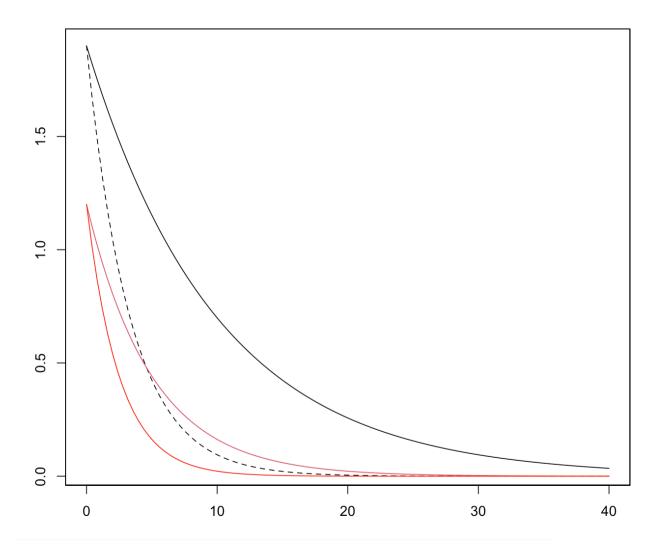
# **Analysis of Environmental Data - Lab 5** Olivia Dinkelacker

```
Q1:

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

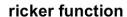
curve(
    exp_fun(x, 2.2, 1/15), add = FALSE, from = 0, to = 50, ann = FALSE, axes = TRUE, ylab = "f(x)"); box()
```

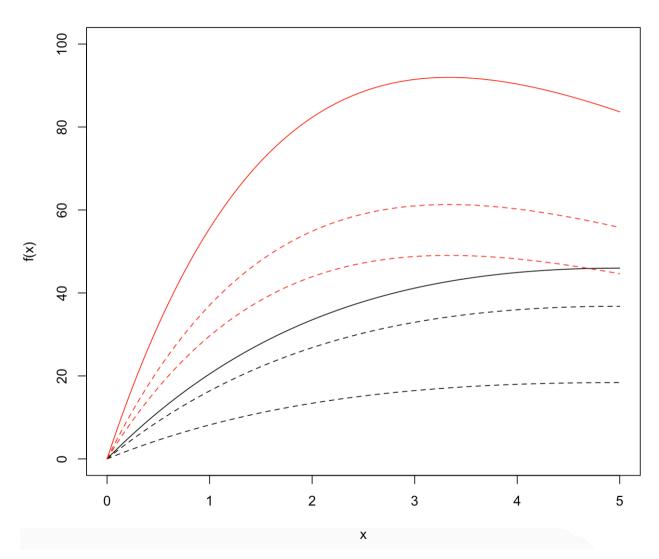
Q2:



Q3: a is the parameter that determines the starting height of the curve.

Q4: The parameter b determines the rate of decay.





#### Q6:

The a parameter is the initial slope.

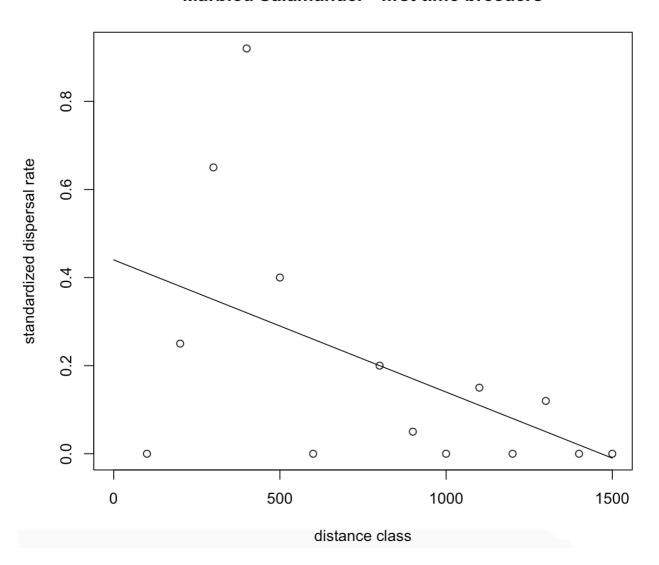
## Q7:

The parameter b determines the height of a graph  $\,$ . The highest point of the curve occurs at an x value of 1/b.

# Q8: curve(line\_point\_slope(x, 800, 0.2, -0.0003), add = TRUE)

I chose the x value by taking a value in the middle of the x axis, and the y axis because it fitted the data well.

## Marbled Salamander - first time breeders

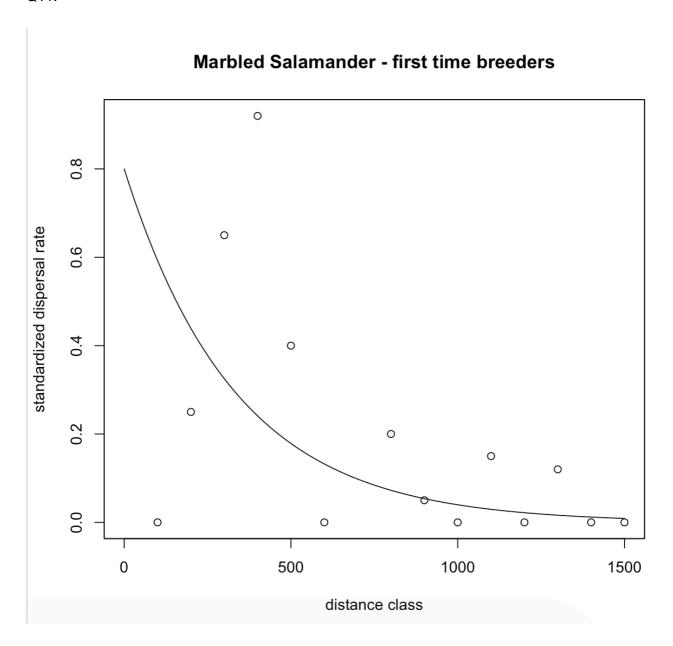


```
Q10:

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

curve(
    exp_fun(x, 0.8, 0.003), add = TRUE, from = 0, to = 1500, ann = FALSE, axes = TRUE, ylab = "f(x)"); box()
```

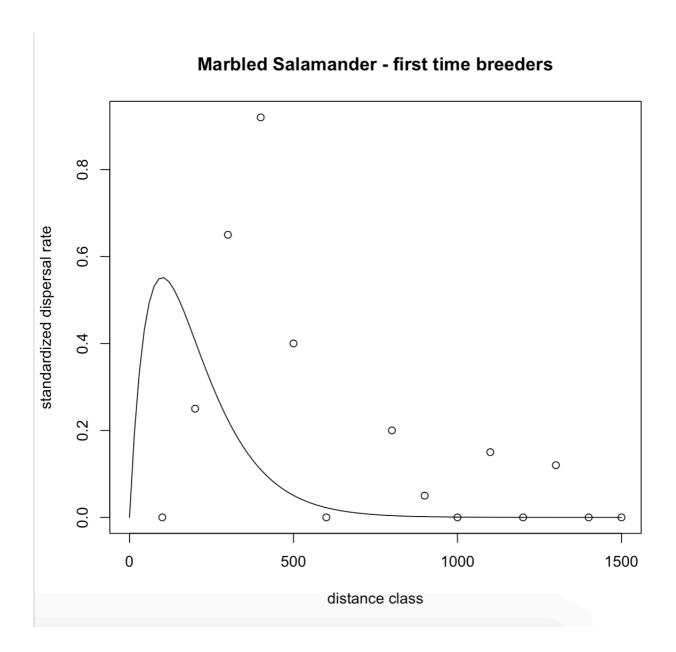
I chose these values because I tested many different ones and they resulted in the best fit.



# Q12: I chose those parameters based on guesses. 0.015 and 0.01 resulted in the best fit.

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

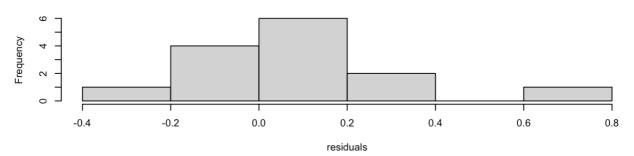
#create curve
curve(
  ricker_fun(x, 0.015, 0.01),
  from = 0, to = 1500, add = TRUE,
  main = "Ricker function: a = 1, b = 1",
  ylab = "f(x)", xlab = "x")
```



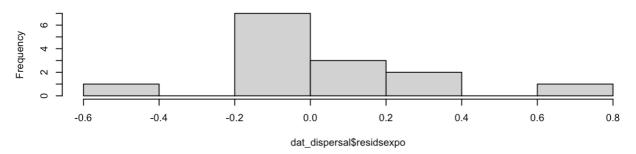
Q14:

dat\_dispersal\$residslinear <- dat\_dispersal\$disp.rate.ftb - predicted dat\_dispersal\$residsexpo <- dat\_dispersal\$disp.rate.ftb - predicted2 dat\_dispersal\$residsricker <- dat\_dispersal\$disp.rate.ftb - predicted3

#### linear residuals



#### exponential residuals



## Histogram of dat\_dispersal\$residsricker

