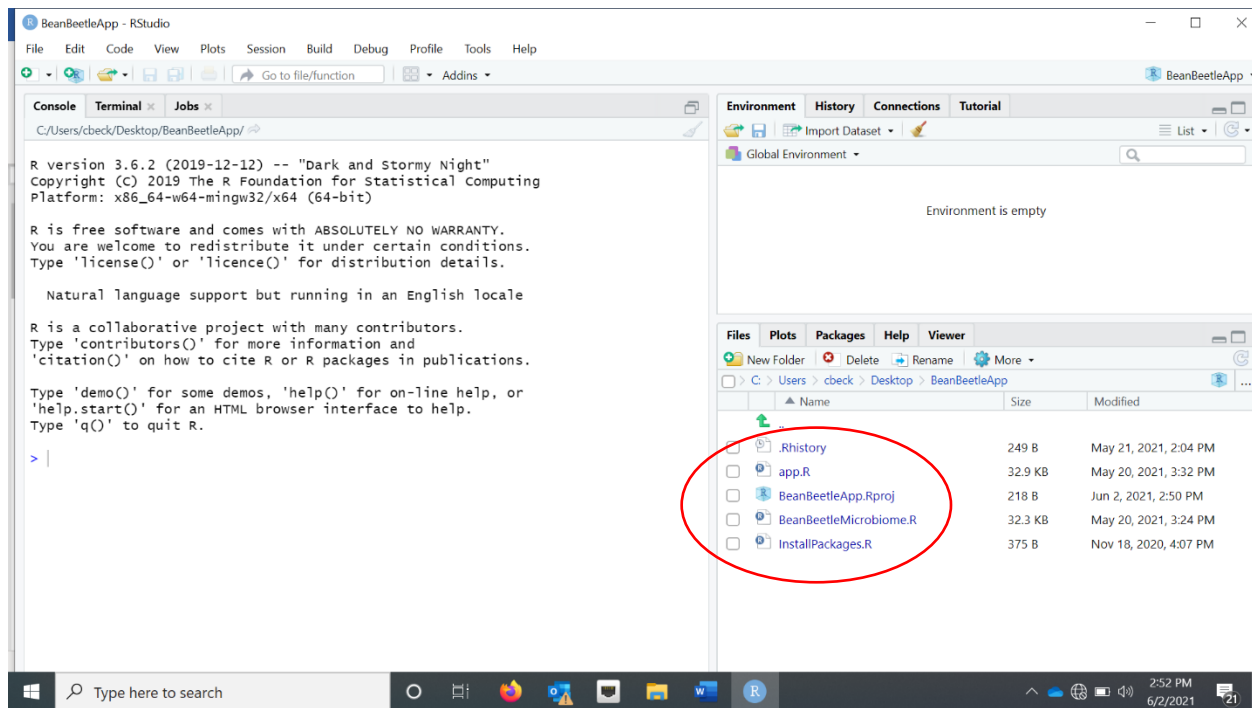
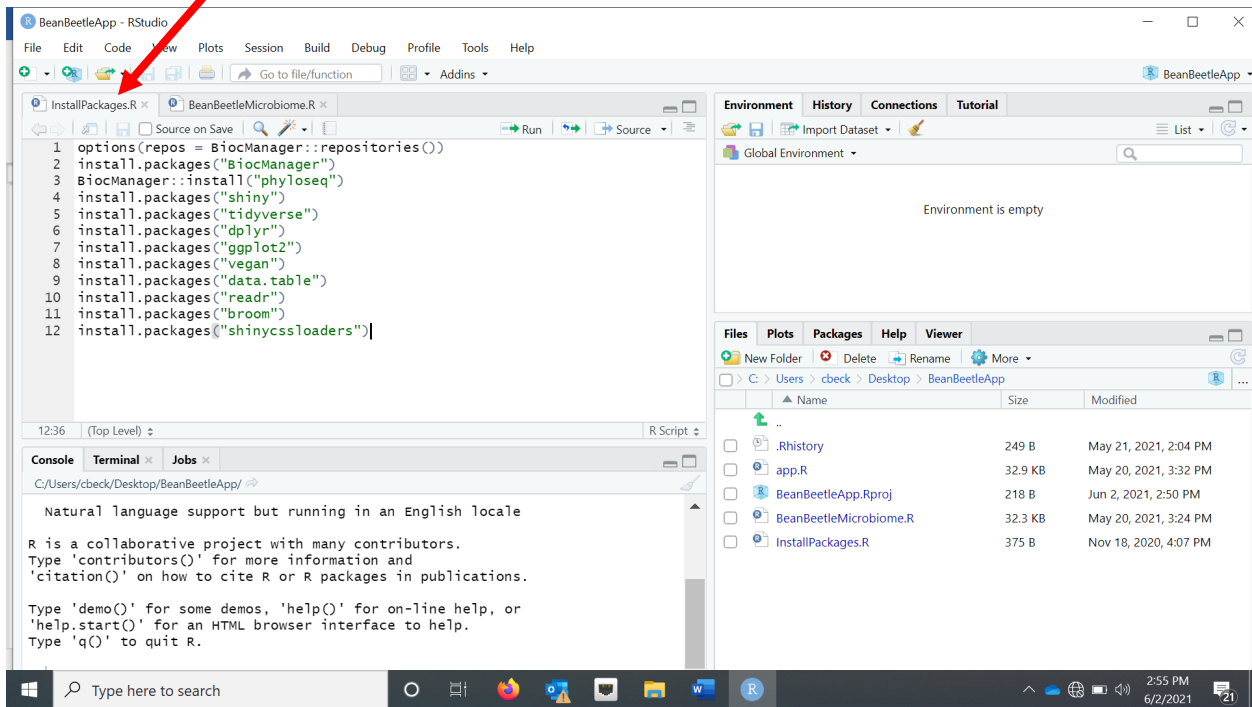


Installing and running BeanBeetleMicrobiome app locally

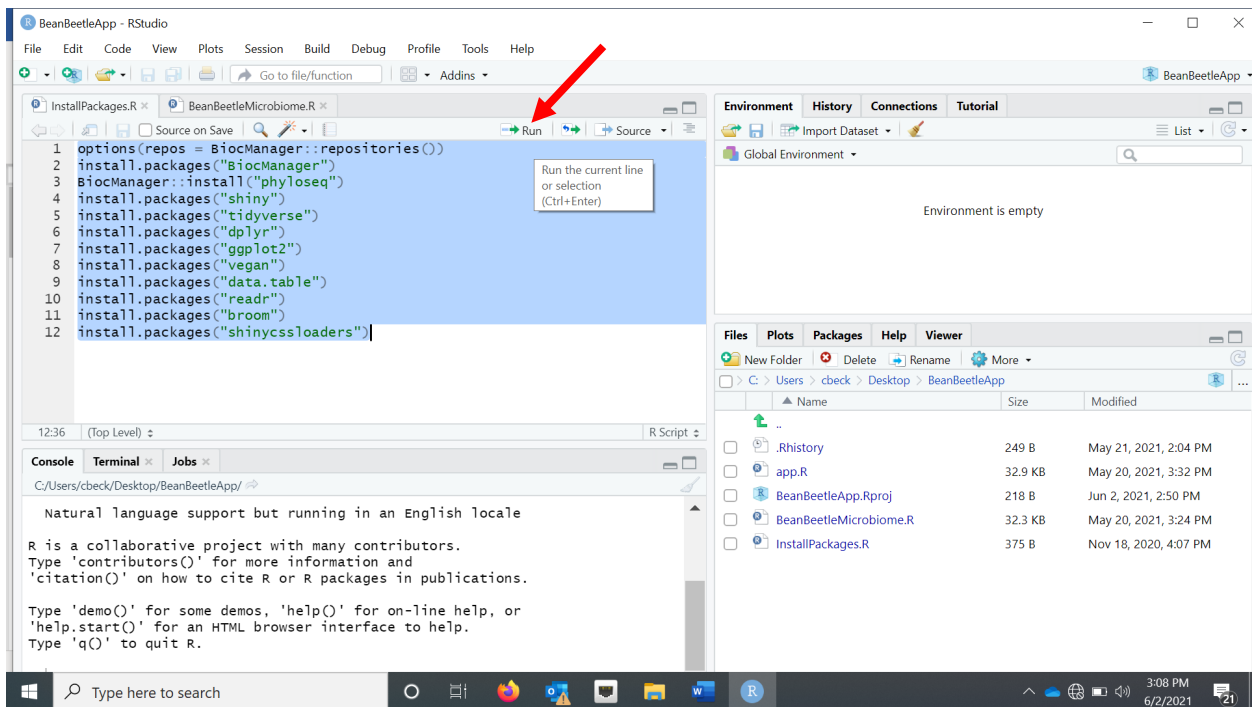
1. Download and install R
2. Download and install RStudio
3. Create a folder for the BeanBeetleMicrobiome app.
4. Download and save the script to install the necessary R packages to the folder that you just created. Make sure that the file is a .R file rather than a .txt file.
5. Download and save the app file to the folder. Make sure that the file is a .R file rather than a .txt file.
6. Open RStudio.
7. In RStudio, create a New Project by clicking File -> New Project. Then, select Existing Directory and navigate to the folder with the script and app files. Then, click Create Project.
8. In the lower right panel, the files in your folder should be listed in the lower right panel. Click on the names to load "InstallPackages.R" and "BeanBeetleMicrobiome.R".



9. In the upper left panel, select the InstallPackages.R tab.



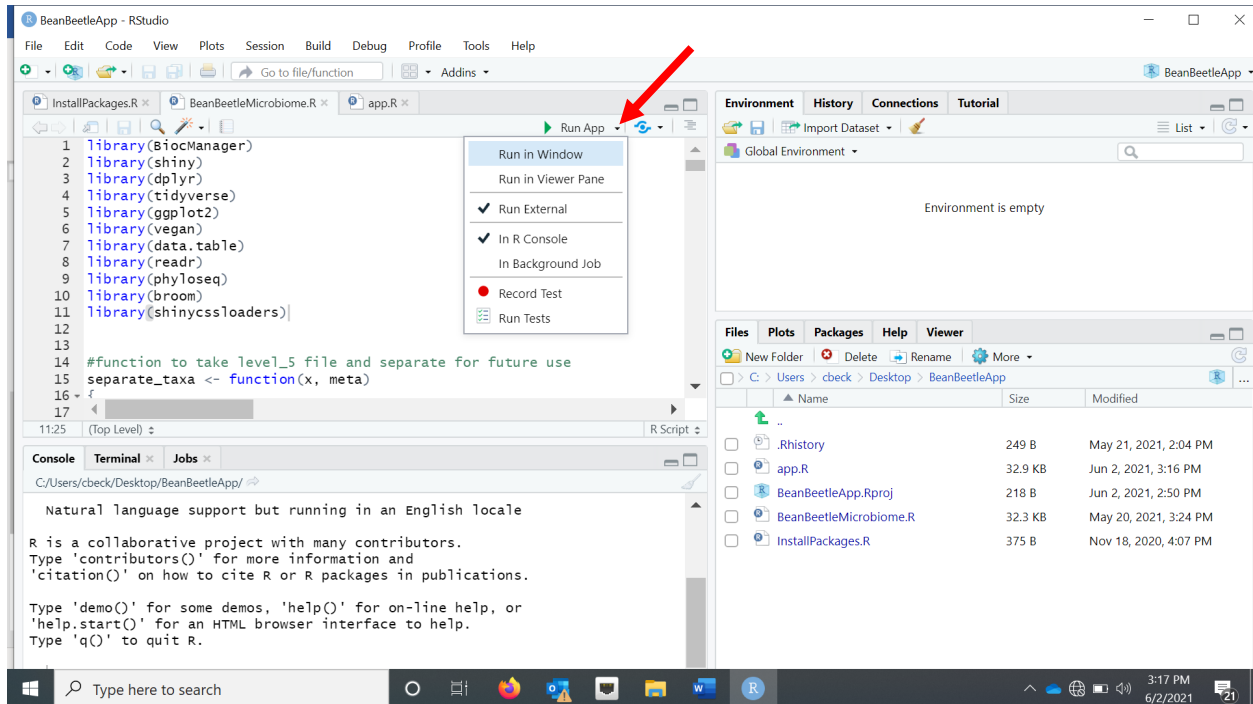
10. Select all of the code in InstallPackages.R and click the Run button. This step will take some time while it loads the packages. If any dialog boxes pop up, select “Yes”.



11. Once the packages are loaded, you should see a “>” in the lower left Console window. At this point, click on the tab for BeanBeetleMicrobiome.R in the upper left. If the file is an R file, you should see a “Run app” button. If it is a text file, I will show “Run” instead. If it shows “Run,” create a new R script by File -> New File -> R Script. Then, copy and paste all of the code in the

BeanBeetleMicrobiome.R window into this new window. Save this as “app.R”. Once you do this, “Run app” should appear.

12. Click the small dropdown arrow to the right of “Run app” and select “Run external”.



13. Finally, click “Run app” button. This will open your default web browser and open the app.