README document

The following source code and data files are provided so that someone with minimal computational skills can reproduce our results or employ different datasets. Some small knowledge of R (<http://www.r-project.org/>) is required to understand/run the code.

List of codes and files included:

1. server.R. The code that calculates the TopS values and produce the histogram, means, standard deviations, correlations and clustering results.
2. ui.R creates a user-interface and display elements on the page
3. The input file must be named: “input\_file.csv” and it must have a header. The first column must include: protein names, gene names or any categorical data. If you want to have a different file name, it must be changed inside of this code at line “14”. Please select the “Comma” separator.
4. An example file for SARS dataset (A SARS-CoV-2-Human Protein-Protein Interaction Map Reveals Drug Targets and Potential Drug-Repurposing by David E. Gordon et al. at https://www.biorxiv.org/content/10.1101/2020.03.22.002386v3.supplementary-material**)** is included to create TopS values.

Workflow of TopS to generate the TS results:

1. First install the devtool library using this command:

install.packages(“devtools”)

install.packages(“gplots”)

install.packages(“gridExtra”)

install.packages(“shiny”)

1. Type:

library(shiny)

1. Run:

runApp()

A user interface should appear and the file input can be selected. TopS generate an output file named: “ouput\_file.txt” that consists of TS values. Please select the Quote: “None”. The file is generated in the directory where the shiny app is running. If a hierarchical clustering of columns (i.e. baits in the example file) is desire for this output file, then select the generated output file for the analysis. TOPS will also generate three pdf figures in the same directory.

If an error occurs: dev.off(): cannot shut down device, please use #dev.off(0 inside the server.R