

Analysis of Forest Composition in the BFEC

What are the questions?

- Are all the forests of the BFEC essentially the same?
- “Sameness” can be measured in terms of:
 - The physical characteristics of trees such as size and density
 - The overlap in identity of the trees among sites
 - The diversity and degree of species dominance in the communities
 - The degree of similarity in ecological characteristics such as whether species are shade-tolerant or are early colonizers
- If there are differences, what best explains those differences?
 - Soil type?
 - Slope?
 - Disturbance history?

Methods I. Using GIS to visualize differences

Start ArcMAP and open your BFEC project (an *.mxd file that should be on your H: drive). Simplify your display by deselecting layers for soils and contours.

You need to be able to edit some class data, so you will need to move some files to your H: drive. This will allow you to make your own changes without altering the files for everyone else. Moving files with ArcCatalog ensures that all the support files are moved as well as the *.shp file.

- Click on the ArcCatalog icon (the file cabinet at the second row)
- Right click on “north forest rndm points.shp” and select “copy”
- Highlight your H: drive and then “paste” the file into it
- Repeat this process for the file, “forest sampling areas.shp”

This is a good time for you to see how we can use GIS to select sampling points. The random points file was generated by a small program that I obtained from the ESRI support web site (the price was right – free!). Because the points are random, some of them are so close that they would essentially sample the same trees. The goal was to identify a set of points that were no closer than 75 feet.

- Use the “+” icon (second row of menu icons) to add “forest sampling area.shp”
- For now, make the fill color “hollow”
- Use the “+” icon to add “north_forest_rndm_points.shp”
- Right click on the points layer and “zoom” to that layer.
- From the “Tools” menu (top row) select the “Buffer Wizard”
- In the Buffer Wizard, select
 - “feature of a layer” and make sure the random points layer shows in the window
 - click “next” and then select . . .
 - “at a specified distance” and enter “75”
 - at the bottom of this window, select “feet” as the units of distance
 - click “next” and select . . .
 - “No” to “dissolve barriers between”

- Save the buffers to your H: drive, as you will not be allowed to save to P:\data. You will need to click on the icon to the right to navigate to your H: drive and then type in a file name such as “random points”.
- Click “Finish”
- Right click on the buffer layer to select “no color” or “hollow” as the fill for the buffer circles.

Now you can see when points are closer than 75 feet. How do you choose a point to remove?

- Move the random points layer to be the top layer in the directory (click on the layer name and drag it above the “buffer” layer).
- Select the information icon (an “i” in a blue circle) from the third row of menu icons
- Using this tool, click on a point that is within the buffer circle of another point. This will indicate the number of that point. Do the same for the other point sharing a buffer area. We will exclude the point with the higher number.
- Click on the downward-pointing triangle in the “Editor” window (4th row) and select “Start Editing”
- Select the “H:” drive files and click “Start Editing”
- Use the solid triangular “editing pointer” to select a point. Then press the “delete” key.
- Now that you see the basic procedure, you can remove the layers for points and buffers.
- End the edit session by going to the “Editor” button and “Stop Edit” – do not save

Now we are ready to visualize the data on tree diversity in the BFEC. First, check out the different study areas.

- Select “properties” of the layer for study sites, and go to the “symbology” tab.
- In the “categories” section, choose “Unique Values” and use “Site” as the value field.
- Click on “add all values” and then “Apply”
- Close the property windows and check out the site locations.

How are the sites different? If you are ambitious you can make the fill for sites hollow and then bring up the soils and contours layers.

We want to examine differences in the forest composition. First, we will examine patterns of distribution for a few different species of trees. See Figure 1 on the next page for an example of the screen appearance.

- Right click on “forest sampling areas” and select properties and “symbology”
- Choose “charts” and “bar/column”
- Under “Field Selection” choose Buckeye, Cottonwood, and Sycamore
- Click on “Background” and select “hollow”
- “OK”

What do you see? Do the sites appear to differ in the abundance of these species? What do these species of tree have in common? What does the number “31” in the key indicate?

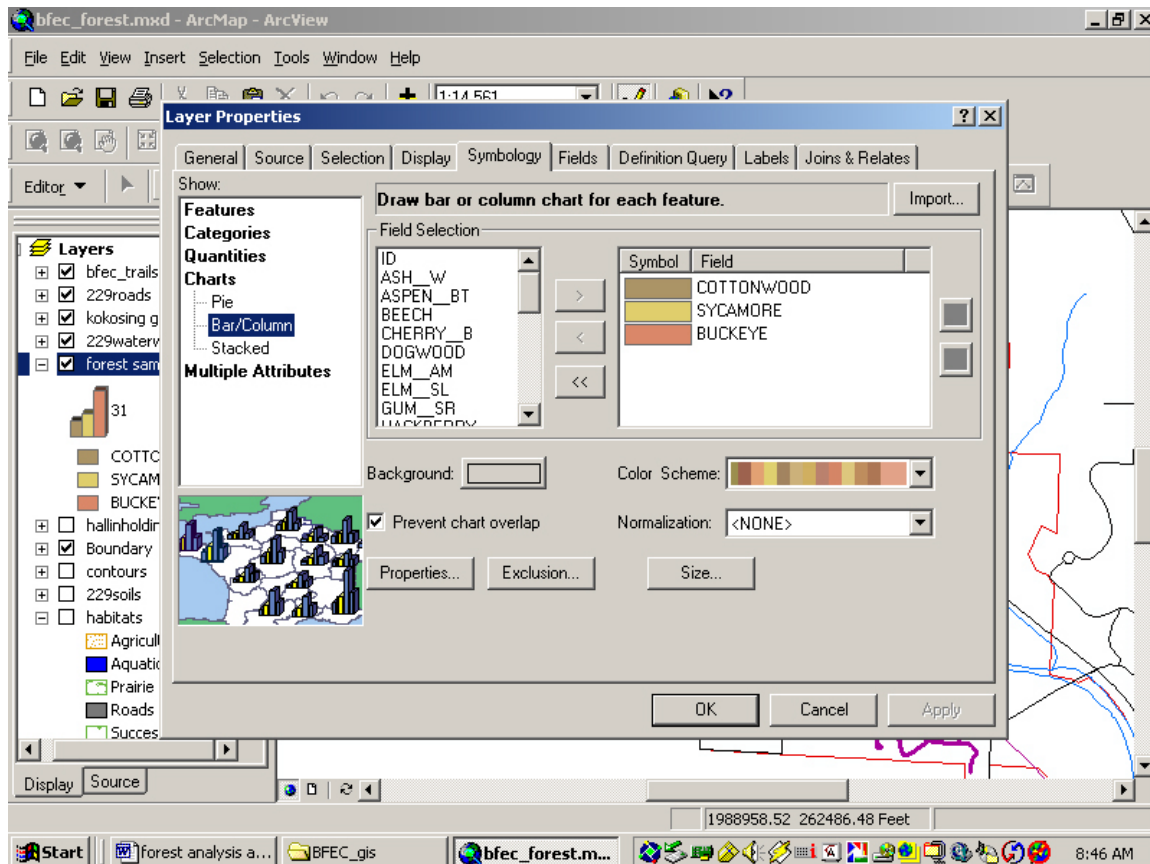


Figure 1. ArcGIS screen to create bar graphs for tree importance values in different study sites.

Often, we want to examine patterns that are “higher order” or the aggregate of some combination of individual data points. For example, we might want to ask whether forest study sites differ in the relative abundances of species that are shade tolerant, as compared to early colonizers. To do that, we need to manipulate the “attribute table” for our tree diversity study.

Our goal is to sum up the importance values for species that are extreme in shade tolerance (beech, linden, white oak, ironwood) and colonizing ability (white ash, hawthorn, red maple, sycamore).

- Open the attribute table for “forest study areas” after “right clicking” on the layer name
- Note the different columns giving the site names and I.V. values for different trees
- Find the “Options” button at the lower, right corner of the attribute table, and click on it
- Choose “add field”
- Enter “Shade” in name and “Float” as the data type. Then click “ok”
- Repeat this to create a field for “Colonizer”
- Now open an “Edit” session as you did earlier
- In the attribute table, select the whole column for “Shade” by clicking on the column name. The column should become highlighted
- Right click on the column for “Shade” and select “Calculate Values” from the drop-down menu

- Select the correct tree species (and select the “+” sign in between) – you are adding the Importance Values for all the “shade-tolerant” tree species
- Click “OK”
- Repeat the process for the “Colonizer” column using the appropriate species
- End the edit session – **Be sure to save your edits**
- Close the Attribute Table

Now you can create another thematic map for Shade and Colonizer species. Repeat the process you used to look at distributions of just three species above. This time, select “**Pie Chart.**”

What is your best hypothesis about mechanisms that created differences in the tree species in the BFEC study sites. How would you test your hypothesis?

GIS is especially good at showing spatial relationships, but other tools are extremely important. In order to evaluate numerical differences among sites, we need to apply other techniques. Statistical analysis will be important in evaluating data on patterns of shared species, differences in tree size and differences in tree density. These techniques are described in the next section.