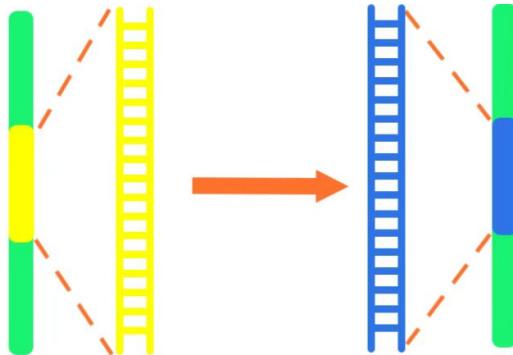


# weIMPUTE: A User-Friendly Web-Based Genotype Imputation Platform

A web-based imputation GUI, weIMPUTE, which supports multiple software including SHAPEIT, Eagle2, Minimac4, Beagle5, and IMPUTE2 for genotype phasing and imputation.



# *weIMPUTE*

This repository provides a Docker Image to run your own instance of the weIMPUTE Imputation Server.

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# Installation

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## Requirements

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[Docker](#) must be installed on your local computer. Please following the [guide](#) step by step to install the latest version.

## Deploy

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## Download

After the successful installation of Docker, Download the suanfa\_v6.tar file from

[http://144.34.160.128:82/suanfa\\_v6.tar](http://144.34.160.128:82/suanfa_v6.tar)

## Deploy weIMPUTE on CentOS

To get started with weIMPUTE on CentOS, make sure your firewall allows ports **9083** and **9085** to be open. You can follow these steps:

```
sudo firewall-cmd --permanent --add-port=9083/tcp
sudo firewall-cmd --permanent --add-port=9085/tcp
sudo firewall-cmd --reload
```

Now, ports 9083 and 9085 have been added to the CentOS firewall rules and are allowed through the firewall.

Run the commands as follow:

```
sudo docker load -i suanfa_v6.tar  
sudo docker run -d --privileged --net=host suanfa:v6
```

It may take several minutes depending on your internet connection and computer resources. Then, your imputation server instance is ready and you are able to access it on.

<http://IP:9083>

and

<http://IP:9085>

IP refers to the IP address of your local computer where weIMPUTE is installed.

## Deploy weIMPUTE on Ubuntu

To get started with weIMPUTE on Ubuntu, make sure your firewall allows ports **9083** and **9085** to be open. You can follow these steps:

```
sudo ufw allow 9083/tcp  
sudo ufw allow 9085/tcp  
sudo ufw enable
```

Now, ports 9083 and 9085 have been added to the Ubuntu firewall rules and are allowed through the firewall.

Run the [DeployonUbuntu.sh](#) command.

Save the file 'DeployonUbuntu.sh' in the same folder as 'suanfa.txt,' then change the execute permission of 'DeployonUbuntu.sh' using the command:

```
sudo chmod 774 DeployonUbuntu.sh
```

After that, execute it using the following command.

```
./DeployonUbuntu.sh
```

It may take several minutes depending on your internet connection and computer resources. Then, your imputation server instance is ready and you are able to access it on.

<http://IP:9083>

and

<http://IP:9085>

IP refers to the IP address of your local computer where weIMPUTE is installed.

## Deploy weIMPUTE on Windows

Ensure that Docker is installed correctly on Windows, and either disable the firewall or open ports 9083 and 9085.

Run the commands as follow:

```
docker load -i suanfa_v6.tar  
docker run -d --privileged -p 9083:9083 -p 9085:9085 --net=bridge suanfa:v6
```

It may take several minutes depending on your internet connection and computer resources. Then, your imputation server instance is ready and you are able to access it on.

<http://localhost:9083>

and

<http://localhost:9085>

## Example Website

---

If you deploy correctly, the local service should match the example website URL.

<http://144.34.160.128:80>

<http://144.34.160.128:81>

Enter the verification code and login as admin with the default admin password:

admin

admin123

## File requirements

---

### Main imputation services

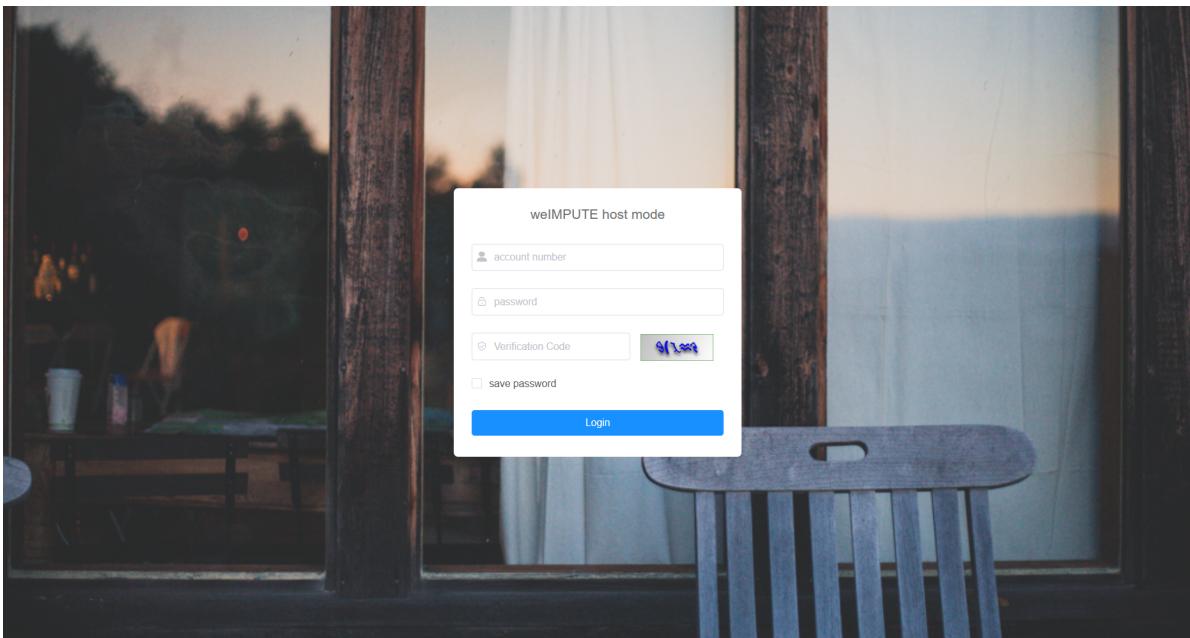
---

- All the genotype files for imputation must be a separated vcf.gz file for each chromosome.
- Variations must be sorted by genomic position.

## Admin Data Preparation

---

Access the admin page on <http://IP:9085>.



Enter the verification code and login as admin with the default admin password:

admin

admin123

## MAP files

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Before using it, the admin needs to upload the map file. A genotype map file is a file used in biological and genetic research, containing information about genotype data for individuals or populations.

Map id	Map name	Software name	File name	File Path	Remarks	Operation
g38.txt	g38.txt	Impute2	g38.txt	/upload/2022/11/18/6ed7...	g38.txt	<a href="#">Delete</a>
g38_chr2.txt	g38_chr2.txt	Shapeit	g38_chr2.txt	/upload/2022/11/18/52eb...	g38_chr2.txt	<a href="#">Delete</a>
plink chr2.GRCh38.map	plink chr2.GRCh38.map	Beagle	plink chr2.GRCh38.map	/upload/2022/11/18/ec06...	plink chr2.GRCh38.map	<a href="#">Delete</a>
genetic_map_hg38_withX.t xt.gz	genetic_map_hg38_withX.t xt.gz	eagle	genetic_map_hg38_withX.t xt.gz	/upload/2022/11/18/b770...	genetic_map_hg38_withX.t xt.gz	<a href="#">Delete</a>
genetic_map_hg38_withX.t xt	genetic_map_hg38_withX.t xt	Minimac4	genetic_map_hg38_withX.t xt	/upload/2022/11/18/ac6e...	genetic_map_hg38_withX.t xt	<a href="#">Delete</a>

Click on the "**File upload**" tab and the "**New**" tab , fill in relevant information. You have to choose the right imputation software from Eagle, Shapeit, Beagle, Impute, or Minimac.

## Add map file

X

Map name	genetic_map_hg38_withX.txt.gz
Map file name	genetic_map_hg38_withX.txt.gz
Software name	eagle
File name	genetic_map_hg38_withX.txt.gz
Pathway	<input type="button" value="Select File"/> genetic_map_hg38_withX.txt.gz
Chromosome number	X
Note	genetic_map_hg38_withX.txt.gz

## Reference genotype data

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The reference genotype data owner can choose to install weIMPUTE to the server or workstation and release web-based imputation service to public users, where the reference data could be used for imputation without sharing. weIMPUTE is a comprehensive imputation platform that provide an easy-to-use solution for the users from a range of research fields. Users can easily build their own imputation server using weIMPUTE cross different operation system.

The screenshot shows the weIMPUTE web interface. The left sidebar has links for Home, System management..., Basic directory, File upload, and Reference ... (which is currently selected). The main content area is titled 'Reference file' and shows a table with one row labeled 'No Data'. There are buttons for '+ New' and 'Delete' at the top of the table. A search bar is located above the table.

Click on the "**Reference file**" tab and the "**New**" tab , fill in relevant information. You have to choose the correct format from .vcf.gz, .m3vcf.gz (Minimac 4), or .zip (Shapeit).

Add reference file management

**File name** reference\_demo\_chr2.vcf.gz

**File type** vcf.gz

**File path** [Pick File](#)

refile.vcf.gz

**Chromosome** 2

**Note** demo

**OK** **Close**

For Minimac4, it is recommended that the data format of the reference panel be in M3VCF format. You can convert it from VCF format to M3VCF format in advance using Minimac3 or m3vcftools. If you choose to use the VCF format directly, that's also possible, as the built-in Minimac3 will automatically convert it to M3VCF. However, please be aware that this will take more time.

## User management

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Click on the "**User management**" tab and the "**New**" tab , fill in relevant information.

The screenshot shows the "User management" section of the weIMPUTE software. The left sidebar has categories like Home, System management, User management (which is selected and highlighted in blue), and Log management. The main area has a search bar with fields for "Please enter a name", "User ID", "Status", and "Create date". Below the search are buttons for "+ New", "Search", "Reset", "Revise", "Delete", "Input", and "Export". A table lists three users:

	User ID	User Name	Status	Create date	Operation
<input type="checkbox"/>	2	ry	<input checked="" type="checkbox"/>	2021-12-31 09:52:47	<a href="#">Revise</a> <a href="#">Delete</a> <a href="#">More</a>
<input type="checkbox"/>	3	comadmin	<input checked="" type="checkbox"/>	2022-09-30 10:35:15	<a href="#">Revise</a> <a href="#">Delete</a> <a href="#">More</a>
<input type="checkbox"/>	8	lml	<input checked="" type="checkbox"/>	2023-03-01 17:24:23	<a href="#">Revise</a> <a href="#">Delete</a> <a href="#">More</a>

At the bottom, there are pagination controls: "Total 3", "10/page", and "Go to 1".

To ensure system security, you must select a user role: "Administrator users" or "Ordinary users"\*\*! !\*\*

Add

* User nickname	testname	Department	Ordinary users
Phone number	Please enter Phone number		
* UserName	test	* Password	*****
User gender	Please select		
Role	Ordinary users		
Remarks	test		

State  Normal  Closed

OK Cancel

Click on the "**More**" tab and the "**Reset**" tab, you can reset the password.

Remind

Please input new passport

OK Cancel

Click on the "**More**" tab and the "**Assign**" tab, You can change account registration permissions.

Home / Assign ID level

nickName	test001	Account	test001	
Serial	Role number	Role name	Permission character	Creation time
1	2	Ordinary users	common	2021-12-31 09:52:48
2	3	Administrator users	platformManager	2022-09-30 10:33:05

Total 2 10page < > Go to 1

Submit Return

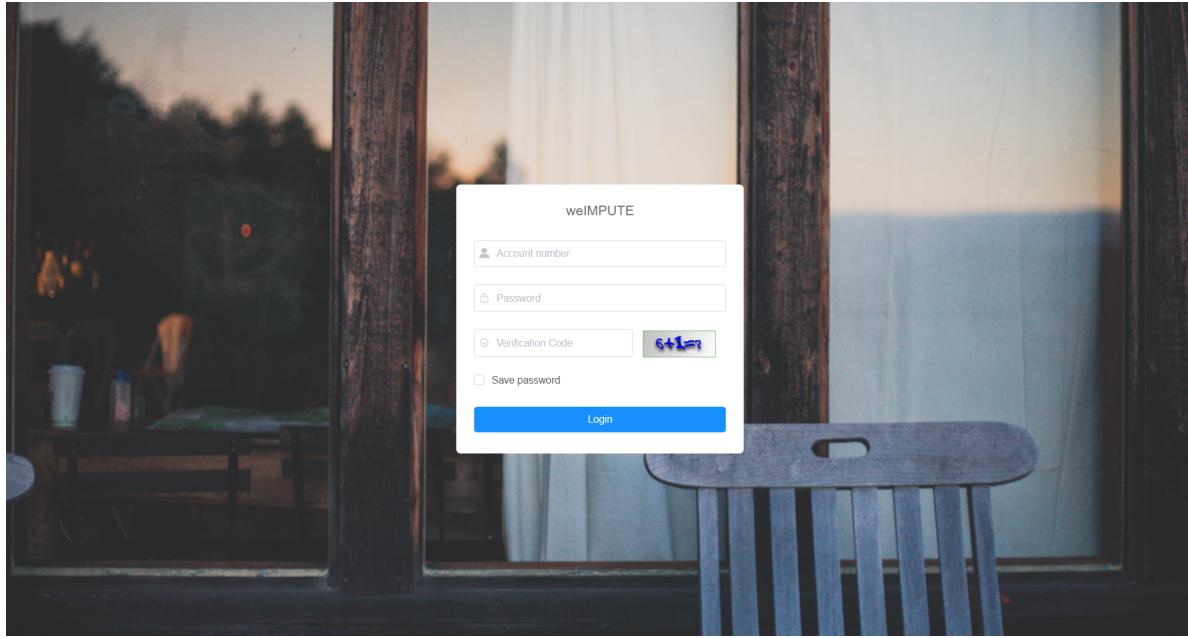
# Step By Step Guide

## Login

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Your Imputation Server instance is ready and you are able to access it on <http://IP:9083>.

Click on the **login** tab and login as **user** with the password which the admin set. If you are the admin ,you can login as **admin** with the admin password .



## Setup your first imputation job

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Click on the **Operation Configuration** tab and you can now start a job by clicking on the **Run Configuration** tab.



The screenshot shows the weIMPUTE interface. On the left, there's a sidebar with two tabs: "Operation Configuration" (selected) and "Operation Records". Below the tabs is a red "Run Configuration" button. The main content area has a title "What is weIMPUTE" and a detailed description of the software's features and workflow.

## LiftOver files

If the Genetic data which will be imputed has the different genomic reference sequence version number, you need to click on the **File update** tab to upload the LiftOver file.

### 1 Reference panel files

This screenshot shows a modal window for uploading reference panel files. It includes a "Upload files" input field, a "File upload" button, a "View uploaded files" button, and a "Done" button.

You can choose to expose the data or not by choose the **Public or not Public**.

LiftOver files can be uploaded either from your local disk or switch type. In both cases, several one file or several one location can be selected at once.

### File Upload

A form field labeled "Data Name" with a placeholder "Please enter the data name".

A dropdown menu labeled "Public or not Public" with an option "Please choose".

A section labeled "File" containing a "switchType" button and a "Select a file" button.

A form field labeled "Remark" with a placeholder "Please enter the data name".

OK

Cancel

## View Uploaded Files

<input type="checkbox"/>	Data Name	File Name	File Address	Public or not Public	Remark	Operate
<input type="checkbox"/>	hg19ToHg38.over.chain.gz	hg19ToHg38.over.chain.gz	/upload/2022/1...	Public	undefined	Delete
<input type="checkbox"/>	hg38ToHg19.over.chain.gz	hg38ToHg19.over.chain(1).gz	/upload/2022/1...	Not Public	hg38ToHg19.o...	Delete
<input type="checkbox"/>	hg19ToHg38.over.chain.gz	hg19ToHg38.over.chain.gz	/upload/2023/0...	Public	hg19ToHg38.o...	Delete

Total 3    10/page    <    **1**    >    Go to     Cancel

Click on the **Done** tab to start the next step.

## Choose Haplotype Phasing Program

Choose the Phasing program from eagle, Shapeit and use the right MAP file the admin uploaded.

② Haplotype Phasing Program

Eagle     Shapeit

Eagle

Reference panel files

No selection

**Done**

Click on the **Done** tab to start the next step.

## Choose Genotype Imputation Program

Choose the Imputation program from Beagle, Impute 2, Minimac 4, and use the right MAP file the admin uploaded.

③ Genotype Imputation Program

Beagle

Reference panel files: genetic

No selection

No selection

Complete

Click on the **Done** tab and Click on the **Start Running** tab.

Operation Configuration

Start Running

And then name it.

Start Running

Operation name: eagle-Beagle\_demo

Remark: chr2

OK Cancel

Click on the **Operation Records** tab , choose the job and click on the **Begin to run** tab.

weIMPUTE

Operation Modules My Calculations My Files

Operation Configuration

Operation Records

+ Begin to run

Start time	Operation name	Create by	Status	Remark	Operate
2023-03-04 15:4...	eagle-Beagle_d...	test001	Unfinished	chr2	<input type="button" value="Stop"/> <input type="button" value="Delete"/>

## Start your imputation job

### Quality Control before Genotype Imputation

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## Upload File

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

The screenshot shows a user interface for a bioinformatics tool. On the left, there's a sidebar with a tree view containing nodes for 'Quality Control before Genotype Imputation', 'Haplotype Phasing Program', 'Genotype Imputation Program', and 'Quality Control after Genotype Imputation'. The main panel is titled 'Quality Control before Genotype Imputation' and has a sub-section titled '① Upload File'. This section includes fields for 'Input file' (with a 'Select a file' button), 'Phasing reference file' (with 'Use private data' and 'Use public data' buttons), and 'Imputation reference file' (with 'Use private data' and 'Use public data' buttons). A green 'Next' button is located at the bottom right of the main panel.

VCF files can be uploaded either from your local disk or switch Type. In both cases, several one file or several one location can be selected at once. Please make sure that all files fulfill the [requirements](#).

### input file

#### Upload VCF files from your computer

When using the file upload, data is uploaded from your local file system to weIMPUTE Imputation Server. By clicking on **Select a file** an open dialog appears where you can select your VCF files.

#### Import VCF files via Path address

Another convenient way to use your data is by importing it directly from the server.

To import a file using a file path address within a Docker container, you will need to first upload the file from the server to the Docker container. This can be done using the "docker cp" command, which will copy the file from the server to the specified destination within the running Docker container. Here's an example command:

```
docker cp /path/to/local/file container_id:/path/to/container/destination
```

In this command, "/path/to/local/file" is the path to the local server file, "container\_id" is the ID of the running Docker container, and "/path/to/container/destination" is the destination path within the container where the file will be copied to.

Once you have copied the file to the container, you can use the container's internal file path address to import the file within your application.

After clicking on the **Switch Type** button, a new dialog appears where you can enter your path address of your file.

Here's an example path address:

/path/to/container/destination/filename

In this example, "/path/to/container/destination" is the path where the file was copied to within the container, and "filename" is the name of the file. A path can be only point to one file.

If the file is large, it is recommended to upload the file to the server first, and then copy it from the server to the Docker container.

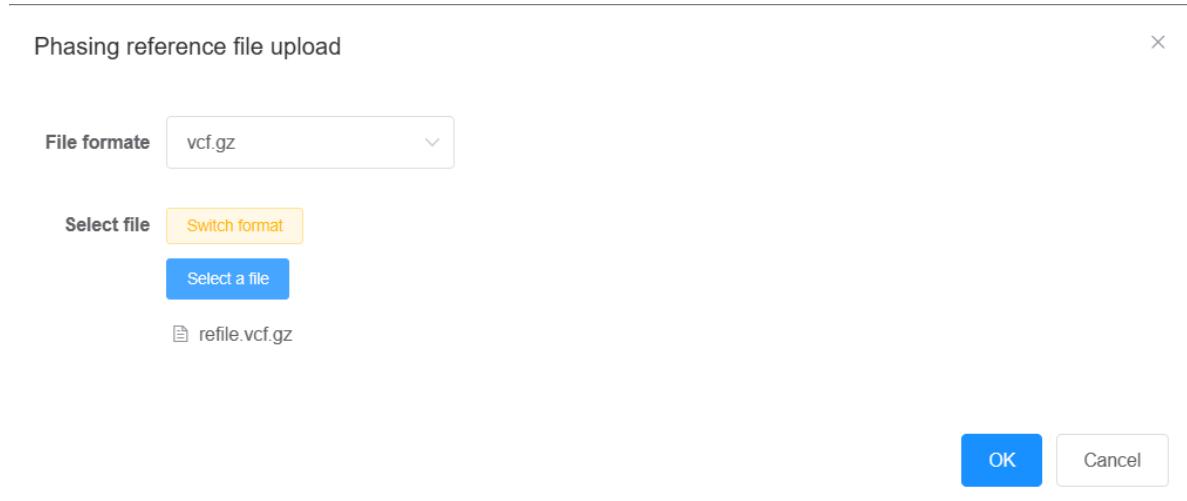
## Reference

You can choose to use a personal reference file or a public reference file.

### personal reference file

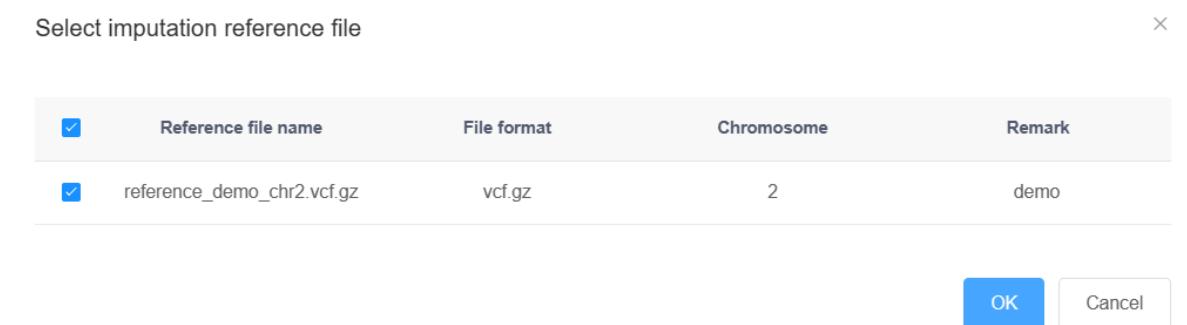
Click on the **Use personal date** tab. You have to choose the right format from .vcf.gz, .m3vcf.gz (Minimac 4), .zip (Shapeit).

You can also upload either from your local disk or switch Type by click on the **Select a file** button or the **Switch Type** button. It is same as [input file](#).



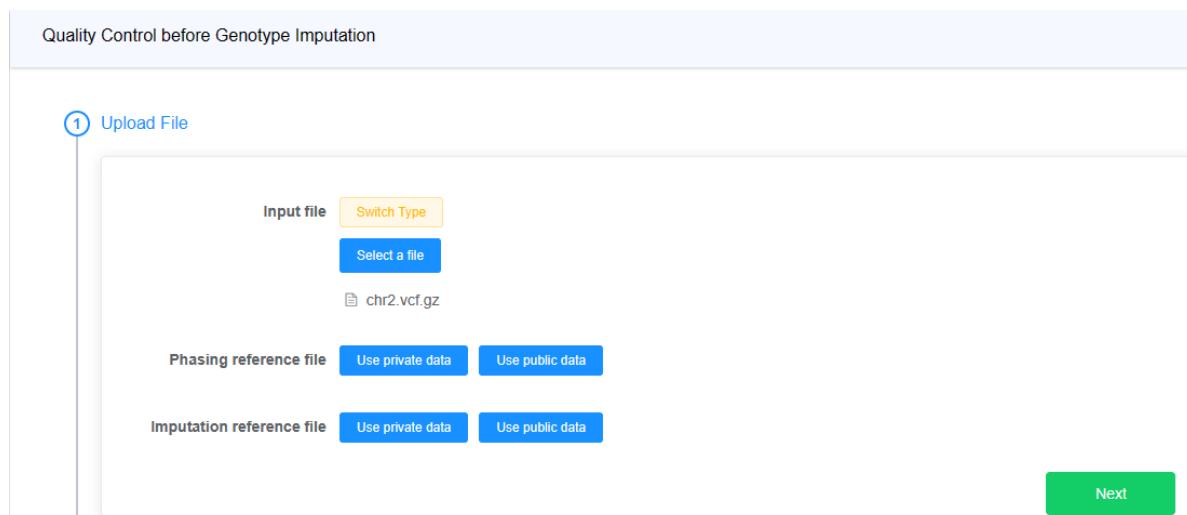
### public reference file

Click on the **Use public date** tab and choose the right reference that the admin uploaded.



Because it is divided into two phase-filled parts, the reference panel file is uploaded separately.

Click on the **Next** tab to upload them.



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

Upload File

Input file Switch Type

Select a file

Phasing reference file Use private data Use public data

Imputation reference file Use private data Use public data

Reload results status

Click on the **Reload results status** tab until the screen shows "Complete".

Upload File

Input file Switch Type

Select a file

Phasing reference file Use private data Use public data

Imputation reference file Use private data Use public data

Complete

## Extracting and Judging Chromosomes

According to the inference files you uploaded, you can choose to split chromosomes or using LiftOver to convert to different map version:

### ② Extracting and Judging Chromosomes

Chromosome extraction 2

Chromosome file chr.vcf.gz;

Human chromosome

Yes

Chromosome

2

No segment

Chromosome transformation judgment

- If the Genetic data which will be imputed has the same genomic reference sequence version number and has been segmented, click on the **chromosomal transformation judgment** tab and Click on the **Ignore**, it will skip the LiftOver step and jump to [segment chromosomes](#).
- If the Genetic data which will be imputed has the different genomic reference sequence version number, click on the **chromosomal transformation judgment** tab , click on the **chromosomal transformation judgment** and click on the **Do not ignore** it will start Transform by LiftOver.

## ② Extracting and Judging Chromosomes

Chromosome extraction 2

Chromosome file chr.vcf.gz;

Human chromosome

Yes

Ignore

Do not ignore

## Transform by LiftOver

Choose the right transformation file uploaded.

### ③ Transform by LiftOver

Chromosome file hg19ToHg38.over.chain.gz

Human chromosome

None

Start Conversion

Restart

Click on the **Start Conversion** tab to transform by LiftOver.

### ③ Transform by LiftOver

Chromosome file hg19ToHg38.over.chain.gz

Human chromosome

None

Reload results status

Restart

Wait a while, click on the **Reload results status** tab until the screen shows "**Complete**".

### ④ Transform by LiftOver

Chromosome file hg19ToHg38.over.chain.gz

Human chromosome

text.name

Complete

Restart

## Haplotype Phasing Program

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Click on the **Haplotype Phasing Program** tab.

## segment chromosomes

Click on the **Add** tab to segment chromosomes.

The screenshot shows the weIMPUTE software interface. On the left, there is a sidebar with several options: Quality Control before Genotype Imputation, Haplotype Phasing Program (which is selected and highlighted in blue), Genotype Imputation Program, and Quality Control after Genotype Imputation. The main area is titled "Haplotype Phasing Program" and contains a sub-section titled "① Segment chromosomes". This section includes a table with columns for "Split file", "File name", "Chromosomes", and "Operate". A button labeled "Add" is located at the top right of this table. Below the table, it says "No Data". At the bottom right of the main area is a green "Next" button.

Put the chromosome number you want to impute from List 1 to List 2 and name the file.

This is a modal dialog box titled "Add split file". It has a header "The segmented name" with a text input field containing "chr2". Below this are two lists: "List 1" and "List 2". "List 1" has a checkbox and "0/0" next to it, with a placeholder "Please enter the chrom" and a note "No data". "List 2" has a checkbox and "0/1" next to it, with a placeholder "Please enter the chrom" and a checked item "2". At the bottom are "OK" and "Cancel" buttons.

The page displays the chromosome. Also, you can delete it and choose another one.

Click on the **next** tab to start the next step.

The screenshot shows the "Haplotype Phasing Program" section again. The "Segment chromosomes" sub-section is visible. In the "Split file" table, there is one entry: "File name" is "chr2", "Chromosomes" is "2", and there is a "Delete" link next to the row. A "Next" button is located at the bottom right of the main area.

## Haplotype Phasing Program

### ① Segment chromosomes

Split file

File name

Chromosomes

Operate

Add

chr2

2

Delete

**Reload results status**

Wait a while, click on the **Reload results status** tab until the screen shows "**Complete**".

## Haplotype Phasing Program

### ② Segment chromosomes

Split file

File name

Chromosomes

Operate

Add

chr2

2

Delete

**Complete**

## Phasing Program

Depending on what you have chosen ([Haplotype Phasing Program](#)), the screen will show the Phasing program.

Click on the **Start judging** tab to determine whether the phasing is complete.

### ② eagle

Judge if phased

**Start judging**

Click on the **Next** tab to start the next step.

### ② eagle

Phased status

**Unphased**

Map file

genetic\_map\_hg38\_withX.b

**Jump phasing**

Advanced setup

Advanced running

**Next**

Also, you can click on the **Advanced set up** tab , Select parameters you want and click on the **Advanced running** tab.

## Phased File

Phasing is in progress, you can download the log file to monitor the running status.

The screenshot shows a user interface for a 'Phased File' task. At the top left is a blue circular icon with the number '3'. To its right is the text 'Phased File'. Below this is a table titled 'Result file'. The table has columns: 'Result file ...', 'Chromosome...', 'Phasing', 'Start time', 'End time', 'Gene start', 'Gene end', and 'Download'. A single row is present in the table, showing 'chr\_chr2\_...' in the first column, '2' in the second, 'Phasing' in the third, and '2023-03-' in the fourth. At the bottom right of the table are two buttons: a blue 'Results status update' button and a green 'Next' button.

Result file ...	Chromosome...	Phasing	Start time	End time	Gene start	Gene end	Download
chr_chr2_...	2	Phasing	2023-03-				<a href="#">Result</a> <a href="#">Log</a>

[Results status update](#) [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.

Click on the **Next** tab to start imputation.

If you just want to phase it, you can download the phasing result and [end the job](#).

This screenshot shows the same 'Phased File' results page as the previous one, but with updated data in the table. The table now shows 'Filled' in the 'Phasing' column and '10180' and '33378' in the 'Gene start' and 'Gene end' columns respectively. The other columns remain the same. The 'Results status update' and 'Next' buttons are also present at the bottom.

Result file ...	Chromosome...	Phasing	Start time	End time	Gene start	Gene end	Download
chr_chr2_...	2	Filled	2023-03-	2023-03-	10180	33378	<a href="#">Result</a> <a href="#">Log</a>

[Results status update](#) [Next](#)

## Genotype Imputation Program

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### segment chromosomes

This step is done to segment the reference panel chromosome. This step is not performed by the main imputation service.

Just Click on the **Next** tab to skip it.

The screenshot shows the 'Genotype Imputation Program' interface. On the left, there's a sidebar with tabs: 'Quality Control before Genotype Imputation', 'Haplotype Phasing Program', 'Genotype Imputation Program' (which is selected), and 'Quality Control after Genotype Imputation'. The main panel is titled 'Genotype Imputation Program' and shows step 1: 'Segment chromosomes'. It has an option 'Close job after running is done:' with a toggle switch set to off. Below it is a section 'Whether detailed segmentation:' with a button labeled 'Detailed segmentation'. A table titled 'Split file:' is present, with columns: File name, Chromos..., Start pos... (with a dropdown menu), End posit..., Split state, and Download. A message 'No Data' is shown below the table. At the bottom are two buttons: 'Results status update' and 'Next'.

## Imputation Program

Choose the right map file and enter the appropriate number of threads. The default number of threads is 4.

Click on the **Next** tab to start imputation.

The screenshot shows the 'Beagle' setup interface. Step 2 is labeled 'Beagle'. It has a 'Map file:' dropdown set to 'plink.chr2.GRCh38.map' and an 'Nthreads:' input field set to '4'. Below these are three buttons: 'Advanced setup', 'Advanced running', and 'Next'.

Also, you can click on the **Advanced set up** tab , Select parameters you want and click on the **Advanced running** tab.

## Complete imputation

When imputation is in progress, you can download the log file to monitor the running status.

The screenshot shows the 'Complete imputation' interface. Step 3 is labeled 'Complete imputation'. It displays a table of results with one entry: 'beagle\_chr...' under 'File name aft...', 'Imputing' under 'Imputing', '2023-03-04...' under 'Start time', 'Unimputed' under 'Imputation r...', and 'Download' with links to 'Log' and 'Result'. There's also a 'Results status update' button. At the bottom is a 'Next' button.

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

Click on the **Next** tab to start Quality Control.

### ③ Complete imputation

A screenshot of a web-based application interface. At the top, there is a green button labeled "Results status update". Below it is a table titled "Result file:" with columns: File name aft..., Imputing, Start time, Imputation r..., End time, and Download. A single row is shown: "beagle\_chr..." under "File name aft...", "Filled" under "Imputing", "2023-03-04..." under "Start time", "Done" under "Imputation r...", "2023-03-04..." under "End time", and two download links under "Download". At the bottom right of the table area is a green "Next" button.

If you just want to impute it, you can download the imputation result and [end the job](#).

## Quality Control after Genotype Imputation

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### Quality Control

After clicking on the ***Close job after running is done*** button and enter the appropriate number of threshold, chick on the ***Start Quality Control*** tab to Start quality control.

A screenshot of the "Quality Control after Genotype Imputation" step. On the left, there is a sidebar with tabs: "Quality Control before Genotype Imputation", "Haplotype Phasing Program", "Genotype Imputation Program", and "Quality Control after Genotype Imputation" (which is highlighted). The main panel shows the "Quality Control" tab with the following interface:

- "Close job after running is done": A toggle switch is turned on.
- "Detailed imputation results": A "Shown in detail" button.
- "Threshold": A input field containing "0.8".
- "Start quality control" and "Reload QC results" buttons.
- "Quality control results" table:

File name	Chromosome	Imputation method	QC status	Results	Download
beagle_chr...	2	Beagle	No QC	<a href="#">Download the result</a>	<a href="#">Quality inspection</a>

At the bottom right of the main panel is a green "Next" button.

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

A screenshot of the "Quality Control after Genotype Imputation" step, similar to the previous one but with updated results. The sidebar and main panel are identical, but the "Quality control results" table shows a completed job:

File name	Chromosome	Imputation method	QC status	Results	Download
beagle_chr...	2	Beagle	Completed	10000,400	<a href="#">Download the result</a>

At the bottom right of the main panel is a green "Next" button.

This result (10,000;400) means: Quality inspection according to the threshold value is filtered out of 10,000 out of 400.

You can download the quality control results.

**The main imputation service is fully complete!!!**

## Job Management

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After clicking on the **Operation Records** tab, a new screen appears which is displaying status, time and other information.

The screenshot shows a user interface for managing operation records. On the left, there's a sidebar with two tabs: 'Operation Configuration' and 'Operation Records'. The 'Operation Records' tab is selected and highlighted in blue. The main area is titled 'Operation Records' and contains a search bar with placeholder text 'Please enter the operation name', a 'Search' button, and a 'Reset' button. Below the search bar is a table with the following data:

	Start time	Operation name	Create by	Status	Completion time	Remark	Operate
<input type="checkbox"/>	2023-03-04 18:3...	test	test001	Running		002	<a href="#">Stop</a> <a href="#">Delete</a>
<input type="checkbox"/>	2023-03-04 16:2...	eagle-Beagle_d...	test001	Done	2023-03-04 18:2...	chr2	<a href="#">Stop</a> <a href="#">Delete</a>
<input type="checkbox"/>	2023-03-04 16:1...	eagle-Beagle_d...	test001	Done	2023-03-04 16:2...	chr2	<a href="#">Stop</a> <a href="#">Delete</a>
<input type="checkbox"/>	2023-03-04 15:4...	eagle-Beagle_d...	test001	Done	2023-03-04 16:1...	chr2	<a href="#">Stop</a> <a href="#">Delete</a>

### Begin to Run

Choose the job and click on the **Begin to run** tab.

### Stop

For projects in progress, if you want to force stop it, click on the **Stop** tab.

### Delete

For completed projects, if you want to delete it, click on the **Delete** tab to free up computer storage space.

## Back office management

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### Log management

#### Operation log

From this page, admins can view details such as **Operator**, **Type**, **Status**, **Operation time**, and other operation records.

You can also use the above information to quickly find out.

<input type="checkbox"/>	Log number	Operation type	Operator	Operation address	Operation location	Operation Data	Operation
<input type="checkbox"/>	1827	Revise	test001	172.16.114.192	Success	2023-03-04 18:34:06	<a href="#">Detailed</a>
<input type="checkbox"/>	1826	Revise	test001	172.16.114.192	Success	2023-03-04 18:34:06	<a href="#">Detailed</a>
<input type="checkbox"/>	1825	Revise	test001	172.16.114.192	Success	2023-03-04 16:22:59	<a href="#">Detailed</a>
<input type="checkbox"/>	1824	Revise	test001	172.16.114.192	Success	2023-03-04 16:22:59	<a href="#">Detailed</a>
<input type="checkbox"/>	1823	Revise	test001	172.16.114.192	Success	2023-03-04 16:11:19	<a href="#">Detailed</a>
<input type="checkbox"/>	1822	Revise	test001	172.16.114.192	Success	2023-03-04 16:11:19	<a href="#">Detailed</a>
<input type="checkbox"/>	1821	Revise	test001	172.16.114.192	Success	2023-03-04 15:41:51	<a href="#">Detailed</a>
<input type="checkbox"/>	1820	Revise	test001	172.16.114.192	Success	2023-03-04 15:41:51	<a href="#">Detailed</a>

## Login Log

From this page, admins can view details such as **Login address**, **User name**, **State**, **Login time**, and other login records.

You can also use the above information to quickly find out.

<input type="checkbox"/>	Access number	User name	Login address	Browser	Operating system	Login status	Login date
<input type="checkbox"/>	864	admin	172.16.114.192	Chrome 11	Windows 10	Success	2023-03-04 18:46:54
<input type="checkbox"/>	863	test001	172.16.114.192	Chrome 11	Windows 10	Success	2023-03-04 18:46:43
<input type="checkbox"/>	862	test001	172.16.114.192	Chrome 11	Windows 10	Success	2023-03-04 18:05:27
<input type="checkbox"/>	861	test001	172.16.114.192	Chrome 11	Windows 10	Success	2023-03-04 15:25:43
<input type="checkbox"/>	860	test001	172.16.114.192	Chrome 11	Windows 10	Fail	2023-03-04 15:25:20
<input type="checkbox"/>	859	admin	172.16.114.192	Chrome 11	Windows 10	Success	2023-03-04 15:24:57
<input type="checkbox"/>	858	admin	172.16.114.192	Chrome 11	Windows 10	Success	2023-03-04 14:45:54

## System monitoring

### Online users

From this page, admins can view who is online and the related information.

## Service monitoring

This page monitors information about CPU, Memory, Server information, Java Virtual Machine Information, Disk status, etc.

Attribute	Value
Number of cores	160
User usage	0%
System utilization	0%
Current idle rate	100%

Attribute	Memory	JVM
Total memory	440.35G	483M
Memory used	8.87G	317.73M
Remaining memory	431.48G	165.27M
Utilization rate	2.01%	65.78%

Server name	ubuntuserver	Operating system	Linux
Server IP	127.0.1.1	System architecture	amd64

Java name	OpenJDK 64-Bit Server VM	Java version	11.0.17
Start time	2023-02-24 09:41:53	Run time	8days, 9hours and41minutes
Installation path	/usr/lib/jvm/java-11-openjdk-amd64		
Project path	/home/suanfa		

Drive letter path	File system	Drive letter type	Total size	Available size	Used size	Percent Used
/	ext4	/	878.2 GB	301.4 GB	576.7 GB	65.67%
/boot/efi	vfat	/dev/sda1	511 MB	504 MB	6.7 MB	1.3%
/space	ext4	/dev/sdb	8313.5 GB	1753.7 GB	6559.8 GB	78.91%
/var/lib/ixcfs	fuse.ixcfs	ixcfs	0 B	0 B	0 B	0%
/media/chuaixi/001E8F771E8F650E	fuseblk	/dev/sdc1	59.8 GB	59.7 GB	96.6 MB	0.16%

## Cache monitoring

This page monitors cache information.

weIMPUTE

Home / System monitoring / Cache monitoring

Home Cache monitoring

Essential information

Redis version	4.0.9	Operating mode	Stand-alone	Port	6379	Number of clients	1
Running time (days)	100	Use memory	836.94K	Use CPU	0.41	Memory configuration	0B
Whether the AOF is on	no	Whether the RDB is done	ok	Key quantity	22	Network entrance/exit	0.00kps/0.00kps

Command statistics

Memory information

Memory consumption: 836.94K

Basic directory

System management

Online users

Service monitoring

Cache monitoring