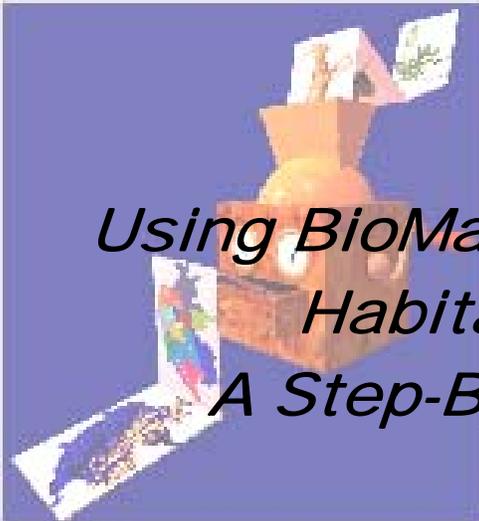


About BioMapper



# BIOMAPPER 3.1

*Version 3.1.5.265*



***Using BioMapper 3 to Create  
Habitat Models:  
A Step-By-Step Guide***

Written by Alexandre Hirzel

Module ENFA based on the work of N. Perrin  
et al. (2000)

(c) Alexandre H. Hirzel (1998-2005),  
Dpt of Ecology and Evolution,  
University of Lausanne, Switzerland



References

Modus operandi

License

OK

Created by: Emil Peter IV  
Created for: Karner Blue Butterfly Habitat Modeling Project  
Forest Landscape Ecology Lab  
Department of Forest Ecology & Management  
University of Wisconsin – Madison  
120 Russell Labs, 1630 Linden Lane  
Madison, WI 53706  
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### Initial Steps...

- Open BioMapper Software
  - o Select **OK** at Slash Screen.
- Add Ecogeographical Variable (EGV) maps.
- Save project. This can be preformed by keying **ctrl + s** at anytime.
- Add workmap (species presence map).
  - o Do this by right-clicking in the workmaps space and selecting **Add Maps**.
  - o After adding map, highlight then right click it, select *Mark as species map*.
- Verify EGVs by right-clicking on any of the maps in this space and selecting *Verify Maps...* By verifying the maps, you are checking that they line up and occupy roughly the same space as each other, as well as making sure the map's values are not too large.

### Run Analysis of maps...

There are two ways of doing this.

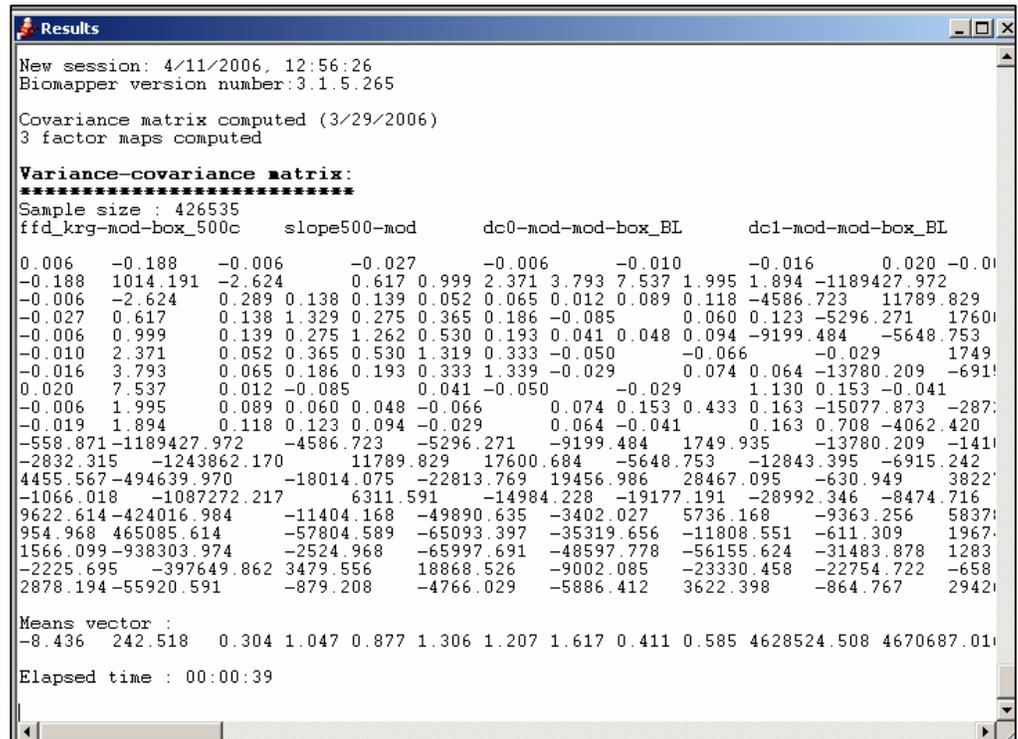
- The first is **Automatic Analysis**.
  - o At the top of the Biomapper window, choose *Factor Analysis, Automatic Analysis...*
  - o A window like this will appear:
  - o Choose which **Processes** you would like to run (the default does not include a Covariance Matrix).
  - o Select your species map.
  - o Choose the method you prefer for the **number of factors** to be chosen.
  - o Select your **Habitat Suitability Algorithm**.
  - o Select your **scaling** method.
  - o Select the number of **Cross-Validation** partitions (k value), then select whether or not to keep the maps after they are used to make the calculations (not keeping the maps saves disk space).
  - o Choose your methods of output and the name of your **Habitat Suitability map** (double clicking the space for the name will give a default name, it is rarely nonsensical). By selecting the majority of output methods, you reduce the number of times you would have to re-run the complete analysis to gain those pieces of information.

The screenshot shows the 'Automatic Analysis' dialog box with the following settings:

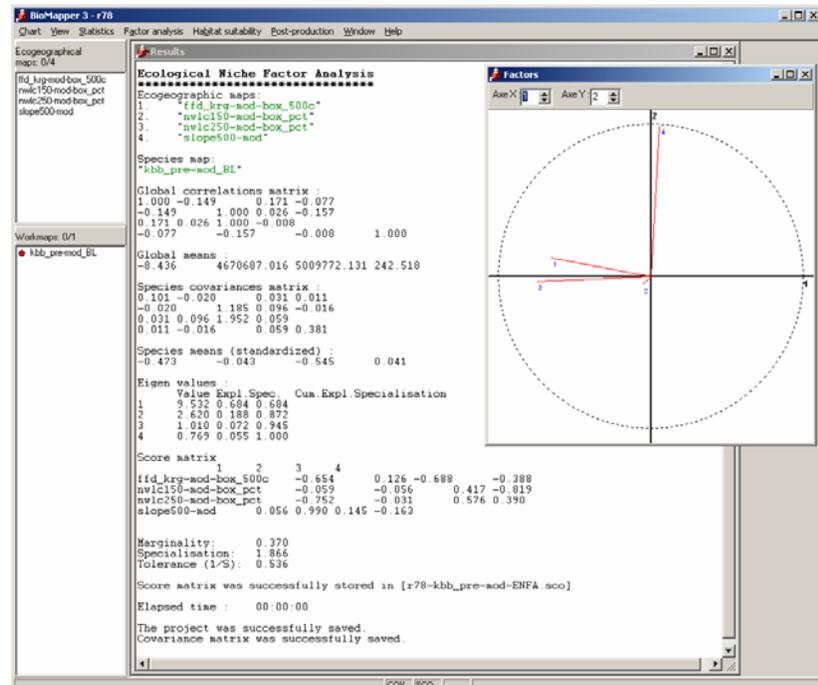
- Processes:** 1. Covariance matrix, 2. ENFA, 3. Factor maps, 4. Habitat Suitability map, 5. Cross-validation (all checked).
- Species maps:** Species: kbb\_pre-mod\_BL
- Factors:** Number of factors chosen by: Broken-stick (selected), Percent of explained variance: 75, Fixed number: 10.
- Habitat suitability algorithm:** Medians
- Scaling:** Isopleths (selected), Stretched to 100 (old method).
- Cross-validation:** Nb of partitions: 10, Keep temporary HS maps (unchecked), Confidence limits maps (checked).
- Output:** Habitat Suitability map: log\_reg\_2-HS-M-kbb\_pre-mod\_BL, Intermediary output (unchecked), Eigenvalues (checked), Score matrix (checked), Factor map list (checked), Factor distributions (checked), EGV species distribution (checked).

Buttons: Cancel, Compute

- The second method of analysis is **Step-By-Step**.
  - Compute Covariance Matrix by selecting from the top menu *Factor Analysis, Covariance Matrices*, then *Covariance Matrix*. BioMapper will then compute the covariance matrix and display it in the Results window.

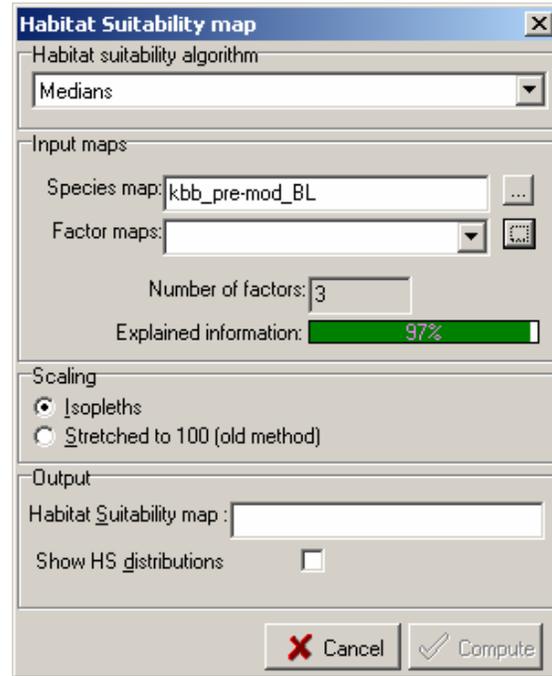


- Save your covariance matrix.
- Compute **Ecological Niche Factor Analysis (ENFA)** by selecting from the top menu *Factor Analysis, Factor Computation, Ecological Niche Factor Analysis (ENFA)*.
- Your results will again be displayed in the Results window along with a factor chart with an X, Y, and Z axis.
- Save project.

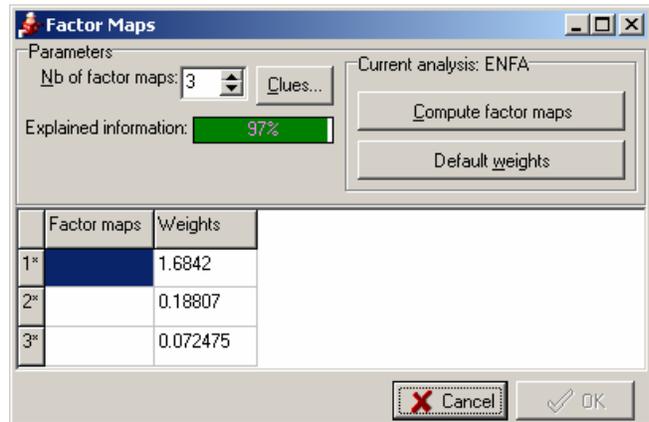


- Compute **Habitat Suitability Map** by selecting *Habitat Suitability, Habitat Suitability map...*

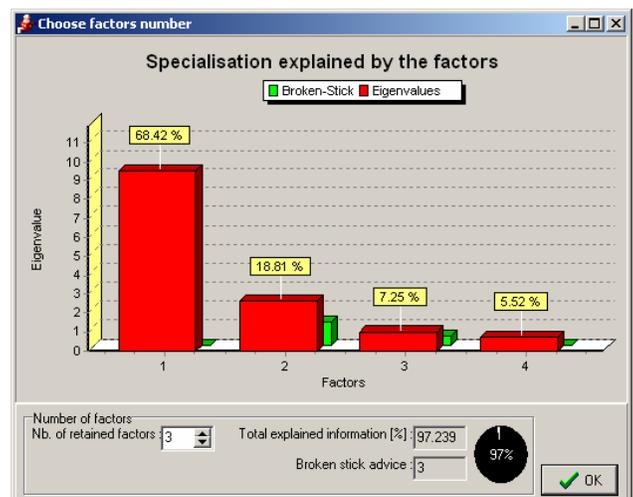
- After verifying the correct **species map** and **Habitat Suitability Algorithm**, you will want to compute your factor maps at this time by clicking the little box next to the drop down menu.



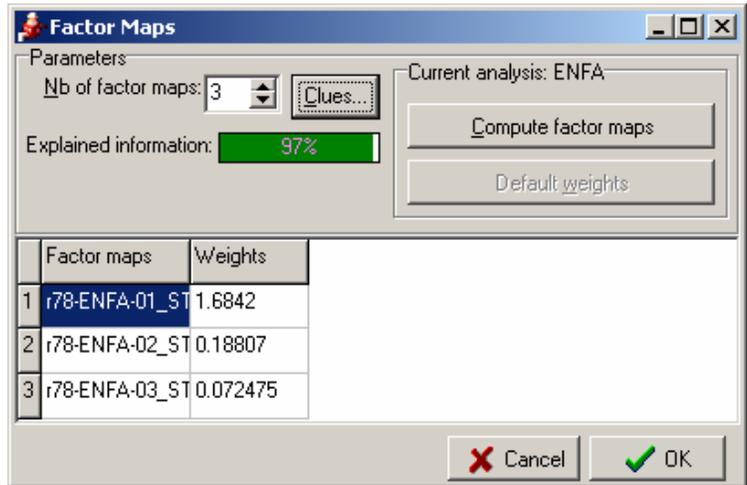
- A window like this will appear:



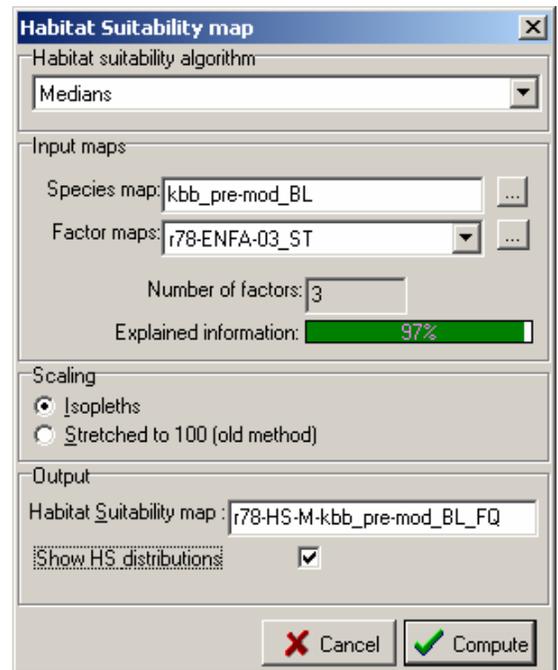
- By selecting the **Clues...** box, a chart that may be helpful to you in selecting the number of factors needed for a complete analysis will appear. You can select the number of factors in this window also, but it is not necessary. Click **OK** to exit.



- Once you have decided how many factors you will need to explain your data, select **Compute factor maps**. Your factor maps will be computed and the *Factor Maps* box will look similar to this:



- Selecting **OK** will move you to the next step.
- Choose your **scaling** method. The default is *Isopleths*.
- Choose your **Output** variables. Double clicking in the **Habitat Suitability map** space will give a default name that you can use or edit to make it more meaningful to you or your project.
- Click **Compute** to calculate map.



- Again, your results are given in the Results window. Double-clicking any of the map names in **red** or **green** will open those maps.

```

Factor map computation
*****
Number of factors : 3
Explained information : 0.972
Explained specialisation : 0.945

Factor 1 map --> "r78-ENFA-01_ST" 12:00:00 AM
Factor 2 map --> "r78-ENFA-02_ST" 12:00:01 AM
Factor 3 map --> "r78-ENFA-03_ST" 12:00:00 AM
Elapsed time : 12:00:03 AM

Habitat suitability map
*****
Factors:
1. 1.684 "r78-ENFA-01_ST"
2. 0.1881 "r78-ENFA-02_ST"
3. 0.07248 "r78-ENFA-03_ST"
Species map:
"kbb_pre-mod_BL"

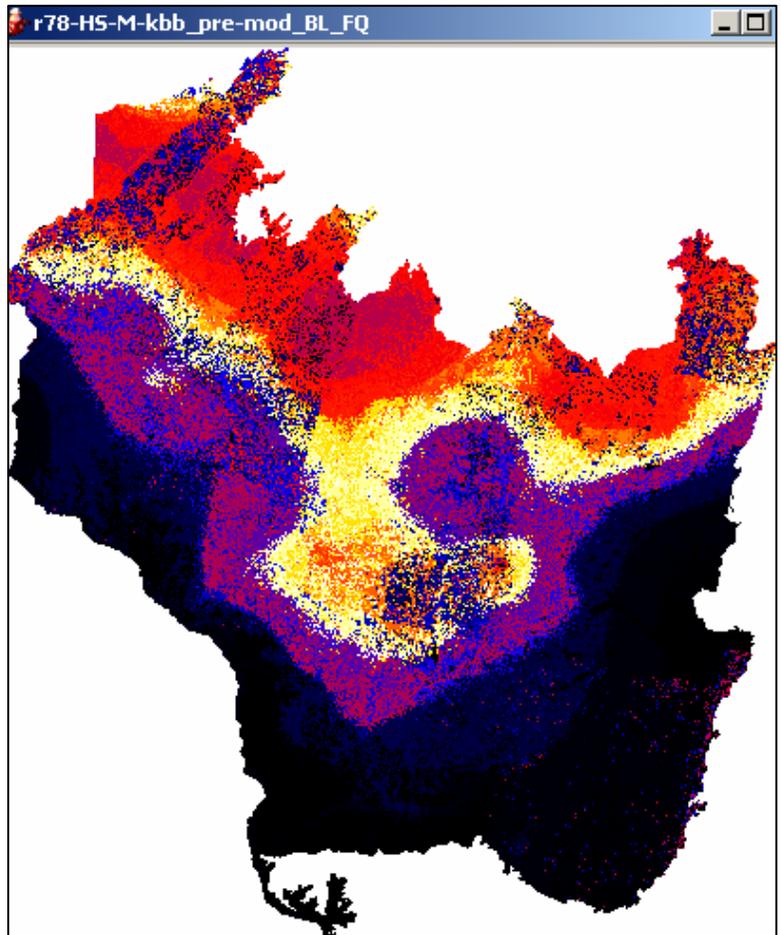
Habitat suitability map:
- Number of factors: 3
- Explained Information: 0.972
- Explained specialisation: 0.945
- Algorithm: Medians
- Number of categories: 20
- HS values computed by isopleths

- Suitability map --> "r78-HS-M-kbb_pre-mod_BL_FQ"

Elapsed time : 00:00:02

```

- Select the habitat suitability map name that is in red by double clicking it. A copy of your map should then come up in a new window.
- Save project.

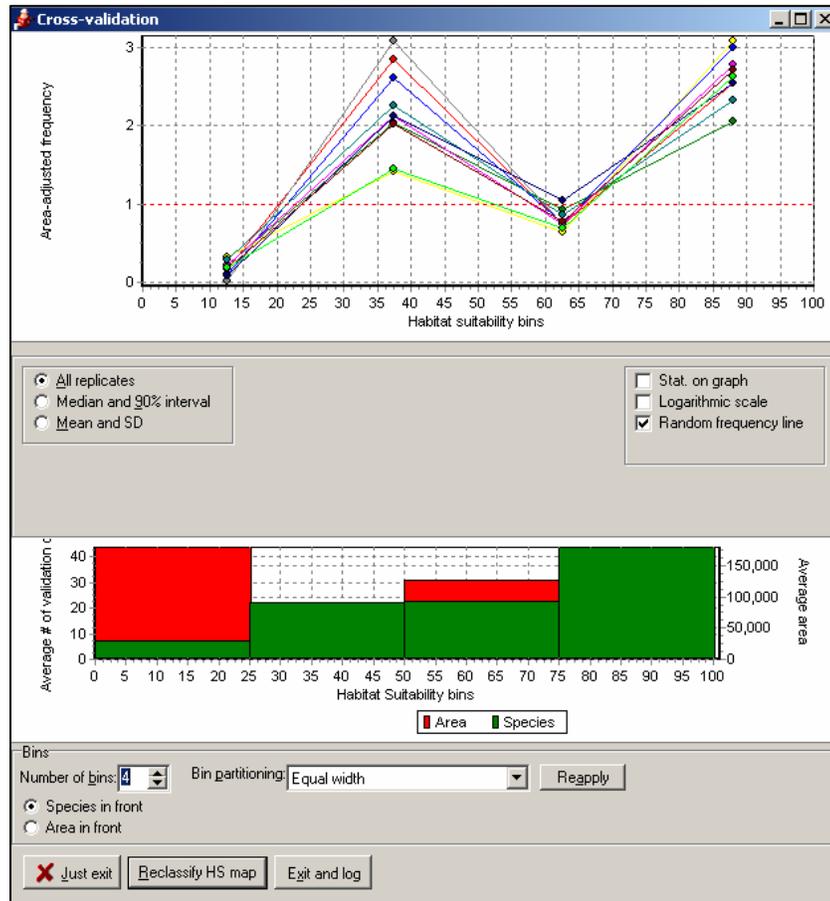


- You are now ready to **Cross-validate** your model. Do this by selecting *Habitat Suitability* from the top menu, then *Area-Adjusted-frequency Cross-validation*.

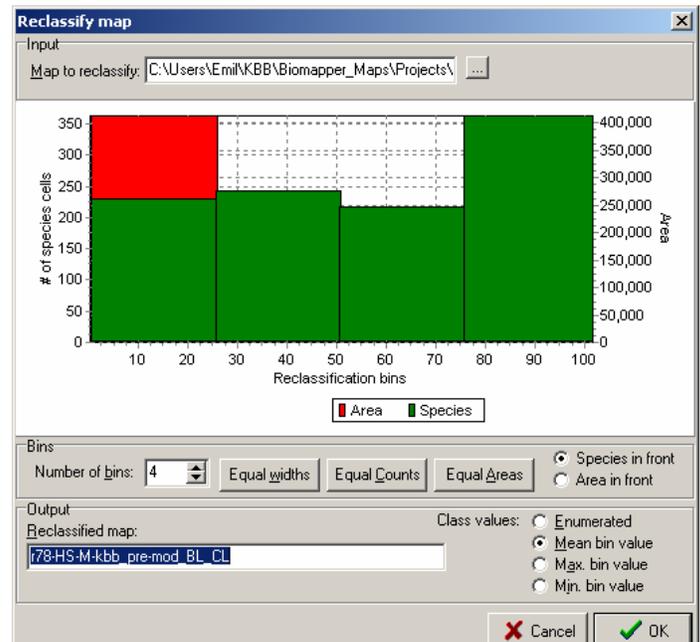
- After choosing your **Habitat Suitability algorithm**, verifying your **Input Maps**, and selecting your **Scaling** method, you will come to the k-fold cross-validation section. Accepting the defaults is good for now, but also select the **Confidence Limits maps** box to compute those as well.

- Click **Compute** to proceed.

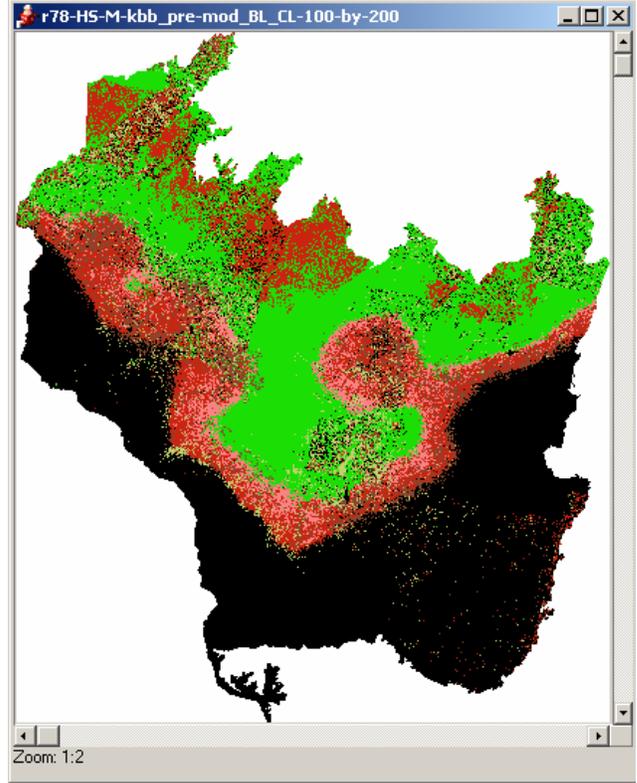
- Your results will be displayed in the **Results** window and a **Cross-Validation** window will appear.



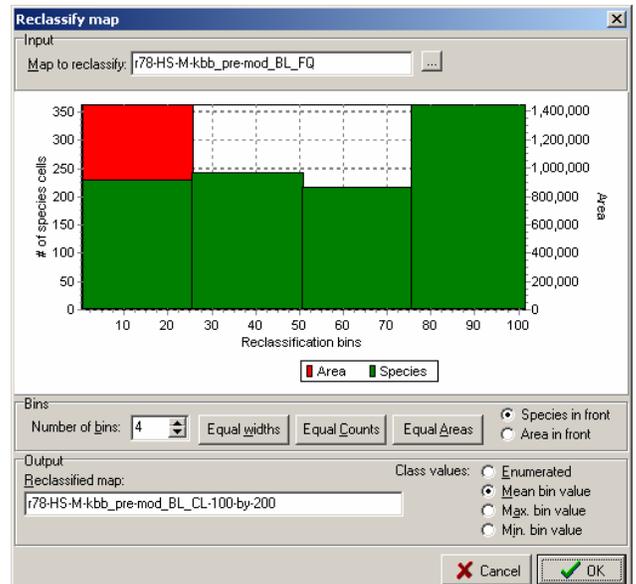
- Select the **Reclassify HS map** button at the bottom.
- In the **Input** section, navigate to the Habitat Suitability map you created earlier and select it for reclassification. Also, verify the name of the **Reclassified Map** in the **Output** section at the bottom to ensure a meaningful name. Again, double clicking in the box will give you a default name.



- Select **OK** then **Exit and Log** to display the results of your reclassification in the **Results** window.
- Save project.
- Your map is now reclassified to have the number of bins and validation points you have chosen.
- You can change the number of bins by choosing from the top menu *Post Production*, then *Reclassify map...*



- The **Reclassify Map** dialogue will reappear and you can change the bin settings there to divide up your data points into as many groups as you would like. Once again, make sure you give your newly reclassified map a meaningful name in order to distinguish it from your other maps, or do not change the name to rewrite the older map.
- Save project.



These are the basic steps needed to make your habitat models in BioMapper. Other processes may be helpful in later analyses, but these will get you started and a good way down the road to determining your habitat suitability.

### ***A Few Words About Automatic Analysis vs. Step-By-Step...***

Though the automatic analysis may offer a seemingly easier route to fly through your data, it has a few drawbacks. The first of which is that you will have to re-run the entire analysis if you decide to change one value, where as with the step by step analysis, you can change the value, discard the changes, and change it again before moving on to the next step. Also, the automatic analysis will stop and discard all changes and results if it encounters an error at any point. So if you have a large amount to get through, automatic analysis may be the way to go for you. As for the step-by-step analysis, it can get tedious if you have multiple models to build, but the ability to scrap your changes and then make corrections on the fly is very handy and has out weighed the ability to punch in settings and click 'GO' countless times. With either route you choose to run your analyses, you will have to play with the settings at some point to figure out how to work with BioMapper until you get the ones you need or understand how BioMapper is working with your data to develop your models.

### ***Model Comparison...***

In order to compare your models, look at the Rs ( $R^2$ ) values of your different models. As  $R^2$  gets closer to 1.0, the model is getting better. The further your  $R^2$  value is from 1.0, the worse your model is at predicting presences dependably<sup>1</sup>. To make your  $R^2$  values easier to track, you should consider putting them into a spread sheet next to each of your model names so you can evaluate them all side by side at once.

### ***Also and maybe most importantly...***

It cannot be stressed enough to save your work when working with BioMapper. If BioMapper encounters a problem, and it will, the problem *may* be fatal. Chances are very good that the problem *is* fatal and BioMapper will need to be shut down and restarted at which point you will wish you had saved your work before taking that last step or last calculation.

<sup>1</sup>NOTE: If your  $R^2$  value is 1.0, you need to increase the number of random seeds or increase your k value. 1.0 is possible only in a perfect world.