

ENCORE README

Thank you for downloading ENCORE (ECHO Native Circadian Ontological Rhythmic Explorer)! ENCORE is an app designed to help you navigate and understand the function of amplitude change categories for circadian rhythms with gene ontologies. This guide will lead you in first time set-up and use. Pictures have been provided for ease of use, using Windows 10. An asterisk indicates the step has an explanation below, and a tilde indicates the step is first-time set up only.

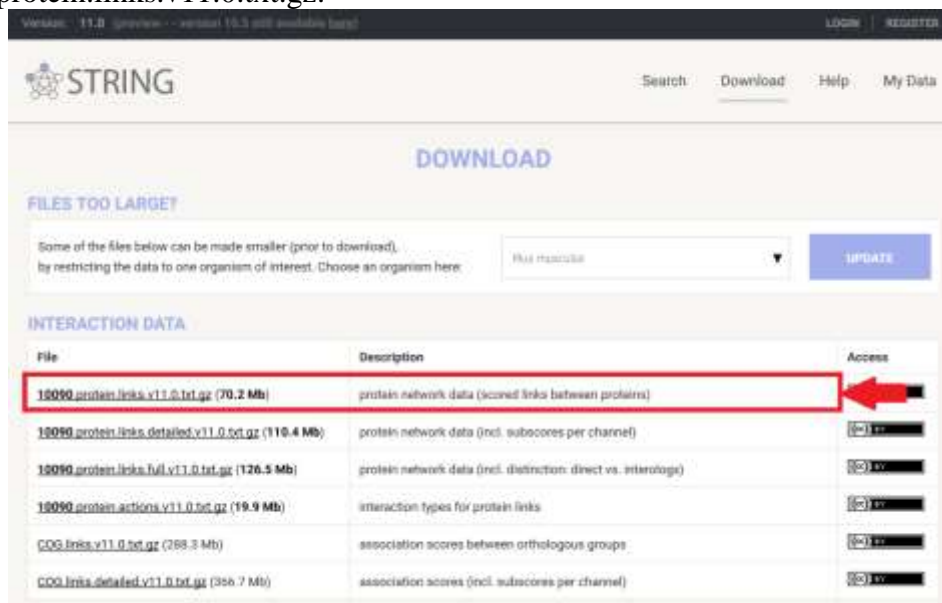
Last updated: 2/8/19 (ENCORE version 0.1)

Steps:

1. *~ Download Firefox (<https://www.mozilla.org/en-US/firefox/new/>) or Chrome (<https://www.google.com/chrome/browser/desktop/index.html>) and make it your default browser.
2. ~ Download the protein links for *your organism* from STRING (<https://string-db.org/cgi/download.pl>). The organisms that are available in this application are:

Organism	Taxonomy Number
Mus musculus	10090
Homo sapiens	9606
Neurospora crassa	5141
Drosophila melanogaster	7227
Anopheles gambiae	7165
Saccharomyces cerevisiae	4932
Escherichia coli K12 substr MG1655	511145

Enter your organism's name in the 'choose an organism' box and click update. You should then see the taxonomy number preceding the file names. Download the file called TAX#.protein.links.v11.0.txt.gz:



Version: 11.2 (previous: - version 10.3 still available here) LOGIN REGISTER







STRING Search Download Help My Data

DOWNLOAD

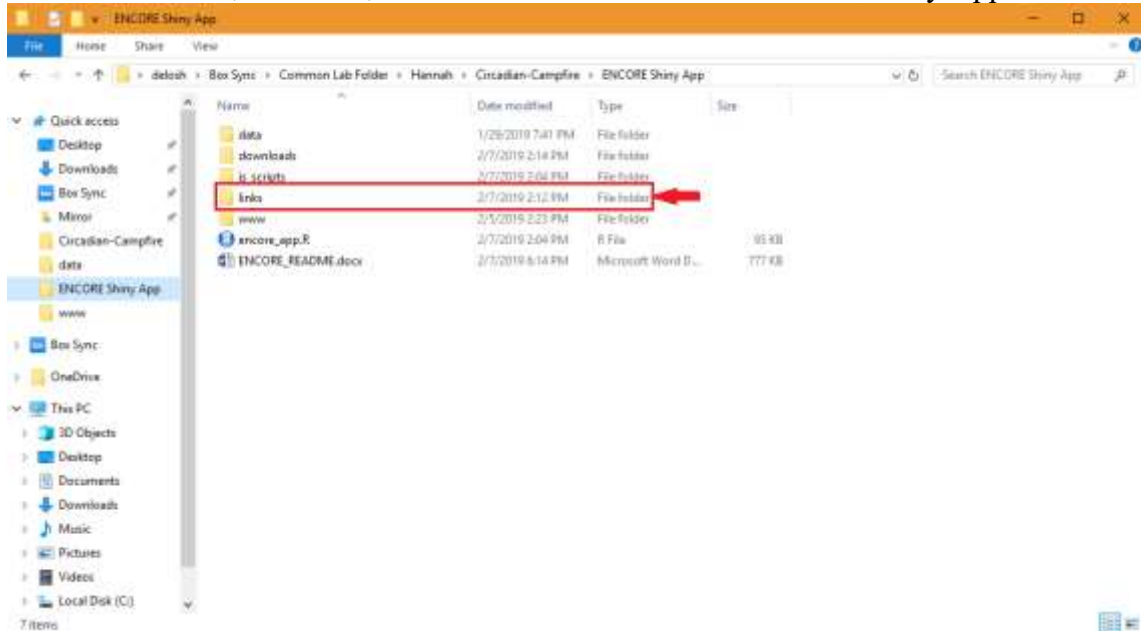
FILES TOO LARGE?

Some of the files below can be made smaller (prior to download), by restricting the data to one organism of interest. Choose an organism here: **UPDATE**

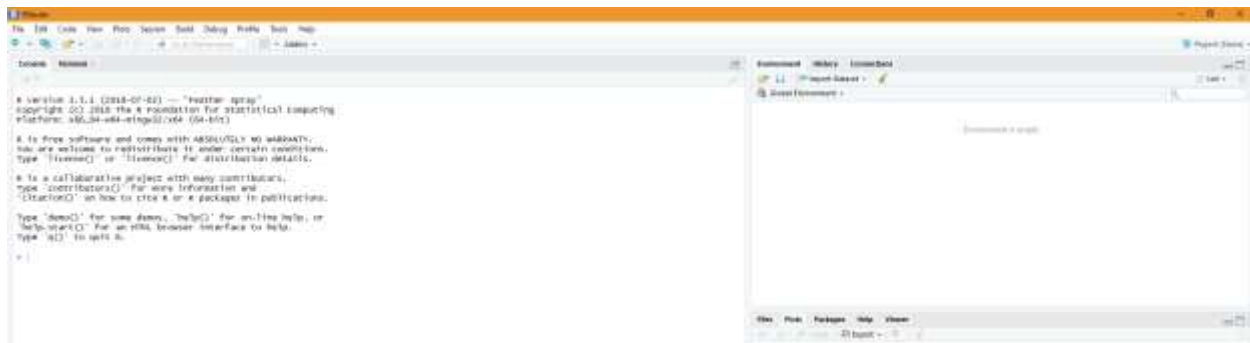
INTERACTION DATA

File	Description	Access
10090.protein.links.v11.0.txt.gz (70.2 Mb)	protein network data (scored links between proteins)	 Download
10090.protein.links.detailed.v11.0.txt.gz (110.4 Mb)	protein network data (incl. subcores per channel)	 Download
10090.protein.links.full.v11.0.txt.gz (126.5 Mb)	protein network data (incl. distinction: direct vs. interologs)	 Download
10090.protein.actions.v11.0.txt.gz (19.9 Mb)	interaction types for protein links	 Download
COG.links.v11.0.txt.gz (288.3 Mb)	association scores between orthologous groups	 Download
COG.links.detailed.v11.0.txt.gz (356.7 Mb)	association scores (incl. subcores per channel)	 Download

3. ~ Once you've downloaded that file, extract the text file. (You may need to download an alternative unzip program that can unzip .gz files, such as 7Zip [<https://www.7-zip.org/>].) Place that text file, unaltered, in the 'links' folder of the 'ENCORE Shiny App' Folder.



4. ~ Download R, if you do not already have it: <https://www.r-project.org/>
5. ~ Download RStudio, if you do not already have it (RStudio Desktop is sufficient): <https://www.rstudio.com/products/rstudio/download/>
6. Plug in your computer, if it is not plugged in already.
7. Open RStudio. It should look something like this:



8. ~ Copy and paste the following text into the console window (bottom right window of the RStudio Session), then press enter:

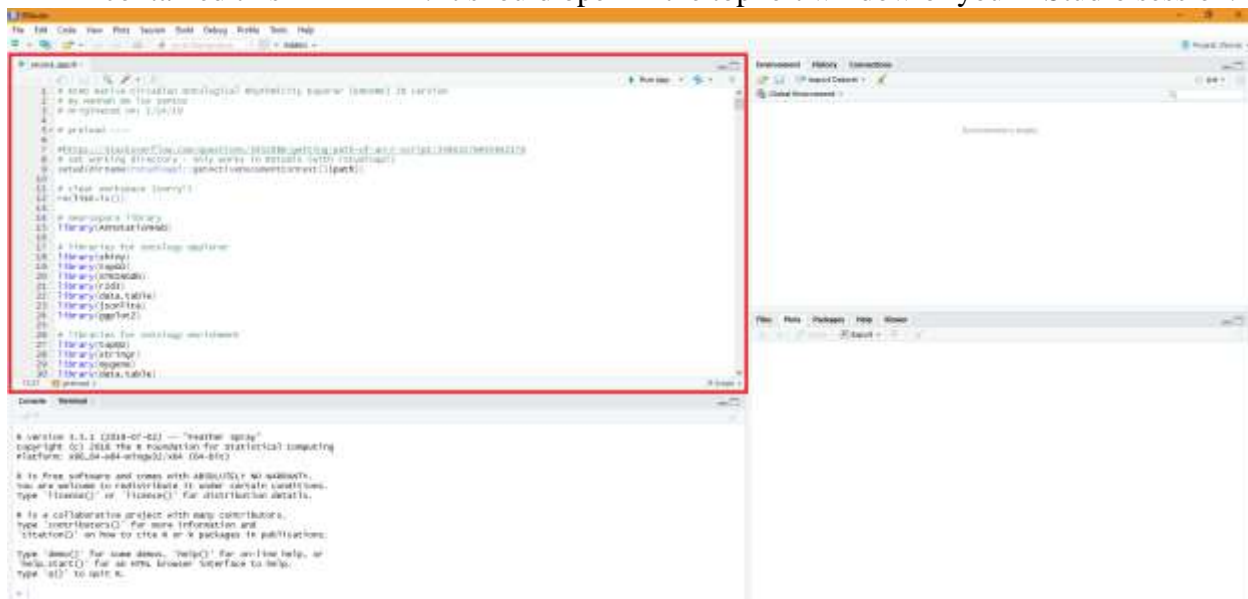
```
install.packages("rstudioapi")
install.packages("shiny")
install.packages("ggplot2")
install.packages("r2d3")
install.packages("data.table")
install.packages("jsonlite")
install.packages("igraph")
install.packages("stringr")
```

Copy each of the following lines in the console separately and press enter for each:

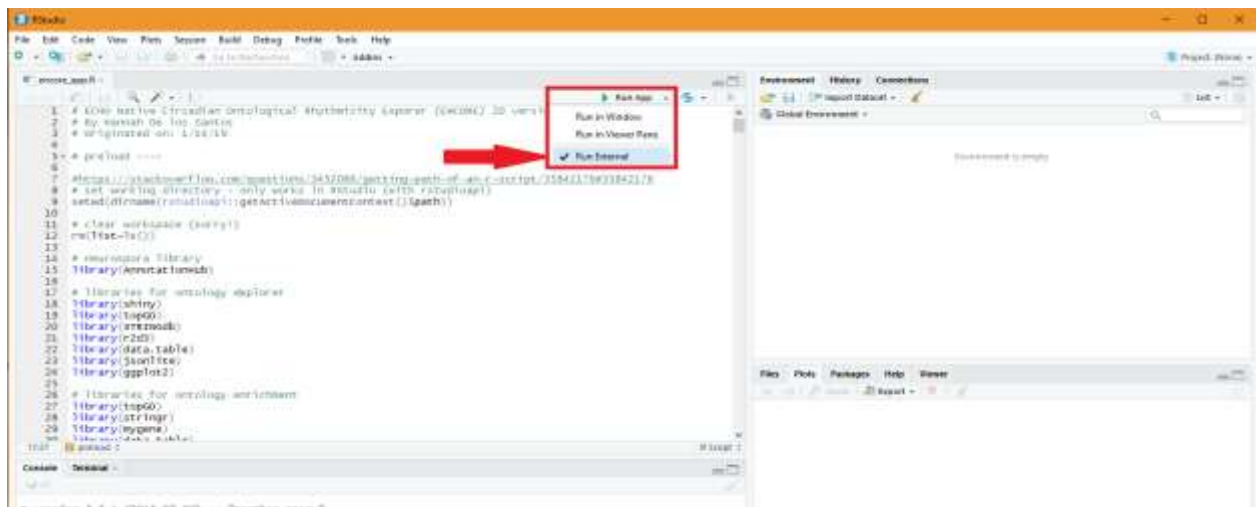
```
if (!requireNamespace("BiocManager", quietly = TRUE))
  install.packages("BiocManager")
BiocManager::install("STRINGdb", version = "3.8")
BiocManager::install("AnnotationHub", version = "3.8")
BiocManager::install("mygene", version = "3.8")
BiocManager::install("topGO", version = "3.8")
BiocManager::install("AnnotationDbi", version = "3.8")
BiocManager::install("org.Ag.eg.db", version = "3.8")
BiocManager::install("org.Dm.eg.db", version = "3.8")
BiocManager::install("org.Hs.eg.db", version = "3.8")
BiocManager::install("org.Mm.eg.db", version = "3.8")
BiocManager::install("org.EcK12.eg.db", version = "3.8")
BiocManager::install("org.Sc.sgd.db", version = "3.8")
```

This will install these packages (a set of functions that this application uses) onto your computer. This may ask for your input, so just say no to the questions asked. If you run into errors saying “no,” just say yes instead. Note: this may take some time.

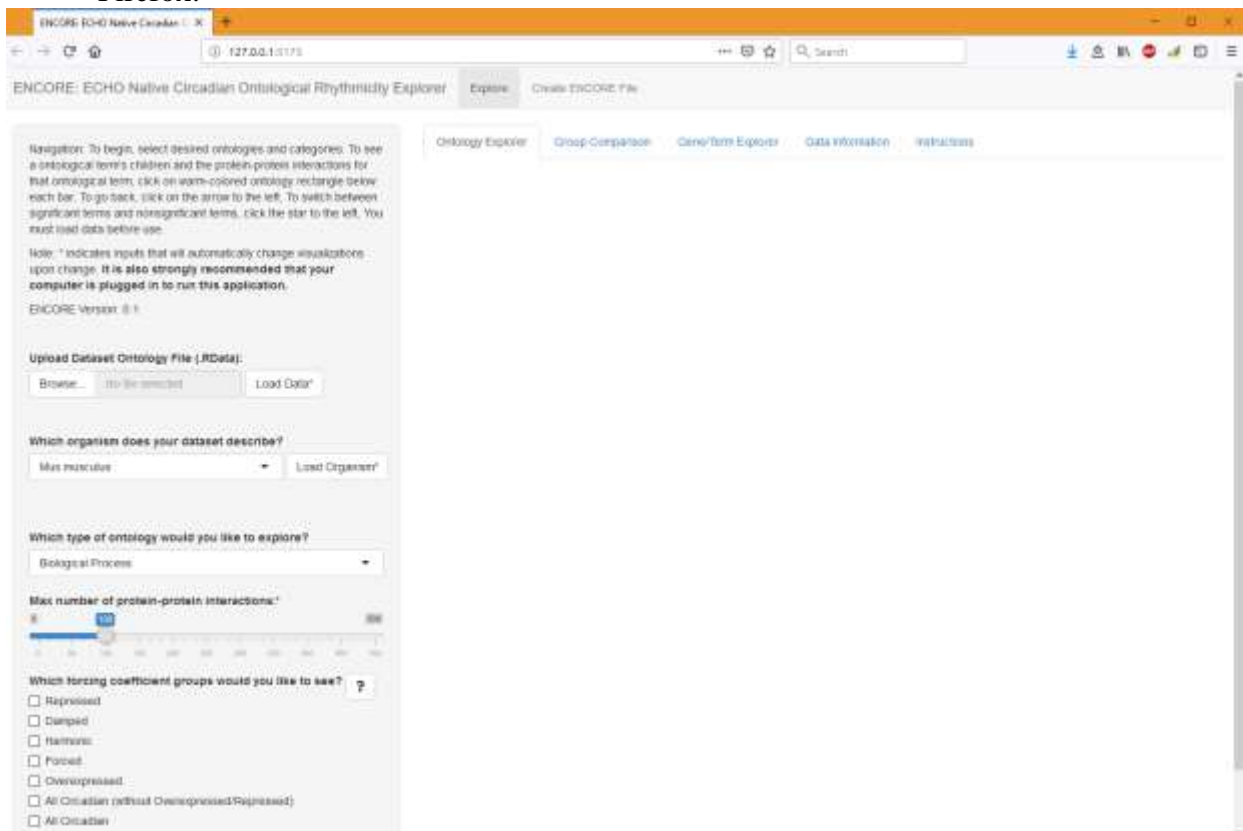
9. Open `encore_app.R`, which should be included in the .zip file you downloaded and also contained this README. It should open in the top left window of your RStudio session.



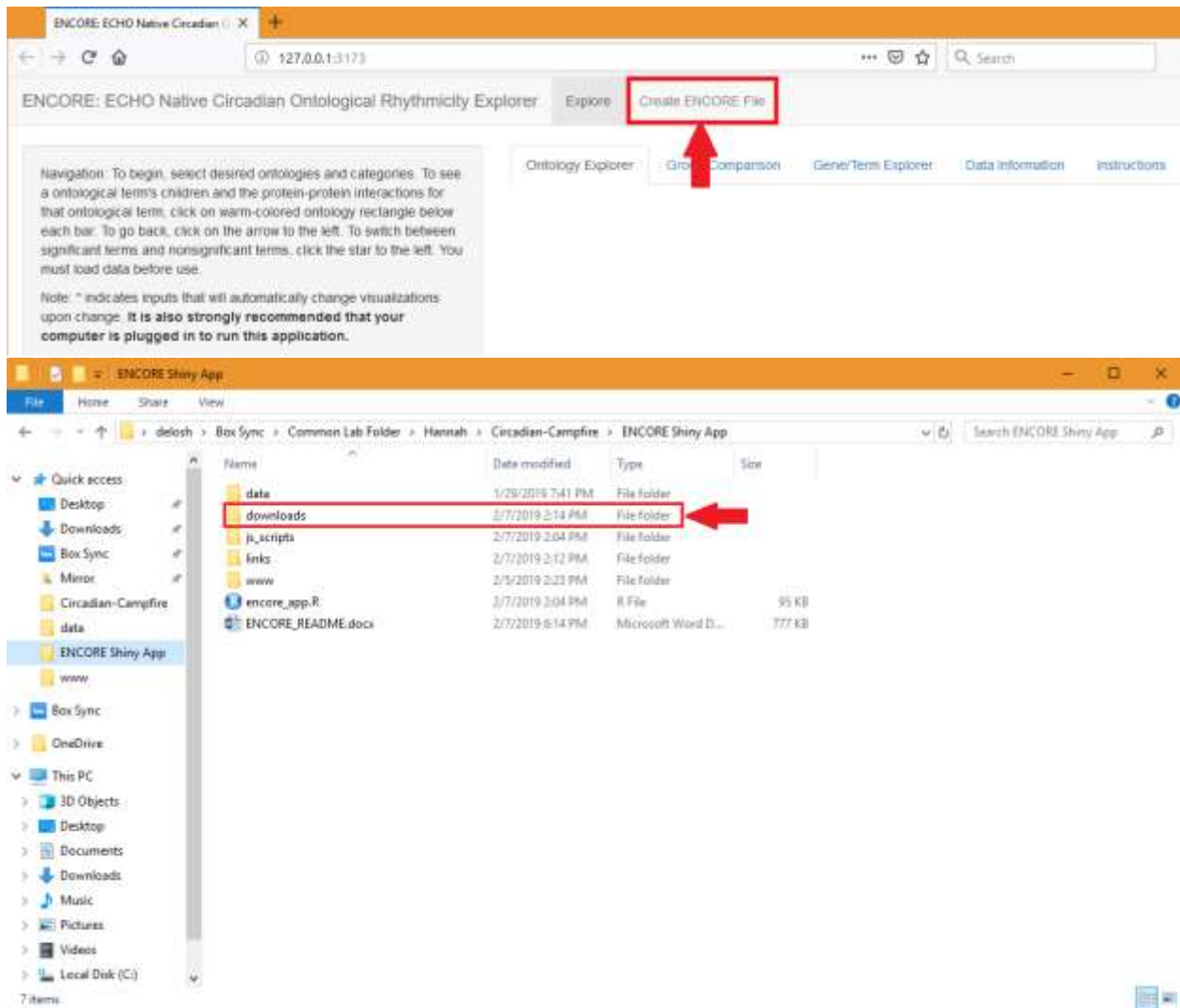
10. In the top right corner of the `encore_app.R` window, you should see the button, “Run App”. Click on the small downwards arrow next to it and choose “Run External”.



11. Now click “Run App”. This should open the ENCORE application in your now default browser window (either Firefox or Chrome). The picture below is a representation in Firefox.



12. Start by choosing the ‘Create ENCORE File’ section to calculate your ECHO (<https://github.com/delosh653/ECHO>) output for ENCORE and download resulting file. ENCORE downloads appear in the ‘downloads’ folder of the ENCORE Shiny App folder that you’ve downloaded.



13. Once you've downloaded the ENCORE file, upload it to the 'Explore' section and proceed, following the navigation instructions.
14. Have fun!

* Why do I have to install either Firefox or Chrome, you ask? Why not Internet Explorer, or some other browser? Well, it is known there are problems downloading files when viewing shiny apps in Internet Explorer, as well as some aspects of d3 not working, so we definitely want to avoid that. However, I have not tested this app in browsers like Microsoft Edge, Safari, etc. If you can verify that these work, please let me know at delosh@rpi.edu.