Supplementary material for: Ben-Horin, T., Lafferty, K.D., Bidegain, G. and Lenihan, H.S. Fishing diseased abalone to promote yield and conservation, *Phil. Trans. R. Soc. B.* doi: 10.1098/rstb.2015.0211

# Mathematical details and Matlab code

## S.1. Endemic equilibrium $N$

We assume $N^* > 0$ and $i^* > 0$. At the endemic equilibrium, from equation (2.4) $N^*$ satisfies the following equation:

$$rN^* - (\mu + cN^* + f_S)S^* - (\mu + cN^* + f_I + \alpha)I^* = 0, \tag{S.1}$$

where S* and I* are the densities of susceptible and infected hosts at the endemic equilibrium. Substituting $S^* = (1 - i^*)N^*$ and $I^* = i^*N^*$ and rearranging, we obtain:

$$N^* = \frac{r-\mu-f_S+i^*(f_S-f_I-\alpha)}{c}. \tag{S.2}$$

## S.2. Estimate of $R_0$ at the disease-free equilibrium

We estimated the basic reproductive number $R_0$ from the next generation matrix approach of Diekmann et al. [S1]. Assuming a completely susceptible population ($S \approx N$), we linearized equations (2.2) and (2.3) around the steady state $\frac{dS}{dt} = 0$ and $I << N$ and $P << N$:

$$\frac{dI}{dt} = \beta NP - (\mu + cN + f_I + \alpha)I \tag{S.3}$$

$$\frac{dP}{dt} = \sigma I - (\delta + \beta N)P, \tag{S.4}$$

Equations (5.3) and (5.4) describe the infection subsystem, as they only describe the production of new infected hosts and changes in the states of already existing infected hosts and their shed parasite stages in the environment. We decomposed the Jacobian matrix describing this linear system of ODEs with the *transmission* matrix $T$, describing the production of new infections, and the *transition* matrix $\Sigma$, describing changes in the state of infected hosts, here through removal by death:

$$T = \begin{pmatrix} 0 & \beta N \\ \sigma & 0 \end{pmatrix} \tag{S.5}$$

$$\Sigma = \begin{pmatrix} -m & 0 \\ 0 & -(\delta + \beta N) \end{pmatrix} \tag{S.6}$$

where $m$ = ($\mu$ + $cN$ + $f_I$ + $\alpha$). The large domain next generation matrix $K_L$ describes new transmissions and transitions:

$$K_L = -T\Sigma^{-1} = \begin{pmatrix} 0 & \frac{\beta N}{\delta+\beta N} \\ \frac{\sigma}{m} & 0 \end{pmatrix}, \tag{S.7}$$

and the dominant eigenvalue of $K_L$ defines $R_0$, where:

$$\lambda = R_0 = \sqrt{\frac{\beta N \sigma}{(\delta+\beta N)m}}. \tag{S.8}$$

Substituting $m$ = ($\mu$ + $cN$ + $f_I$ + $\alpha$):

$$R_0 = \sqrt{\frac{\beta N \sigma}{(\delta+\beta N)(\mu+cN+f_I+\alpha)}}. \tag{S.9}$$

In the case where the lifespan of parasite stages outside hosts is limited, the loss of parasite stages to host contacts is negligible compared to parasite mortality in the water column (i.e. $\beta NP << \delta P$). Equation (S.4) becomes:

$$\frac{dP}{dt} = \sigma I - (\delta + \beta N)P, \tag{S.10}$$

and the transition matrix $\Sigma$ (equation S.6) becomes:

$$\Sigma = \begin{pmatrix} -m & 0 \\ 0 & -\delta \end{pmatrix}. \tag{S.11}$$

The large domain next generation matrix $K_L$ describing new transmissions and transitions is:

$$K_L = -T\Sigma^{-1} = \begin{pmatrix} 0 & \frac{\beta N}{\delta} \\ \frac{\sigma}{m} & 0 \end{pmatrix}, \tag{S.12}$$

and the dominant eigenvalue of $K_L$ defines $R_0$, where:

$$\lambda = R_0 = \sqrt{\frac{\beta N \sigma}{\delta m}}. \tag{S.13}$$

Substituting $m = (\mu + cN + f_I + \alpha)$:

$$R_0 = \sqrt{\frac{\beta N \sigma}{\delta(\mu + cN + f_I + \alpha)}}. \tag{S.14}$$

## References

S1 Diekmann, O., Heesterbeek, J.A.P. and Roberts, M.G. 2010. The construction of next-generation matrices for compartmental epidemic models. *J. R. Soc. Interface.* **7**, 873-885. (doi:10.1098/rsif.2009.0386)

**Matlab code for equations (2.1) – (2.3)**

```
function dY = SIP(t,init,p)

%% Specification of the simple fisheries model
% Tal Ben-Horin September 2015

%% State Variables
S = init(1); %initial susceptible red
I = init(2); %initial infected red
P = init(3); %initial RLO

%% Parameters
r = p(1); %intrinsic population growth
mu = p(2); %natural mortality rate
c = p(3); %density dependent parameter
f = p(4); %fishing mortality
fi = p(5); %targeted fishing mortality
alpha = p(6); %disease mortality
s = p(7); %fomite production
d = p(8); %decay of parasites
b = p(9); %beta

%% ODE
dS = r*(S+I) - (mu + c*(S+I) + f)*S - b*S*P;
dI = b*S*P - (mu + c*(S+I) + fi + alpha)*I;
dP = s*I - (d+b*S)*P;

%% Output
dY  = [dS;dI;dP];
```

```
function [Ps, Is, Ts] = paramsSIP()

%% Parameter file for the simple fisheries model
% Parameter values are described in the manuscript text
% Tal Ben-Horin Sept 2015

%% Parameters
Ps={%   Value       Name        Description
        0.32,       'r',        'intrinsic population growth';
        0.15,       'mu',       'intrinsic population growth';
        0.025,      'c',        'density dependent parameter';
        0.0,        'f',        'fishing mortality';
        0.0,        'fi',       'targeted fishing mortality';
        0.2,        'alpha',    'disease mortality';
        1000,        's',        'fomite production';
        50,         'd',        'decay of parasites';
        0.03,       'beta',     'coefficient of disease transmission';%0.03
        };


%% Initial Values
Is={%   Value   Name    Description
        3.0,   'S_0', 'Initial susceptible';
        1.0,   'I_0', 'Initial infected';
        1.0,   'P_0', 'Initial parasite';
        0.5,   'H_0', 'Initial harvested';
};

%% Time
Ts={%   Value   Name    Description
        0.0,    'T0',   'Start Time (years)';
        0.0027, 'Inc',  'Time Increment (day)';
        1000.0,   'T_F',    'Finish Time (years)'
};
```