Shiny PCA

1. **Installation**

Requires miniconda or anaconda installed in for the user.

1.1 Run the install.bat file to create env and install necessary dependencies.

1.2 Manual install

Dependencies

r-base v 4.4.3

r-essentials

r-shiny

r-plotly

r-htmlwidgets

r-biocmanager

r-reactable

CMD:

```
conda create -n shiny_pca
conda activate shiny_pca
conda install -c conda-forge r-base=4.4.3 r-essentials r-shiny r-plotly
r-htmlwidgets r-biocmanager r-reactable
```

1.3 Use R to install deseq2

CMD:

```
BiocManager::install("DESeq2")
```
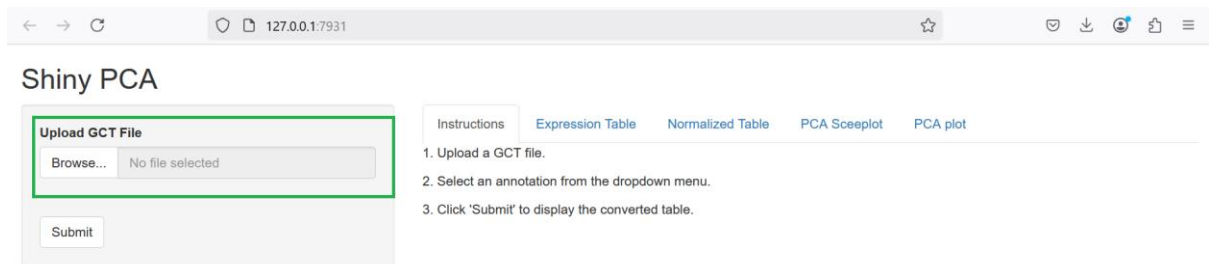
2   App usage manual

2.1 To launch the application run the following commands in powershell.

```
conda activate shinyPCA
run_shinyPCA.bat
```

The above command will start the shiny app.

2.2 Input Data

The app takes gct file as input, upload the file in the marked section
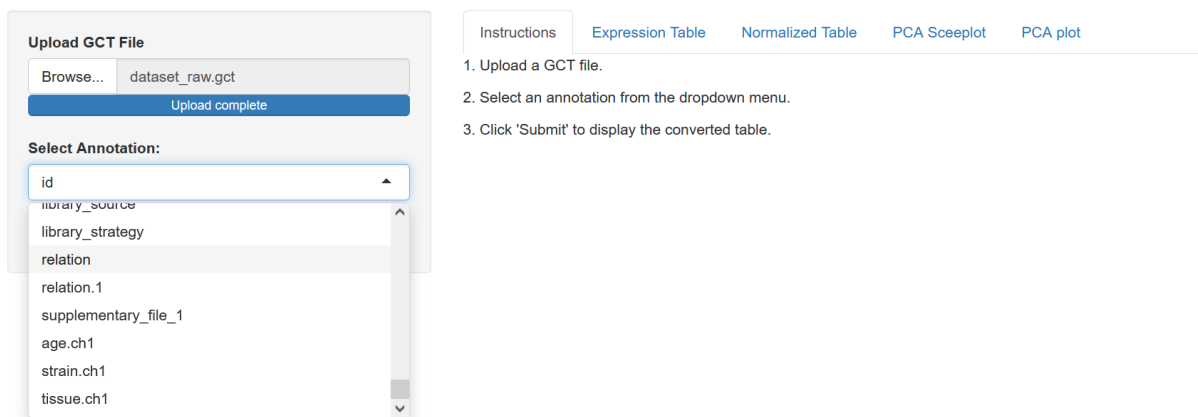
Once uploaded, user will be provided with the option to select metadata/annotation from the available information in gct file
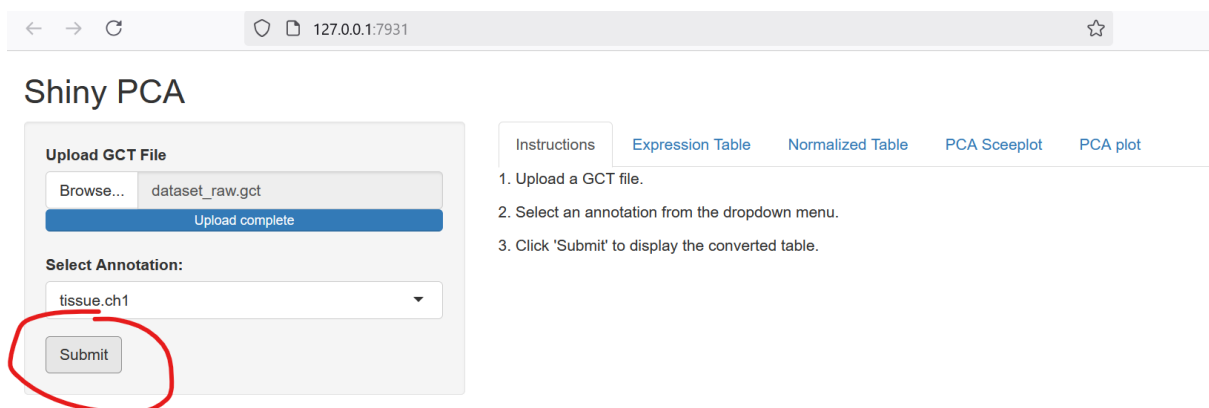
Select desired metadata from the drop down menu and click submit.

Once submitted users can browse the tabs on the main page to browse the result.