

GCTA MANUAL

Once you have downloaded the GCTA file, you need to do the following steps:

Add ENVIRONMENT VARIABLE:

a. Before running the program, find environment variable file ".zshrc". You can open it with command "**vim ~/.zshrc**" in your terminal.

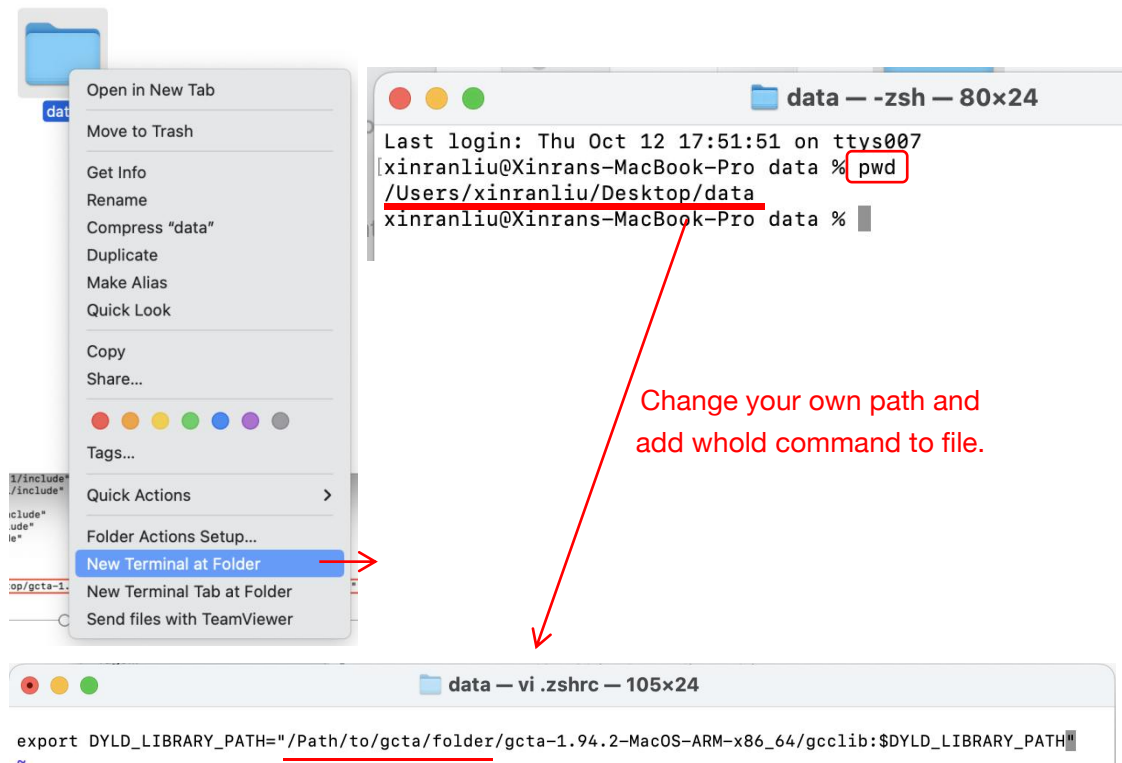


```
xinranliu — zsh — 80x24
Last login: Thu Oct 12 17:33:42 on ttys008
xinranliu@Xinrans-MacBook-Pro ~ % vim ~/.zshrc
```

b. Then add command:

```
export DYLD_LIBRARY_PATH="/Path/to/gcta/folder/gcta-1.94.2-MacOS-ARM-x86_64/gcclib:$DYLD_LIBRARY_PATH"
```

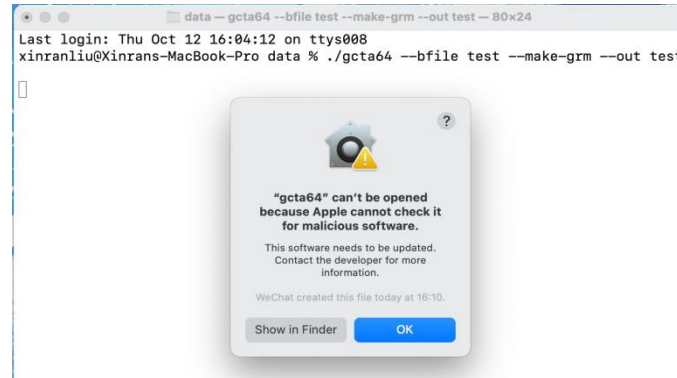
to your ".zshrc" file. Note: **/Path/to/gcta/folder** needs to be replaced with the directory where your gcta folder resides, you can find the path by command "**pwd**"



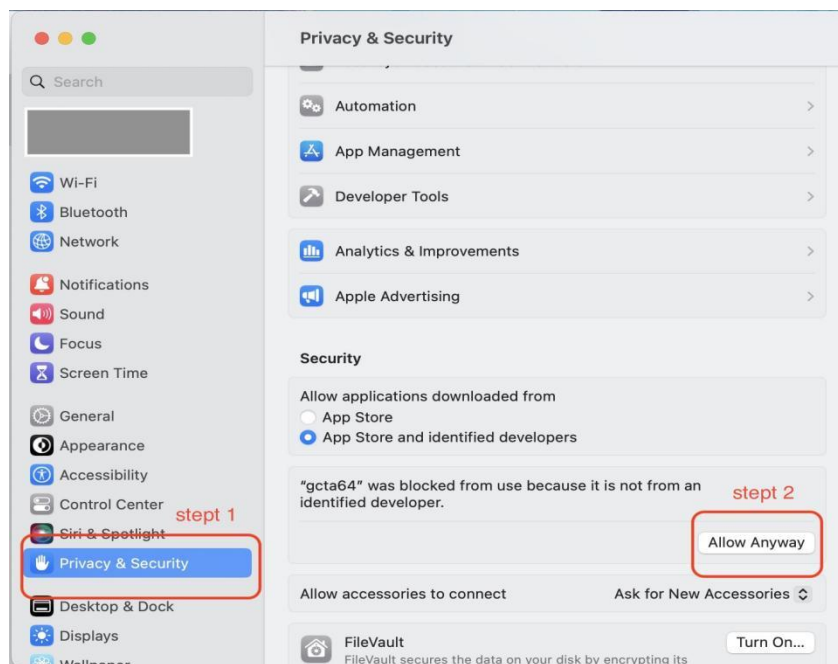
c. run command "**source ~/.zshrc**", then you can run GCTA as normal.

Notes :

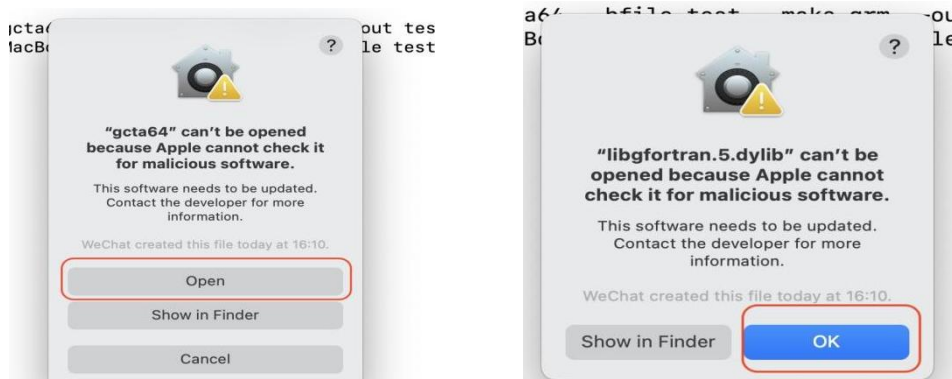
When you first use the GCTA, you may encounter the following situation:



You can solve this by following two steps in "**System Settings**":

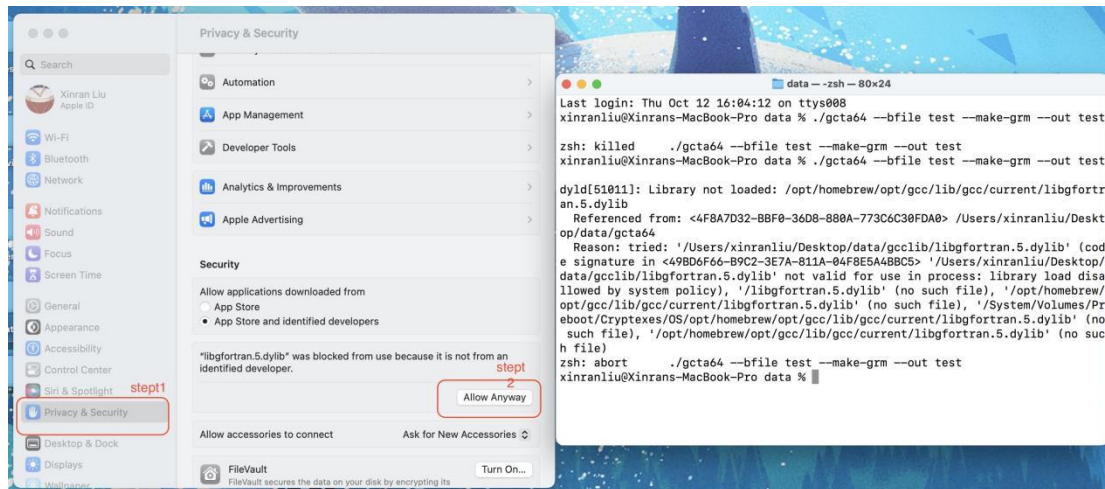


Then run your gcta command, there may be some pop ups like:



And your Settings will continue prompt you to allow the libraries, you need to click

them for several times. Then you can continue to run your command, and repeat the operations until there are no pop ups any more.



Finally you can find your app run smoothly like this:

```
data — zsh — 86x42
Last login: Thu Oct 12 18:18:53 on ttys005
xinranliu@Xinrans-MacBook-Pro data % ./gcta64 --bfile test --make-grm --out test
*****
* Genome-wide Complex Trait Analysis (GCTA)
* version v1.94.1 Mac
* (C) 2010-present, Yang Lab, Westlake University
* Please report bugs to Jian Yang <jian.yang@westlake.edu.cn>
*****
Analysis started at 18:20:20 CST on Thu Oct 12 2023.
Hostname: Xinrans-MacBook-Pro.local

Options:
--bfile test
--make-grm
--out test

Note: GRM is computed using the SNPs on the autosomes.
Reading PLINK FAM file from [test.fam]...
3925 individuals to be included from FAM file.
3925 individuals to be included. 1643 males, 2282 females, 0 unknown.
Reading PLINK BIM file from [test.bim]...
1000 SNPs to be included from BIM file(s).
Computing the genetic relationship matrix (GRM) v2 ...
Subset 1/1, no. subject 1-3925
  3925 samples, 1000 markers, 7704775 GRM elements
IDs for the GRM file have been saved in the file [test.grm.id]
Computing GRM...
  100% finished in 0.1 sec
1000 SNPs have been processed.
Used 1000 valid SNPs.
The GRM computation is completed.
Saving GRM...
GRM has been saved in the file [test.grm.bin]
Number of SNPs in each pair of individuals has been saved in the file [test.grm.N.bin]

Analysis finished at 18:20:20 CST on Thu Oct 12 2023
Overall computational time: 0.25 sec.
xinranliu@Xinrans-MacBook-Pro data %
```