Run the following commands in your R console.

```
> View(infert)
> ?infert
> infert.glm <- glm( (spontaneous > 0) ~ age, data=infert, family=binomial)
> summary(infert.glm)
> plot( (spontaneous > 0) ~ age, data=infert)
```

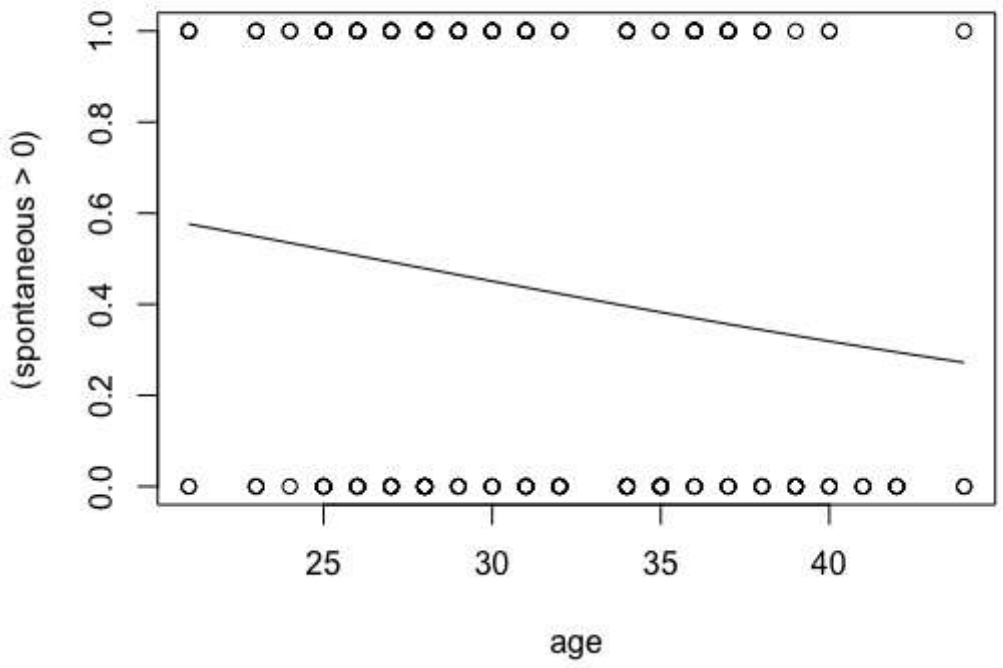
What values should be used in place of b0 and b1 in the following command to place the logistic curve on the plot you now have in R?

```
> curve( exp(b0 + b1*x)/(1 + exp(b0 + b1*x)), add=TRUE)
> #This code only works if you replace b0 and b1 with numbers.
```

b0 = 1.487

b1 = -0.05616

Notice that when you make the correct plot, it looks as follows. This shows that the logistic regression is not very useful for these data because the curve does not approach 0 or 1 within the range of the data. (To see when a logistic regression gives useful information, you should look at the plot in the **challenge** example. There you will see a nice logistic curve going from 1 down to 0 witnessing that logistic regression is very useful for that data.)



Run the following code in R.

```
> table(infert$age)
```

Which of the following codes performs the appropriate goodness of fit test for these data?

(See your R Instructions for Simple Linear Regression for the answer.)

- (●) > pchisq(residual deviance, df for residual deviance, lower.tail=FALSE)
  Where the summary(infert.glm) output contains the values for residual deviance and df.
- ( ) > hoslem.test(Y, pi)
  Where Y is located in infert.glm$y and pi is located in infert.glm$fitted

Perform the correct goodness of fit test in R to test to see if there is evidence that the above logistic regression model is not a good fit for the data.

The p-value of the test, to the 5th decimal place is 0.00016 .

Note that since the p-value is significant , the conclusion of the test is that the logistic model is not a good fit for these data. In other words, the null hypothesis was that the logistic regression was a good fit, but we have sufficient evidence to reject that assumption and conclude that logistic regression is not very useful for these data. We already saw this in the plot above, this just reaffirms our previous conclusion.)