User need to have python >=3.5+ install in their system.

User can install all dependencies for the application using requirements.txt file present in the folder.

One can use following command for same :

**python3 -m pip install --user -r /path\_where\_project/searchProject/requirements.txt**

User also need to have R installed in their system beforehand.

R related packages required : **GenomicRanges**

Rpy2 library used in this project creates a bridge between R and python.

In order to install tkinter which provides GUI for the app, user needs to install it using following command :

**apt-get install python3-tk**

Finally user can run the application by reaching into the searchProject folder and running following command :

"**python3 scepisearch.py"**

If all dependencies work well, user can see the GUI.

Note : If user runs into the error "OSError: cannot load library '/home/cell/R/lib/R/lib/libR.so': libBblas.so: shared Cannot open object file: there is no such file or directory "

Solution : User needs to add path : **export LD\_LIBRARY\_PATH = "/path-to-R-installation/lib/R/lib:$LD\_LIBRARY\_PATH"**

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**If user is executing from location machine, GUI will work fine.**

Otherwise if user is executing from remote server, Following process has to be followed :

1. If local system is windows, User needs to install Xming from : https://sourceforge.net/projects/xming/

 Afterwards, user should login to remote server from putty and tick X11 forwarding :

 

2. If user is accessing remote server from linux based local system, then user can login to remote server with -X ssh login.

For eg, ssh -X username@192.168.X.X