

Quick Start Guide

This guide provides you an example on how to quickly get started with the imputation service.

The instructional video that complements this guide can be found at the end of the [GitHub README](#).

Here we use our example website to illustrate the detailed steps of imputation service. You could deploy the service locally by following the deployment guidance, <http://144.34.160.128:80>.

DemoFile Preparation

Please download the demonstration file.

[chr2.vcf.gz](#)

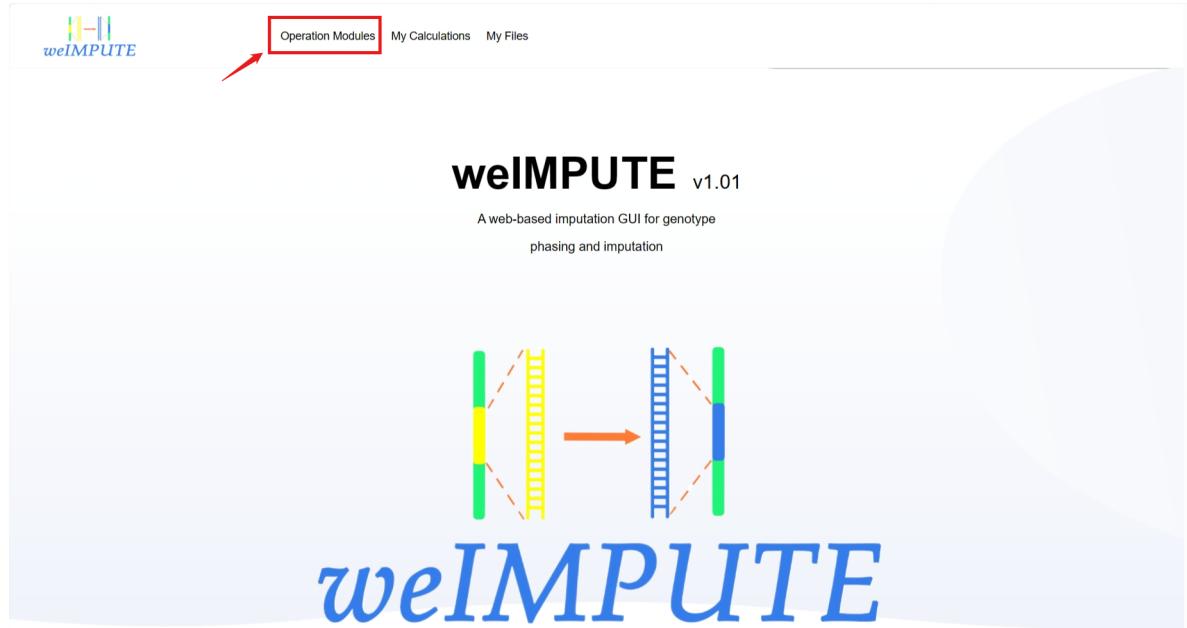
[refile.vcf.gz](#)

The other supporting files have been configured on the server.

Log in

Access the demo server at <http://144.34.160.128:80>.

Click on the "Operation Modules" tab.

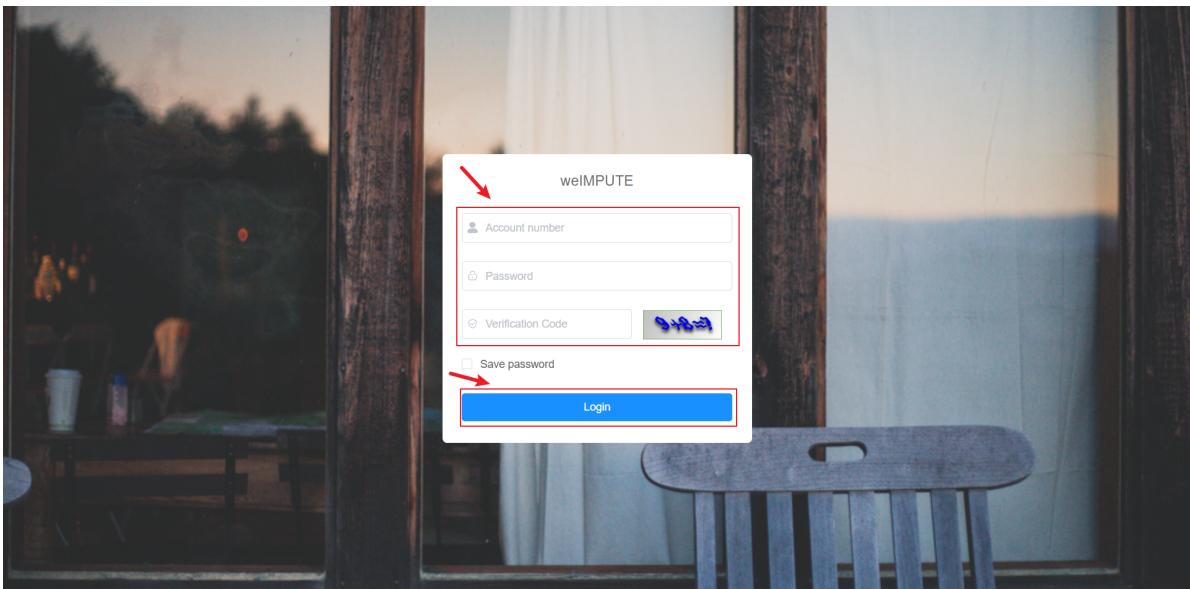


Login as admin with the default admin password:

admin

admin123

And enter the verification code.



Operation Configuration

Click on the "Run Configuration" tab.

weIMPUTE

Operation Modules My Calculations My Files

Operation Configuration

Run Configuration

What is weIMPUTE

weIMPUTE is a web-based imputation GUI, weIMPUTE, which supports multiple software including SHAPEIT, Eagle, Minimac4, Beagle, and IMPUTE2 for genotype phasing and imputation. weIMPUTE has a whole workflow including quality control and data format converting that make the process of imputation accessible to both novice and advance users.

As an example of using Eagle for phasing and Beagle for imputation, click in the order indicated by the diagram.



Operation Configuration

Start Running

1. Done

2. Eagle

3. Done

4. Beagle

5. Complete

Operation Configuration

Reference panel files

Upload files File upload View uploaded files

Haplotype Phasing Program

Eagle Shapeit

Reference panel files genetic_map_hg3

No selection

Genotype Imputation Program

Beagle Impute2 Minimac4

Reference panel files g

No selection No selection

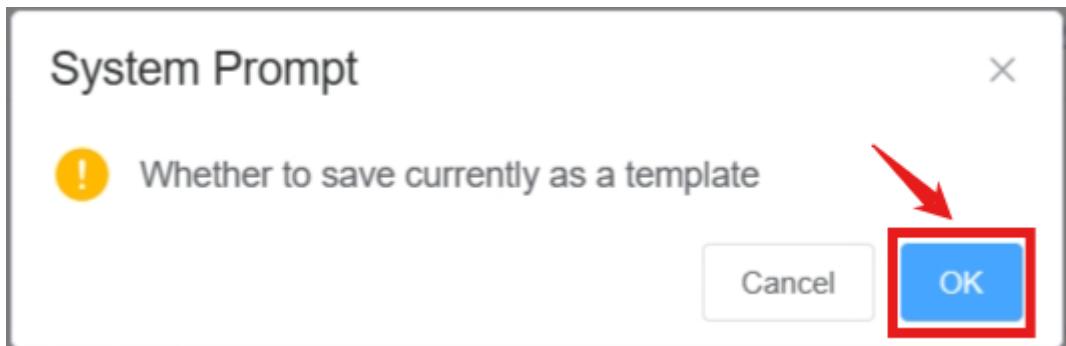
Done

Done

Complete

The screenshot shows the 'Operation Configuration' page with three main sections: 'Reference panel files', 'Haplotype Phasing Program', and 'Genotype Imputation Program'. In the 'Reference panel files' section, there is a 'File upload' button and a 'View uploaded files' button. In the 'Haplotype Phasing Program' section, 'Eagle' is selected (radio button highlighted). In the 'Genotype Imputation Program' section, 'Beagle' is selected (radio button highlighted). Each section has a 'Done' button at the bottom right. A green vertical line with checkmarks connects the top of each section to the 'Done' buttons. A red box highlights the 'Done' button in the 'Haplotype Phasing Program' section. A red arrow points to the 'Done' button in the 'Genotype Imputation Program' section. A red box highlights the 'Done' button in the 'Genotype Imputation Program' section. A red box highlights the 'Complete' button at the bottom right.

At the pop-up window, click "OK" to save the template for future use.



Then, return to the top of the page and click "Start Running".

At the pop-up window, name the job and add the remark, then click "OK" to save.



Click on the left-hand side "Operation Records", select the project you just created, and click "Begin to run" to enter the project.

(Note: Make sure that all other projects, except the one you just created, have a status of "Done". If not, click "Stop" or "Delete" to stop or delete other projects.)

	Start time	Operation name	Create by	Status	Completion time	Remark	Operate
<input type="checkbox"/>	2023-08-28 22...	quick_start	admin	Unfinished		demo chr2	<input type="button"/> Stop <input type="button"/> Delete
<input type="checkbox"/>	2023-08-23 08...	test	admin	Done	2023-08-23 0...		<input type="button"/> Stop <input type="button"/> Delete
<input type="checkbox"/>	2023-07-25 03...	Demo_test	admin	Done	2023-07-25 0...	SHAPEIT+MI...	<input type="button"/> Stop <input type="button"/> Delete

Quality Control before Genotype Imputation

Click on the "Quality Control before Genotype Imputation" tab.

Upload File

Click "Select a file" and choose the previously downloaded chr2.vcf.gz file from your local computer.

Click "Use private data" and select the downloaded refile.vcf.gz file from your local computer.

Click "Use private data" again and choose the downloaded refile.vcf.gz file from your local computer.

Click "Next", wait for a moment, then click "Reload results status" to proceed to the next step.

Quality Control before Genotype Imputation

① Upload File

Input file 1. Select a file

Phasing reference file 2. Use private data Use public data

Imputation reference file 3. Use private data Use public data

4. Next

Extracting and Judging Chromosomes

Since the genomic sequence versions of the demo files are consistent, LiftOver conversion is not needed.

Click on the "chromosomal transformation judgment" tab and Click on the "Ignore" , it will skip the LiftOver step and jump to segment chromosomes.

2 Extracting and Judging Chromosomes

Chromosome extraction 2

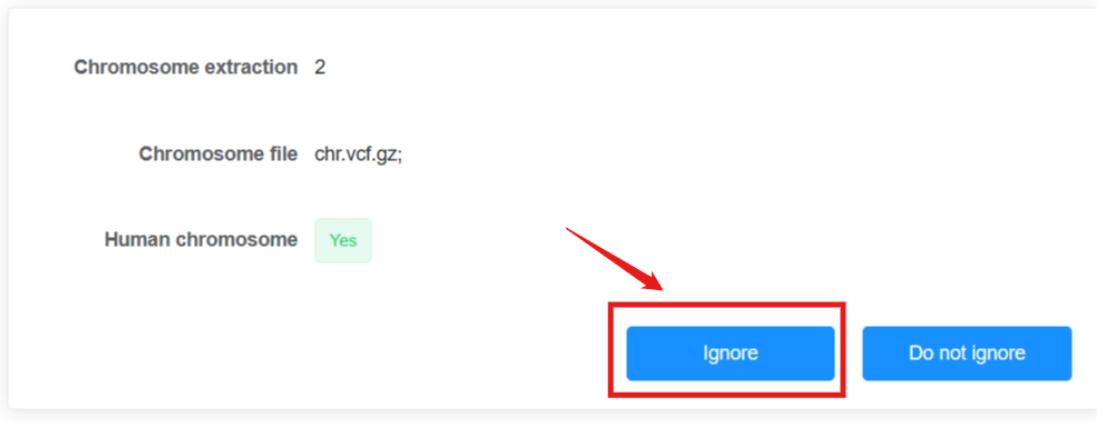
Chromosome file chr.vcf.gz;

Human chromosome Yes

Chromosome 2

No segment Chromosome transformation judgment

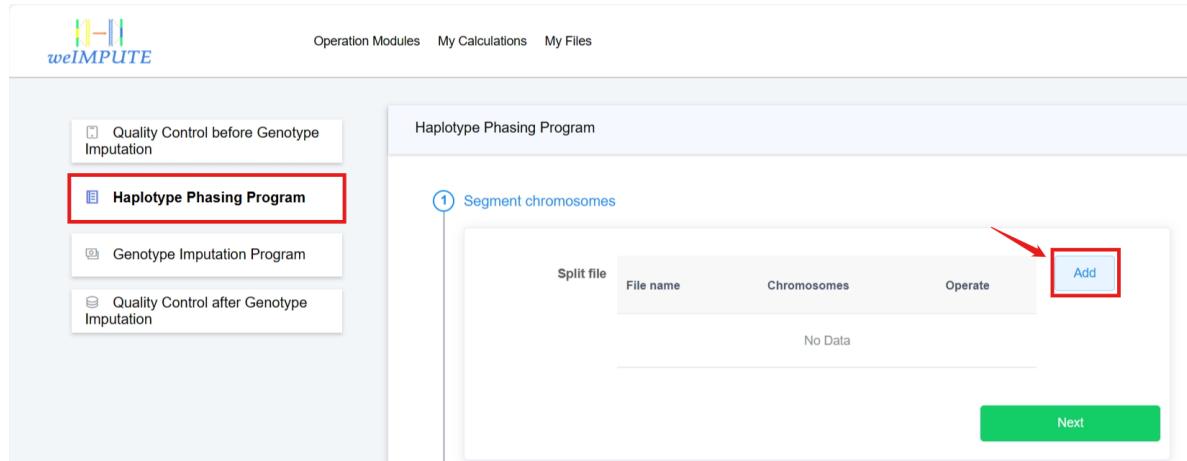
② Extracting and Judging Chromosomes



Haplotype Phasing Program

Click on the "Haplotype Phasing Program" tab on the left-hand side.

Click on the "Add" tab.



In the pop-up window, move the chromosome number you want to impute from List 1 to List 2 and give it a name.

Click on the "OK" tab.

Add split file

X

3. The segmented name

1. 2

2. < >

List 1 0/1
Please enter the chromo

List 2 0/0
Please enter the chromo
No data

4. OK Cancel

Ensure there is only one chromosome file, then click "Next".

Wait for a moment, then click "Reload results status" to proceed to the next step.

① Segment chromosomes

Split file		
File name	Chromosomes	Operate
chr2	2	<input type="button" value="Delete"/>

Phasing

Click on the "Start judging" tab.

② eagle

Judge if passed

Select the Map file "genetic_map_hg38_withX.txt.gz" that has been pre-configured on the server.

Then, click "Next" to start phasing.

② eagle

Phased status Unphased

1. Map file Please select

genetic_map_hg38_withX.txt.gz

2. Next

Depending on your Internet connection and date size, it could take different times. Click on the "results status update" tab to update the results.

③ Phased File

Result file

Result file ...	Chromo...	Phasing	Start time	End time	Gene start	Gene end	Download
chr_chr2_...	2	Phasing	2023-03-...				Result Log

Results status update

Next

When more information appears, and the "Result" download button turns blue, you can click "Result" to download the phasing result file, and click "Log" to download the log file.

Click on the "Next" tab to start imputation.

③ Phased File

Result file

Result fi...	Chromo...	Phasing	Start time	End time	Gene start	Gene end	Download
chr_chr...	2	Filled	2023-0...	2023-0...	10180	33378	Result Log

Results status update

Next

Genotype Imputation Program

Click on the "Genotype Imputation Program" on the left.

No additional processing is required for the file, so simply click "Next".

Imputation

Choose the right map file and click on the "Next" tab to start imputation.

Depending on your Internet connection and date size, it could take different times.

Click on the "Results status update" tab to update the results.

When more information appears, and the "Result" download button turns blue, you can click "Result" to download the imputation result file, and click "Log" to download the log file.

③ Complete imputation

[⟳ Results status update](#)

Result file:	File name...	Imputing	Start time	Imputatio...	End time	Download
	beagle_c...	Filled	2023-08...	Done	2023-08...	↳ Log ↳ Result

[Next](#)

The main imputation service is fully complete!!!