

Lab 4: Path dependencies

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Coupled Human-Natural Systems

ENVS 80.10/ EEES 181 Winter 2020

Dartmouth College

Due: Thursday 2/6/2020 at 2:25pm to Canvas

Your submission should be a single PDF or Word file (no need to submit your code). A printed copy of a partial answer key will be made available before the deadline. You will self-assess your assignment and post your edited version of the lab exercises to Canvas by the due date.

Please consult the syllabus for any accessibility concerns.

This week we discussed path dependencies. In this lab we will take a closer look into these complex dynamics starting with fisheries as an example.

Exercise 1: Developing modeling intuition

In this class we are slowly cultivating an intuition for how to model coupled human-natural systems. As a test for that intuition let's start by having you consider the following questions:

This week in lecture and our readings we discussed the collapse of cod fisheries in the North Atlantic and the serious impacts of that overfishing on both human and fish populations.

- a.) If you were to model this system, what would be the key dynamic variables (those that change over time as a function of one another) that we should keep track of?
- b.) Given your answer to 1a, draw a conceptual diagram where each of the dynamic variables are represented by a circle labeled with a unique letter corresponding to that variable (provide a key please). Draw arrows with positive and negative signs indicating how each variable influences the other.
- c.) Should any of these variables influence themselves? Are these effects positive, negative or neutral? Explain your reasoning. Are there any flows in the system that don't involve relationships with other dynamic variables? If so, how could you indicate this in your diagram?
- d.) Choose 2 of your dynamic variables and convert the rest, for now, into constants. Try to write two equations, one for each variable changing over time to describe the processes you deem important in the system. Write a key to describe what each parameter in the equation you developed means.

$$\frac{dA}{dt} =$$

$$\frac{dB}{dt} =$$

The `$$` in R markdown script are used to stylize display equations using Latex. Check out your Rmarkdown cheatsheet on Canvas to help you format your equations here.

Let's compare your model to some that have been developed by others to describe fisheries, the first is called the Ricker Model, created by Bill Ricker in 1954:

$$N_{t+1} = N_t e^{r(1 - \frac{N_t}{k})}$$

This model has 1 dynamic variable : N, the population size of the fish. It also has 2 other parameters that are static constants, r = growth rate of the fish, k = carrying capacity of the fish.

Exercise 2: Ricker model

a.) What are the differences between your model and the Ricker model. How could you edit the Ricker model to be more like what you conceived of in Exercise 1?

Let's see what we can infer from the Ricker model itself by first creating a vector of N values called **n**. We will just create a list of of initial N values from 0 to 50:

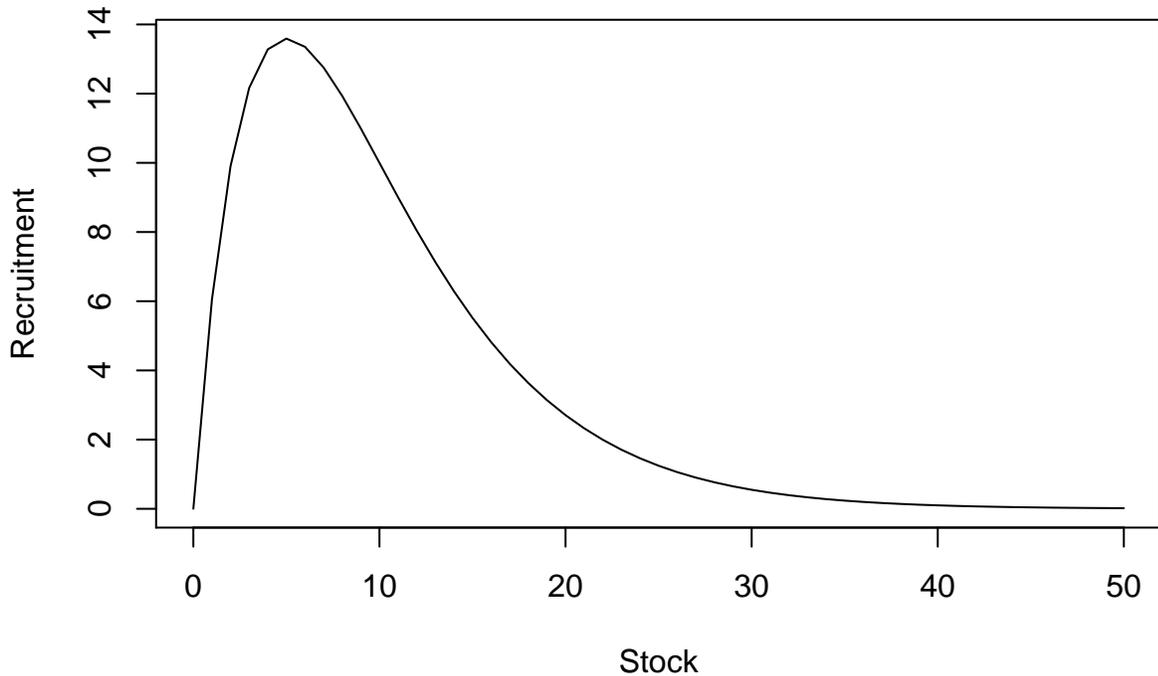
```
n<-seq(0,50)
#check out the new list here:
n
## [1] 0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24
## [26] 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49
## [51] 50
```

b.) Use your experience over the last few labs (check Canvas if you have to) to write an R function for the Ricker function. Call your function “ricker.” Create the function so that the output of the function gives you $N[t+1]$ from inputs of r, k and n parameters.

Hint: It should start something like: ricker<-function(r,k,n)

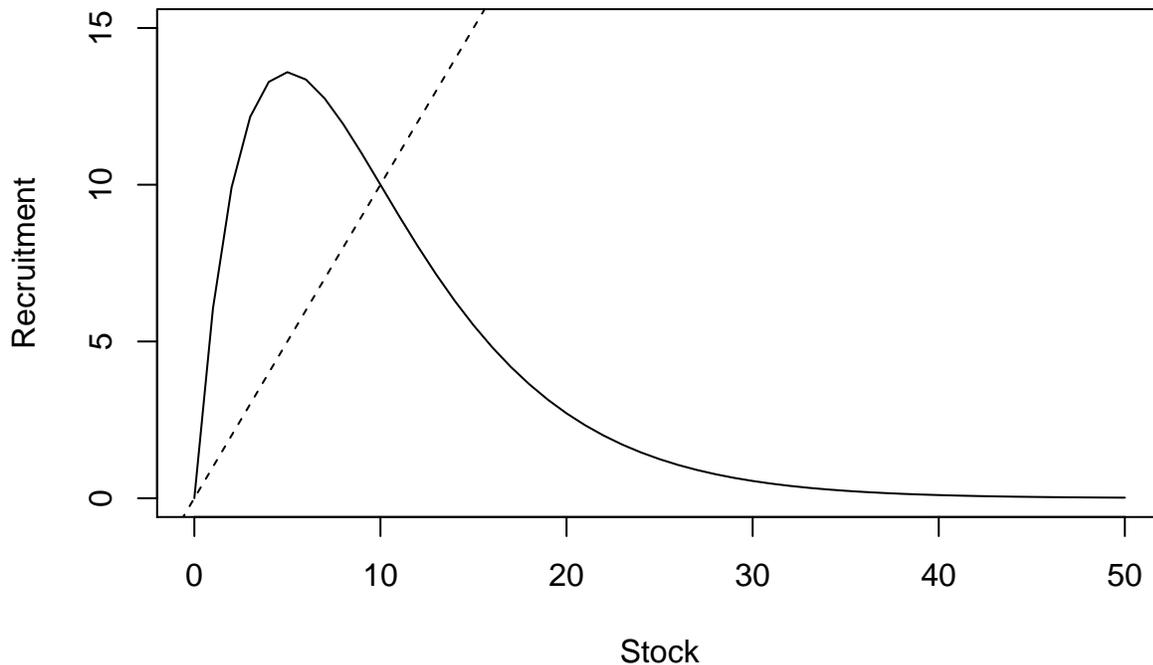
Test out your ricker function and plot a phase diagram of N_t vs. N_{t+1} for the following parameters:

```
plot(n, ricker(r=2,k=10,n=n), type="l",xlab="Stock",ylab="Recruitment")
```



Add a 1:1 line, which represents the replacement line in this fisheries context.

```
plot(n, ricker(r=2,k=10,n=n), type="l",xlab="Stock",ylab="Recruitment",ylim=c(0,15))
abline(a=0,b=1,lty=2)
```



c.) Now this model is very similar to the logistic population model we looked at in the first lab. However, in the context of fisheries the results can be interpreted very differently. Explain why we labeled the x and y axes ‘Stock’ and ‘Recruitment.’ What is the significance of the 1:1 line labeled as the ‘replacement line’?

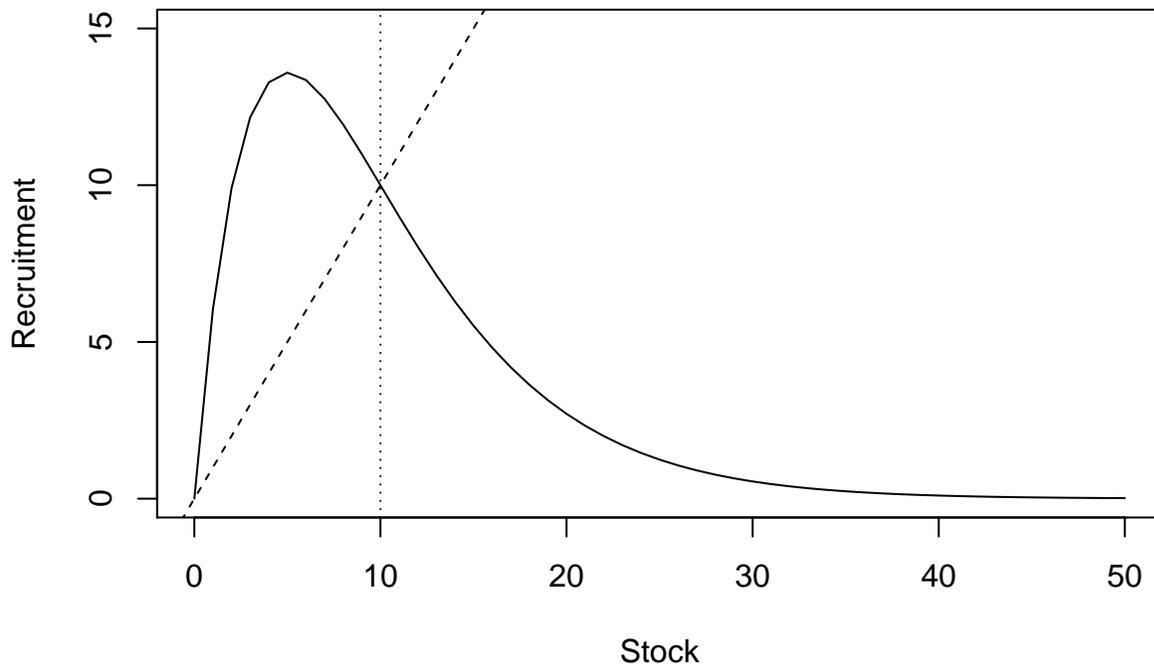
d.) Notice that recruitment declines with stock size. What is a biological reason to expect this?

Now this model may seem a little one-dimensional because humans are absent. However, fisheries managers have used this model extensively to decide how much fish should be harvested. Let’s examine how this limit is determined. First we will mark the point where recruitment is equal to stock size. We can solve for that point by opening up Mathematica and running the following command:

```
Solve[n*E^(r*(1 - n/k)) == n, n] /. {r -> 2, k -> 10}
```

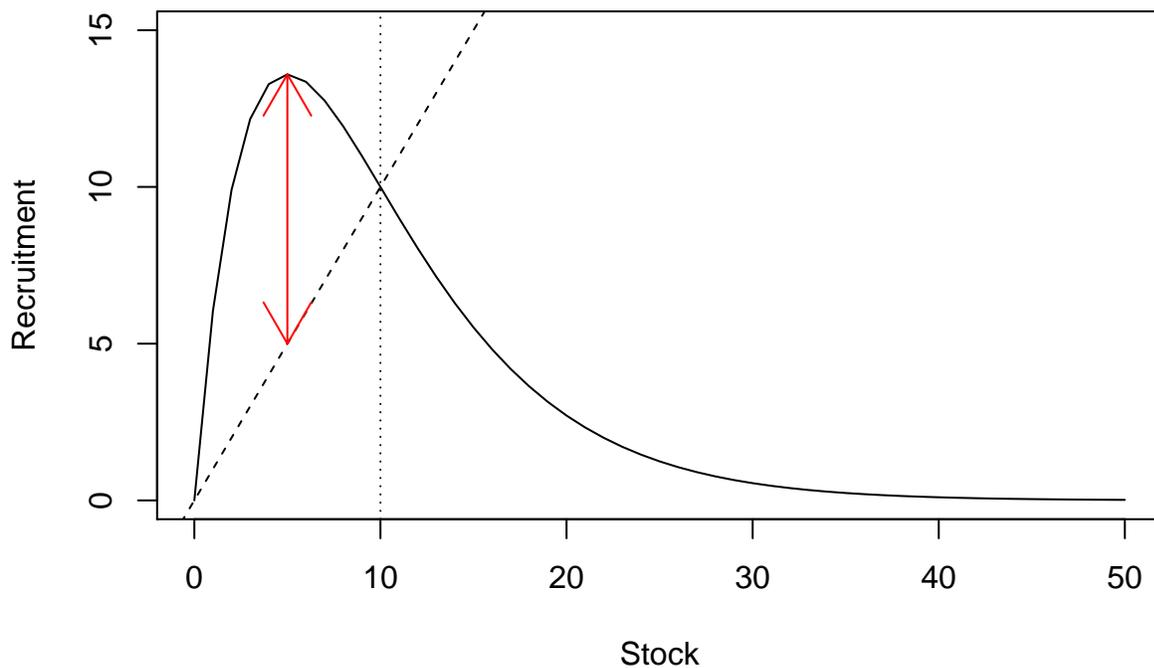
Make sure your cursor is in the line of the code then click shift+enter to run, or Evaluation> Evaluate Cells on the menu bar.

Replot your Ricker curve/replacement line in R and draw in a horizontal line with `lty=3` for where stock and recruitment are equal (other than 0). Your plot should look something like this:



If fishing happens to the left of this new vertical line we plotted, it is possible to take out fish without decreasing recruitment below replacement. We can use the `arrows` function to draw a double-headed arrow marking the maximum sustainable yield, defined as the maximum number of fish that we could harvest before reducing recruitment below replacement, for a stock size of 5.

```
plot(n, ricker(r=2,k=10,n=n), type="l",xlab="Stock",ylab="Recruitment",ylim=c(0,15))
abline(a=0,b=1,lty=2)
abline(v=10,lty=3)
arrows(x0=5,y0=5,x1=5,y1=ricker(r=2,k=10,n=5),code=3,col="red")
```



We can write an equation that describes this MSY (max sustainable yield):

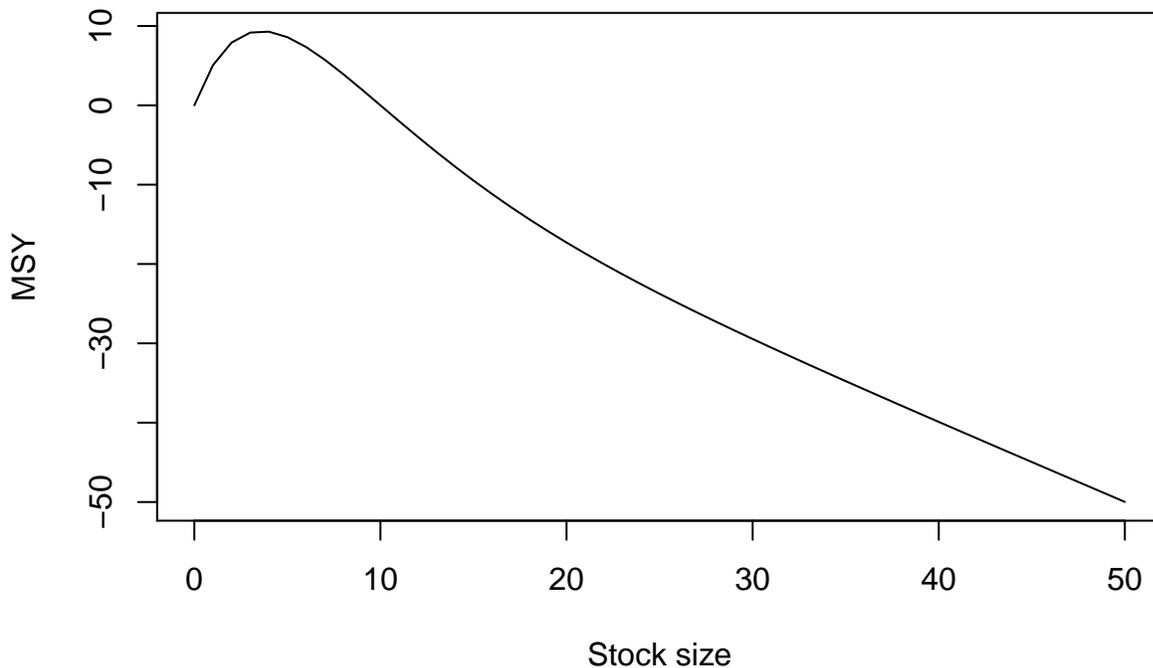
MSY= Recruitment-Stock

and create a function that represents this in the context of the Ricker function:

```
msy<-function(r,k,n){  
  n*exp(r*(1-n/k))-n  
}
```

Let's plot MSY as a function of Stock size:

```
plot(n,msy(2,10,n),type="l",xlab="Stock size",ylab="MSY")
```



So far we've only looked at a static picture of the system, but time is an important component. How does MSY change as a function of time? Let's track changes in MSY for a 100 year time span.

```
msy_t<-rep(0,100)  
msy_t[1]<-msy(r=2,k=10,n=5)  
  
for(t in 1:length(msy_t)){  
  msy_t[t+1]<-msy(2,10,msy_t[t])  
}
```

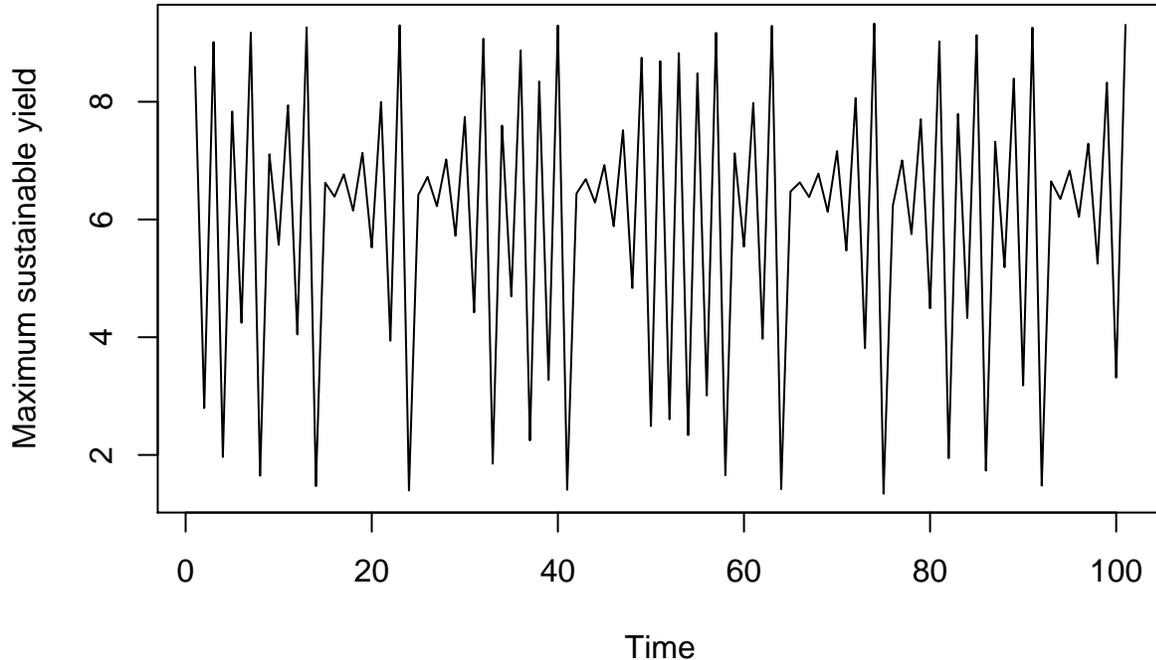
msy_t

```
## [1] 8.591409 2.795689 9.014242 1.964462 7.834986 4.245626 9.174615 1.646696  
## [9] 7.106612 5.569296 7.940424 4.047285 9.263695 1.469743 6.624387 6.387722  
## [17] 6.767690 6.150311 7.132097 5.524593 7.997042 3.940203 9.299123 1.399291  
## [25] 6.416197 6.722820 6.225211 7.019061 5.721838 7.740856 4.421444 9.071644  
## [33] 1.850854 7.594061 4.693093 8.871640 2.245986 8.344408 3.275385 9.295186  
## [41] 1.407123 6.439807 6.685433 6.287230 6.924097 5.885419 7.516450 4.835376  
## [49] 8.748502 2.488162 8.689439 2.603984 8.826065 2.335724 8.481906 3.008979  
## [57] 9.171140 1.653594 7.124262 5.538350 7.979711 3.973022 9.289241 1.418947  
## [65] 6.475233 6.629036 6.380105 6.779654 6.130256 7.162048 5.471885 8.062671  
## [73] 3.815599 9.328565 1.340711 6.235837 7.002877 5.749857 7.703163 4.491501  
## [81] 9.024669 1.943837 7.792806 4.324563 9.131079 1.733067 7.321591 5.188172
```

```
## [89] 8.393850 3.179781 9.259461 1.478161 6.648634 6.347925 6.829999 6.045481
## [97] 7.287154 5.249820 8.325179 3.312508 9.306497
```

Let's plot these results

```
plot(msy_t, type="l", xlab="Time", ylab="Maximum sustainable yield")
```



Exercise 3: Sensitivity to initial conditions

We learned in class that when systems are path dependent, initial conditions are very important in determining the state of the system.

- Replot your last figure and include different initial stock conditions ($n=5,2,1.4,7$) each plotted as a different colored line on the same graph. Include a key using the `legend` function.
- Does the system appear path dependent? Can you tell from this graph alone? What does this mean for fishers and fisheries management?

BONUS EXERCISE: BROWNIE POINTS

If more than half of you complete the following, I will bake brownies for our next break time! (please let me know if you have allergies to any foods here or if you prefer a different treat too!)

- Create a new Ricker function that includes what happens when fishers take out a certain proportion of the maximum sustainable yield. Make sure to give it a unique name.
- Adjust the % MSY catch from 0 to 100% in 25% intervals and plot how this change should influence recruitment through time on one graph with a legend. Assume the same initial conditions (N_0), r and K values as before. Make sure to label your plot!

Exercise 4: Syndromes of production

For this last exercise, we will use Mathematica to run a continuous time ordinary differential equation model of syndromes of production in agriculture. This is based on a paper by Vandermeer and Perfecto in 2012:

“Syndromes of production in agriculture: prospects for social-ecological regime change” *Ecology and Society*. You can find a copy of it on Canvas if you’re interested in a good read.

The paper constructs a theory for why there seems to be two major “syndromes of production” in agriculture, one that relies heavily on technology and external inputs (synthetic fertilizers, pesticides, etc.) and one that relies primarily on traditional indigenous practices with low inputs.

The authors propose a very general relationship between technology (E) and human population density (N). They suggest that

$$\frac{dE}{dt} = N - g(E)$$

$$\frac{dN}{dt} = f(E) - N$$

This model proposes that technology is determined by the density of the population minus some function g of the current technology, which represents the sustainable population.

$$g(E) = N_{sustainable}$$

Population change is determined by some function f of technology, the necessary population, minus the population density.

$$f(E) = N_{necessary}$$

- a.) Give a reason why when sustainable population is greater than N , technology declines?
- b.) Provide an argument for why when the necessary population is greater than N , population increases?

Let’s assume $g(E)$ and $f(E)$ are linear for now. Use Mathematica to plot the following:

```
Manipulate[ Plot[{ge*env, fe*env + b}, {env, 0, 15}, Epilog -> {PointSize[0.04],
Point[{-2/(fe - ge)}, -(2 ge)/(fe - ge)}], VertexColors -> {ColorData[97, 8],
Black}}, AxesLabel -> {"Environment (technology of production)", "Population
density"}, PlotStyle -> {ColorData[97, 1], ColorData[97, 3]}, ImageSize -> Large,
PlotRange -> {{0, 15}, {0, 15}}, {ge, .75, 1}, {fe, 0.5, 1}, {b, 2}]
```

The green line is the necessary population size, ge , and the blue line is the sustainable population size, fe as functions of the environment, which in this case is the technology of production.

- c.) Add a vector field to your plot and assess the stability of the equilibrium point. Submit a screenshot here in your Markdown doc.
- d.) How does changing the slope of $g(E)$ and $f(E)$ affect the equilibrium levels of N/E ? Does it make practical sense given your understanding of food systems? Why or why not?

Vandermeer and Perfecto argue in their paper that the shape of the sustainable population function is likely nonlinear. Plot their interpretation of the relationship with the following code in Mathematica:

```
Manipulate[Show[ Plot[{Log[ge*env/(14 - env)] + 4.6, fe*env + 2}, {env, 0, 15}, AxesLabel
-> {"Environment (technology of production)", "Population density"}, PlotStyle
-> {ColorData[97, 1], ColorData[97, 3]}, ImageSize -> Large, PlotRange -> {{0, 15},
{0, 15}}, StreamPlot[{n - (Log[ge*env/(14 - env)] + 4.6), (fe*env + 2) - n},
{env, 0, 15}, {n, 0, 15}, StreamPoints -> Coarse, StreamStyle -> Black]], {ge, 1,
10}, {fe, 0.2, .8}]
```

Play with the sustainable population function $g(E)$ and the necessary population function $f(E)$ by moving the scroll bar back and forth.

- d.) How many equilibria are in the system maximum and minimum, how do the stabilities change as you adjust the functions $g(E)$ and $f(E)$?
- e.) Does hysteresis occur in the system, if so, how and why? Start from the default values of $g(E)$ and $f(E)$ and hand-draw a bifurcation diagram that indicates how changing $f(E)$ should influence N . Show in this same plot how then going from high to low slopes of $f(E)$ affect values of N .
- f.) What does this imply for transitions from low tech to high tech agriculture and vice versa? How might we encourage transitions towards low input technology and are there any negative consequences of such a transition?

HW 3: Evidence of hysteresis

Complete the following on your own time and upload your homework to the appropriate assignment slot on Canvas. This HW has the same deadline as Lab 4.

It is pretty difficult to confirm hysteresis with a static view of the world. Yet sometimes, that's all we have access to.

We are going to access a dataset from Doering et al.'s *Nature Ecology & Evolution* paper titled: "Social tipping points in animal societies in response to heat stress" in 2018.

I found the data for this on **Dryad**, an open access repository for databases used in peer-reviewed publications. You may find this useful for your final project: <https://datadryad.org>

This paper experimentally manipulated temperature in groups of spiders and assessed effects on aggression. Though this paper considers spider aggression, note that similar arguments have been made about people in a hotter world.

Back to R now!

Setup

First download the data file from canvas titled "spiders.csv" and place in in the same folder that your .Rmd file lives in.

In R we can load data with the following script, making sure to call our data something, I choose "spiders"

```
spiders<-read.csv("spiders.csv")
```

Let's take a look at the structure of the data:

```
head(spiders)
```

```
##   Colony.ID Colony.Size Composition Trial Direction Temperature X..Interactions
## 1      A1          6 Aggressive    1      Up          27.0             1
## 2      A1          6 Aggressive    1      Up          27.5             3
## 3      A1          6 Aggressive    1      Up          28.0             1
## 4      A1          6 Aggressive    1      Up          28.5             6
## 5      A1          6 Aggressive    1      Up          29.0             0
## 6      A1          6 Aggressive    1      Up          29.5             3
##   X..Agg Prop.Int.Agg
## 1      0           0
## 2      0           0
## 3      0           0
## 4      0           0
## 5      0           0
## 6      0           0
```

```
summary(spiders)
```

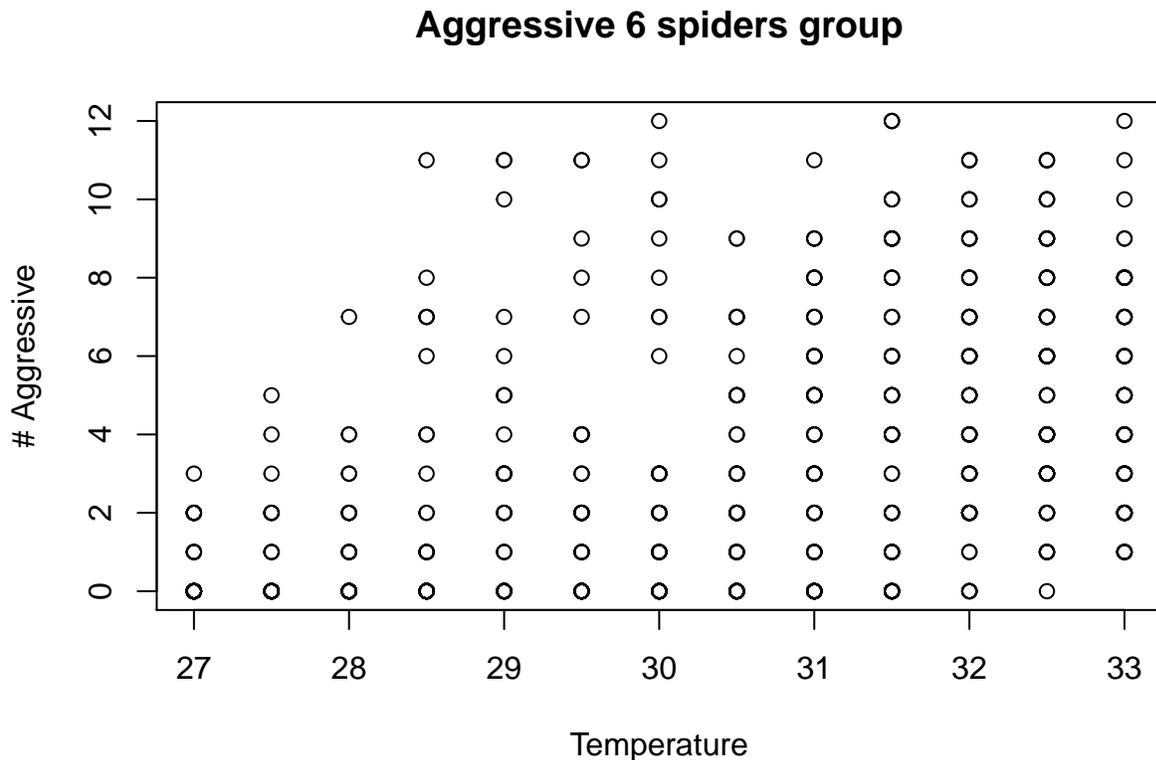
```
## Colony.ID Colony.Size Composition Trial Direction
## A1 : 52 Min. :6 Aggressive:312 Min. :1.00 Down:468
## A2 : 52 1st Qu.:6 Docile :312 1st Qu.:1.75 Up :468
## A3 : 52 Median :6 Mixed :312 Median :2.50
## A4 : 52 Mean :6 Mean :2.50
## A5 : 52 3rd Qu.:6 3rd Qu.:3.25
## A6 : 52 Max. :6 Max. :4.00
## (Other):624
## Temperature X..Interactions X..Agg Prop.Int.Agg
## Min. :27.0 Min. : 0.000 Min. : 0.000 Min. :0.0000
## 1st Qu.:28.5 1st Qu.: 2.000 1st Qu.: 0.000 1st Qu.:0.0000
## Median :30.0 Median : 5.000 Median : 1.000 Median :0.1250
## Mean :30.0 Mean : 5.733 Mean : 2.304 Mean :0.2675
## 3rd Qu.:31.5 3rd Qu.: 9.000 3rd Qu.: 4.000 3rd Qu.:0.5000
## Max. :33.0 Max. :16.000 Max. :12.000 Max. :1.0000
##
```

There are 4 different 'Compositions,' which represent groups of 'Aggressive,' 'Docile,' and a 50:50 'Mixed' assortments of spiders. There are also 2 colony sizes, 6/20 and 2 directions that the temperature was changed experimentally: 'Up' and 'Down.'

Let's take a look at only the Aggressive spiders that were placed in groups of 6 individuals, I'll call this subset of data `agg6`:

```
agg6<-subset(spiders, Colony.Size==6&&Composition=="Aggressive")
```

```
plot(agg6$Temperature,agg6$X..Agg,xlab="Temperature",ylab="# Aggressive",
     main="Aggressive 6 spiders group",ylim=c(0,12))
```



should first average aggression by colony:

We

```
agg6means<-aggregate(agg6[,8], list(agg6$Colony.ID,agg6$Temperature,agg6$Direction), mean)

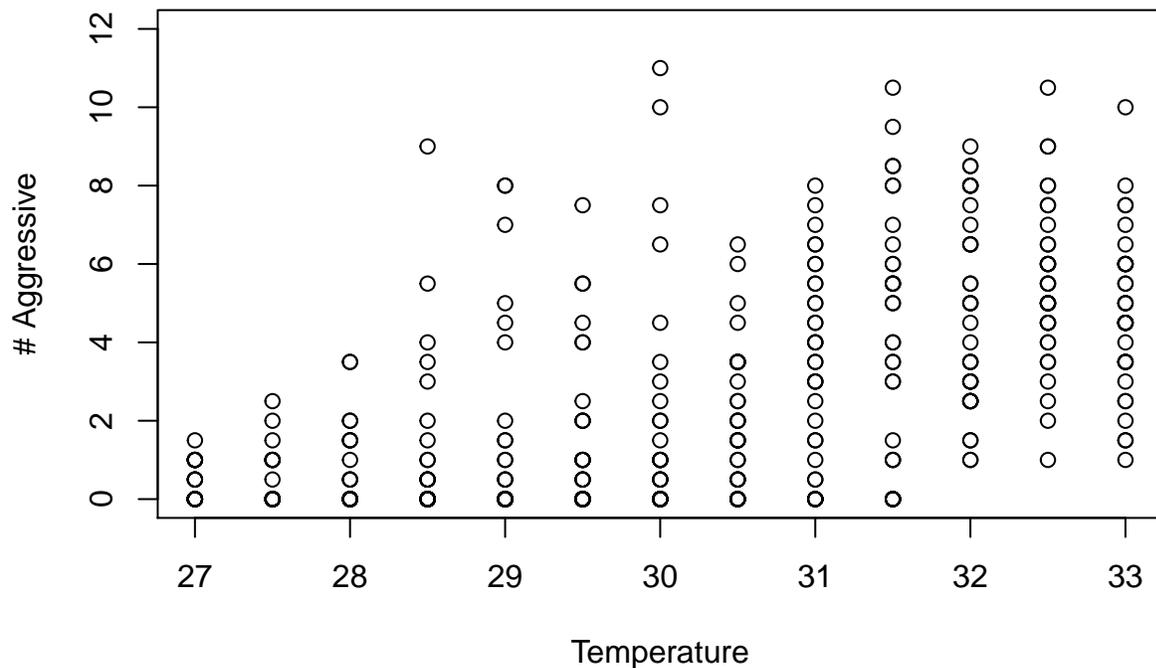
dimnames(agg6means)[[2]]<-c("Colony.ID","Temperature","Direction","NoAggressive")

head(agg6means)
```

```
## Colony.ID Temperature Direction NoAggressive
## 1 A1 27 Down 0.0
## 2 A2 27 Down 0.0
## 3 A3 27 Down 0.0
## 4 A4 27 Down 1.5
## 5 A5 27 Down 0.5
## 6 A6 27 Down 0.5
```

```
plot(agg6means$Temperature,agg6means$NoAggressive,xlab="Temperature",ylab="# Aggressive",
     main="Aggressive 6 spiders group",ylim=c(0,12))
```

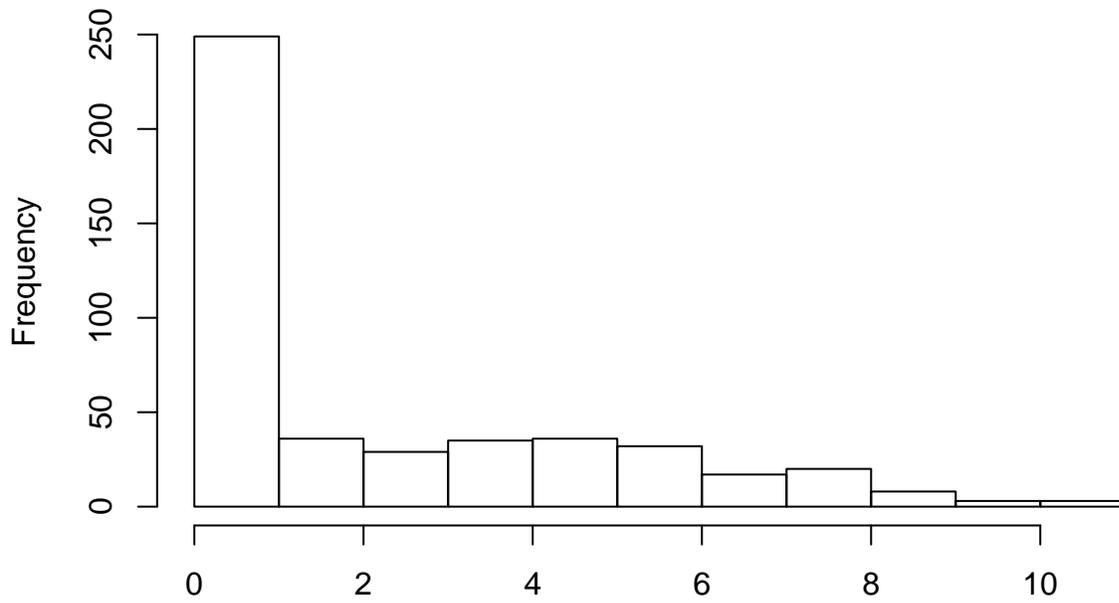
Aggressive 6 spiders group



1.) Based off of the above graph alone is there evidence of hysteresis? Explain your answer.

Let's plot a histogram of the agg6means data, which is a graph of the frequency of the data according to their size (here # aggressive spiders):

```
hist(agg6means$NoAggressive,xlab="# Aggressive spiders",main="")
```



Aggressive spiders

We call

these distributions right skewed because most of the data is on the left where frequency is low but some of it skews right where frequency is quite high.

2.) From this histogram, what was # of aggressive spiders was most commonly found? Is there evidence for two distinct 'modes' that may lead you to believe there are differences between up and down directions?

To test our suspicions, let's actually separate the up and down directions and plot them in different colors:

```
agg6_up<-subset(agg6means, Direction=="Up")
agg6_down<-subset(agg6means, Direction=="Down")

plot(agg6_up$Temperature,agg6_up$NoAggressive,xlab="Temperature",ylab="# Aggressive",
     main="Aggressive 6 spiders group",col=rgb(1,0,0,1),ylim=c(0,12))

points(agg6_down$Temperature,agg6_down$NoAggressive,xlab="Temperature",ylab="# Aggressive",
      main="Aggressive 6 spiders group",col=rgb(0,0,1,1),pch=3)
```

