…

library(raster)   
 library(dismo)   
   
 r <- raster(nrows = 100, ncols = 100, xmn = 0, xmx = 100, ymn = 0, ymx = 100)   
 r[] <- 0   
   
 steps <- 500   
 n <- 100   
   
 locations <- data.frame(matrix(ncol = n, nrow = steps))   
   
 pp <- randomPoints(r,n)   
 cell <- cellFromXY(r, pp)   
 infected <- 1:10   
 pob <- 1:n   
 ratio <- data.frame(1:steps, NA)   
 pob\_inf <- list()   
   
 for (j in 1:steps){   
 print(j)   
 locations[j,] <- cell   
   
 for(i in 1:n){   
   
 cell[i] <- adjacent(r, cell[i], 8)[round(runif(1,0.51,nrow(adjacent(r, cell[i], 8))+0.49),0),2]   
   
 }   
   
 new\_inf <- cell %in% cell[infected]   
 infected <- pob[new\_inf]   
 ratio[j,2] <- length(infected)   
 pob\_inf[[j]] <- infected   
   
 }   
   
 locations2 <- data.frame(matrix(ncol = n, nrow = steps))   
   
 cell2 <- cellFromXY(r, pp)   
 infected2 <- 1:10   
 pob2 <- 1:n   
 ratio2 <- data.frame(1:steps, NA)   
 pob\_inf2 <- list()   
   
 for (j in 1:steps){   
 print(j)   
 locations2[j,] <- cell2   
   
 for(i in 1:25){   
   
 cell2[i] <- adjacent(r, cell2[i], 8)[round(runif(1,0.51,nrow(adjacent(r, cell2[i], 8))+0.49),0),2]   
   
 }   
   
 new\_inf2 <- cell2 %in% cell2[infected2]   
 infected2 <- pob2[new\_inf2]   
 ratio2[j,2] <- length(infected2)   
 pob\_inf2[[j]] <- infected2   
   
 }

Let’s make some plots to put them together in a GIF and better visualize the results…

num <- seq(1,500,4)   
   
 for (p in 1:125){   
 id <- sprintf("%03d", num[p])   
 png(paste("corona\_",id,".png", sep=""), width=780, height=800, units="px", pointsize = 15)   
 layout(matrix(c(1,1,2,3),2,2,byrow = TRUE))   
 plot(ratio[1:num[p],],pch=19, xlim = c(0,500), ylim = c(0,100), ylab = "nº of infected",   
 xlab = "time", col = "red", cex.axis = 1.4, cex.lab = 1.4, main = "Infected curves", cex.main = 2)   
 points(ratio2[1:num[p],],pch=19,col="blue")   
 legend("topright", legend = c("free movement", "restricted movement"),lwd = c(4,4), col = c("red","blue"), cex = 1.5 )   
 plot(r, col = "white", legend = FALSE, axes = FALSE, main = "free movement", cex.main = 1.8)   
 points(xyFromCell(r,as.numeric(locations[num[p],])), cex = 1.2, col = "grey40", pch = 18)   
 points(xyFromCell(r,as.numeric(locations[num[p],]))[pob\_inf[[num[p]]],], pch = 18, col = "red", cex = 1.4)   
 plot(r, col = "white", legend = FALSE, axes = FALSE, main = "restricted movement", cex.main = 1.8)   
 points(xyFromCell(r,as.numeric(locations2[num[p],])), cex = 1.2, col = "grey40", pch = 18)   
 points(xyFromCell(r,as.numeric(locations2[num[p],]))[pob\_inf2[[num[p]]],], pch = 18, col = "blue", cex = 1.4)   
   
 dev.off()   
 }

Done!

