

# hostsynch

## Methods

For host species  $i$ , let us assume that the recruitment of new susceptibles ( $B$ ) is described with the Ricker equation:

$$B(N_{i,t}) = N_{i,t} \exp(r_{i,t}(\frac{1 - N_{i,t}}{K_i})). \quad (1)$$

Here,  $r_t$  is the intrinsic growth rate and is time-dependent;  $K$  is the specieses' carrying capacity. Including infection:

$$S_{i,t+1} = N_{i,t} \exp(r_t(\frac{1 - N_{i,t}}{K_i})) - \sum_{j=1}^n \beta_j S_{i,t} I_{j,t} - \mu_i S_{i,t}, \quad (2)$$

the susceptible individuals can be infected by members of its own species as well as by members of other species. The transmission coefficient  $\beta$  can be unique to the species and will determine the species' competence. The total number of new infections is:  $\sum_{j=1}^n \beta_j S_{i,t} I_{j,t}$ .

As the susceptibles enter into the infected class:

$$I_{i,t+1} = \sum_{j=1}^n \beta_j S_{i,t} I_{j,t} - (\gamma_i + \mu_i) I_{i,t}, \quad (3)$$

where individuals recover at the rate of  $\gamma$ . When individuals recover, we have:

$$R_{i,t+1} = \gamma_i I_{i,t} - \mu_i R_{i,t}, \quad (4)$$

fully-recovered hosts cannot get reinfected.

```
ricker_SIR_model <- function(r = 0.5){}
```

## Varying temporal fluctuations

We model the intrinsic growth rate of each species as being seasonal:

$$r_{(i,t)} = r_0 + \sin(\omega t + o_i) + \epsilon_t, \quad (5)$$

For our mathematical model, we assume the following:

1. The

```
n_sp = 100
```