**Download**

**Executable Files**

The executable files below only support a 64-bit operating system on the x86\_64 CPU platform.

Linux [gcta\_1.93.3beta.zip](http://172.16.13.142/software/gcta/bin/gcta_1.93.2beta.zip)

Windows [gcta\_1.93.2beta\_win.zip](http://172.16.13.142/software/gcta/bin/gcta_1.93.2beta_win.zip) (v1.93.3beta will be available soon)

Mac [gcta\_1.93.2beta\_mac.zip](http://172.16.13.142/software/gcta/bin/gcta_1.93.2beta_mac.zip) (v1.93.3beta will be available soon)

The executable files are released under the MIT license. We recommend to use the Linux version because the Windows and Mac versions have not been fully tested. The Linux version of GCTA only supports kernel version >= 2.6.32 (released 10 years ago), otherwise one may receive an error message: "FATAL: kernel too old". The Windows and Mac versions are tested under the most recent system versions only.

Note: GCTA 1.93.3beta is a beta version under testing. We have fixed a few bugs in the previous versions. If you find any bug in this version, please report it to Jian Yang at [jian.yang@westlake.edu.cn](mailto:jian.yang@westlake.edu.cn).

**Source code**

[gcta\_1.93.2\_src.zip](http://172.16.13.142/software/gcta/pre_gcta/gcta_1.93.2_src.zip)

The source code are released under GPL v3.

**Update log**

**Version 1.93.3beta (1 Jun 2021)**

* Added a new module [fastGWA-GLMM](http://172.16.13.142/software/gcta/index.html#fastGWA-GLMM) (a resource-efficient generalized linear mixed model association tool for biobank-scale data).
* Added a new module [fastGWA-BB](http://172.16.13.142/software/gcta/index.html#fastGWA-BB) (a burden test for binary traits under the fastGWA-GLMM framework).
* Added a new module [ACAT-V](http://172.16.13.142/software/gcta/index.html#ACAT-V) (a very efficient set-based test that only requires GWAS summary statistics, originally proposed by [Liu et al, 2019](https://www.sciencedirect.com/science/article/pii/S0002929719300023)).