**M**eta**G**ene 1.0

Documentation

Table of Contents

Introdiction

MetaGene 1.0 is developed as a research project on bio-informatics domain. The main requirement of metagene is to act as a visualization platform, is capable of visualizing various plots that is used in bioinformatic domain. The sources for plots are micro array gene expression data which are present as data set which are very large in size. MetaGene facilitates scientists,biologists and students a visualization platform. Observing gene expression data without the aid of graphs is hectic and almost impossible as these datasets perhaps comprise of millions of rows.

MetaGene is implemented as a web application based on client server architecture using python bokeh[2] as a visualization libraray. Data sets are acquired from the Gene Expression Omnibus archive.[1] A user can enter an accession number present on GEO archive and have the relevant plots plot by metagene.

Plotting Using MetaGene

A user is first directed to the home page where user can enter the GEO accession number. After entering the accession number data is fetched from GEO archive. Then the user is asked to enter the type of the graph that he wants to be plot. Thereafter, the system prompts for relevant parameters and generate the visualization. After generating the visualization user is directed to the canvas and the visualization is displayed there along with the meta data of the dataset
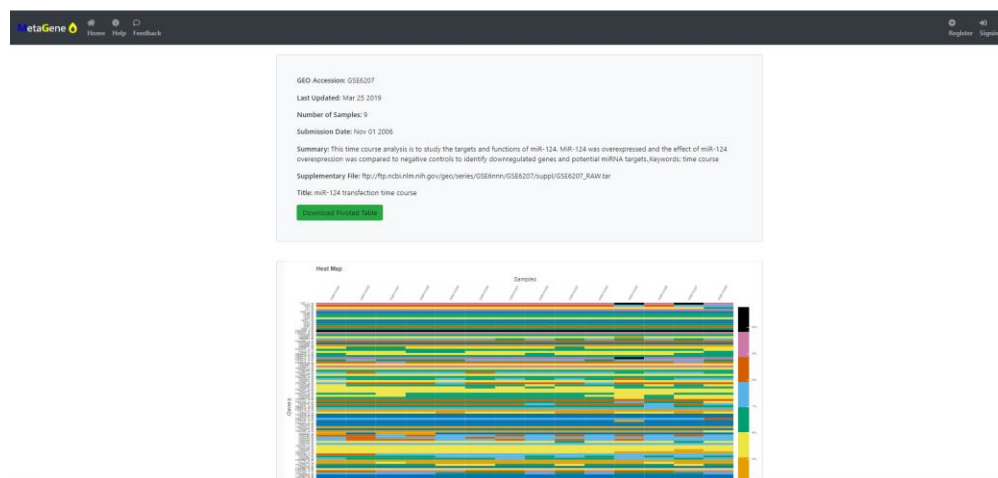
User can perform activities such as zooming in, slicing on the visualization using the tool bar below the visualization. In addition, using the export icon user can export the plot in png format.

Sign in, register and Dashboard

User can register and sign-in using the icons on far right of the navbar. When a user is signed in, he is directed to the dashboard which comprises if privileges that are only available to registered members. Version 1 .0 doesn't consist of more functionality in dashboard. However, in version 2.0 there will be added functionalities to improve the user experience.

Support and Feedback

A user can submit a support ticket using the help section. To use this privilege user has to be signed in first. In addition, a user can give feedback about the system using feedback section.

References

[1]"Home-GEO - NCBI", Ncbi.nlm.nih.gov, 2019. [Online]. Available: https://www.ncbi.nlm.nih.gov/geo/. [Accessed: 19- May- 2019].

[2] B. contributors, "Welcome to Bokeh — Bokeh 1.1.0 documentation", *Bokeh.pydata.org*, 2019. [Online]. Available: https://bokeh.pydata.org/en/latest/. [Accessed: 19- May- 2019].