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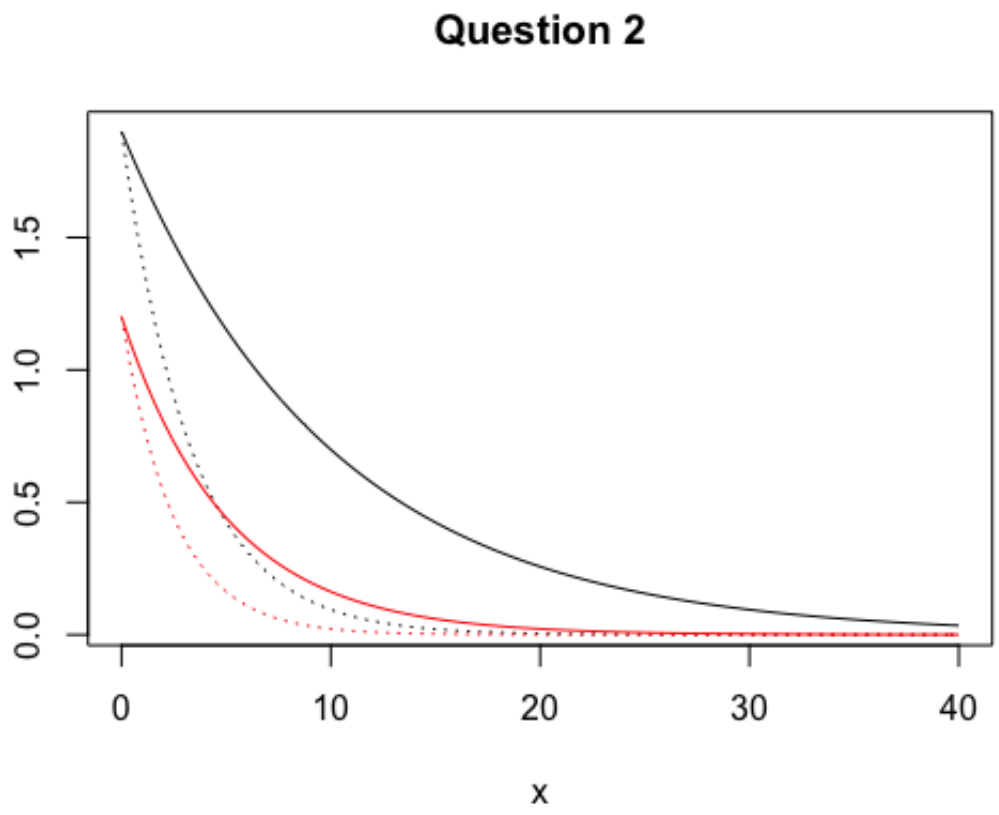
Analysis of Environmental Data
Lab 5
October 17, 2021
Worked with Juliana Berube

1: Show the R code you used to create exp_fun()

```
require(here)
dat = read.csv(here("data", "dispersal.csv"))

exp_fun = function(x, a, b)
{
  return(a * exp(-b*x))
}
plot(dat$disp.rate.ftb, dat$dist.class)
curve(
  exp_fun(x, 1700, 5), add = TRUE, from = 0, to = 1,
  ann = FALSE, axes = TRUE, ylab = "f(x)"); box()
```

2: In your lab report, include a single figure containing four negative exponential curves with these parameter values:



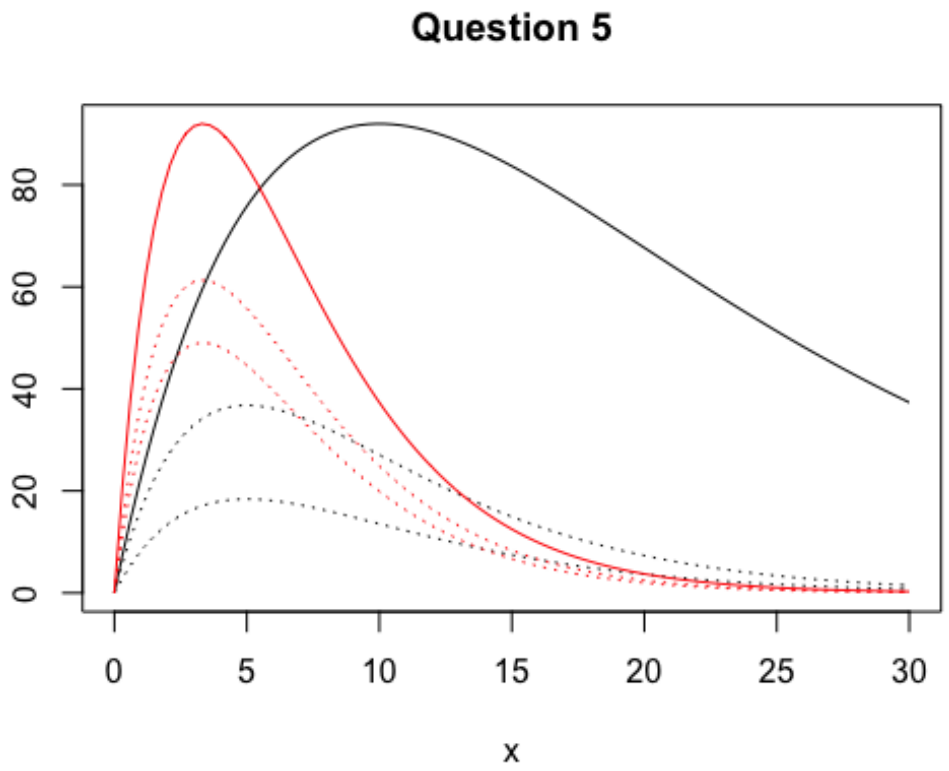
3: Observe how the curves vary as you change the two parameters' values. Qualitatively describe what happens to the curve as you vary parameter a

When x = 0, a = y. This is the “beginning” of the exponential curve. When a was changed from 1.9 to 1.2, the “beginning” of the curve started lower on the y-axis.

4: Observe how the curves vary as you change the two parameters' values. Qualitatively describe what happens to the curve as you vary parameter b

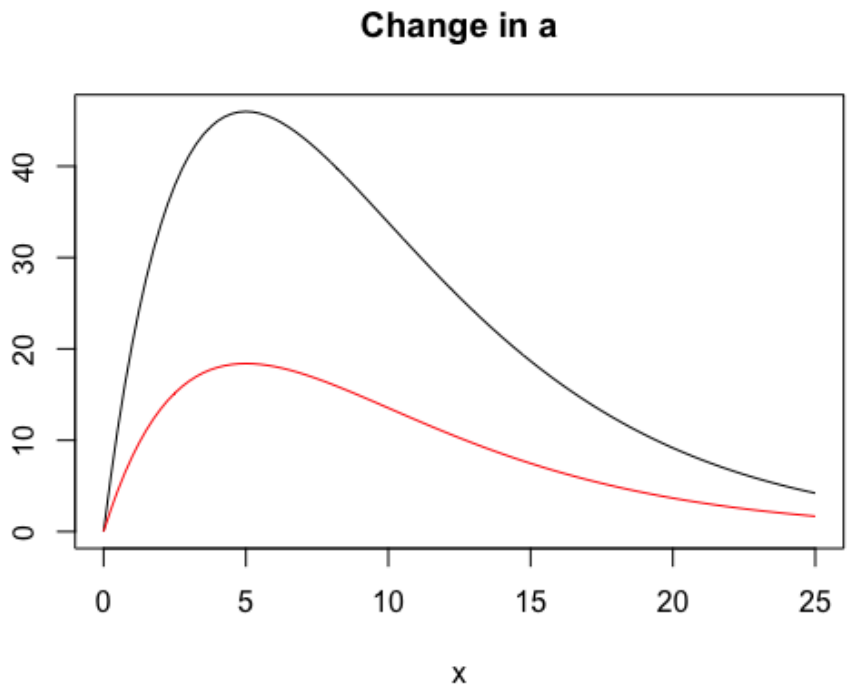
B is the “steepness” or how straight or curved the exponential curve is. The larger the b, the more dip in the curve.

5: In your lab report, include a single plot containing 6 Ricker curves with these parameter values:



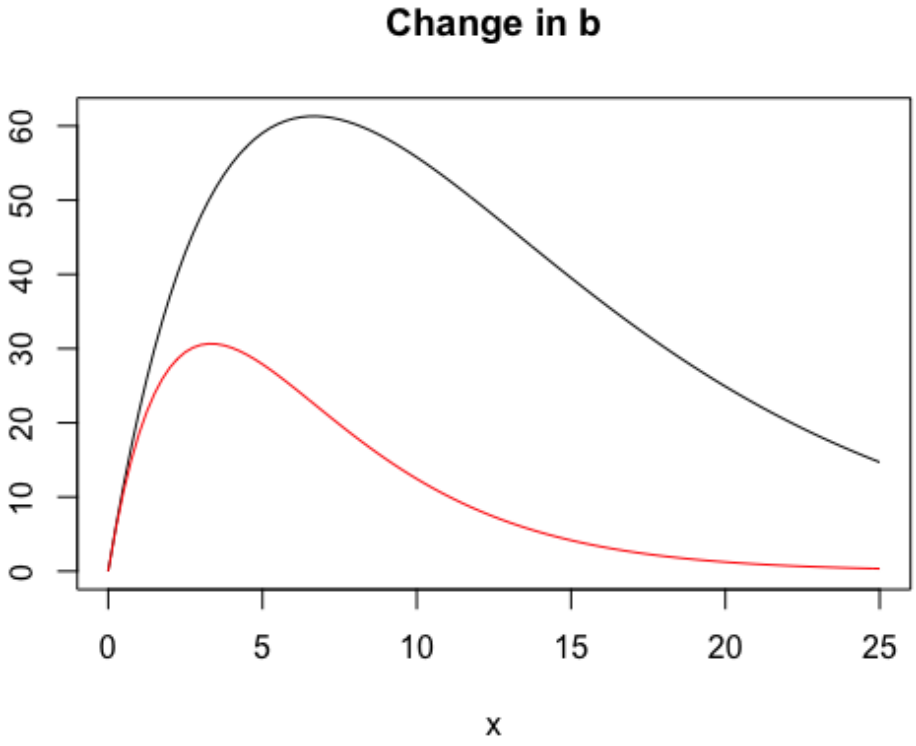
6: Observe how the curves vary as you change the two parameters' values. Qualitatively describe what happens to the curve as you vary parameter a

a determines the height of the tip of the curve. If the a is raised when the b is consistent, the curve is steeper and reaches a higher maximum y-value (on the left side of the curve).



7: Observe how the curves vary as you change the two parameters' values. Qualitatively describe what happens to the curve as you vary parameter b

B determines where on the x-axis the tip of the curve is. The larger the b-value, the lower the x-value where the peak of the curve is.

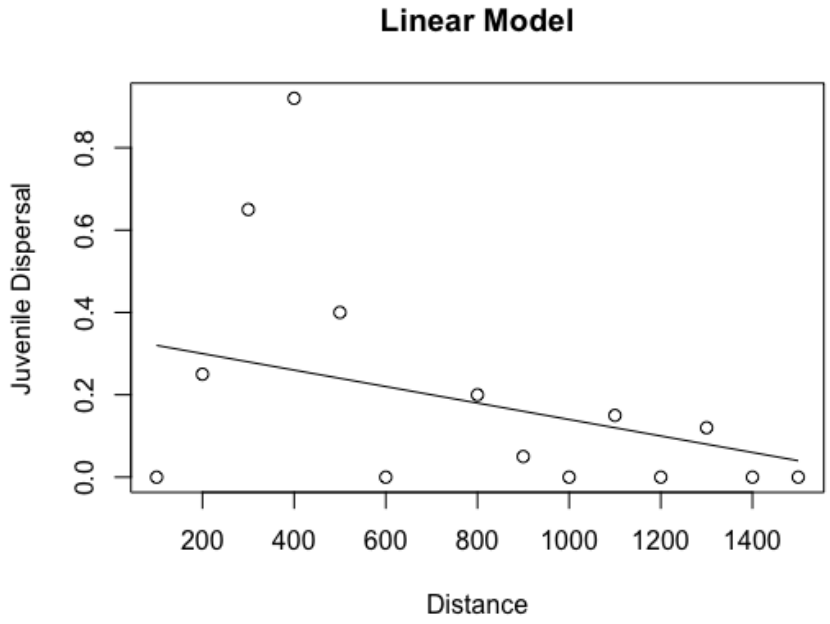


Q8 (2 pts): Linear Model. Provide the values of the slope, x1 and y1 parameters you chose. Briefly describe how you chose the values.

X = 700
Y = 0.2
Slope = -0.0002

I chose x and y based on the location that I thought the line would run through (700 , 0.2). After that I knew the slope had to be negative and represent rise/run. I played around with different slopes until I felt the linear model was a good visual representation.

Q9 (2 pts): In your lab report, include a scatterplot of the salamander data with your fitted linear model.

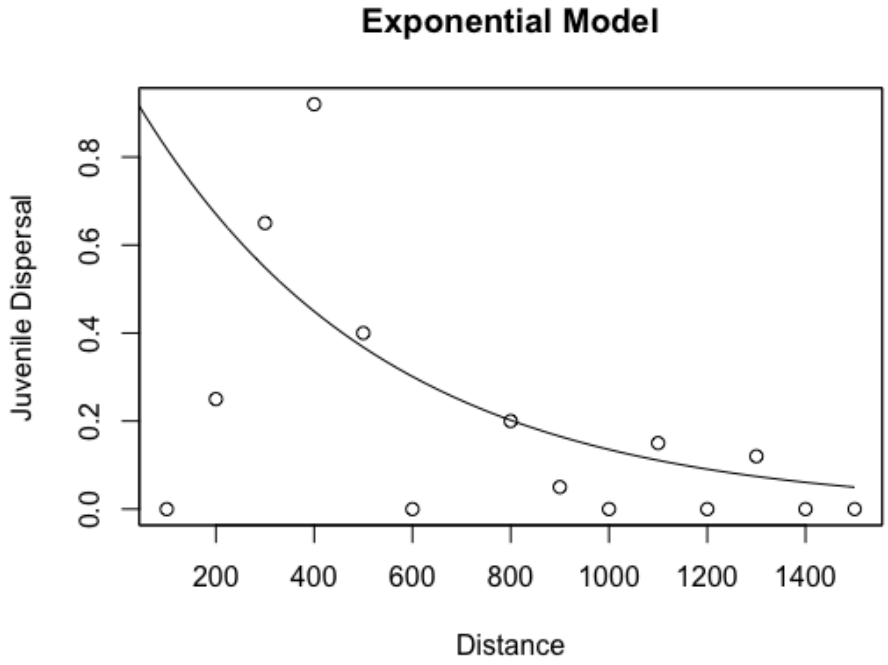


Q10 (2 pts): Exponential Model. Provide the values of the a and b. Briefly describe how you chose the values.

A = 1
B = 0.002

I initially started out with finding my b-value. I thought a good place for the curve to change directions was around x = 500. To find my b, I did 1/500 = 0.002. A is the beginning of the curve (where x and y intercept on the plot). I wanted the start of the curve to be at 1.

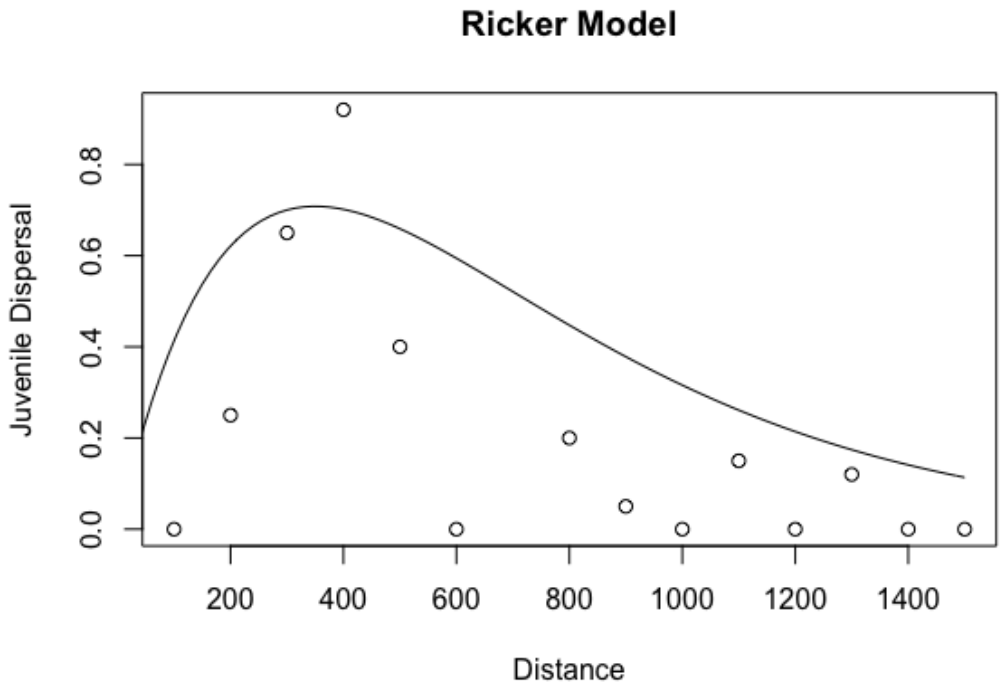
Q11 (2 pts): In your lab report, include a scatterplot of the salamander data with your fitted exponential model.



Q12 (2 pts): Ricker Model Provide the values of the a and b. Briefly describe how you chose the values.

A= 0.0055
B= (1/350)
I again started with the b-value. I chose what x-value I wanted the peak of the curve to be. I chose x = 350, so my b would be (1/350). Then I chose what y-value I wanted the peak of the curve to be. I chose y = 0.7. Then I rearranged the ricker formula to get a = (0.7 * (1/350)) / e^{-1}
. That is equal to a = 0.0054 (I made a = 0.0055 because its prettier).

Q13 (2 pts): In your lab report, include a scatterplot of the salamander data with your fitted ricker model.



Q14 (4 pts): Show the R code you used to create your data frame of model residuals.

```
pred_linear = line_point_slope(dat$dist.class, 700, .2, -
0.0002)
resids_linear = (pred_linear - dat$disp.rate.ftb)

pred_exp = exp_fun(dat$dist.class, 1, .002)
resids_exp = (pred_exp - dat$disp.rate.ftb)

pred_ricker = ricker_fun(dat$dist.class, .0055, (1/350))
resids_ricker = (pred_ricker - dat$disp.rate.ftb)

dat$resids_linear <- resids_linear
dat$resids_exp <- resids_exp
dat$resids_ricker <- resids_ricker
```

Q15 (3 pts.): In your lab report, include histograms of the residuals for each of your three models. You may create a single figure with three panels, or include three separate figures.