Working Document for Breakout Group on Day 1
Single Population, Single Species Infectious Model

1 Introduction

The first step in the creation of the abalone disease model is to represent the early infection processes. For this model, susceptible animals become infected by contact either with live or dead infected or by contact in some fashion with particles that are released by live or dead infected animals.

2 Questions

The following set of questions should be answered to design an appropriate model.

- What is the disease mortality rate?
- Does the disease mortality rate depend on any other parameters (e.g., time since infection)?
- Are infective particles produced primarily from infected living individuals, dead individuals, or both?
- If infective particles are produced primarily from infected living individuals, what is the release rate?
- If infective particles are produced primarily from dead individuals, how many particles are released per dead animal?
- If infective particles are produced primarily from dead individuals, are there any scavengers that might consume and inactivate the infective particles? If so, is this particle sink important?
- What does the infective particle transmission rate depend upon beyond the number of infective particles impinging the susceptible individual?
- Are the particles passively taken up as a function of their water-column concentration (say, based on the surface area of the animal) or are they actively concentrated from the water column by the susceptible individual (say, by filtration)?

- Does a dose-response relationship exist? If so, does the susceptible individual have any mechanism to inactivate absorbed particles?
- What is the mortality or deactivation rate of infective particles in the water column?

3 Model Equations

The time and length units for this model are days and meters, respectively. Model variables represent number of animals per volume (m^3) (or per area (m^2) on the bottom for benthic species). The variables are S (susceptible [number/m^2]), I (infected [number/m^2]), D (dead of infection [number/m^2]) and P (particles [number/m^3]). The particle concentration is integrated vertically to have the number of particles per bottom area which assumes that all particles in the volume above an area can transmit the disease to susceptible animals.

3.1 Particle Contact Model

The governing equations for this model are

$$\begin{aligned}
\frac{d\,S}{dt} &= -\beta_p\,P\,S - \beta_i\,I\,S - \beta_d\,D\,S - m_b\,S \\
\frac{d\,I}{dt} &= \beta_p\,P\,S + \beta_i\,I\,S + \beta_d\,D\,S - m_i\,I \\
\frac{d\,D}{dt} &= m_i\,I - e\,D \\
\frac{d\,P}{dt} &= c_i\,I + c_d\,D - r\,P
\end{aligned}$$

Particle based transmission occurs in proportion to the number of particles in the environment and the number of susceptibles. Contact transmission occurs based on the number of infected animals (alive or dead) along with a contact probability. The transmission parameters (β_p, β_i, β_d) have units number of infected produced per day per susceptable per particle or infected or dead.

Disease causes mortality at a rate m_i [per day]. For completeness, a natural or background mortality is included on susceptible with a rate m_b [per day].

Particles are released into the environment by alive infected at a rate c_i and by dead infected at a rate c_d. Both of these parameters have units of particles released per day per animal.

Particles in the environment become inactive (or non-infective) at a rate r [per day]. The inactivation can represent biological degradation of the particle, removal of the particle by sinking, filtration by other animals, or removal from the local volume by flow or diffusion.

This model assumes that a single contact by a susceptible to a single infective particle, infected or dead is sufficient to cause an infection. This representation is based on a probability of a susceptible encountering an infective particle or animal.

3.2 Body Burden Particle Transmission Model

Another infection scenario is that the susceptible animals constantly encounter infectious particles but are able to avoid an infection if the number of particles is sufficiently small. This might be due to an immune system or some other reason.

The transmission model is based on the fact that susceptible animals will have some (non-zero) level of body burden [internal infectious particles per animal] of infectious particles before they are considered "infected". Furthermore, we assume a few susceptibles have a relatively large body burden while most will have a small body burden.

The distribution of the number of animals with each level of body burden (B) is assumed to be

$$S(B) = S_o e^{-a\,B},$$

a distribution with a long tail allowing a few uninfected animals to have large body burden. The tail is limited by an imposed maximum body burden (B_m) for an animal to be considered uninfected. A second body burden (B_i) is chosen as the lowest body burden at which animals are likely to be identified as infected.

At any time, there will be some number of susceptible animals (S) and a total absorbed internal pool of infectious particles (IP). We use these values to determine how many animals should become infected.

The total number of animals at any time is

$$S = \int_0^{B_m} S(B)\,dB = \int_0^{B_m} S_o\,e^{-a\,B}\,dB = \frac{S_o}{a}(1 - e^{-a\,B_m}).$$

The total body burden for the population is

$$\begin{aligned} IP &= \int_0^{B_m} B\,S(B)\,dB = \int_0^{B_m} S_o\ B\,e^{-a\,B}\,dB = \frac{S_o}{a^2}(-1-a\,B)\,e^{-a\,B}|_0^{B_m} \\ &= \frac{S_o}{a^2}(1-(1+a\,B_m)\,e^{-a\,B_m}) \end{aligned}$$

The values of IP and S are both known at any model time step, so the values of S_o and a can be calculated. For body burdens up to several hundred, $1/a$ is a good approximation for the average body burden (S/IP), which is the value used in the model.

The total number of susceptibles to be converted to infected is

$$t_S = \int_{B_i}^{B_m} S_o\,e^{-a\,B}\,dB = \frac{S_o}{a}(e^{-a\,B_i} - e^{-a\,B_m}).$$

The total number of infectious particles that should be removed from the susceptible internal pool is

$$\begin{aligned} t_{IP} &= \int_{B_i}^{B_m} B\,S_o\,e^{-a\,B}\,dB = \frac{S_o}{a^2}(-1-a\,B)\,e^{-a\,B}|_{B_i}^{B_m} \\ &= \frac{S_o}{a^2}((1+a\,B_i)\,e^{-a\,B_i}) - (1+a\,B_m)\,e^{-a\,B_m}). \end{aligned}$$

Note that since the heavily infected susceptibles are the ones that become infected, a large number of internal infectious particles should be removed from the internal pool of susceptibles.

Based on these calculations, a fraction t_S/S of the susceptibles need to be moved to the infected pool and t_{IP}/IP of the internal infectious particles need to be removed from the susceptible internal pool. These changes are assumed to occur at a rate of about 10% per day, so the exponential rate is $\alpha = 2.3$. The terms in the governing equations representing disease transmission have the form,

$$\begin{aligned} \frac{dS}{dt} &= -\alpha\,t_S/S \qquad + \text{other terms} \\ \frac{dI}{dt} &= +\alpha\,t_S/S \qquad + \text{other terms} \\ \frac{dIP}{dt} &= -\alpha\,t_{IP}/IP \qquad + \text{other terms} \end{aligned}$$