This code takes in all the species that are in all the surveys you put in the Data folder. It does this by looking for the names of all the files in the Data folder and then looping through them all. It arranges the species in 4 ways.

1. A giant list of all the unique species found in all the sites
2. A list of all the unique species found on each survey. This is a list where the names of the elements are the sitecode_year and the values are vectors of all the unique species found on that survey.
3. A list of all the unique species found on each site. This is another list with each element having a name as the site code and the value as a vector of all the unique species names. It is essentially an amalgamation of all the survey lists where the site code is the same.
4. Finally, there is a list where each element name is the survey and the values is a list of species, exactly as it is entered on the 'whole plot data' tab in the excel survey file. These are in the same order with the same gaps.

Then all of these strings in these containers are fixed for typos. Entries which just a genus are changed to "genus sp.", and lots of simple fixes are made like trailing spaces. Finally, a set of manual name changes are made from the file "rename.csv" in the folder dataframes. Here the first column is a list of potential typos and the second column is what they should be. If you leave the second column blank it changes the typo to NA. You can add to this list of manual name changes and it will work for all future surveys. The output file "Missing_species.csv" will tell you all the species which haven't been picked up with this code. Copy these into the first column of rename.csv and enter what they should be, then rerun the code.