

paraGSEA tutorial

Shunyun Yang

September , 2016

1 Build instructions

paraGSEA runs on Mac and Linux as a command line application. You can download the source code of paraGSEA from Github with the following command on a standard terminal.

git clone <https://github.com/ysycloud/paraGSEA.git>

Note that this requires that you already have a Github account and that the computer you are working on has an SSH key registered on Github. If this is not the case, follow the instructions from <https://help.github.com/articles/generating-ssh-keys/>.

This should download a directory named paraGSEA. To build paraGSEA, execute the following.

cd paraGSEA

make all

make install

This should succeed on most Linux systems because make is available by default. If this is not the case, you can obtain it by typing **sudo apt-get install make** on Ubuntu. Other Linux systems can also easily obtain the *make* tool by some simple commands. On Mac, you need to install *XCode*, which may take some time. First, you will need an Apple ID, then you will need to download it from the developer website of Apple <https://developer.apple.com/xcode/downloads/>. Then, you may need to follow the instructions shown on the following link to install the command line version of *make*. <http://stackoverflow.com/q/10265742/1248687>.

Calling make should create some executable files. Note that you need root authority to run **make install** command, then you can running the commands of paraGSEA in any path of this system. If you cannot, the application can be only used in paraGSEA/bin directory. To check that the building is successful, execute the following command.

./quick_search_serial

If you obtain the output shown below, then everything went fine and you are done with the build. If not, then something went wrong. In this case, you can explain how to reproduce the problem on <https://github.com/ysycloud/paraGSEA/issues>. Then, we will solve it for you as quick as possible.

Usage: quick_search_serial [options]

general options:

-n --topn: The first and last N GSEA records ordered by ES
input/output options:
-i --input: input file/a parsed profiles's file from pretreatment stage.
-s --sample: input file/a parsed sample sequence number file from pretreatment stage.
-r --reference: input a directory includes referenced files about genesymbols and cids.

2 paraGSEA basics

Coming soon...