

GAPIT

GAPIT is a Genome Association and Prediction Integrated Tool freely available for Public since 2011. It has been updated frequently to incorporate the state of art methods for Genome Wide Association Study (GWAS) and Genomic Selection (GS). The first two milestones of implementations were documented by the [Bioinformatics paper](#) led by [Dr. Alex Lipka](#) in 2012, and the [Plant Genome paper](#) led by Dr. You Tang and Dr. Xialolei Liu in 2016. Currently, Dr. Jiabo Wang is leading the new development, GAPIT version 3. In addition to the methods implemented in version 1 and 2 (e.g. [Q+K](#), [Compressed MLM](#), and [SUPER](#)), the new version implemented two new GWAS methods ([FarmCPU](#) and [BLINK](#)) and two new GS methods ([sBLUP](#) and [cBLUP](#)) published since 2016. All GAPIT documents are hosted at [GitHub](#), including source code, user manual, demo data and demo code. The previous versions of source code are archived at [Dr. Zhiwu Zhang Lab](#) (GAPIT [achieve](#)). [GAPIT Forum](#) is available for asking questions or giving comments. Please maximize the usage of the forum for benefit of our user community before contacting the current leading author (Dr. Jiabo Wang, email: wangjiaboyifeng@163.com).