Working Document for Breakout Group on Day 3 b) Multi-Species, Single Population Model

1 Introduction

The main focus of this model development is a single population consisting of sevaral species. One setup is to have each species act independently in terms of infections, infective particles, recruitment and so forth. This would be the same as using model 2 for each species.

The more interesting case is to have the species interact in various ways. Competition for resources for reproduction would be one interaction. Another case would be to have different species host different life stages of a disease. Specifically, species 1 would create infectious particles that infect species 2 (but not species 1). Species 2 would then release infectious particles that would infect only species 1.

Recruitment is added to this model in the same fashion as model 2. The species do not compete for resources so each has a separate carrying capacity. This can easily be changed.

2 Questions

- Do we include the sum of all species in the local compensation of recruitment; that is, is resource limitation species specific?
- Are there any other important between-species interactions?
- Is there a disease reservior species? If so, do we need to include the natural (non-disease) mortality rate for different species?

3 Model Equations

The basic interaction between individuals follows the pattern of the earlier models, except more species can be part of the ecosystem. Both susceptible and infected individuals die at different rates. Particles are released by both infected and dead individuals at different rates. Both particles and dead individuals are removed from the environment. The infection is spread by contact with infected or dead infected individuals or with infectious particles in the environment. For multiple species, the disease transmission rate is a table with entries like $\beta(i, s)$ where *i* indicates the species causing the infection and *s* indicates the species being infected. There is a different transmission parameter for infected contact, dead contact and infectious particle contact.

The following interactions are active for a given species, s. The symbol Σ_i indicates a sum over all species.

$$\frac{d S(s)}{dt} = -\sum_{i} \beta_{p}(i, s) h P(i) S(s)
-\sum_{i} \beta_{i}(i, s) I(i) S(s)
-\sum_{i} \beta_{d}(i, s) D(i) S(s)
+max(0, [1 - (S + I)/k)] (a_{s} S + a_{i} I) - m_{b} S(s)
+max(0, [1 - (S + I)/k)] (a_{s} S + a_{i} I) - m_{b} S(s)
+\sum_{i} \beta_{p}(i, s) h P(i) S(s)
+\sum_{i} \beta_{i}(i, s) I(i) S(s)
+\sum_{i} \beta_{i}(i, s) I(i) S(s)
-m_{i} I
$$\frac{d D(s)}{dt} = m_{i} I - e D
\frac{d P(s)}{dt} = c_{i} I + c_{d} D - r P$$$$