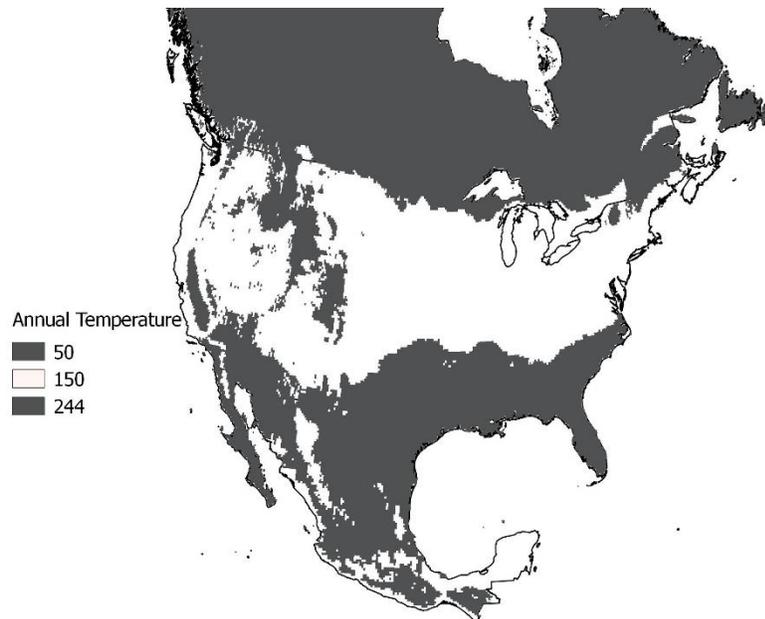


## Lab 7: Bottom-Up Ecological Niche Modeling

### Introduction

Today we are going to use another form of ecological niche modeling to determine the species distribution of the American bullfrog. As introduced in last week's lecture, bottom-up models use physiological performance measured in the lab. We then scale the lab measurements up by looking at climate patterns across the landscape. The logic here is that if we know how hot is too hot based on lab experiments, we can mark off areas on the map where it is too hot. We will be using QGIS, one of the climate layers from last week, and our thresholds calculated from the physiology lab. Output files (after doing some cleaning) look like a map with areas where it is too hot or cold blocked off. See below for an example using simulated data, where white represents areas of potential habitat:

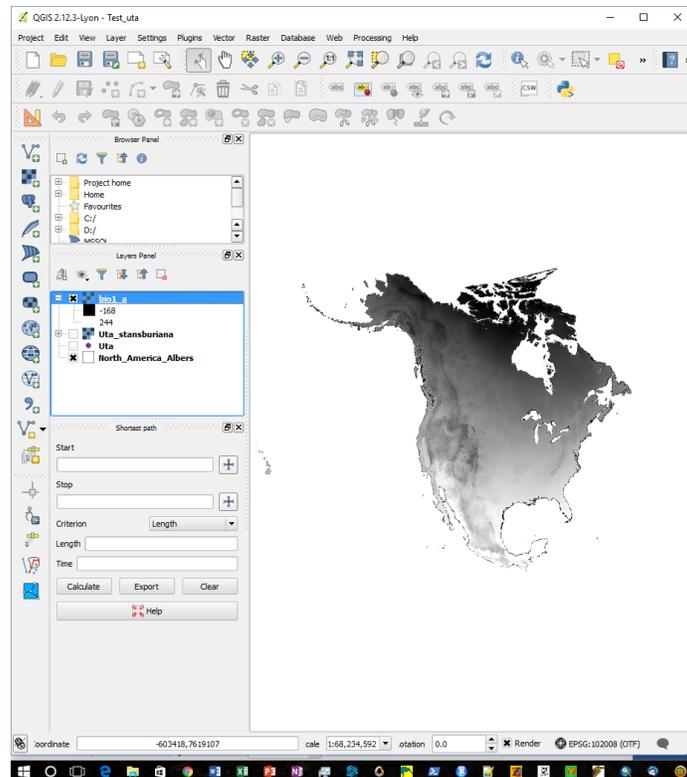


Note that this image is rather misleading without a figure caption, which we will discuss later. The goal for today's lab is to load in the annual temperature data that was clipped and reprojected from the last lab, and then color coding areas of the map that are acceptable based on the physiological thresholds you calculated from the EcoPhys lab. I am going to walk you through doing this with annual temperature and resting BPM, but you are expected to make the maps for the other calculated thresholds that fit the Gaussian curve. **The overall goal of your final paper is to have maps based on physiological measurements, a map based on Maxent/correlations with climate, and maps that compare the two. These will serve as your figures for the second lab report.**

## Adding and Color Coding Climate Layers

1) Open QGIS Desktop with GRASS and start a new project. This fresh start will make things simpler as we no longer have to deal with the clutter from last week. First, add the North America Albers shapefile from previous weeks and set the project coordinate system to EPSG: 102008. If you are unclear on these two steps please reference last week's lab.

2) Click Layer, Add Layer, Add Raster Layer. Now, select the .asc raster for bio1. Bio1 is annual temperature. As a default, you should see something like this:



Currently, the raster is set to display as a continuous variable, with darker colors being colder. Under the layer panel you can see that black is set to -171.2 and white is 242.7. **Remember, Bioclim layers are in tenths of a degree Celsius, so really black is -17.1 average annual temperature and white is 24.2 degrees Celsius.**

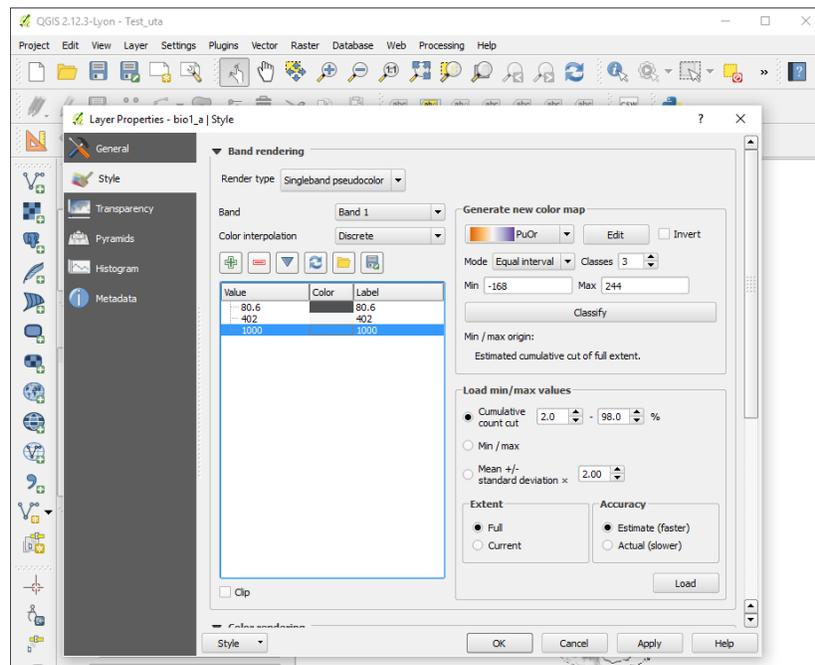
2) Because we calculated thresholds, we do not want this continuous image of temperature. For this lab and the bottom up model, **use a calculated threshold of 50% from the physiology lab** and model for each response variables you will be mapping. So, what we are doing is "cutting out" areas on the map that are too hot or too cold. Note that we are not actually going to be cutting our raster, just changing how it is displayed. If you have not done your threshold calculations, do them now before proceeding.

3) Now that we know what temperatures are too hot and too cold, we are ready to change how our map displays. For the rest of the lab I am going to use a cut off of 14.6 and 64.8 degrees Celsius which was calculated from the resting BPM data. Right click bio1 in the Layers Panel and select Properties. Navigate to the style tab.

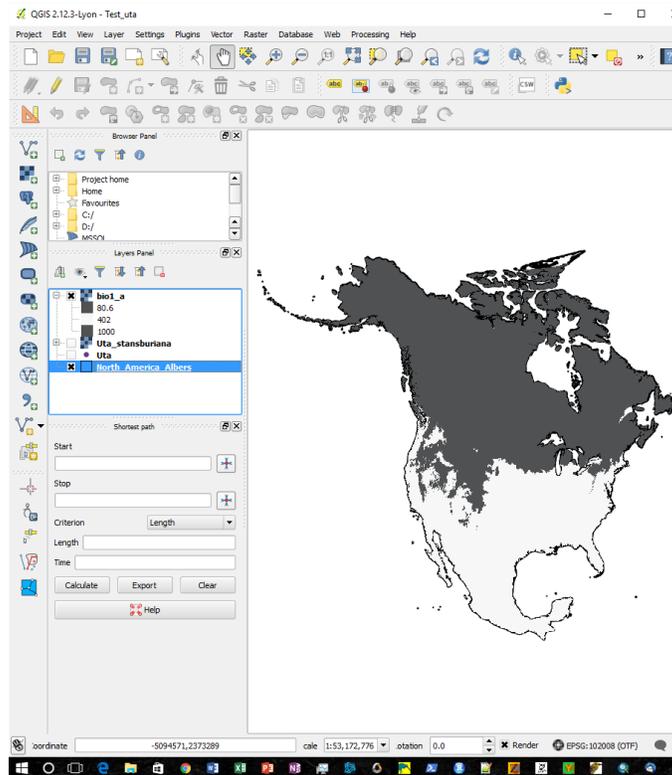
- 4) Change Render type to "Singleband pseudocolor". We only have one band of data and we want to customize our color scheme, so this is the best choice.
- 5) Change color interpolation from "Linear" to "Discrete".
- 6) Under Generate new color map, you are going to change mode from "Continuous" to "Equal interval" and classes to 3. This is telling the program we want 3 discrete categories and not a continuous blend of colors.
- 7) Click the "Classify" button if the program does not automatically update.
- 8) You will now see the classification scheme for the raster. The value column is what value is given each color, color is what color that value is displayed, and label is how that value and color will be displayed in your legend. We want to change the values to reflect our thresholds. In QGIS, the value you enter is the maximum value that color will be displayed. So, if you were to have a raster with values from 0 to 10, and one color was classified as 5, that color would display for all values from 0 to 5.

Because of this, we are going to set maximum values for each of these values. Set the lowest color to 146. Remember, these layers are in tenths of a degree Celsius. The second color should be 648. The highest value can be set to any arbitrary large value (1,000). This may seem strange because we are going beyond the raster value of 244, but we are setting values based on the physiological tolerances and based on these numbers we are simply not going to observe areas that are too hot *when using average annual temperature*. Change the colors (by double clicking) to either highlight appropriate areas or areas that are too hot or cold. The example map on the first page went with the second option. Choose colors that you think are appropriate (making nice maps is an art).

Your window should look like this if you are going with the second option:



9) Click "OK," the following settings will give a similar map to the one below:



10) Go to Project, Save, and Export as an image.

11) Repeat this process for the other metrics that you provided figures for in your physiology paper and calculated thresholds for.

12) You might notice that there is no legend. To add legends and really work through exporting a nice map, go to "Project" and then "Composer Manager." **This is not a requirement, but I wanted to include the information here in case you use QGIS in the future. Because I am not requiring a legend, make sure you do an excellent figure caption.**

### **Creating a Top Down vs. Bottom Up Comparison**

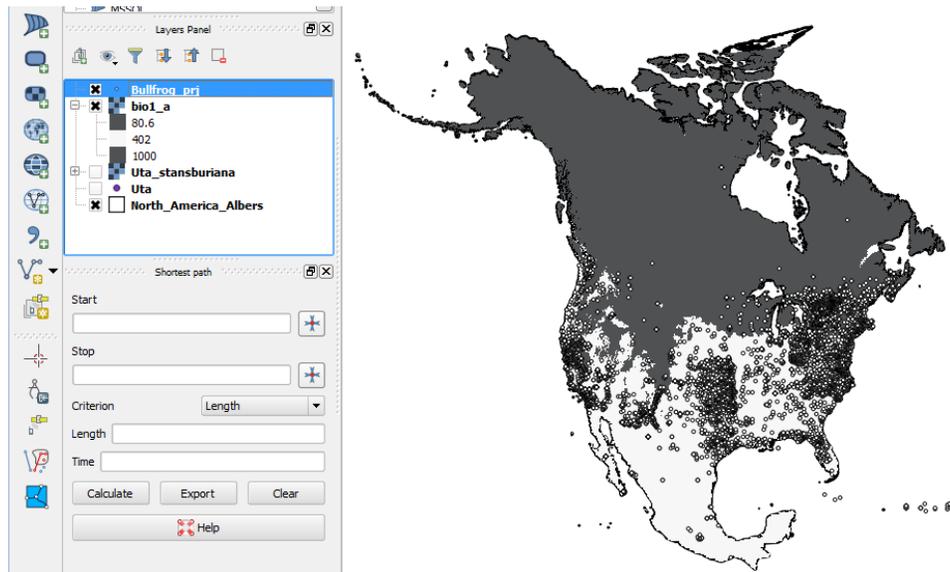
1) Next we want to see how different our two models are as well as how well they match the known occurrence points. Let us start with the occurrence points.

2) Click Layer, Add Layer, Delimited Text File. Select the points that you transformed to meters from last week. Default settings are fine, so click "OK."

3) You will be prompted to select the coordinate system. Make sure to select EPSG 102008.

4) Just like going to Style (under Properties) for the raster let us change how things look, we can do the same thing the points. Make them slightly less intrusive (e.g. changing color and size,

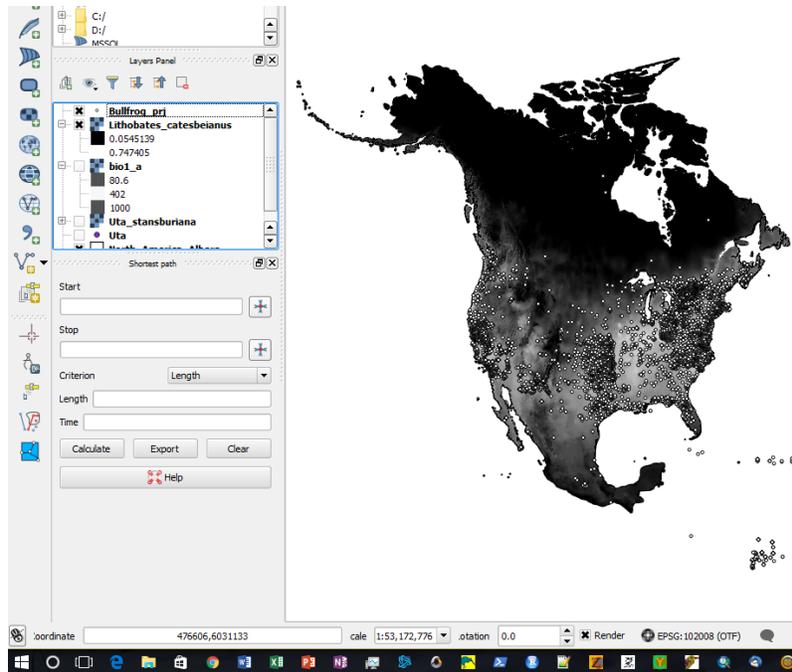
which is in the upper-right of the menu). You should see something like this (note that I have extra layers in my panel, just ignore them):



You may need to adjust the draw order in the layers panel by dragging the point file to the top. You will notice that the points in the Northeast frequently extend beyond the limit our model predicts, but the West seems to do all right. At this point you should also notice that we have no southern edge. Why might this be? Think about the layer we are using and other factors that may control the range of a species. For the map in your report you don't need to include the points, but it is a good way to think about how well the model may be performing.

5) Next, let us see how the ENM from Maxent compares. Click the little X next to your bio 1 layer so that it disappears. Next, add the ENM from Maxent (the .asc file). If you are unsure of how to do this, please refer to Lab 5 from last week.

6) Leaving the defaults and just adjusting the drawing distance as necessary, you should see something similar to this:



This looks like it might fit a bit better, as there are fewer points overlapping areas of poor habitat in the Northeast.

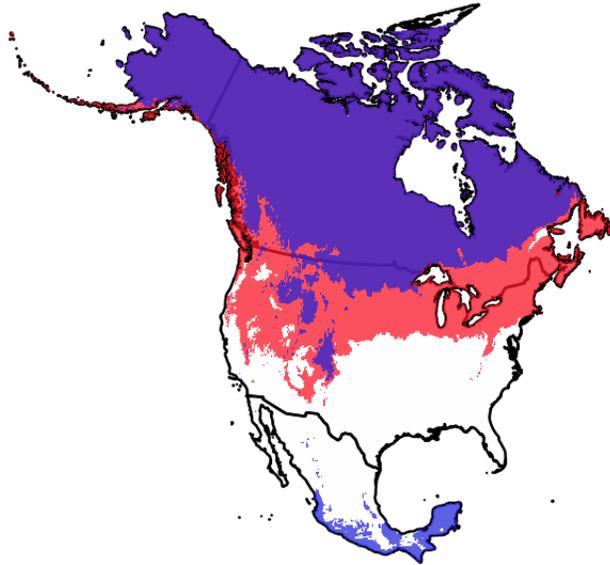
7) Comparing this continuous layer to our physiology discrete model is a little odd though. So, next we want to change how this layer appears. Follow the same instructions as before, but only do 2 discrete colors. Set the values to 0.25 and 1, and select colors you think will allow this image to be informative. This will give us a cut-off of relative probability of presence of 25%. This is only slightly arbitrary. As best practice you normally look at the range of ENM values for locations with known presence and then set a threshold. I've done that for you.

8) You should now have a map that looks a bit more similar to the bottom-up physiology lab map we created above that highlights suitable regions.

9) We really do want to see both maps compared, so for your next map we need to make it so both layers can be seen. The easiest way to do this is to change the transparency of the map. Go under properties **for both layers**, and click the transparency bar. Change the global transparency slider to 50%. This makes it so you can now see areas predicted for presence by both models (in white), by one model (in light gray), or neither model (in dark gray). The shades of gray are a bit annoying, so try changing your colors to things that make sense (such as one to blue and one to red, so the area of crossover is purple). Feel free to play with the transparency options and get creative!

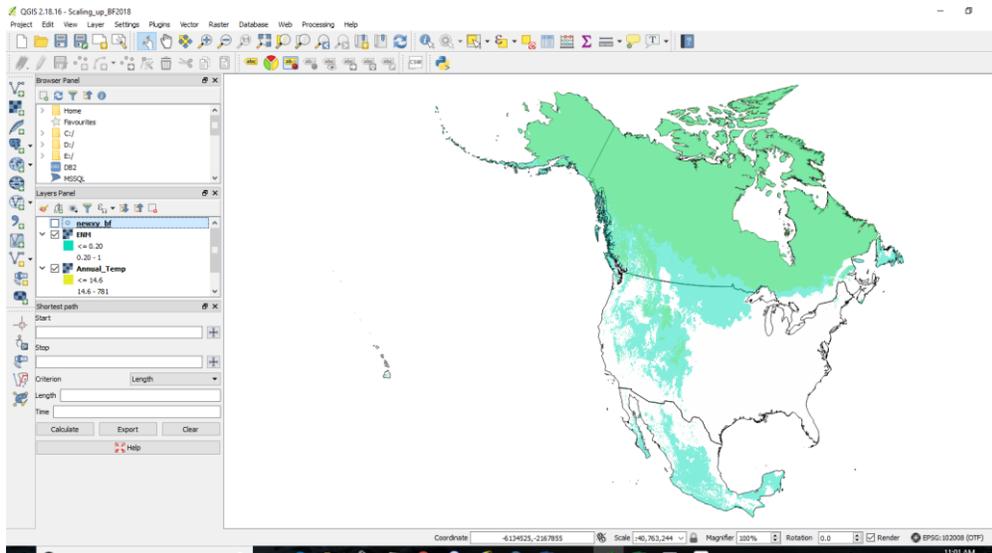
10) As with the other maps, export as an image and save your project.

Here is an example with the simulated data I had at the start of the lab:



This image will allow me to visually compare the two models. Note that this made up data shows a much greater mismatch of the two models than you might see.

Here is an example screenshot from me working the bullfrog data. You will notice I renamed the layers so I was less likely to confuse myself:



## The Report and Advice on Writing Modelling Papers

### What to Do

To make things clear, your paper should have multiple maps: the map from Maxent, the map for each physiological threshold/trait measured, and a combination map of each physiological threshold/trait measured with the ENM. The ENM by itself should be continuously shown with color-coded colder to warmer colors and the other maps should use discrete color categories. So, if you have two traits to consider, you should have 5 maps. You can combine multiple maps into single figures to make things easier. You can easily combine figures and make figure captions in PowerPoint and then simply Save As an image file.

In addition to the maps, you should also compare the response curves of the physiology model compared to the Maxent model. The Maxent .html file outputs response curves for you (unless you forgot to check the check box before running the model). If you don't remember response curves, please review Lab 5 from last week. You do not have to include your figures from the physiology lab, but one way that would be informative would be to show the response curves with each bottom-up model. Remember the final goal of these papers is to synthesize your two different studies—one focused on estimating physiological thresholds, the other on finding correlates with known locations—into a single-coherent report. As such you will need to **include a description of the response curve of annual temperature from Maxent** (what value is the max roughly at? where does the response curve drop below 50% of the max?) **in the Results section**. In the **Discussion section**, you should compare this to **the figures from your physiology paper paper** (do they predict the same max? the same threshold value?).

## How to Do That

First and foremost, read through and re-familiarize yourself with the instructions on how to write a lab report and look at the rubric to make sure that you start out on the right foot.

To write a methods and results section, the best advice I have to give you is to look in the literature and see what other people have done. I have uploaded a published paper that I worked on to give you an idea of what needs to be included. Remember, the goal of the methods is to allow your work to be repeatable, so you should include things like:

- Software used and version
- Where the location points came from
- How many location points were used
- Where did the climate layers come from
- What projection and coordinate system was used
- What values did you select for the shown colors
- Number of replicates the model was run for

THIS IS NOT AN EXHAUSTIVE LIST

The results should state what was observed and determined, and should *not* include interpretation. As an example, you might state in your results that the physiology model aligned similarly with the Maxent model along the East coast or that the model showed unsuitable habitat along the East coast where bullfrogs are found based on your presence points or that the physiology model showed no southern range edge. Then, in the discussion, you should talk about why these things may be and bring in the deeper interpretation of the model.

There is a lot to potentially discuss, but at a minimum you should think about:

- How do the northern and southern range edges differ between models
- Where, specifically, do the models align and misalign
- How do the models compare to our known presence points
- What may be occurring that is reducing how much each model's map align with the points. Think about the assumptions of each model
- Model fit (AUC value)

AGAIN, THIS IS NOT AN EXHAUSTIVE LIST NOR IS IT THE ORDER YOU SHOULD USE

Not to be too repetitive, but if you are struggling or having doubts, look in the literature. Simply plugging "Maxent" into a search engine for scholarly articles will give you lots of examples.

As a final note, don't forget detailed figure captions that allow your beautiful maps to stand completely alone. You should follow the general instructions from before; it is crucial that you include the aspects that explain the model (such as software used, point number).