***Introduction to Theoretical Ecology Assignment 4***

Ricker Logistic Growth Model

One unrealistic feature of the discrete logistic growth equation is that *Nt+1* will become negative when *Nt* >> *K*. An alternative approach is to follow the Ricker logistic equation (Ricker, 1952), a well-known model in fisheries:



1. Show analytically the equilibrium points and determine their stability criteria. Compare the stability criteria for this model to those for the standard discrete logistic model. (6 pts)

***Solution:***

1. Find the equilibrium points:
2. Analyze the stability by taking the derivative of the right hand side with respect to *N* and evaluate it at the equilibrium points:

* : unstable; the population will monotonically divert away from the equilibrium

1. If : *K* is stable; the population will approach the equilibrium monotonically
2. If : *K* is stable; the population will approach the equilibrium with damped oscillations
3. If : *K* is unstable; the population will oscillate around the equilibrium but never approach it
4. The stability criteria for Ricker model are the same as those for the standard discrete logistic model (*N\** = 0 is unstable and *N\* = K* is stable when 0 < *r* < 2). This suggests that Ricker model is probably a better alternative to the discrete logistic model since it avoids the possibility of getting negative population size.
5. Plot the population trajectories under three growth scenarios *r* = 0.5, *r* = 1.5, and *r* = 2.7 (*N0* = 10, *K* = 500, 100 time steps for each simulation). Please include the R code you used to generate the results. (4 pts)

***Solution:***

1. *r* = 0.5: monotonically approaching the carrying capacity *K*

r0.5.tiff

1. *r* = 1.5: damped oscillations towards the carrying capacity *K*

**r1.5.tiff**

1. *r* = 2.7: bounded oscillations (chaos)

**r2.7.tiff**

**R Code**

**library(tidyverse)**

**Ricker <- function(r){**

**# Set the parameters**

**r <- r**

**K <- 500**

**N0 <- 10**

**time <- 100**

**# Ricker logistic growth equation**

**log\_fun <- function(r, N, K){N\*exp(r\*(1-N/K))}**

**# for loop**

**pop\_size <- numeric(time)**

**pop\_size[1] <- N0**

**for (i in 2:time) {pop\_size[i] <- log\_fun(r = r, N = pop\_size[i - 1], K = K)}**

**pop\_data <- pop\_size %>%**

**as.data.frame() %>%**

**rename(., pop\_size = `.`) %>%**

**mutate(time = 0:(time-1)) %>%**

**relocate(time)**

**head(pop\_data)**

**# Population trajectory**

**ggplot(pop\_data, aes(x = time, y = pop\_size)) +**

**geom\_point() +**

**geom\_line() +**

**geom\_hline(yintercept = K, color = "red", size = 1.2, linetype = "dashed") +**

**geom\_text(x = time\*1.02, y = K+50, label = "italic(K)", color = "red", size = 6.5, parse = T) +**

**labs(y = expression(italic(N)), title = paste0("Discrete logistic growth", "\n", "(r = ", r, ", K = ", K, ", N0 = ", N0, ")")) +**

**scale\_x\_continuous(limits = c(0, time\*1.05), expand = c(0, 0)) +**

**scale\_y\_continuous(limits = c(0, max(pop\_size)\*1.1), expand = c(0, 0)) +**

**theme\_bw(base\_size = 15) +**

**theme(plot.title = element\_text(hjust = 0.5))**

**}**

**Ricker(r = 0.5)**

**ggsave("r0.5.tiff", width = 5.5, height = 4.5, dpi = 600, device = "tiff")**

**Ricker(r = 1.5)**

**ggsave("r1.5.tiff", width = 5.5, height = 4.5, dpi = 600, device = "tiff")**

**Ricker(r = 2.7)**

**ggsave("r2.7.tiff", width = 5.5, height = 4.5, dpi = 600, device = "tiff")**