Biostats 518 Homework 2

1. Question 1

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| **Type** | **Sample Size** | **Mean LDL (sd) mg/dl** |
| Died within 5 years | 119 | 118.7 (36.2) mg/dl |
| Survived at least 5 years | 606 | 127.2 (32.9) mg/dl |

* 1. The samples seem to be similar in magnitude. They are both in the hundreds number set. The standard deviations are also similar with an absolute difference of 3.3 mg/dl.

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| **Type** | **Mean LDL** | **Standard Error** | **95% CI [low, high]** |
| Died within 5 years | 118.7 mg/dl | 3.3 | [112.1, 125.3] |
| Survived at least 5 years | 127.2 mg/dl | 1.3 | [124.5, 129.8] |

* 1. The point estimates seem to be similar in magnitude. The standard errors are also similar in magnitude, however there is an absolute difference of 2 mg/dl between them. The standard error for the group that died within 5 years is larger because the sample size is smaller. The standard error for the group that survived at least 5 years is smaller because the sample size is larger.
	2. The overlap between the high end of the 95% CI for the folks who died within 5 years and the low end of the 95% CI for the folks who survived at least 5 years seems to be minimal (0.8 mg/dl). Based on this, we can conclude that there is a significant difference between the groups.
	3. Assuming the means of the two groups are different but the variances are equal, the best estimate for the standard deviation would be the standard deviation from a geometric mean of the LDL.

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| **Type** | **Mean LDL mg/dl** | **Standard Error** | **95% CI [low, high]** |
| Difference | 8.5 mg/dl | 3.5 | [1.4, 15.5] |

* 1. The p-value that the groups don’t have equal mean LDLs is 0.0186, so the p-value that the groups do have equal mean LDLs is 0.9814. Based on all of the data and analysis we’ve conducted thus far, I can conclude that there is a significant association between serum LDL and 5-year all cause mortality.
1. Question 2
	1. Both of the models are not saturated because we have more data points (119 for died within 5 years and 606 for survived at least 5 years) than estimated parameters in our polynomial equation 🡪 E(ldl|deadin5) = 127.2-8.5\*deadin5
	2. Using the model based off of those who died in 5 years (deadin5), the group who survived at least 5 years have an LDL value of 127.2 mg/dl. This is the exact same answer we got when we ran a t-test in question 1.
	3. Using the model based off of those who died in 5 years (deadin5), the group who survived at least 5 years have a 95% CI of 124.5 mg/dl on the low end and 129.8 mg/dl on the high end. These are the exact estimates derived from the t-test in question 1.
	4. Using the model based off of those who died in 5 years (deadin5), the group that died within 5 years have an LDL value of 118.7 mg/dl. This is the exact same answer we got when we ran a t-test in question 1.
	5. Using the model based off of those who died in 5 years (deadin5), the group that died within 5 years have a 95% CI of 109.4 mg/dl on the low end and 124.5 mg/dl on the high end. These estimates, however, seem to be a little different from the values I derived in question 1. There seems to be an absolute difference of 2.7 mg/dl on the low end and 0.8 mg/dl on the high end.
	6. For the first model, the deadwithin5 group seems to have a standard deviation of 4.65 and the ones who survived at least 5 years seem to have a standard deviation of 1.3. The standard error we obtained in question 1 is the same for the group that survived at least 5 years, but greater than the value for the deadwithin5 group (3.3). For the second model, the deadwithin5 group seems to have a standard deviation of 6.36 and the ones who survived at least 5 years seem to have a standard deviation of 9.66. These results are different from what we obtained in question 1. The estimates from this model are much higher, probably because there are fewer data points so the standard error is higher.
	7. Both of the models seem to be the identical on the surface, but in reality they give us different results from each other. It seems like a lot hinges on the data the model was generated from.
	8. E(LDL|deadin5) = 127.2 – 8.5(X)
		1. When X (aka deadin5) is equal to 0 (the person survived at least 5 years), the mean LDL is 127.2 mg/dl.
	9. When X (aka deadin5) is equal to 1 (the person died within 5 years of the first MRI), the mean LDL is 8.5 mg/ml less.

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| Type | Mean LDL mg/dl | Standard Error | 95% CI [low, high] |
| Model1 | 127.2 mg/dl | .3 | [-15,.1 -1.9] |

* 1. The p-value testing whether the populations are the same is equal to the square of the r-squared value (0.0088^2) = 7.7e-5. We can again conclude that there is a significant association between LDL and 5-year all cause mortality. This matches the conclusion that was drawn in question 1.
1. For the deadin5 group, the p-value seems to be smaller and the confidence intervals seem to be more narrow (compared to the results from question 1). For the group that survived at least 5 years, the p-value seems to be larger and the confidence interval seems to be wider (compared to the results from question 1).
2. For the deadin5 group, the 95% CI seems to be more narrow than the results we saw in question 3. For the group that survived at least 5 years, the 95% CI seems to be wider than compare to question 3. These trends seem to match what we expect based on the analyses we’ve done so far and the observation that t-test and regression can be interchangeable for this data set.
3. Question 5

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| **Type** | **Sample Size** | **Mean** | **Standard Deviation** | **Min** | **Max** |
| LDL (mg/dl) | 393 | 101.25 | 19.29 | 11 | 129 |
| Age (years) | 225 | 74.69 | 5.25 | 65 | 92 |
| Male  | 107 | 0.55 | 0.49 | 0 | 1 |

* 1. Descriptive stats above communicate the very basic knowledge required to assess whether or not there is a relationship between LDL and age (and whether sex is a confounder)
	2. I used simple regression to create a model that relates LDL and age. The process includes plotting age on the X-axis and LDL (mg/dl) level on the Y-axis, and then creating a best-fit line to summarize the data points. Best being defined by having the lowest sum of square residuals value as possible (because we are using Ordinary Least Squares). Sometimes RMSE or root mean squared error is also used to communicate how “well” a model is fit to its data.
	3. A saturated model is one where the number of parameters is equal to the number of data points. The answer is no, this model is not saturated. There are 725 data points in this model and only one parameter.
	4. E(LDL|age) = 132.5 – 0.09(AGE)
		1. 132.5 – 0.09\*70 = 126.2 mg/dl
	5. 132.5 – 0.09\*71 = 126.11 mg/dl. The answer to this question is a little lower (by 0.09 mg/dl, or 1 unit) than the previous answer. The slope is an averaged estimation of all of the data points used to fit the model from part c.
	6. 132.5 – 0.09\*75 = 125.75 mg/dl. As age increases, the mean LDL value seems to decrease at a rate of 0.09 mg/dl. Again, the slope is an average of the general trend of the data.
	7. The root mean squared error (RMSE) in my model is 33.62 (mg/dl). In general, RMSE refers to how close the model fit line is to the actual data points. What this means in particular to my model is that the trend line has a leeway of 33.62 mg/dl.
	8. There is meaning in the intercept. It means every person in our model will have a mean LDL value of at least 132.5 mg/dl.
	9. There is also meaning in the slope. It means a person in the model will have 0.09 mg/dl lower mean LDL serum values for each year they age.
		1. Method: I used simple linear regression to fit the model and used ordinary least squares to understand how well the model was fit to the data.
		2. Inference: Based on the model, there seems to be the trend that the older a person is, the lower their mean LDL serum value is. The p-value is about 4e-8 (r-squared\*r-squared), which is definitely denotes a significant association.
	10. When calculating the point estimate and 95% CI for the mean difference across groups that differ by 5 years, I would report
		1. Point estimate difference = 0.45 mg/dl
		2. 95% CI = [-2.7, 1.8]
	11. The correlation between LDL serum value and age seems to be -0.0146. This seems to indicate that there is a very weak relationship between those two variables. This is contrary to the conclusion I previously came to when viewing the data solely through the lens of regressions and descriptive statistics.