the limiting population in advance.

This is an autonomous equation, and <u>we will study its critical points.</u> The effect of this equation depends upon the value of the parameter γ. (From now on we'll assume $s > 0$, as it is in the application at hand; in fact, in our application $0 < s < 1$.) <u>First, draw the graphs of $s - 1$ and of $\ln s$.</u> They are tangent at $(1, 0)$. Multiplying $\ln s$ by the positive constant γ <u>stretches this graph vertically</u> by a factor of $\gamma > 0$. It still meets the graph of $s - 1$ at $s = 1$, but if $\gamma \neq 1$ the graphs meet one additional time, at $s = s_{\text{crit}}$. <u>If $\gamma > 1$, $s_{\text{crit}} > 1$; if $\gamma < 1$, $0 < s_{\text{crit}} < 1$.</u>

The equation $s_{\text{crit}} - 1 = \gamma \ln |s_{\text{crit}}|$ <u>can't be solved</u> analytically for s_{crit} in terms of γ, but we can find γ in terms of s_{crit} (which we will restrict to be positive!):

$$\gamma = \frac{s_{\text{crit}} - 1}{\ln s_{\text{crit}}}.$$

It can be plugged into MATLAB. Let's do that.

MATLAB contains a powerful and accurate ODE solver, called `ode45`. If you fire up MATLAB and type `help ode45` you'll get a screenful of command summaries, from which the following is extracted.

```r
library(deSolve)
library(ggplot2)
library(dplyr)

# Define the ODE system
SIR <- function(t, state, parameters) {
  with(as.list(c(state, parameters)), {
    dS <- - beta * S * C
    dC <- beta * S * C - alpha * C
    dR <- alpha * C
    list(c(dS, dC, dR))
  })
}

# Parameters and initial conditions
parameters <- c(alpha = 0.14, beta = 0.23)
state <- c(S = 0.999999, C = 0.000001, R = 0)
times <- seq(0, 330, by = 1)

# Solve
out <- ode(y = state, times = times, func = SIR, parms = parameters)

# Plot with ggplot2
out_df <- as.data.frame(out)
ggplot(out_df, aes(x = time)) +
  geom_line(aes(y = S, color = "Susceptible")) +
  geom_line(aes(y = C, color = "Contagious")) +
  geom_line(aes(y = R, color = "removed")) +
  labs(title = "SIR in R", x = "time", y = "Population", color = "Compartment") +
  theme_minimal()
```

In order to use `ode45` you will have to create and store a file containing a description of the function $F(x,t)$ occuring in the ODE $\dot{x} = F(x,t)$. Here's the file:

```
function sdot=sir(t,s,flag,beta,gamma);

sdot = beta*s*(s-1-gamma*log(s));
```

(Remember, the semicolons suppress the screen printout of the answers.)

Now let's pick some values. Reasonable values are $\gamma = .5$, $\beta = 1$. Take as initial value $s = .999999$ (so only one in a million is contagious). We might watch the evolution of the disease over 75 time units. All this is accomplished by typing:

```
[t,s]=ode45('sir',[0,75],.999999,[],1,.5)
```

When you hit ⟨enter⟩, a list of pairs of numbers should stream across the screen. Those are values of t followed by corresponding computed values of s. This command has defined two lists of numbers, t and s, of the same length.

We want to plot s against t. This is easy: type

```
plot(t,s)
```

A window appears with a graph on it. The graph is somewhat deceptive; it probably doesn't extend all the way down to $s = 0$. To make it extend to zero, declare explicitly what you want your axis dimensions to be:

```
axes([0,75,0,1])
```

To line things up with the eye a little better, add a grid, using `grid`. Notice how long it takes for the susceptable population to get enough below 1.0 to be visible on this plot!

Finally, let's add to this the graph of c, the contagious population. First compute it using **(d)** above:

```
c=(.5)*log(s)-s+1
```

Again a list of numbers will stream across the screen. To plot it against t, on the same graph, type `hold on` (which makes future graphing commands plot on the same window instead of a new one) and then `plot(t,c)`. Again, note how long it takes for the contagious population to become noticeable!

(e) From the graph, estimate the time at which the contagious population is a maximum, and what that maximum is. Also, estimate the

fraction of the population which is left susceptible as $t \to \infty$. Print out and hand in the plot you made (by selecting File/Print on Figure No. 1).

Further comments:

The significance of (1) depends upon the value of γ. The tangent line to $c = \ln|x|$ at $(1,0)$ is given by $c = s - 1$ and lies above the curve. If $\gamma > 1$, $\gamma \ln|s|$ passes through the same point but more steeply, and intersects $c = s - 1$ at $s = 1$ and again at a point $s > 1$, which is not meaningful in our application. If $\gamma > 1$, $c < 0$ when $0 < s < 1$. What happens here is: nothing, the epidemic never gets started, since the rate of decay of contagiousness is too large relative to the transmission rate of the disease. On the other hand if $\gamma < 1$, the epidemic flares and dies off, with little effect if γ is near 1 and with more devastating effect if γ is small. Small γ reflects a slow decay rate of contagiousness relative to the transmission rate of the desease. The specific values of α and β determine the speed with which the epidemic spreads, but its trajectory in the (s, c) plane depends only on the quotient γ.

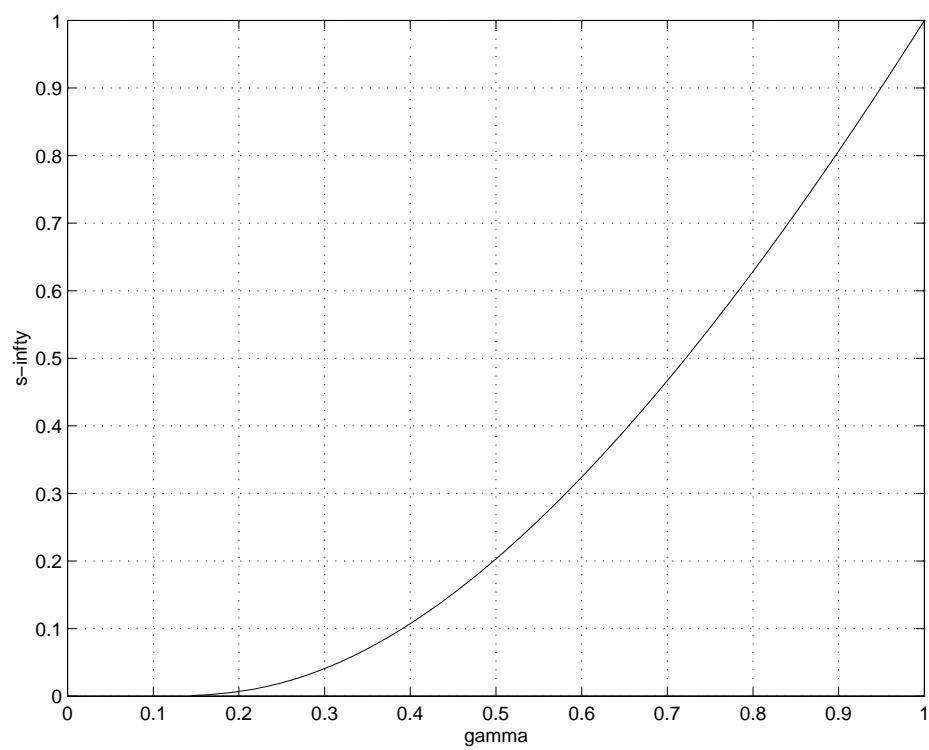The limiting value of s, as $t \to \infty$, can be found by setting $c = 0$ in (1). It satisfies the equation

(3)
$$\gamma = \frac{s_\infty - 1}{\ln s_\infty}$$

This can't be solved for s_∞ in elementary functions, but it's easy to use Matlab to compute γ in terms of s_∞ and then plot the inverse function. One finds that if $\gamma < .2$ then $s_\infty < .01$: more than 99% of the population is infected. As $\gamma \uparrow 1$, $s_\infty \uparrow 1$: the epidemic affects a very small portion of the population if γ is near 1. In any case, some fraction of the population will always survive.

The differential equation $\dot{c} = \beta s c - \alpha c$ tells us where to find the center of the epidemic: the maximum of c occurs when $s = \gamma$, and thus, by (1), is given by

(4)
$$c_{\max} = 1 - \gamma + \gamma \ln \gamma.$$

The invariant γ is thus available to doctors monitoring the disease, assuming they can recognize contagious individuals: they have to watch for the number of contagious individuals to peak. Knowing this peak, they can use (4) to find γ and then (3) to find s_∞—that is, to predict the eventual fraction of the population which will be infected and rendered immune or dead. (Since $c \to 0$, this is $1 - s_\infty$.)

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