LVToxinModel.R

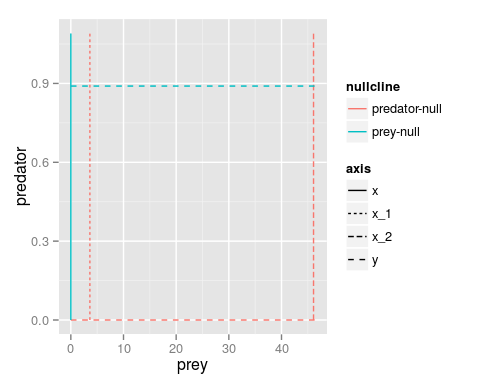
josue

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rm(list=ls())  
 library(deSolve)

##   
## Attaching package: 'deSolve'  
##   
## The following object is masked from 'package:graphics':  
##   
## matplot

library(ggplot2)  
 library(reshape)  
  
# parameters  
  
mu <- 0.1;   
gamma <- 0.3;  
c <- 0.3;  
sigma <- 0.5;  
beta <- 1;  
delta <- 1;  
T0 <- 1-mu  
T1 <- ((sigma\*gamma\*c + 2\*beta\*delta\*sigma) - 2\*sigma\*sqrt(beta\*delta\*(beta\*delta+c\*delta\*gamma)))/(c\*c\*gamma)  
  
  
# others  
TX <- 0.01;   
Delta <- ifelse(TX == T1, 0, ((sigma - TX\*c)^2)\*(gamma^2) - 4\*gamma\*TX\*beta\*delta\*sigma)  
  
nullclines <- function() {  
 nullcline <- c()  
 axis <- c()  
 prey <- c()  
 predator <- c()  
 # x-null  
 x\_x <- 0  
 x\_y <- (max(0,1-TX) - mu)/beta  
   
 # y-null  
 y\_x\_1 <- 0  
 y\_x\_2 <- 0  
 if ( Delta > 0 ) {  
 y\_x\_1 <- ( (sigma - TX\*c)\*gamma - sqrt(Delta) )/(2\*gamma\*TX\*beta)  
 y\_x\_2 <- ( (sigma - TX\*c)\*gamma + sqrt(Delta) )/(2\*gamma\*TX\*beta)  
 }  
   
 if (Delta == 0) {  
 y\_x\_1 <- ( (sigma - TX\*c))/(2\*TX\*beta)  
 }  
 y\_y <- 0  
   
 xf <- max(x\_x,y\_x\_1,y\_x\_2) + 0.2  
 yf <- max(x\_y,y\_y) + 0.2  
   
 nullcline <- c(nullcline, c("prey-null","prey-null"))  
 axis <- c(axis, c("x","x"))  
 prey <- c(prey, c(x\_x,x\_x))  
 predator <- c(predator, c(0,yf))  
 if ( x\_y > 0) {  
 nullcline <- c(nullcline, c("prey-null","prey-null"))  
 axis <- c(axis, c("y","y"))  
 prey <- c(prey, c(0,xf))  
 predator <- c(predator, c(x\_y,x\_y))  
 }  
   
 if ( y\_x\_1 > 0) {  
 nullcline <- c(nullcline, c("predator-null","predator-null"))  
 axis <- c(axis, c("x\_1","x\_1"))  
 prey <- c(prey, c(y\_x\_1,y\_x\_1))  
 predator <- c(predator, c(0,yf))  
 }  
   
 if ( y\_x\_2 > 0) {  
 nullcline <- c(nullcline, c("predator-null","predator-null"))  
 axis <- c(axis, c("x\_2","x\_2"))  
 prey <- c(prey, c(y\_x\_2,y\_x\_2))  
 predator <- c(predator, c(0,yf))  
 }  
   
 nullcline <- c(nullcline, c("predator-null","predator-null"))  
 axis <- c(axis, c("y","y"))  
 prey <- c(prey, c(0,xf))  
 predator <- c(predator, c(y\_y,y\_y))  
 df <- data.frame(nullcline, axis, prey, predator)  
 df  
}  
  
g <- ggplot()+  
 geom\_path(data = nullclines() ,  
 aes(x = prey, y = predator, colour = nullcline, linetype = axis))   
g



if ( (sigma/c -TX)>0 ) {  
 print("Se cumple la condición 1")  
 }else {  
 print("No se cumple la condición 1")   
 }

## [1] "Se cumple la condición 1"