***Exploring how climate will impact plant-insect distributions***

***and interactions using open data and informatics***

**Class 2: Tips for students to overcome commonly encountered errors in R**

* Before beginning, be sure you set your **working directory** to where your scripts are located so R can access the files you are trying to execute.
* Changes to your script files:
  + If you received an error such as: "**Error in if (!cl) {missing value where TRUE/FALSE needed**" then you may have made a mistake in your script file. On page 3 of the SP2 instructions under ***3. Making changes to your script file*** you were supposed to replace MY\_SPECIES.csv with the name of your csv file you downloaded from iNaturalist. The final line in the script should still have **data/** in front of that file name and be surrounded by quotations - so the text on line 14 should look like **infile <- "data/Adelpha\_eulalia\_data.csv"** where only **Adelpha\_eulalia\_data.csv** is replaced with your file name. The same goes for all of the script files (some this is line 14 and some it is line 13 and 14).
  + In the same script file you were also supposed to replace "**MY\_SPECIES**" on line 15 with your species name. The species name should still have quotations around it (e.g. "Adelpha\_eulalia"). The same premise holds for all script files.
* Any error with the phrases: "**cannot find input data file**", "**file does not exist**", "**object 'infile' not found**", "**no such file or directory**" suggest one of two common errors. Please keep in mind the error message could say a lot more but if any part of the error message contains one of the aforementioned phrases this is likely pointing to the same problem.
  + ***Misspelling***: The wrong spelling could be how you wrote the name of the file in the script - open the script file again and make sure the edits you made spell the names exactly as they appear in the file names.
  + ***Misspelling***: It might have just been that you misspelled the script file in the source(file = "scripts/filename-sdm-single.R") command in your console window.
  + ***Quotations*** were deleted somewhere. Check through the commands to make sure you have quotations wherever you are supposed to have quotations! This could be in the script files themselves or in the **source(file = "scripts/filename-sdm-single.R")** command.
  + ***File location.*** Your files may not be where you think they are. Make sure data files (the csv files) are in the **data** folder and the script files are in the **script** folder. If not, the easiest way to move them is to open the **biodiversity-sdm-lesson** folder on your computer and move them.
* Remember to read error messages carefully - just because you got an error message doesn't mean that it is the same error as before. Approach this with patience and see if you can work out some of the errors you encounter using the guidelines above.

### **Class 2: Additional Resources**

* The GitHub repository for this exercise has troubleshooting tips available at:

<https://github.com/jcoliver/biodiversity-sdm-lesson/blob/master/docs/troubleshooting.md>

* Some additional troubleshooting tips for Git/RStudio integration can be found at: <http://happygitwithr.com/troubleshooting.html>
* YouTube video on how to setup and configure R and RStudio on a Mac: <https://www.youtube.com/watch?v=cmj8Oi6PFe0> (16:18)
* YouTube video with brief navigation introduction to RStudio on a Mac: <https://www.youtube.com/watch?v=bGBgjZd6YHw> (2:21)