# 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/RobotSeq

In the TrendyShiny folder there are the following dataset options:

Human and mouse time-courses sampled for 600 minutes:

- $\bullet \ \ mouseRobot\_scaled0to1\_trendyForShiny.RData$
- humanRobot scaled0to1 trendyForShiny.RData

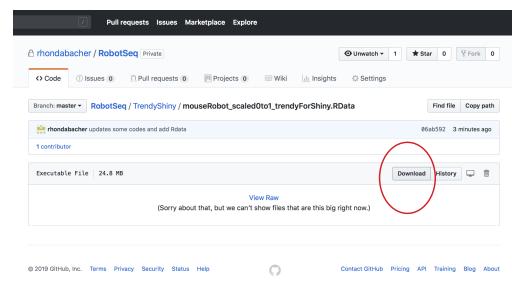
Human control time-course sampled for 600 minutes:

 $\bullet \ \ humanRobotControl\_scaled0to1\_trendyForShiny.RData$ 

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

- mouseRobot scaled0to1 trendyForShiny.RData
- humanRobot scaled0to1 trendyForShiny.RData

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

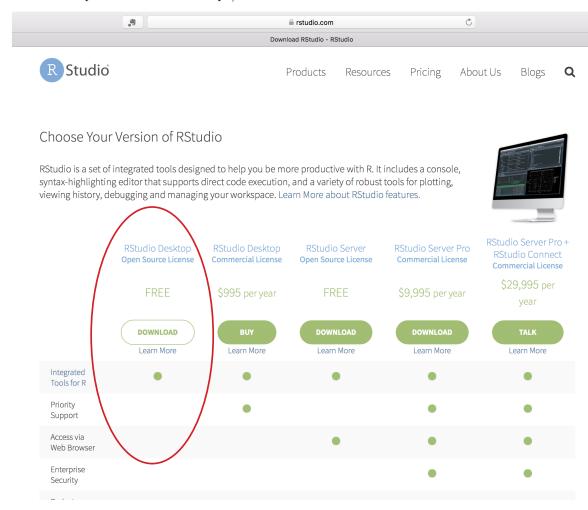


## Step 2:

Open a session of R or RStudio.

If you do not have RStudio, it can be downloaded for free at: https://www.rstudio.com/products/rstudio/download/

(Select the free option "RStudio Desktop").

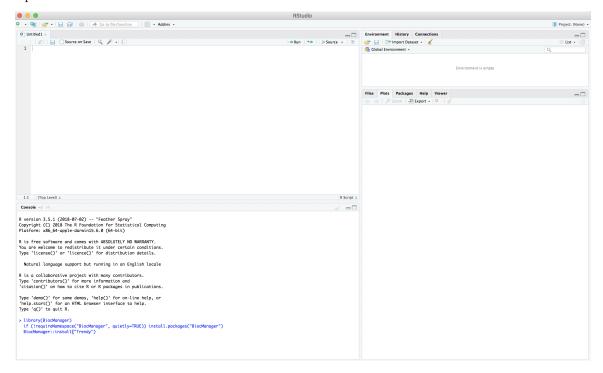


### Step 3:

To install Trendy, type the following into the Console:

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

#### Example:

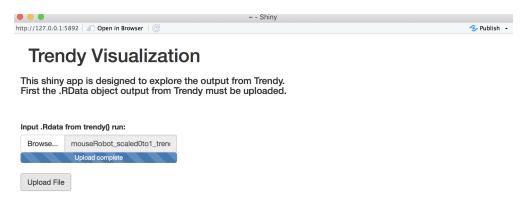


## Step 4:

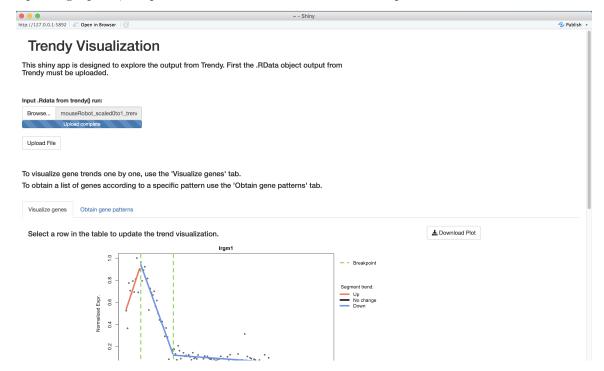
To open the Trendy Shiny App, type the following into the console:

```
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/RobotSeq/issues