

Quick Start Guide

Following this guide, you can complete the imputation service on the server.

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

To demonstrate sample data, you can choose to deploy it locally on your server or log in to the example website.

DemoFile Preparation

Please download the demonstration file.

[chr2.vcf.gz](#)

[refile.vcf.gz](#)

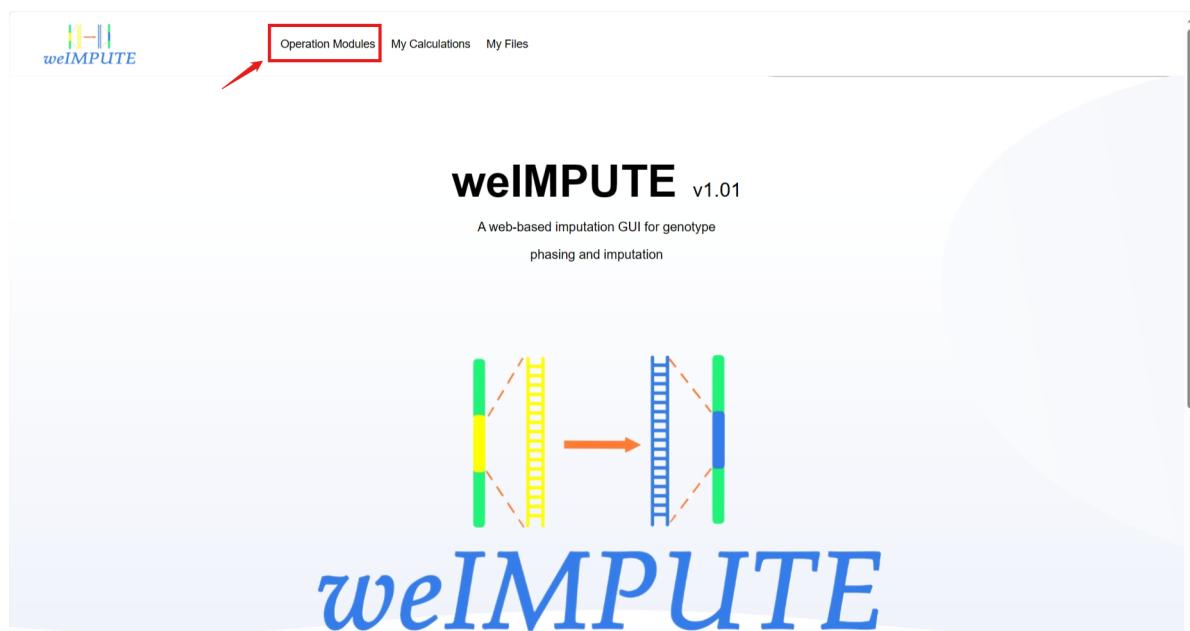
The other supporting files have been configured on the server.

Log in

Access the example server for a quick fill service.

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

Click on the "Operation Modules" tab.

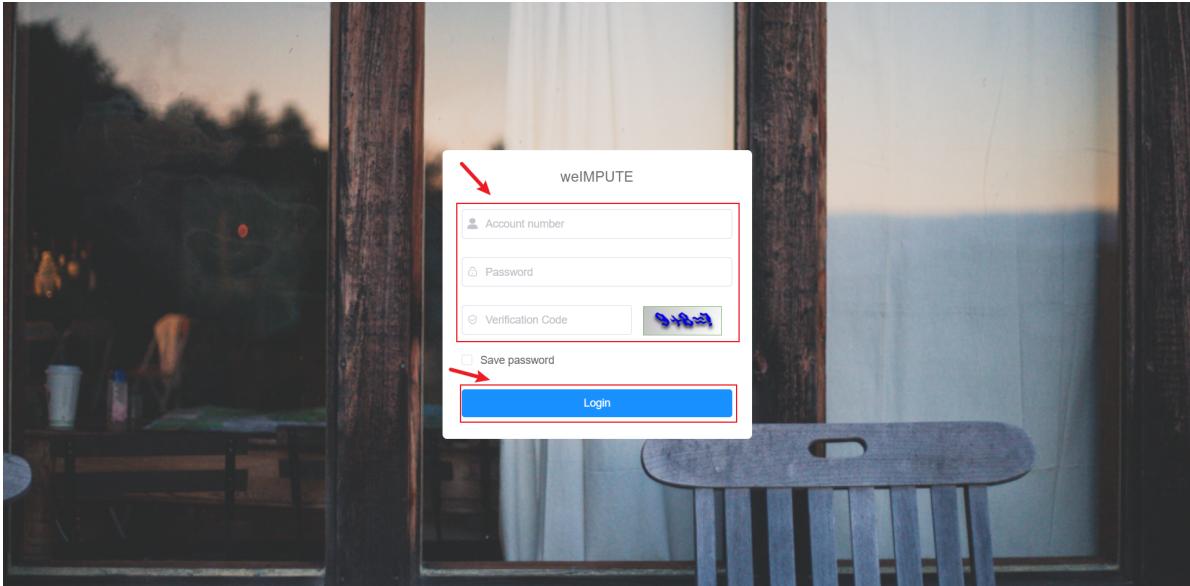


Login as admin with the default admin password:

admin

admin123

And enter the verification code.



Operation Configuration

Click on the "Run Configuration" tab.

weIMPUTE 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.

Click in the order indicated by the diagram.


[Operation Modules](#)
[My Calculations](#)
[My Files](#)

[Start Running](#)

[Operation Configuration](#)
[Operation Records](#)

Operation Configuration

1. Done

Reference panel files

Upload files File upload View uploaded files

2. Eagle

Eagle toggle

Reference panel files | genetic_map_hg3 ✓

No selection

3. Done

Genotype Imputation Program

4. Beagle

Beagle toggle

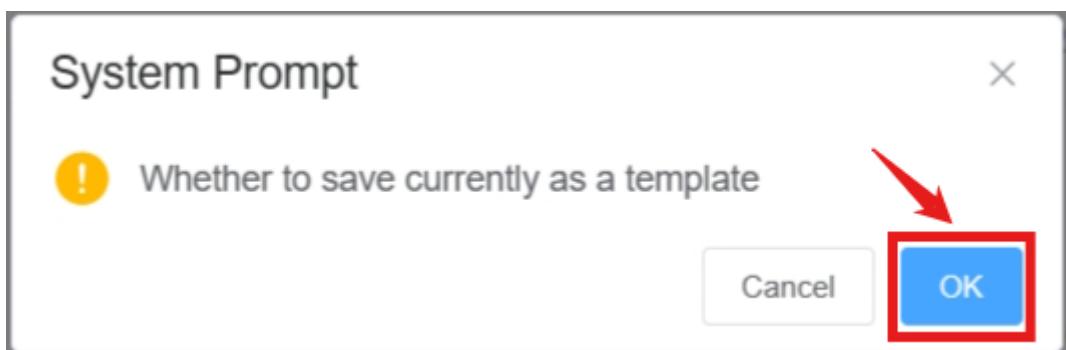
Reference panel files | g ✓

No selection

No selection

5. Complete

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.

The screenshot shows the 'Quality Control before Genotype Imputation' interface. On the left, there's a sidebar with three options: 'Haplotype Phasing Program', 'Genotype Imputation Program', and 'Quality Control after Genotype Imputation'. The third option is currently selected. The main area has a title 'Quality Control before Genotype Imputation' and a step-by-step process. Step 1 is 'Upload File'. It contains three sub-steps: 1. 'Input file' with a 'Switch Type' button and a red box around the 'Select a file' button; 2. 'Phasing reference file' with 'Use private data' and 'Use public data' buttons, and a red box around 'Use private data'; 3. 'Imputation reference file' with 'Use private data' and 'Use public data' buttons, and a red box around 'Use private data'. Step 4 is a green 'Next' button at the bottom right.

Extracting and Judging Chromosomes

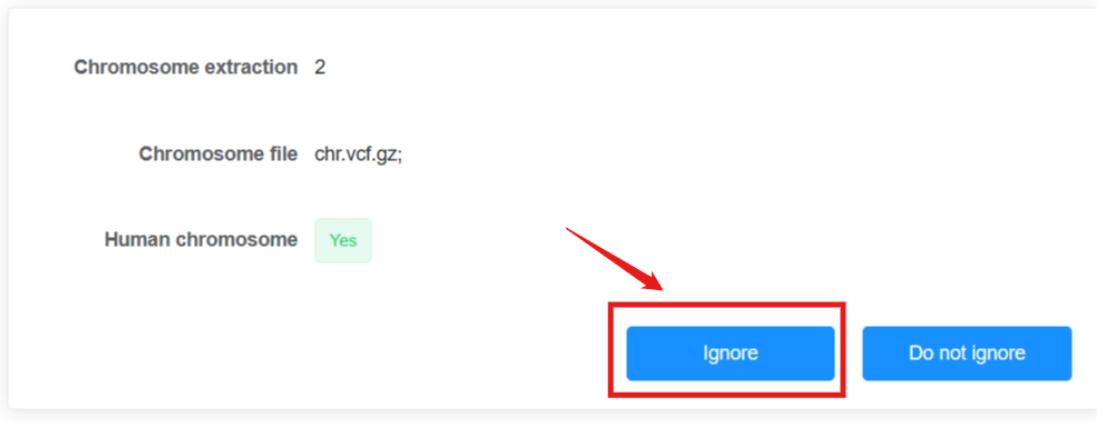
The demo file versions are consistent, and LiftOver conversion is not needed.

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

The screenshot shows the 'Chromosome extraction 2' interface. It has a title 'Chromosome extraction 2' and a sub-section 'Chromosome file: chr.vcf.gz;'. Below that, there's a 'Human chromosome' section with a 'Yes' button. Underneath is a 'Chromosome' dropdown menu set to '2'. At the bottom, there are two buttons: a red 'No segment' button and a green 'Chromosome transformation judgment' button. A red arrow points from the text above to this green button.

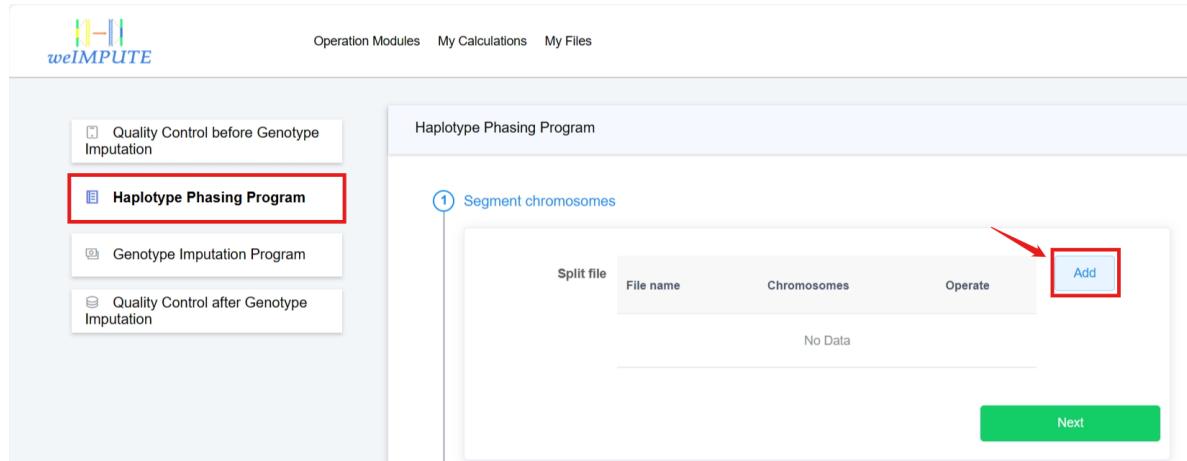
② Extracting and Judging Chromosomes



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. 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 preconfigured 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.

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

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!!!