

## Working Document for Breakout Group on Day 3

### a) Single Species, Multi-Population Model

## 1 Introduction

The main focus of this model development is on a single species with multiple isolated subpopulations. The previous models are expanded to allow spatially distributed subpopulations which are isolated from each other. Contact infections are still allowed within each subpopulation. Infectious particles that are released into the environment can move between subpopulations creating remote infections. The purpose of these models is to analyze the spread of an infection due to freely drifting infectious particles.

Recruitment can easily be added to this model. Larval transmission can also be added which will use the same exchange processes as is used for the infectious particles.

## 2 Questions

- Do the different subpopulations cover different areas? Are they separated by different distances?
- Is a  $2 \times N$  array sufficient; that is,  $N$  sites alongshore, but simply an offshore and inshore site perpendicular to shore?
- Do we impose a distance dependent mortality rate on infective particles? If so, what is the relationship?
- How do we define the recruitment process in the metapopulation? Assuming that the allee effect is always local, can we assume that compensation is also local; that is, can compensation be modeled as local resource limitation?
- Do we impose a distance dependent mortality rate on potential recruits (=larvae)? If so, what is the relationship?
- Presumably the alongshore distance is latitudinal, so that temperature differences are implicit in the parameters. What population and

disease processes vary enough with temperature that their parameterization will vary in the alongshore direction? Can we impose a simple temperature gradient and Q10 temperature relationship for these processes?

- What circulation process do we invoke? If the California coast is our example system, it has a southward drift for most of the year with east-west exchange in both directions.

### 3 Model Equations

The basic interaction within each subpopulation follows the pattern of the earlier models. The populations are assumed to be distributed in the horizontal (2 dimensional) in a grid of volumes indicated by indexes  $(y, x)$ , similar to an array or table. For transfers, the boxes exchange with neighbors, in keeping with the array distribution of populations (details below). More complicated connectivity can be imposed, but this should be a reasonable starting place.

The infection is spread by contact with infected or dead infected individuals or with infectious particles in the environment. 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 following interactions are active within each subpopulation.

$$\begin{aligned} \frac{dS(y, x)}{dt} &= -\beta_p h P(y, x) S(y, x) - \beta_i I(y, x) S(y, x) - \beta_d D(y, x) S(y, x) \\ &\quad - m_b S(y, x) \\ \frac{dI(y, x)}{dt} &= \beta_p h P(y, x) S(y, x) + \beta_i I(y, x) S(y, x) + \beta_d D(y, x) S(y, x) \\ &\quad - m_i I(y, x) \\ \frac{dD(y, x)}{dt} &= m_i I(y, x) - e D(y, x) \\ \frac{dP(y, x)}{dt} &= c_i I(y, x) + c_d D(y, x) - r P(y, x) \end{aligned}$$

The basic idea for the geometry of this model is the US west coast where there are populations distributed along the coast and at certain distances

away from the coast. Each box is identified by a pair of integers  $(y, x)$  indicating the east and north displacement of the box. To align with an  $(x, y)$  coordinate system, the origin is south and offshore, so box  $(1, 1)$  is the southern offshore box. The  $x$  coordinate increase towards the east; the  $y$  coordinate increases to the north. At the present time, all of the subpopulations have the same volume (this can change). All parameters in the model can have different values for different subpopulations, but the present test solutions use the same value for all subpopulations.

Exchange between the subpopulations is represented by a directed exchange (flow-like motion of infective particles). An exchange parameter is specified between each population which represents east-west exchange ( $Uex$ ) or north-south exchange ( $Vex$ ). These exchange parameters are specified between subpopulations and can be either positive or negative. The parameters have units of 1/day and are defined by an average flow speed [km/day] and a distance [km] between the centers of the subpopulations.

Specifically, if  $Uex(y, x)$  is positive, then particles will move from subpopulation  $(y, x)$  to subpopulation  $(y, x + 1)$ . If  $Uex(y, x)$  is negative, then the exchange is from  $(y, x + 1)$  to  $(y, x)$ . A similar exchange is specified for  $Vex$ . The  $Uex(y, x)$  exchange parameter is specified at the eastern edge of subpopulation  $(y, x)$  while  $Vex(y, x)$  is the exchange at the northern edge of subpopulation  $(y, x)$ . For the present, all of these exchange parameters are assumed not to change with time (this can change).

This exchange is implemented by calculating  $NUex = .5 * (abs(Uex) - Uex)$  which is nonzero only if the exchange parameter is negative, and  $PUex = .5 * (abs(Uex) + Uex)$  which is nonzero only if the exchange parameter is positive. For any given location, only one of these two parameters is non-zero.

The transfer part of the model equations have the following form.

$$\begin{aligned} \frac{dP(y, x)}{dt} = & -PUex(y, x) P(y, x) + NUex(y, x) P(y, x + 1) \\ & +PUex(y, x - 1) P(y, x - 1) - NUex(y, x - 1) P(y, x) \\ & -PVex(y, x) P(y, x) + NVex(y, x) P(y + 1, x) \\ & +PVex(y - 1, x) P(y - 1, x) - NVex(y - 1, x) P(y, x) \\ & +\text{other terms} \end{aligned}$$

Another option for exchange is diffusive exchange where the difference in

concentration between adjacent cells and a diffusion coefficient control the spread of the infectious particles. In the present model, only the directed exchange is implemented. It is a simple extension to set up a diffusive exchange.