

weIMPUTE_GWAS Analysis Software Configuration and User Manual

1. Overview of the weIMPUTE_GWAS Tool

The weIMPUTE_GWAS tool is used to configure and manage GWAS (Genome-Wide Association Studies) tools such as GAPIT, allowing users to upload files, set parameters, start GWAS analysis, and visualize the results via a graphical interface. It is integrated with the weIMPUTE and weIMPUTE_GWAS platforms to enhance the user's workflow.

2. System Requirements

Operating System: Linux / macOS / Windows

Java Version: openJDK 17

Software Requirements: R (GAPIT),

Dependencies: The relevant directory structure and configuration files for weIMPUTE_GWAS should already be set up.

3. How to Use

Example URL: You can access the service via the following address: <http://144.34.160.128:8080/>.

The screenshot displays the weIMPUTE_GWAS web interface. On the left is the weIMPUTE logo. The main area contains several file upload fields, each with a 'Browse...' button and a 'Done' status bar. The fields are: Genotype_file (required), Trait_file (required), Kinship_file--Optional (optional), Covariate_variables_file--Optional (optional), and Tools:GLM,MLM,SUPER,MLMM,FarmCPU,Blink (optional). Below these is a 'Submit' button. At the bottom, there is a table with 7 columns: X, SNP, Chr, Pos, Pvalue, MAF, and traits. The table shows 6 rows of data. To the right of the table is a 'result target' section with a download icon.

X	SNP	Chr	Pos	Pvalue	MAF	traits
851	PZAD3640.1	2	195212071	8.293984e-06	0.04819277	GLM.EarDia
1220	PZD00004.3	3	199478329	2.095929e-06	0.07831325	GLM.EarDia
1459	PZAD3311.5	4	153293454	2.669441e-06	0.03815261	GLM.EarDia
1481	PZAD0453.7	4	166281276	4.997222e-06	0.10441767	GLM.EarDia
1483	PZAD3379.2	4	167650309	1.236051e-07	0.02811245	GLM.EarDia
1506	PZB00282.2	4	178735388	1.36774e-05	0.32329317	GLM.EarDia

Showing 1 to 6 of 10 rows 6 rows per page

3.1 Detailed Operation Steps for weIMPUTE_GWAS Analysis Software

① Input Genotype File:

On the main interface, upload your genotype file. The supported file formats are:

VCF Format: Suitable for most genomic data.

Hapmap Format: You can upload .hapmap.txt files.

② Input Phenotype File:

Upload your phenotype data file, which should contain individual information and phenotype data corresponding to the genotype file.

③ Optional Step: Upload Kinship Matrix:

If you need to use a kinship matrix for analysis, you can upload a kinship matrix file. This is usually a text file containing data on the relationships between individuals.

The kinship matrix is used to estimate the genetic similarity between individuals and is applicable for methods like MLM.

④ Optional Step: Upload Covariate File:

If your analysis requires covariates (such as environmental factors, experimental conditions, etc.), you can upload a covariate file.

The covariate file should include additional feature data corresponding to the individuals in the genotype and phenotype files.

⑤ Select Analysis Model:

Choose the GWAS analysis methods you would like to use (e.g., **GLM, MLM, SUPER, MLMM, FarmCPU, Blink**).

You can select one or more analysis methods. If selecting multiple, separate them with commas “,”.

⑥ Click Submit to Start GWAS Analysis:

After completing the above steps, click the Submit button, and the system will begin performing the GWAS analysis.

The system will calculate based on the chosen analysis method(s).

⑦ View Analysis Results:

Once the analysis is complete, the results will be displayed on the interface, including statistical table.

You can also download the result.tar.gz compressed file, which contains all the analysis results.

Additional Notes:

GAPIT software serves as the core for processing genotype, phenotype, kinship matrix, and covariate data, supporting multiple GWAS analysis methods.

For detailed formats and instructions for phenotype files, kinship matrices, and covariate files, please refer to the GAPIT official documentation.

3.2 Starting the weIMPUTE_GWAS Service

Upload the required scripts and configuration files to the corresponding directories:

Upload your GWAS analysis scripts (e.g., vcf2hmp.txt, gapit.txt) to the config directory.

Upload necessary resource files (e.g., charts, images) to the data directory.

Build and Run weIMPUTE_GWAS:

Use Maven to build the project:

mvn clean install

Once the build is complete, run the packaged JAR file:

java -jar weIMPUTE-GWAS-V0.1.jar

The system will start a web service, which by default will listen on `http://IP:8080`. You can access the service through your browser at this address.

3.3 Using the Interface

Upload Files:

Access the `weIMPUTE_GWAS` service, and you will see a graphical interface where input fields for file uploads and parameter entries will be automatically generated.

Follow the instructions to upload the `Genotype_file` (genotype data), `Trait_file` (trait data), and optionally the `Kinship_file` and `Covariate_variables_file`.

Choose the Analysis Tool:

In the Tools field, select the GWAS analysis method you wish to use (e.g., GLM, MLM, Blink).

Start the Analysis:

After completing the configuration, click the "Start Analysis" button. The system will automatically execute the selected script and generate the analysis results.

View the Results:

The results will be displayed on the interface, including tables and charts.

Users can download the `result.tar.gz` compressed file, which contains all the analysis results.

4. Summary

`weIMPUTE_GWAS` provides a simple graphical interface for command-line tools. Integrated with the `weIMPUTE` and `weIMPUTE_GWAS` platforms, it enhances the user's workflow and makes it easier to configure, execute, and visualize GWAS analysis. By properly configuring the input, execution order, and output paths, you can conveniently perform GWAS analysis and view the results through the visual interface.

For more information or to access the service, visit <http://144.34.160.128:8080/>.