

Instructions to view Trendy Shiny Application

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Below are step-by-step instructions on how to interactively view the data using the Trendy Shiny App.

Step 1:

Download the dataset from the manuscript's Github page:

<https://github.com/rhondabacher/RobotNeuralDiffPaper>

In the [TrendyShiny](#) folder there are the following dataset options:

Human and mouse time-courses sampled for 600 minutes:

- humanRobot_scaled0to1_trendyForShiny.RData
- mouseRobot_scaled0to1_trendyForShiny.RData
- mouseRobot_trendyForShiny.RData (expression was not scaled)
- humanRobot_trendyForShiny.RData (expression was not scaled)

Human and mouse time-courses sampled for 600 minutes alignment to the intron reads:

- human_remap_intronScaled_trendyForShiny.RData
- mouse_remap_intronScaled_trendyForShiny.RData

Human control time-course sampled for 600 minutes:

- humanRobotControl_scaled0to1_trendyForShiny.RData

Human and mouse time-courses from Barry et al., 2017:

- Human_Barry2017_scaled0to1_trendyForShiny.RData
- Mouse_Barry2017_scaled0to1_trendyForShiny.RData
- Human_Barry2017_trendyForShiny.RData
- Mouse_Barry2017_trendyForShiny.RData

Download the file that you want to look at in the Shiny application by clicking Download:

Step 2 :

Open a session of R or RStudio.

If you do not have R installed, it can be installed for free at: <https://cran.r-project.org>

Then to install RStudio, it can be downloaded for free at: <https://www.rstudio.com/products/rstudio/download/>

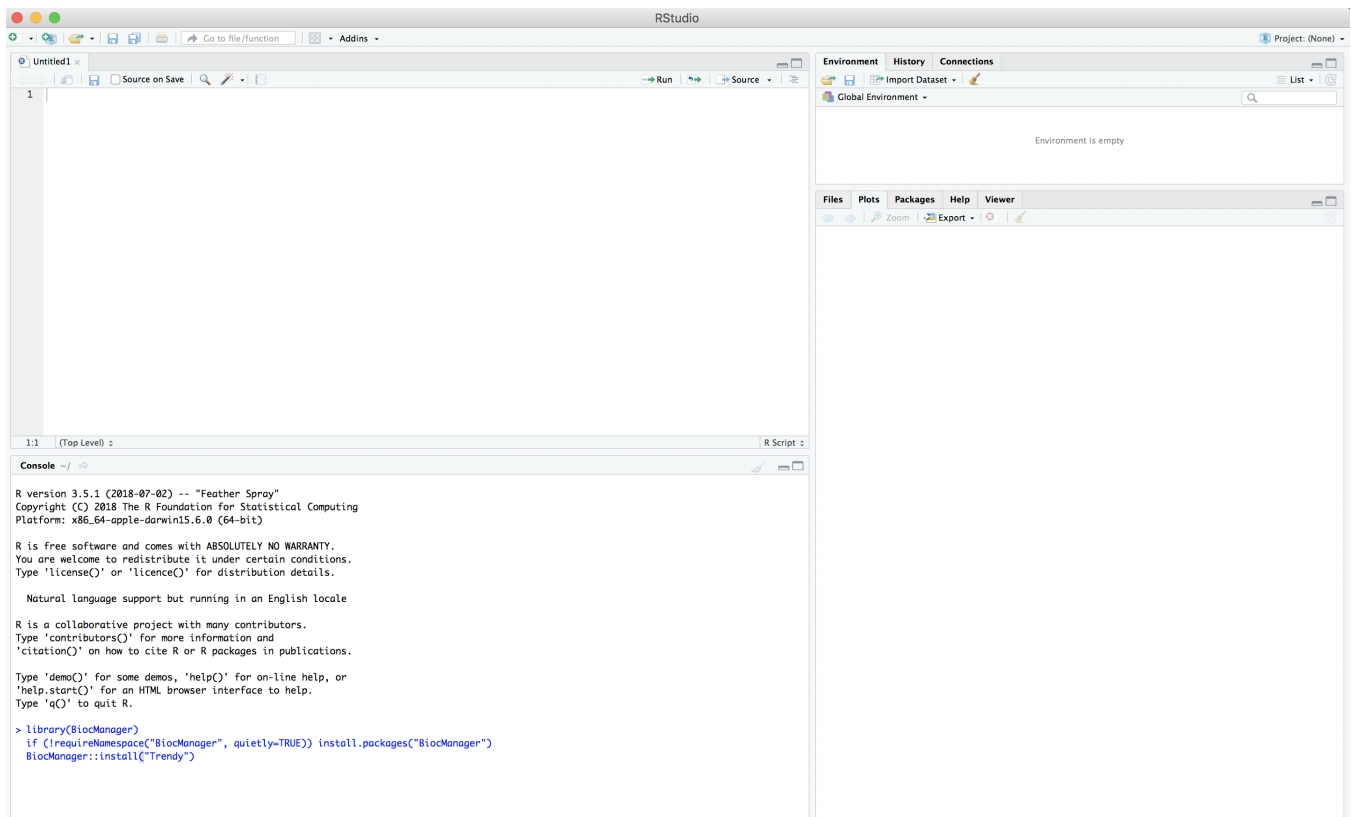
(Select the free option "RStudio Desktop").

Step 3:

To install Trendy, type the following into the Console:

```
library(BiocManager)
if (!requireNamespace("BiocManager", quietly=TRUE)) install.packages("BiocManager")
BiocManager::install("Trendy")
```

Example:



Step 4:

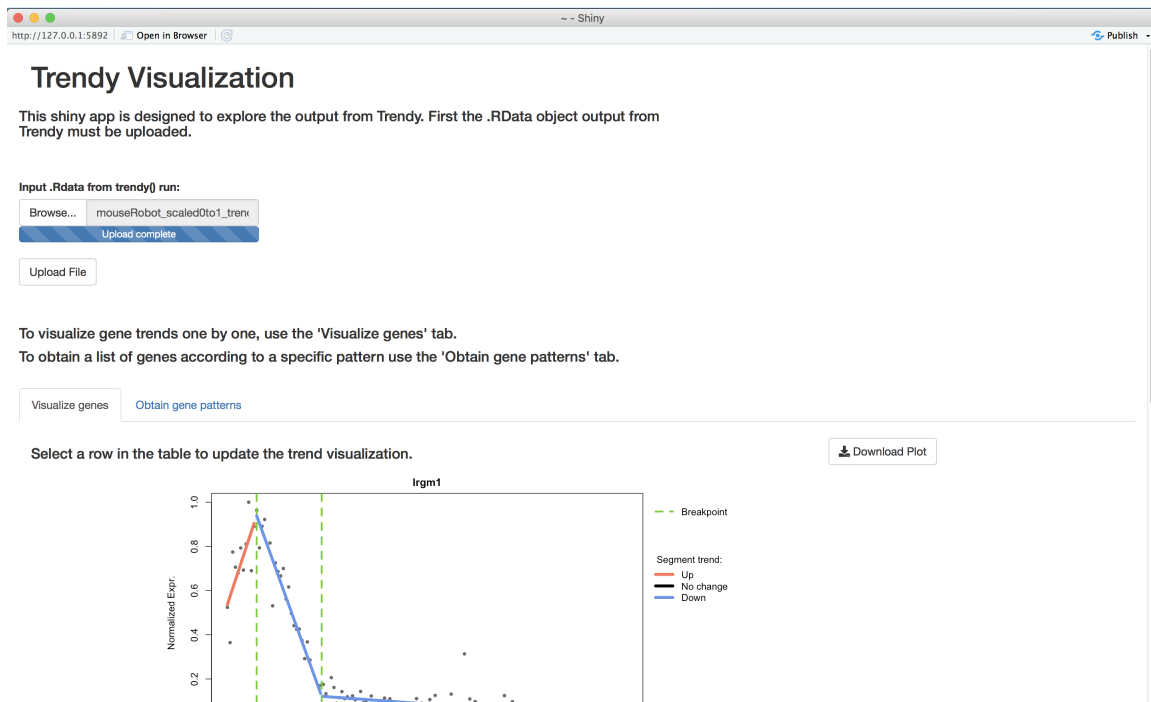
To open the Trendy Shiny App, type the following into the console:

```
library(Trendy)
trendyShiny()
```

A page will then pop-up, which allows you to input the dataset downloaded in Step 1:



After pressing Upload, the plots will load and allow for interactive exploration.



Questions?

Any questions may be emailed directly to rbacher@ufl.edu or submitted on Github as an Issue here: <https://github.com/rhondabacher/RobotNeuralDiffPaper/issues>