Outline for Single Species Model: abalone1

- Processes
- Equations Defining Model
- MATLAB Code for Model
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    - ODE stucture (RHSabalone1.m)
    - Parameters (PARabalone1.m)
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Single Species Model (abalone1)

- Simplest SI model with one species (S, I, and D) and infectious particles (P)
- Infection comes from 3 possible processes:
  - contact with Infected (I),
  - contact with Dead Infected (D)
  - contact with Infectious Particles (P).
- Infectious Particles can come from Infected (I) or Dead Infected (D) or both.
- Natural and disease mortality are allowed.
- Dead animals disappear by scavengers or decay.
- Infectious particles disappear, dissipate or become noninfectious.

Model Equations

Governing equations representing the processes are

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

Notice that dead S are no longer accounted for (although they could be).

Procedure for model solution

1. Specify the structure of the ODE,
2. Specify the values of the parameters,
3. Specify initial conditions,
4. Specify a time span for the solution,
5. Run the ODE solver to obtain the solution,
6. Plot and analyze the results

MATLAB code for model

The MATLAB code is in four parts:

- The main driver routine (abalone1.m) runs the model.
- The structure of the model (the RHS of the ODE) is defined in RHSabalone1.m
- The values for the parameters are held in a collective variable (a structure) called PAR, which is defined in PARabalone1.m
- A general model graphics routine is provided in PLOTabalone1.m. This routine also calculates diagnostics for some models.

abalone1.m (part 1)

The main driver routine:

```
% abalone1
% SI model of abalone in a single population
% The model considers a number of benthic animals in a volume of water
% Infectious particles can be released which spread the infection
% Units:
% time is in days
% populations are in number of animals/m2
% concentrations are in number/m3
% variables are
% y(1): S, susceptible, uninfected individuals [number/m2]
% y(2): I, infected individuals [number/m2]
% y(3): D, dead infected animals [number/m2]
% y(4): P, infectious particles close to the susceptible population [number/m3]
% PARabalone1.m sets the values of the various model parameters
% RHSabalone1.m defines the equations and interaction
```

abalone1.m (part 2)

```
global PAR % makes PAR available to all routines
nVar=4; % number of variables in the model
% array indexes of variables
iS=1;iI=2;iD=3;iP=4;
PAR=PARabalone1; % call the routine defining model parameters
y0=zeros(nVar,1); % initial conditions
y0(iS)=100;y0(iI)=1;y0(iP)=0;
tspan=[0 100]; % time span
[t,y]=ode45(@RHSabalone1,tspan,y0); % call the ODE solver
% rename model results
S=y(:,iS);I=y(:,iI);D=y(:,iD);P=y(:,iP);
```

RHSabalone1.m

```
function ydot=RHSinfct1(t,y)
% RHSabalone1
% define the RHS of the model equations.
% array indexes of variables
nVar=4;iS=1;iI=2;iD=3;iP=4;
global PAR
ydot=zeros(nVar,1);
% time changes for susceptable animals
ydot(iS)= - PAR.IPinfect * PAR.depth * y(iP) * y(iS) ...
- PAR.Iinfect * y(iI) * y(iS) ...
- PAR.Dinfect * y(iD) * y(iS) - PAR.Bmort * y(iS);
% time changes for infected animals
ydot(iI)= PAR.IPinfect * PAR.depth * y(iP) * y(iS) ...
+ PAR.Iinfect * y(iI) * y(iS)...
+ PAR.Dinfect * y(iD) * y(iS)- PAR.Imort * y(iI);
% time changes for dead infected animals
ydot(iD)= PAR.Imort * y(iI) - PAR.DeadDecay * y(iD);
% time changes of infectious particles
ydot(iP)= PAR.Irelease * y(iI) + PAR.Drelease * y(iD) ...
- PAR.IPremove * y(iP);
```

PARabalone1.m (part 1)

```
function PAR=PARabalone1
% define model parameters and values
PAR.case = '1';
PAR.depth = 1; % vertical dimension of the volume (m)
% infection rate by contact with infections particles [infected produced/infectious
particle/day]
PAR.IPinfect = 0.003 ;
% infection rate by contact with infectious individuals [infected produced/suscepti
animal/day]
PAR.Iinfect = 0.001 ;
% infection rate by contact with dead infectious individuals [infected produced/sus
animal/day]
PAR.Dinfect = 0.0008 ;
```

PARabalone1.m (part 2)

```
% mortality rate of infected [1/day]
PAR.Imort = 8.d-2;
% background mortality rate of susceptibles [1/day]
PAR.Bmort = 0;
% removal rate of dead [1/day]
PAR.DeadDecay = 1.5 ;
% infectious particles released by infected [particles/animal/day]
PAR.Irelease = .015;
% infectious particles released by dead [particles/animal/day]
PAR.Drelease = 1.0;
% removal rate of IP from the environment [1/day]
PAR.IPremove = 0.001;
```

PLOTabalone1.m (part 1)

```
% PLOTabalone1.m
% analyze and plot the model results
LW=2;FS=14;FW='demi';
figure
subplot(2,2,1)
plot(t,S,'k-','LineWidth',LW)
title('Susceptable','FontSize',FS,'FontWeight',FW)
ylabel('number/m2','FontSize',FS,'FontWeight',FW)
```

PLOTabalone1.m (part 2)

```
subplot(2,2,2)
plot(t,I,'k-','LineWidth',LW)
title('Infected','FontSize',FS,'FontWeight',FW)
ylabel('number/m2','FontSize',FS,'FontWeight',FW)
subplot(2,2,3)
plot(t,D,'k-','LineWidth',LW)
title('Dead Infected','FontSize',FS,'FontWeight',FW)
xlabel('day','FontSize',FS,'FontWeight',FW)
ylabel('number/m2','FontSize',FS,'FontWeight',FW)
subplot(2,2,4)
plot(t,P,'k-','LineWidth',LW)
title('Infect Particles','FontSize',FS,'FontWeight',FW)
xlabel('day','FontSize',FS,'FontWeight',FW)
ylabel('number/m3','FontSize',FS,'FontWeight',FW)
set(gca,'LineWidth',LW,'FontSize',FS,'FontWeight',FW)
print('-dpng',['Figures/Ab' PAR.case 'Num.png'])
```

PLOTabalone1.m (part 5)

```
figure
infP=PAR.IPinfect * PAR.depth * P .* S;
infI=PAR.Iinfect * I .* S;
infD=PAR.Dinfect * D .* S;
plot(t,infP,'k-',t,infI,'k--',t,infD,'k-.','LineWidth',LW)
title('Infection rate (num/day): P(-) I(--) D(-.)'...
,'FontSize',FS,'FontWeight',FW)
xlabel('day','FontSize',FS,'FontWeight',FW)
ylabel('number/day','FontSize',FS,'FontWeight',FW)
set(gca,'LineWidth',LW,'FontSize',FS,'FontWeight',FW)
print('-dpng',['Figures/Ab' PAR.case 'InfRate.png'])
```