***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* (you’ve probably saw this when playing with the shiny app). 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 of this model to those of 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; monotonically away from equilibrium)

1. If (*K* is stable; a small displacement will monotonically approach the equilibrium)
2. If (*K* is stable; a small displacement will show damped oscillations towards the equilibrium)
3. If (*K* is unstable; a small displacement will oscillate around the equilibrium but not approach it)
4. The stability criteria of Ricker model are the same as those of the standard discrete logistic model. This suggests that Ricker model is probably a better alternative to the discrete logistic model.
5. Plot the population trajectories under two 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

**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")**