library(NetLogoR)
#install.packages("nnls")
#install.packages("lcmix", repos="http://R-Forge.R-project.org")
#install.packages("MASS")
library(lcmix)
library(MASS)

# AGENTS
# Create a square landscape of 9 by 9 cells (81 cells total)
# Cell values are randomly chosen either 1 or 2
land <- createWorld(minPxcor = 1, maxPxcor = 9,
                     minPycor = 1, maxPycor = 9,
                     sample(c(1, 2), 81, replace = TRUE))
plot(land) # visualize the landscape
# Create three moving individuals (three turtles)
# Place the turtles in the middle of the landscape just created
t1 <- createTurtles(n = 3, world = land)
# Visualize the turtles on the landscape with their respective color
points(t1, pch = 16, col = of(agents = t1, var = "color"))
# Define a variable
distRate <- 0.5

# MODEL
for(i in 1:10){ # run the model 10 times
    # Identify the cells the turtles are on
    cellTurtle <- patchHere(world = land, turtles = t1)
    # And the values of these cells
    distMove <- of(world = land, agents = cellTurtle)
    # A turtle moves with a mean of 1 or 2-cell distance
    # at the time (distMove), drawn from a multivariate gamma
    # distribution to show that all turtles move similar
    # distances, i.e., part of a social group or affected by
    # unmeasured conditions
    distShape <- distMove * distRate
    rho <- matrix(rep(0.8, length = nrow(t1) * nrow(t1)), ncol = nrow(t1))
    diag(rho) <- 1
    distMoveRan <- rmvgamma(2, distShape, distRate, rho)[1, ] # vector
    # The turtles t1 move with a step length of distMoveRan (one value
each)
    # The landscape is not a torus (torus = FALSE)
    # and the turtles cannot move outside of the landscape (out = FALSE)
t1 <- fd(turtles = t1, dist = distMoveRan,
             world = land, torus = FALSE, out = FALSE)
    # Then the turtles rotate with a multivariate normal turn angle,
# based on the mean of the group, correlated at 0.8
meanHeading <- mean(of(agents = t1, var = "heading"))
Sigma <- matrix(rep(0.8 * meanHeading, length = nrow(t1) * nrow(t1)),
               ncol = nrow(t1))
diag(Sigma) <- meanHeading
angleInd = mvrnorm(n = 1, mu = rep(meanHeading, nrow(t1)), Sigma = Sigma)
# Turtles rotate to the right if angleInd > 0
# or to the left if angleInd < 0
t1 <- right(turtles = t1, angle = angleInd)
# Visualize the turtles' new position
points(t1, pch = 16, col = of(agents = t1, var = "color"))
}