

Heather Siart

ECO-634 Environmental Data Analysis – Lab

10/27/2021 – LATE

Partners: Jahiya Clark

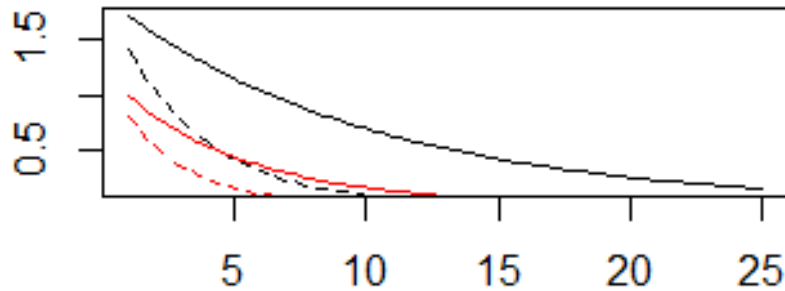
Lab 5: Uncertainty, Samples, and Populations

Q1:

```
Exp_fun = function (x, a, b)
{
  return(a * exp ( -b * x ))
}
```

```
curve(
  exp_fun(x, 0.3, (1.15)), add = FALSE, from = 0, to = 50,
  ann = FALSE, axes = TRUE, ylab = "f(x)"); box()
```

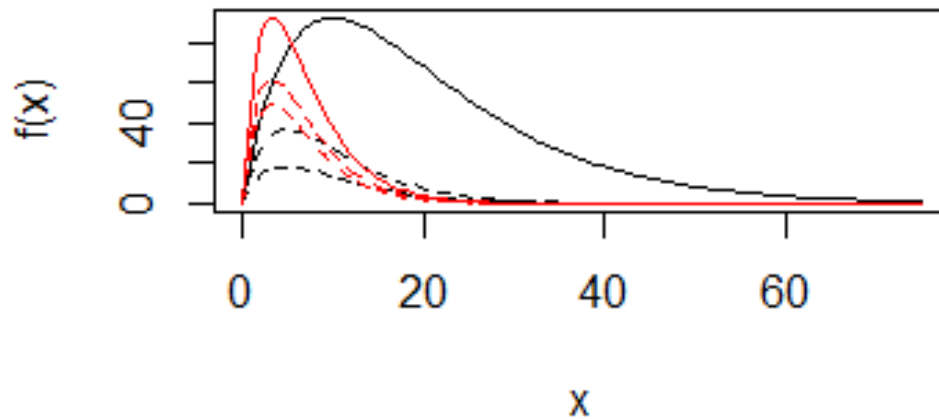
Q2:



Q3: When you change parameter “a” the line begins at a different height on the y axis.

Q4: When you change parameter “b” it causes a drastic curve in the line along the x axis.

Q5:

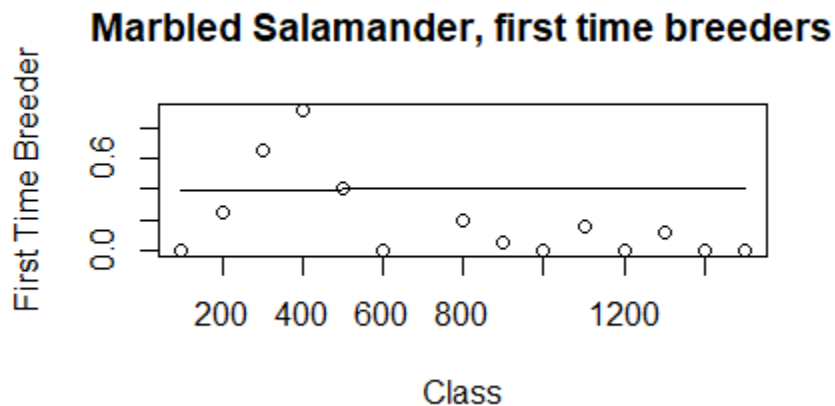


Q6: By changing parameter “a” you change the slope of the line. The red lines have a much more dramatic curve where the black lines are rounder, and softer.

Q7: Changing parameter “b” changes how high the peak of the curve is on the graph.

Q8: To figure out the values for my line I used locator(1) and tried to pick a location that visually looked balanced within the data. This gave me an x value of 503.032, and a Y value of 0.3993503.

Q9:



Q10: I used 0.97 for parameter “a” and 1/350 for parameter “b”. I chose both of these values by changing them around and seeing visually what curve fit the data points best.

Q11:


```
dat_dispersal$resids_exp <- c(0.728, 0.531, 0.399, 0.307,  
  0.241, 0.175, 0.135, 0.096,  
  0.0961, 0.069, 0.056, 0.0301,  
  0.0301, 0.0301, 0.043)
```

```
View(dat_dispersal)  
resid_linear <- c(dat_dispersal$disp.rate.ftb - dat_dispersal$resids_linear)  
resid_exp <- c(dat_dispersal$disp.rate.ftb - dat_dispersal$resids_exp)  
resid_ricker <- c(dat_dispersal$disp.rate.ftb - dat_dispersal$resids_ricker)
```

```
disp_resids <- data.frame(dat_dispersal$resids_linear, dat_dispersal$resids_exp,  
  dat_dispersal$resids_ricker)
```

```
require(here)  
png(  
  filename = here("images", "lab_05_hist.png"))
```

```
par(mfrow = c(3, 1))  
hist(resid_linear, main = "Histogram of Linear Resids", xlab = "", col = "darkorange1", xlim = c(-0.5, 0.5))  
hist(resid_exp, main = "Histogram of Exponential Resids", xlab = "", col = "coral2", xlim = c(-0.5, 0.5))  
hist(resid_ricker, main = "Histogram of Ricker Resids", xlab = "", col = "darkgoldenrod2", xlim = c(-0.7,  
  0.3))
```

```
dev.off()
```

Q15:

