In epidemiology, the basic reproduction number, R_0, of an infection can be though of how many new cases are generated from a single infectious individual over the course of its infectious period in an entirely uninfected population. Usually it is the case that if we can determine that $R_0 > 1$ then the infection/disease continuous on for all time and spreads in a population. However if we can determine that $R_0 < 1$ then the disease is expected to die out in the long run. The larger the value of R_0 the harder it is to attempt to control or contain the disease. On actually calculating R_0 will vary heavily depending what your model actually looks like. When the SARS epidemic broke, R_0 for that model was calculated to be approximately 3.6. This meant that without strong controls such a quarantines, hospitalization, and/or treatment, this disease was expected to last forever. Once the intense control measures were implemented, the new R_0 for a new model became 0.7. This meant that enough control/work had been done that the disease would eventually die out overtime.

1. Example

If we look at a simple example where each infectious individual makes β contacts per unit time and that the infection has a mean infections period of $\frac{1}{\gamma}$ then $R_0 = \frac{\beta}{\gamma}$

More generally we have the following properties:
R_0 is proportional to the length of the infection
R_0 is proportional to the number of contacts that an infectious individual makes
R_0 is proportional to the change of transmitting the infection during an encounter with a susceptible host
$R_0 \propto \frac{infection}{contact} * \frac{contact}{time} * \frac{time}{infection}$
Often in models the last two parts are/can be combined into a single parameter, like in the SIR case where β is the transmission probability which includes both the number of contacts and the chance of transmitting the disease.

2. vaccination

If the model also includes control methods, such as vaccination then you come up with a new R_0 denoted as R_C where
$R_C = R_0(1 - hf)$
where h is the vaccine efficacy (proportion of people vaccinated who will have complete protection)
f is the vaccine coverage (proportion of the population that you expect to actually receive the vaccine).

Note if we want the disease to die out we require the $R_0 < 1$. In this case of vaccination, we can rearrange this equation to get the following:
$f > \frac{R_0 - 1}{hR_0}$
The reasoning for this is once a vaccine is developed, all the terms on the right are now known, and we then just need to figure out what percentage of the population we require to vaccine to help eradicate the disease.
Some real life examples of f required to grant herd immunity.
Measles and Rubella 83-94 percent.
Pertussis 92-94 percent.

3. Next Generation Matrix

The larger the model the more difficult it can become to calculate R_0. What we'll now look at is an algorithm for trying to calculate R_0 for larger matrices. Consider the next generation matrix G. It is composed of two parts, F and V^{-1}, where F is the matrix of new infection, and V is the transfers of infections from one compartment to another. R_0 will simply be the dominant eigenvalue of FV^{-1}

4. SEI Model

$$\frac{dS}{dt} = \mu - \beta SI - \mu S$$
$$\frac{dE}{dt} = \beta SI - (\alpha + \mu)E$$
$$\frac{dI}{dt} = \alpha E - (\gamma + \mu)I$$

Then we have to look at the two infected compartments E and I. We write down F, which defines the rate of NEW infections in different compartments differentiated with respect to E and I, and then evaluated at the disease free equilibrium.

$$F_1 = \beta SI$$
$$F_2 = 0$$
$$F = \begin{bmatrix} \frac{dF1}{dE} & \frac{dF1}{dI} \\ \frac{dF2}{dE} & \frac{dF2}{dI} \end{bmatrix}$$
$$= \begin{bmatrix} 0 & \beta S^* \\ 0 & 0 \end{bmatrix}$$
$$= \begin{bmatrix} 0 & \beta \\ 0 & 0 \end{bmatrix}$$

We write a new matrix V that defines rate of transfer of invectives from one compartment to another.

$$V_1 = (\mu + \alpha)E$$
$$V_2 = (\mu + \gamma)I - \alpha E$$
$$V = \begin{bmatrix} \frac{dV1}{dE} & \frac{dV1}{dI} \\ \frac{dV2}{dE} & \frac{dV2}{dI} \end{bmatrix}$$
$$= \begin{bmatrix} \mu + \alpha & 0 \\ -\alpha & \mu + \gamma \end{bmatrix}$$

```
beta=sym('beta');
lambda=sym('lambda');
mu=sym('mu');
alpha=sym('alpha');
gamma=sym('gamma');
A=[0 beta; 0 0];
B=[alpha+mu 0; -alpha gamma+mu];
B^{-1}
A*B^{-1}
eig(A*B^{-1})
```

```
4

ans =

[                     1/(alpha + mu),               0]
[ alpha/((alpha + mu)*(gamma + mu)), 1/(gamma + mu)]


ans =

[ (alpha*beta)/((alpha + mu)*(gamma + mu)), beta/(gamma + mu)]
[                                        0,                  0]


ans =

                                         0
 (alpha*beta)/((alpha + mu)*(gamma + mu))
```

FIGURE 1. Last part shows the 2 eigenvalues, where the nonzero one will be R_0