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

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

**SP-3: Future Species Distribution Models and Hypothesis Evaluation**

**- Instructions -**

**I.** **Brief Summary**: Climate change is happening fast impacting the abundance and distribution of many plants and animals. Descriptive models may be insufficient tools for policy makers and land managers because the speed and scope of climate change has not been seen in recent human memory. Predictive models using information on future climatic variables may be an important tool to estimate where and when a species may occur in the next 25, 50, or 100 years from now. Here we estimate future species distribution models for the year 2070 using open data provided by citizen scientists and government funded sensors. Specifically, we are using the GFDL-ESM2G model with a 4.5 increase in CO2 for the year 2070 which seems to perform well across a variety of continents (McSweeney et al., 2015). GFDL refers to the Geophysical Fluid Dynamics Laboratory that developed the model. ESM refers to an Earth System Model which models a variety of atmospheric variables and cycles, as well as plant ecology and land use. You can read more about the GFDL’s Earth Systems Models at <https://www.gfdl.noaa.gov/earth-system-model/>. We evaluate the quality of these estimates and compare the results to our hypotheses generated in the last session.

McSweeney, C.F., R.G. Jones, R.W. Lee, D.P. Rowell. 2015. Selecting CMIP5 GCMs for downscaling over multiple regions. *Climate Dynamics*. 44(11-12): 3237-3260.

**II.** **Learning Goals & Objectives:**

1. Use research computing tools (Citizen science crowd sourced data, R programming language, GitHub collaborative web platform, data visualization) to study a butterfly-host plant interaction.

f. Generate forecast maps for species distribution models in 2070 using R from open source biodiversity data

g. Evaluate the hypothesis using present and forecast SDMs

**III.** **Generate a Forecast Species Distribution Map Using Future Climate Variables:**

1. If you look in the **scripts** folder you will see the new script – **run-future-sdm-pairwise.R** which we will need to make your 2070 maps.
2. Open the **scripts** folder within the **biodiversity-sdm-lesson** folder on your computer (not in RStudio) and make a duplicate copy of **run-future-sdm-pairwise.R**. Replace **run** with your butterfly name and delete any extra words such as ‘copy’ that were added to the file name. You file name should look something like: **Adelpha-future-sdm-pairwise.R**
3. Back in RStudio, open the file you just created, (e.g. **Adelpha-future-sdm-pairwise.R)** by going to **File** -> **Open file**. Navigate to the **scripts** folder within the **biodiversity-sdm-lesson** folder and open the file.
4. On line 14 you need to change **BUTTERFLY\_DATA.csv** to the name of your butterfly data file name that you downloaded from iNaturalist. Be very careful to spell this correctly. Also, do not delete the quotations or data/ - these are both needed for R to understand where to find your data. The final line should look something like this:

**butterfly.data.file <- “data/Adelpha\_eulalia\_data.csv”**

1. On line 15 you need to change **PLANT\_DATA.csv** to the name of your plant data file name that you downloaded from iNaturalist. Be very careful to spell this correctly. Also, do not delete the quotations or data/ - these are both needed for R to understand where to find your data. The final line should look something like this:

**plant.data.file <- “data/Quercus\_gambelli\_data.csv”**

1. On line 16 you need to change **MY\_SPECIES** to a file name that you will recognize. My recommendation is to use the genera names of the butterfly and plant followed by 2070 (e.g., **AdelphaQuercus2070**). Again, retain the quotations. The final line should look something like this:

**Outprefix <- “AdelphaQuercus2070”**

1. Save the changes to the script file.
2. In the Console window, run this script file using the following command:

**source(file=“scripts/<species>-future-sdm-pairwise.R”)**

Replace <species> with your butterfly genus name so it matches the exact name of the script file (in the example above I had: **Adelpha-future-sdm-pairwise.R**). Hit enter – the file will have finished running when you see the blue carrot (>) return to the screen. (PS: be patient!). Write down the amount the range will be occupied.

1. Your map should appear as a PDF in the **output** folder in the **biodiversity-sdm-lesson** folder.
2. If you are feeling ambitious, you are welcome to modify and use the **run-future-sdm-single.R** scripts to generate 2070 maps for your species individually. Follow the same protocol as above but this time you will either call on your butterfly or your host plant data so you make one map at a time (similar to the other work with did with the single scripts).
3. Use the data you have generated to complete the **SP-3** assignment.