My first point of contribution was coming up with the idea of analyzing the effects of life history traits on diversification and performing some rough regressions between number of species in an order and the different traits in the dataset to see if it was a real effect when my group was in an early stage where we each came up with an idea for the project to present to each other so we could choose which one to do. I also found three papers from the literature that supported the hypothesis. Once diversification was chosen I then cleaned up the dataset and created new data frames that just listed genus and just listed order with the trait values being the average of all the species in the clade, as well as having a new column for the number of species in that genus or order. Once we decided as a group to use genus rather than order as our level of analysis I then used the code chunks form the lectures as a basis for writing code for performing linear regression between gestation period and number of species per genus and a randomization test comparing the slope of this relationship to the slope when gestation period values are randomly redistributed between all the species in the dataset, which was used as a template by the other group members for their own randomization tests. I also helped another group member who was having trouble adapting this template for her own test. The next stage of the statistical analysis I did myself was the drop-one tests, where I used dplyr to remove four different orders form the analysis one at a time that I thought might have had an impact on the results to see if the relationship between life history traits and diversification was still true with the specific orders removed.

For the paper I wrote most of the initial outline along with Hanatu and contributed to group decision making on structuring the paper and what figures we should include. When we individually fleshed out and added different sections I wrote the data description section, describing the dataset, the changes we made to it, and why we chose to look at genus rather than species level. I also wrote the majority of the discussion section, though the rest of the group also contributed to parts of it, interpreting results and addressing potential sources of error and the biological and ecological factors that could explain our results. I also contributed to the results section, giving input on the tests that I worked on, as well as ran through the paper and corrected some grammar and word choice errors. For our presentation I wrote the discussion slide and presented the discussion section as well as the section on the randomization tests, since I was the one who wrote the code for the randomization tests and most of the discussion section.