Population stability analysis for Balanus improvisus

2019-04-19

Functions to determine proportion of overall survival that is transferred between classes (gamma), and the probability of surviving and staying in the same class is and the probability of surviving and transferring between classes is (From Caswell 2001).

gamma\_i <- function(sigma\_i, lam, T\_i){  
 res <- ((sigma\_i / lam) ^ T\_i - (sigma\_i / lam) ^ (T\_i - 1)) /  
 ((sigma\_i / lam) ^ T\_i - 1)  
}  
  
  
P\_i <- function(p, T\_i){  
 p \* (1 - p ^ (T\_i - 1) ) / (1 - p ^ T\_i)  
}  
  
G\_i <- function(p, T\_i) {  
 p ^ T\_i \* (1 - p) / (1 - p ^ T\_i)  
}

The overall survival for each stage (sigma), and the duration of each stage (T) in units of 6-hour timesteps.

balanus\_lh <- list("larva" = list("sigma" = 0.515, "T" = 44),  
 "cyprid" = list("sigma" = 0.94, "T" = 12),  
 "juvenile" = list("sigma" = 0.58, "T" = 84),  
 "adult" = list("sigma" = 0.998, "T" = 2192))

The function used to estimate the value for for an overall dominant eigenvalue of 1.0006.

balanus\_fit <- function(log\_gamma\_3) {  
 lam <- 1.0006  
  
 sigma\_1 <- balanus\_lh[["larva"]][["sigma"]]  
 gamma\_1 <- 1/balanus\_lh[["larva"]][["T"]]  
 P\_1 <- sigma\_1 \* (1 - gamma\_1)  
 G\_1 <- sigma\_1 \* gamma\_1  
  
 sigma\_2 <- balanus\_lh[["cyprid"]][["sigma"]]  
 gamma\_2 <- gamma\_i(sigma\_i = sigma\_2, lam = lam,  
 T\_i = balanus\_lh[["cyprid"]][["T"]])  
  
 P\_2 <- sigma\_2 \* (1 - gamma\_2)  
 G\_2 <- sigma\_2 \* gamma\_2  
  
 sigma\_3 <- balanus\_lh[["juvenile"]][["sigma"]]  
  
 gamma\_3 <- exp(log\_gamma\_3)  
 P\_3 <- sigma\_3 \* (1 - gamma\_3)  
 G\_3 <- sigma\_3 \* gamma\_3  
  
 sigma\_4 <- balanus\_lh[["adult"]][["sigma"]]  
  
 gamma\_4 <- gamma\_i(sigma\_i = sigma\_4, lam = lam,  
 T\_i = balanus\_lh[["adult"]][["T"]])  
  
 P\_4 <- sigma\_4 \* (1 - gamma\_4)  
  
 F\_4 <- 13.69 # 10000 eggs per season  
  
 A <- matrix(c(P\_1, 0, 0, F\_4,  
 G\_1, P\_2, 0, 0,  
 0, G\_2, P\_3, 0,  
 0, 0, G\_3, P\_4), nrow = 4, byrow = TRUE)  
 gammas <- c("gamma1" = gamma\_1, "gamma2" = gamma\_2, "gamma3" = gamma\_3,  
 "gamma4" = gamma\_4)  
 res = list(A = A, gammas = gammas)  
}

gamma\_min\_function <- function(gamma) {  
 A\_local <- balanus\_fit(gamma)[["A"]]  
 A\_local[is.nan(A\_local)] <- .Machine$double.eps  
  
 res <- (1.0006 - eigen.analysis(A\_local)$lambda1)^2  
}

The function to minimize.

gamma\_min\_function <- function(gamma) {  
 A\_local <- balanus\_fit(gamma)[["A"]]  
 A\_local[is.nan(A\_local)] <- .Machine$double.eps  
  
 res <- (1.0006 - eigen.analysis(A\_local)$lambda1)^2  
}  
  
  
res <- DEoptim(gamma\_min\_function, lower = -7, upper = 0,  
 control = list(trace = 0))

The resulting population transition matrix is

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | larva | cyprid | juvenile | adult |
| larva | 5.032955e-01 | 0.00000e+00 | 0.000000e+00 | 1.369000e+01 |
| cyprid | 1.170450e-02 | 8.85717e-01 | 0.000000e+00 | 0.000000e+00 |
| juvenile | 0.000000e+00 | 5.42830e-02 | 5.726674e-01 | 0.000000e+00 |
| adult | 0.000000e+00 | 0.00000e+00 | 7.332600e-03 | 9.979913e-01 |

with of each stage as:

|  |  |
| --- | --- |
|  |  |
| larva | 2.27273e-02 |
| cyprid | 5.77479e-02 |
| juvenile | 1.26423e-02 |
| adult | 8.70000e-06 |

After submitting the population transition matrix to a model where there is no ship movement, the average population size for each lifestage in the seed ports is shown as:

