#Use your judgment and be ambitious about learning new code and commands to improve commands

#If you get stuck early, middle or late of figuring things out, Google aggressively!

# And, possibly we can set up a time to Skype

First thing to do: Caroline Dolt prepared a full and a brief report about last summer.

Download from Git Hub Repository (Summer 2019) - there's a folder with report files.

Read the reports. Peruse some of the other documents (spreadsheet).

You'll learn about how Caroline obtained and compiled her data about living collections. To start, I think it's best to focus on analyses that she conducted using the package VEGAN. Remember we worked with Vegan in Digital Lab One in the class.

Note that Caroline's analyses are not at the level of species. She worked at higher levels of taxonomy: genus, family and order. We may want to go back to species. One reason she started with genus: many lists have specimens that are identified only to the genus level. For now, let's go right to genus lve.

The Goal: Repeat a lot of Caroline's work, ADDING THINGS THAT ARE MISSING. Mainly, that means three different inventory lists for the Barnard greenhouse (one recent, the other two historical). I also want to add another historical list (the Glass Flower Collection at Harvard, read about it here ) and also two other collections: Smith College and the University of Wyoming.

Preliminary steps to do before starting to repeat her Vegan work:

Assemble three Barnard lists at levels of genus and family. I'm not sure why they are not in her files, but it's a good project to learn to do this.

Her Notebook is "Taxize Tools" but you may also want to look at code we learned in class during Digital Lab Four.

The three Barnard lists to process, converting them to lists of genus and to list of families:

Barnard Sinnott

Barnard 2000

Barnard binomials

Plus also do this for three other lists: Harvard Glass Flowers, Smith, and U-Wyoming

CLEAN AND WORK WITH TAXISE

You'll find a folder on GitHub with Species Binomial lists, and you'll need to download them all into a File Directory on your computer.

I would recommend using stuff from our Digital Lab 4, when we learned these things:

1. Look up species binomials - are they accepted names? Or are they synonyms?

2. Correct so that you have all accepted names

3. For now, ignore if only genus is listed

4. For every taxon on the list, look up the genus, and family and order. Add to a big dataframe

Once you have complete set of lists that add these six to what Caroline used last summer -- then you can start re-doing some of her Vegan analyses.

And, in the meantime, I'll think of some ways to further extend this analysis.

My main idea is to figure out a list of 25-50 that are most often represented in college greenhouse collections, and to focus on their ethnobotany and economic botany significance, or something along those lines.