Working Document for Breakout Group on Day 2
a) Single Population Model with Recruitment
b) Two Population Model with Exchange and Recruitment

1 Introduction

The previous single population infectious model can only analyze the development of an epidemic because the model will go to a state where all susceptibles become infected and then die or the infectious processes will end leaving the remaining susceptible population. For a persistent infection, new animals must recruit to the susceptible population. One recruitment mechanism is that the local population (both susceptible and infected) can reproduce, perhaps at different rates. We assume that the recruits from the infected animals do not carry the disease. A second recruitment possibility is that there are two populations of animals, one of which remains uninfected but is able to exchange recruits, say through freely drifting larvae or migration. Each of these cases will be considered.

Other processes from the single population model remains active in this model.

2 Questions

- How does recruitment depend upon population abundance? Is there a compenstory process (carrying capacity). Is there an allee effect? What low abundance triggers deconpensation.

- Can recruitment (above the abundance level that triggers decompensation – allee effect) be modeled as a Beverton-Holt process? If so, what is the value for steepness? How do we define carrying capacity?

- Is it necessary to introduce a lag effect between transmission and mortality? That is, are there infected individuals that have low mortality (recent infections) and infected individuals that have high mortality (old infections)? Is this differential if it exists important for any population dynamics process beyond mortality?

- Are other population processes important? For example, does infection reduce individual fecundity so that the broodstock estimated for Beverton-Holt is not equivalent to adult abundance?

3 Model Equations

3.1 Single Population model with recruitment

To avoid a runaway population, we assume that recruitment is controlled by a carrying capacity (k) which includes both S and I. Note that the carrying capacity term can only slow the reproduction at high population levels, it can not become negative if $S + I > k$. The recruitment rates $(a_s$ and $a_i)$ for susceptible and infected can be different.

$$
\begin{aligned}
\frac{d\,S}{dt} &= -\beta_p\,h\,P\,S - \beta_i\,I\,S - \beta_d\,D\,S - m_b\,S \\
&\quad + max(0, [1 - (S + I)/k])\,(a_s\,S + a_i\,I) \\
\frac{d\,I}{dt} &= \beta_p\,h\,P\,S + \beta_i\,I\,S + \beta_d\,D\,S - m_i\,I \\
\frac{d\,D}{dt} &= m_i\,I - e\,D \\
\frac{d\,P}{dt} &= c_i\,I + c_d\,D - r\,P
\end{aligned}
$$

3.2 Two Population model with exchange

This model includes a second population of susceptible animals $(S2)$ which grows under the control of a carrying capacity $(k2)$ and exchanges with the diseased population in two possible ways: immigration and diffusion. Immigration simply involves import of animals from the remote population as some fixed rate (b_i) depending on the size of the remote population. Diffusion brings in animals from the remote population at a fixed rate (b_d) proportional to the difference in the populations.

$$
\begin{aligned}
\frac{d\,S}{dt} &= -\beta_p\,h\,P\,S - \beta_i\,I\,S - \beta_d\,D\,S - m_b\,S \\
&\quad + b_d\,max[0, (S2 - S)] + b_i\,S2
\end{aligned}
$$

$$\frac{d\,S2}{dt} = a_2\,max[0,(1-S2/k2]\,S2 - b_d\,max[0,(S2-S)] - b_i\,S2$$

$$\frac{d\,I}{dt} = \beta_p\,h\,P\,S + \beta_i\,I\,S + \beta_d\,D\,S - m_i\,I$$

$$\frac{d\,D}{dt} = m_i\,I - e\,D$$

$$\frac{d\,P}{dt} = c_i\,I + c_d\,D - r\,P$$