Our softwares is divided into two part: (1)set of web pages; (2)R package ‘BANFFVisual’

(1)

If the users only have adjacency matrix file and raw information file of gene and don’t have the json file needed, you may have to install python 2.7 and run adj2graph.py and graph2json.py script to generate the json file. adj2graph.py has three arguments to run, first one is the adjancy matrix file name, second one gene ID file, third one is the ouput file you want. graph2json.py also needs three arguements: the output file generated by adj2graph.py; raw information file of genes and the final output json file used in our visualizatoin.

Our main page is index.html. Users can easily open it and will see our visualization of the gene networks. Users can move and zoom-in and zoom-out displaying area using mouse. Either clicking on the nodes or typing the gene ID in the search box will highlight the selected gene. A slider bar is provided to adjust the size of the nodes. There are several options in the left sidebar. Users can click on submit button after choosing these options to go the other pages. In other pages, users can go back to this main page by clicking on return button.

(2)

The package is attached and please just install it on R and use the codes according to the report.