Instructions for Debugging Laughlin & Grabowski’s Project:

Accessing Data:

Navigate to Ty Laughlin’s BIO247 github repository or use the following link:

<https://github.com/laughlintc/BIO247/tree/master/Project>

Once within this repository, navigate to the folder titled "ProjectData&Code”. Once within this folder, download the six .csv data files. These files are named according to the following convention:

* EB\_visitation\_<honeybees/wildbees>\_<year data was collected>.csv

An example of one of these files is:

* EB\_visitation\_honeybees\_2014.csv

Accessing Code:

After all 6 .csv files are downloaded, then access the R markdown file contained within the same folder, "ProjectData&Code”, titled GrabowskiLaughlinBIO-247Project.Rmd. Once this file is downloaded, open it and ensure your working directory is set to the location where you downloaded the 6 data files too. Once that is done, download Benchmark\_GrabowskiLaughlinBIO247Project.Rmd to test the code and data. Run the coding chunks. The chunk with the header “##Honey Bees 2014” was run successfully if the following graph is yielded:

Chart, histogram

Description automatically generated

If the graph was made correctly, you can begin debugging, if not please reach out to Ty Laughlin or Jonathan Grabowski for assistance.