Climatic Envelope Modeling using BIOCLIM (through the DIVA-GIS interface) and a Comparison of the Number of Environmental Variables Used in the Modeling Process
(tuturial, no points; assigned 9 mar 2009)

A. Import and view data.

1) Open DIVA-GIS.

2) Add data layers (here, shapefiles, .shp) for the following:

   North American administrative boundaries (i.e., countries), US states, and US counties.

   In the table of contents (left side in DIVA), rename these layers as above.

3) Make a copy (copy and paste) of the Lycopodiella.csv file you used for the MAXENT procedure.

4) Open this file using *DATA>Import points to shapefile*.
   Double click on this layer and alter properties (take points to size 6, change the color of the points to your liking).

5) You have just created a map displaying the distribution of specimens from our herbarium.

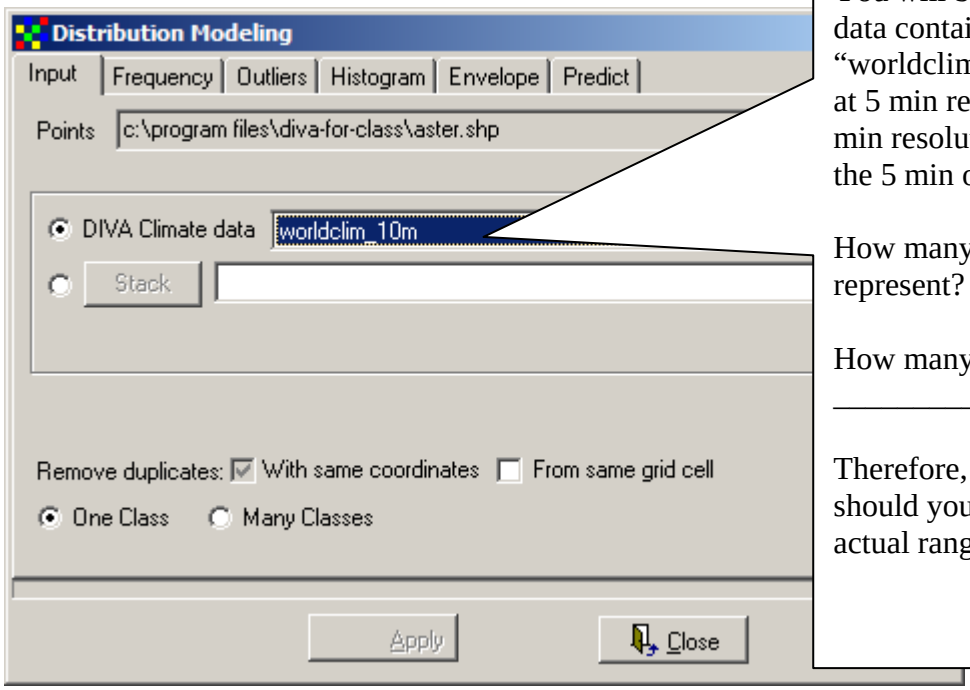
   From which state(s) are our specimens?

   From which PA counties are our specimens?

   What is the PA county with the most specimens?

B. Model the distribution (climatic envelope).

1. With the occurrence records layer active and using the menu option MODELING>Bioclim/Domain, open the following window:



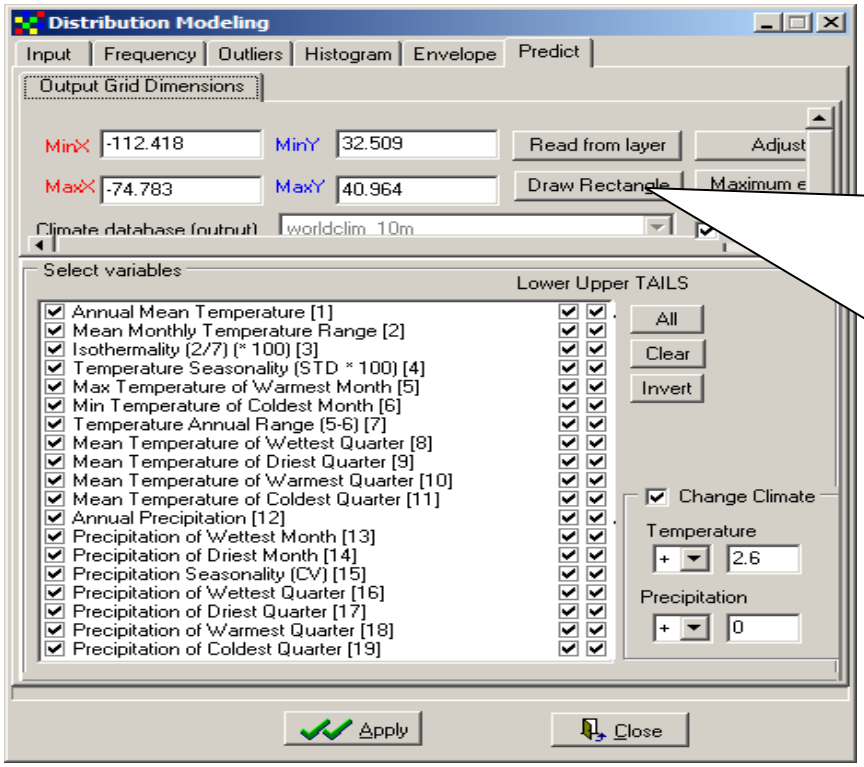
You will be using the climate data contained in "worldclim_5m.clm" (which is at 5 min resolution; use the 10 min resolution climate model if the 5 min one is not available).

How many degrees does this represent? _____

How many degrees wide is PA? _____

Therefore, to what resolution should you be able to model the actual range of your genus?

2. Select the "Predict" tab on the far right of this window to bring up the following window:

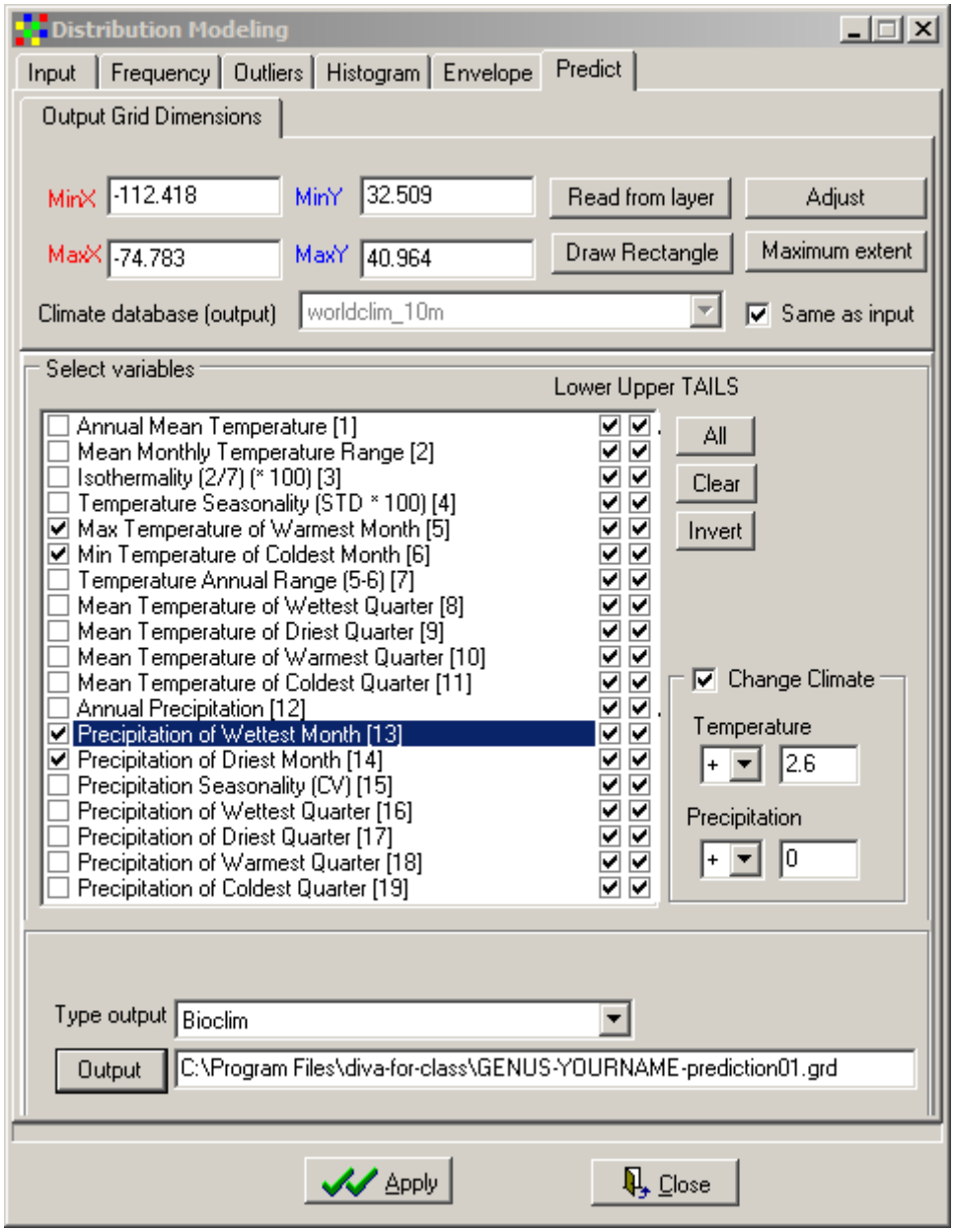


The default is to make a range prediction restricted to a bounding box defined by the geographical limits of your specimen records. However, use this button, followed by click-and-dragging the mouse to define a rectangle encompassing North America only.

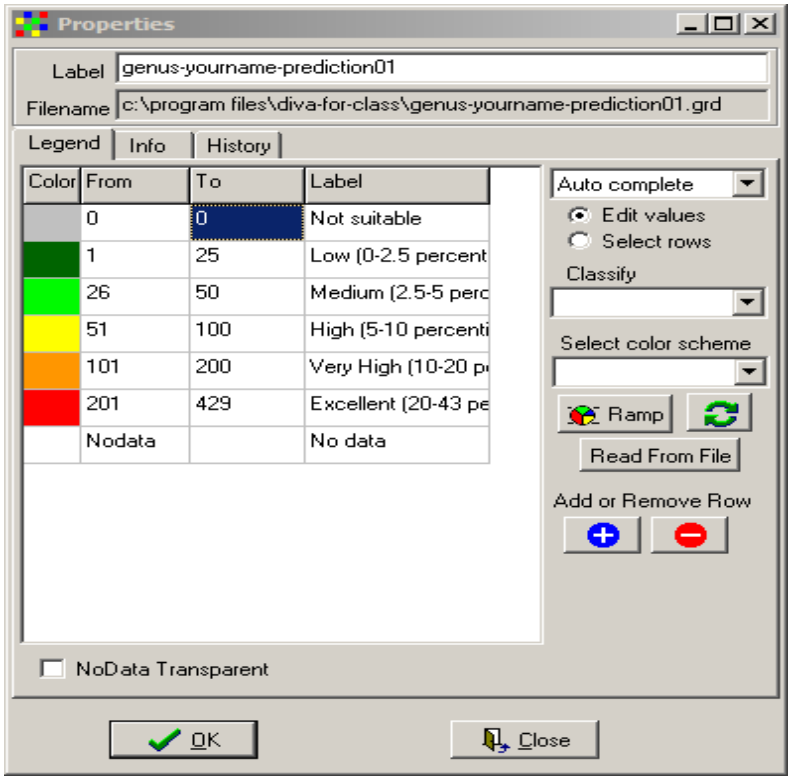
DO NOT yet press "Apply".

3. In the window below, clear all climatic variables except for the same climate variables used for MAXENT (see the MAXENT procedure and that procedure's Table 1).

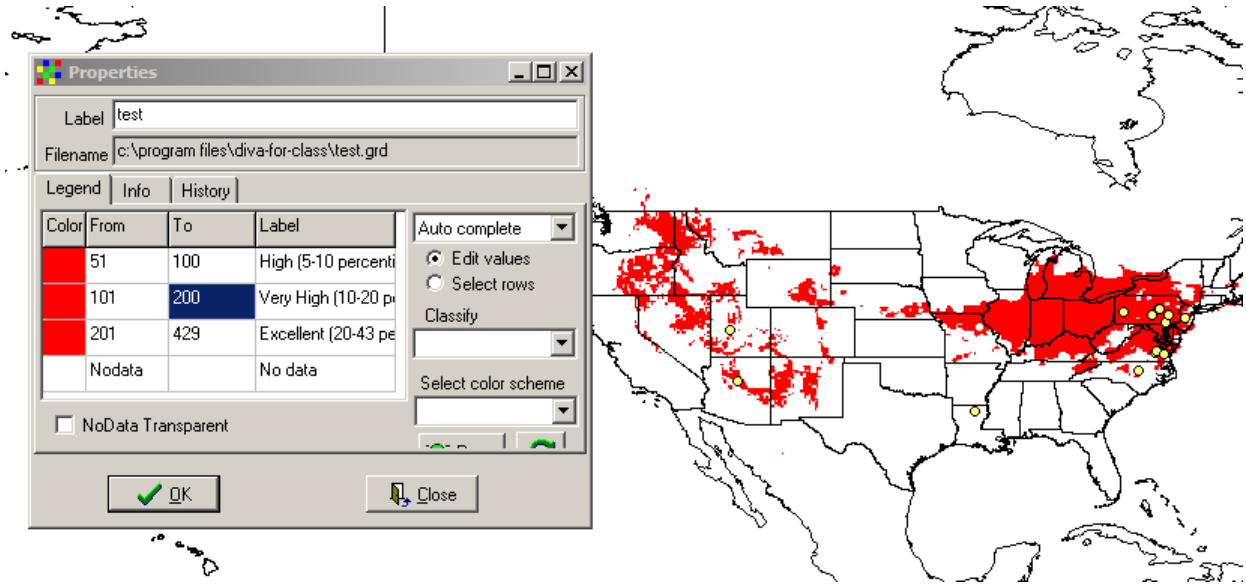
On your folder on the desktop, Save output gridfile as "BIOCLIM-Ly-appressa-6variables.grd". Click APPLY. You've just predicted the possible range for this genus based on these climatic variables.



4. Modify the PROPERTIES of this new layer using the following box.
Remove the rows for NOT SUITABLE, LOW, and MEDIUM. Change the color of all others (i.e., high to excellent) to red. Click OK. You've just produced a color map of the predicted range, showing all areas with high probability of occurrence in red.



After moving the state and country boundary layers on top, your map should look something like this:



What are some of the states predict for your taxon to occur in that we do not have records for?

5. Now, with the original "genus" layer active, do steps C1-C4 again, only this time use ALL CLIMATIC VARIABLES, and make the predicted High probability range blue. Name this new layer appropriately.

Is the distribution predicted now larger, smaller, or about the same area as that the first time around?

_____

Is this expected? Explain. _____

6. Zoom in to PA. Make the county boundaries layer visible again.

Based on the climate predictions made using all climatic variables, what counties is your taxon predicted to occur in for which we do not currently have specimens?

_____

7. Summary Questions:
How could this procedure be used to monitor and manage the health of rare species in Pennsylvania?

Describe some of the limitations of our predicted ranges? Think about limitations in the datasets (occurrences, environmental data) we used.

What is the effect of the number of environmental variables used on the predicted size of the distribution? How do you think you might choose which is an appropriate number of variables?