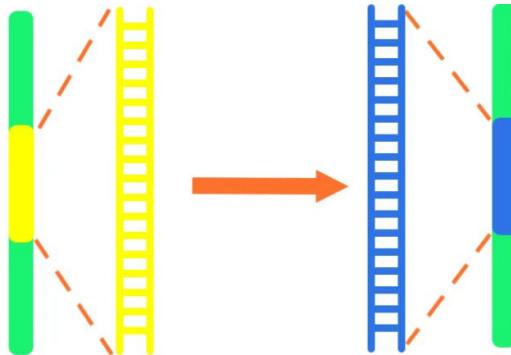


# weIMPUTE: A User-Friendly Web-Based Genotype Imputation Platform

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 weIMPUTE Imputation Server.

## Authors:

You Tang and Meng Huang

## Contact:

E-mail: [tangyou@jlnku.edu.cn](mailto:tangyou@jlnku.edu.cn)

## Contents

- [Installation](#)
  - [Requirements](#)
  - [Deploy](#)
  - [Sample Website](#)
- [File requirements](#)
  - [Main imputation services](#)
- [Admin Data Preparation](#)
  - [MAP files](#)
  - [Reference genotype data](#)
  - [User management](#)
- [Step By Step Guide](#)
  - [Login](#)

- [Setup your first imputation job](#)
  - [LiftOver files](#)
  - [Choose Haplotype Phasing Program](#)
  - [Choose Genotype Imputation Program](#)
- [Start your imputation job](#)
  - [Quality Control before Genotype Imputation](#)
  - [Haplotype Phasing Program](#)
  - [Genotype Imputation Program](#)
  - [Quality Control after Genotype Imputation](#)
- [Job Management](#)
  - [Begin to Run](#)
  - [Stop](#)
  - [Delete](#)
- [Back office management](#)
  - [Log management](#)
    - [Operation log](#)
    - [Login Log](#)
  - [System monitoring](#)
    - [Online users](#)
    - [Service monitoring](#)
    - [Cache monitoring](#)

# Installation

---

[back to top](#)

## Requirements

---

[back to top](#)

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

## Deploy

---

[back to top](#)

## 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.

Next, load the docker image and deploy the service on your server. Run the following commands:

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

It may take several minutes depending on your internet connection and computer resources. Then, your imputation server instance is ready and you can access it through the following address.

Front-end service server: <http://IP:9083>

and

Back-end Management server: <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.

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

Next, Run the [DeployonUbuntu.sh](#) command to deploy the service on your server.

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.

```
sudo sh DeployonUbuntu.sh
```

It may take several minutes depending on your internet connection and computer resources. Then, your imputation server instance is ready and you can access it through the following address.

Front-end service server: <http://IP:9083>

and

Back-end Management server: <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.

Next, 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 can access it through the following address.

Front-end service server: <http://localhost:9083>

and

Back-end Management server: <http://localhost:9085>

## Remove the service

If you no longer wish to use this service and want to uninstall it, please enter the following command:

```
sudo docker ps -a      # To query the container ID  
  
sudo docker stop <container_id>  
  
sudo docker rm <container_id>
```

## Example Website

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

Front-end service server: <http://144.34.160.128:80>

Back-end Management server: <http://144.34.160.128:81>

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

admin

admin123

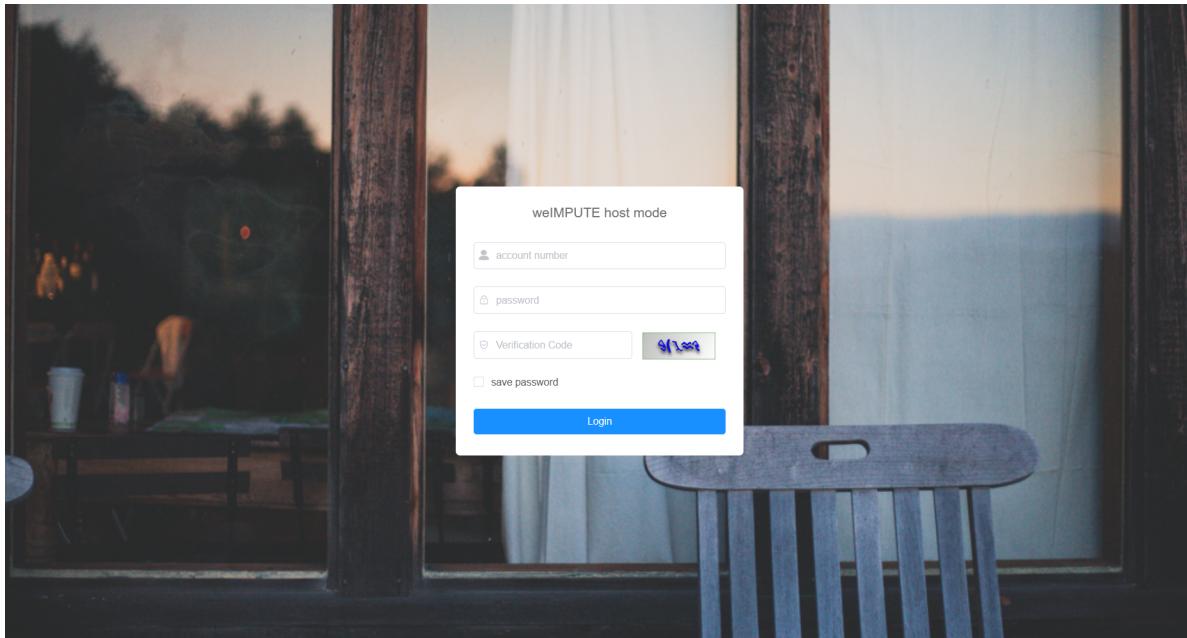
## File requirements

### 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.

# Back-end Data Preparation

Access the back-end management server page on <http://IP:9085>.



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

Account: admin

Password: admin123

## MAP files

[back to top](#)

Before using the service, map files need to be uploaded by administrators. 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	
g38_chr2.txt	g38_chr2.txt	Shapeit	g38_chr2.txt	/upload/2022/11/18/52eb...	g38_chr2.txt	
plink chr2.GRCh38.map	plink chr2.GRCh38.map	Beagle	plink chr2.GRCh38.map	/upload/2022/11/18/ec06...	plink chr2.GRCh38.map	
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	
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	

Click on the "**File upload**" tab and the "**New**" tab , fill in relevant information. You have to choose the corresponding 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"/> <input type="file" value="genetic_map_hg38_withX.txt.gz"/>
Chromosome number	X
Note	genetic_map_hg38_withX.txt.gz

## Reference genotype data

[back to top](#)

The reference genotype data owner can choose to install weIMPUTE to a server or a workstation and release the 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 provides an easy-to-use solution for the users from a range of research fields. Users can easily build their own imputation server using weIMPUTE across different operating systems.

The screenshot shows the weIMPUTE web application interface. On the left is a dark sidebar with navigation links: Home, System management, Basic directory, File upload, and Reference ... (which is currently selected). The main content area has a header 'Home / Basic directory / Reference file'. Below this is a search bar with 'File name' input ('Please enter a file name'), 'Search' button, and 'Reset' button. There are also '+ New' and 'Delete' buttons. A table follows, with columns: File name, File type, Chromosome, Note, Upload time, and Operation. The table displays the message 'No Data'.

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 it will take more time.

## User management

[back to top](#)

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

The screenshot shows the weIMPUTE software interface with the "User management" tab selected. The left sidebar includes sections for Home, System management (with User management and Log management), and System monitoring. The main content area displays a table of users with columns for User ID, User Name, Status, Create date, and Operation. The table shows three entries: User ID 2 (Name: ry, Status: Enabled, Created: 2021-12-31 09:52:47), User ID 3 (Name: comadmin, Status: Enabled, Created: 2022-09-30 10:35:15), and User ID 8 (Name: lml, Status: Enabled, Created: 2023-03-01 17:24:23). Action buttons for Revise, Delete, and More are available for each user entry. Navigation buttons at the bottom include 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		
<span style="float: right;">OK Cancel</span>			

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

Remind

Please input new passport

<span style="float: right;">Cancel OK</span>
--

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

Assign ID level					
nickName		Account		Operation	
1	<input checked="" type="checkbox"/>	2	test001	Ordinary users	common
2	<input type="checkbox"/>	3	test001	Administrator users	platformManager
Total 2	10page	<	1	>	Go to 1
<span style="float: right;">Submit Return</span>					

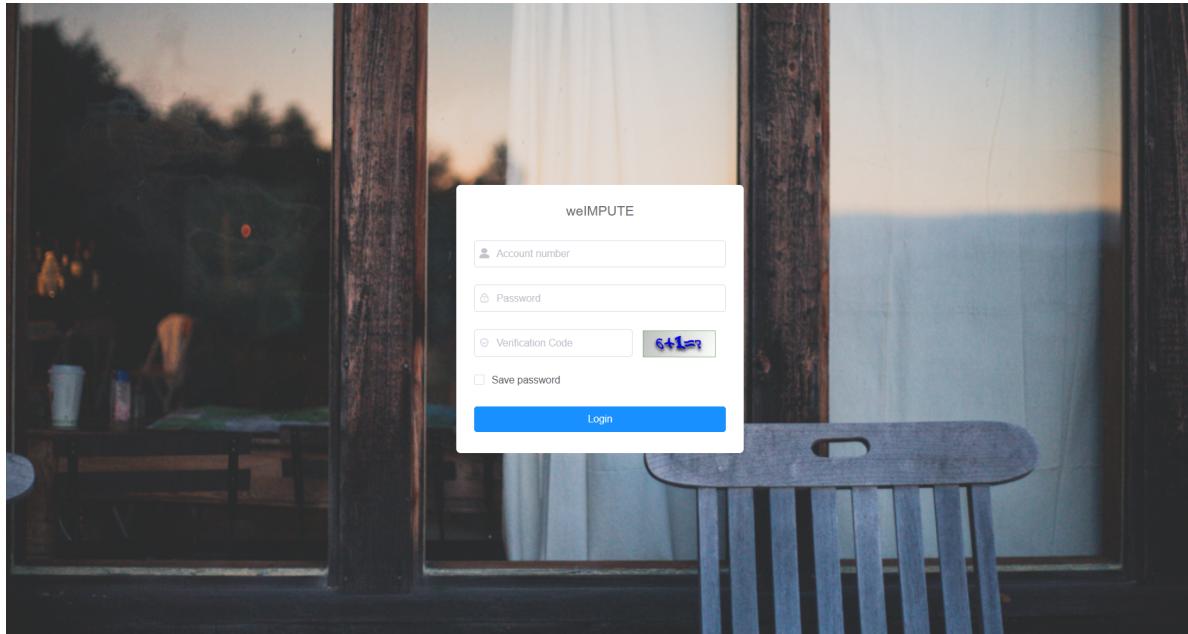
# Step By Step Guide

## Login

[back to top](#)

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

Use your account name and password to login in and then ready to explore the service.



## Setup your first imputation job

[back to top](#)

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 web-based imputation GUI. At the top, there is a navigation bar with links for 'Operation Modules', 'My Calculations', and 'My Files'. Below the navigation bar, there is a sidebar with two buttons: 'Operation Configuration' (selected) and 'Operation Records'. The main content area is titled 'Operation Configuration' and contains a button labeled 'Run Configuration'. Below this, there is a section titled 'What is weIMPUTE' which provides a brief description of the software's features and workflow.

## LiftOver files

If the Genetic data which to be imputed has a different genomic reference sequence version number. A LiftOver file comprises two primary components: coordinates from the source version (such as hg19 or GRCh37) and coordinates from the target version (such as hg38 or GRCh38). You need to click on the **File upload** tab to upload the LiftOver file.

The screenshot shows the 'File upload' tab for 'Reference panel files'. It features a large input field labeled 'Upload files' with a blue 'File upload' button next to it. To the right of the input field is a yellow 'View uploaded files' button. In the bottom right corner of the tab, there is a yellow 'Done' button.

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

LiftOver files can be uploaded either from your local disk or switch type. In either case, only a single file could be uploaded at one time.

## File Upload

X

Data Name	Please enter the data name	
Public or not Public	Please choose	
File	switchType	Select a file
Remark	Please enter the data name	
<div style="text-align: right;">OK Cancel</div>		

## View Uploaded Files

X

<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 1

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

The screenshot shows a configuration interface for the Haplotype Phasing Program. At the top, there are two radio button options: 'Eagle' (selected) and 'Shapeit'. Below this, under the 'Eagle' section, there is a toggle switch labeled 'Eagle' which is turned on (green). A dropdown menu labeled 'Reference panel files' contains the option 'genetic\_map\_hg38\_with'. To the right of the Eagle section, a message says 'No selection'. In the bottom right corner of the main area, there is a yellow 'Done' button.

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

The screenshot shows a configuration interface for the Genotype Imputation Program. At the top, there are three radio button options: 'Beagle' (selected), 'Impute2', and 'Minimac4'. Below this, under the 'Beagle' section, there is a toggle switch labeled 'Beagle' which is turned on (green). A dropdown menu labeled 'Reference panel files' contains the option 'genetic'. To the right of the Beagle section, a message says 'No selection'. To the right of the Impute2 and Minimac4 sections, both also say 'No selection'. In the bottom right corner of the main area, there is a yellow 'Complete' button.

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

The screenshot shows a 'Operation Configuration' screen. On the left, there is a text input field containing 'Operation Configuration'. On the right, there is a red 'Start Running' button.

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.

Start time	Operation name	Create by	Status	Completion time	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

[back to top](#)

#### Upload File

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

VCF files can be uploaded either from your local disk or switch Type. In either case, only a single file could be selected at one time. 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.

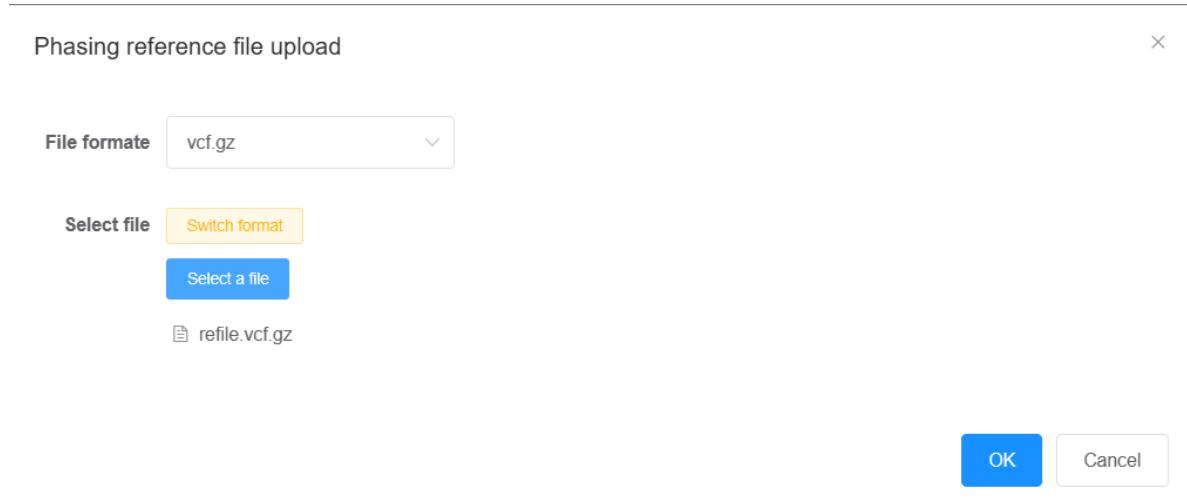
## Reference

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

### personal reference file

Click on the **Use personal data** 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 administrator uploaded.

Select imputation reference file

<input checked="" type="checkbox"/>	Reference file name	File format	Chromosome	Remark
<input checked="" type="checkbox"/>	reference_demo_chr2.vcf.gz	vcf.gz	2	demo

**OK**   **Cancel**

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

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

Quality Control before Genotype Imputation

① Upload File

Input file Switch Type

Select a file

chr2.vcf.gz

Phasing reference file Use private data Use public data

Imputation reference file Use private data Use public data

Next

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

Phasing reference file

Imputation reference file

## 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 Genotype data to 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 Genotype data to be imputed has a 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

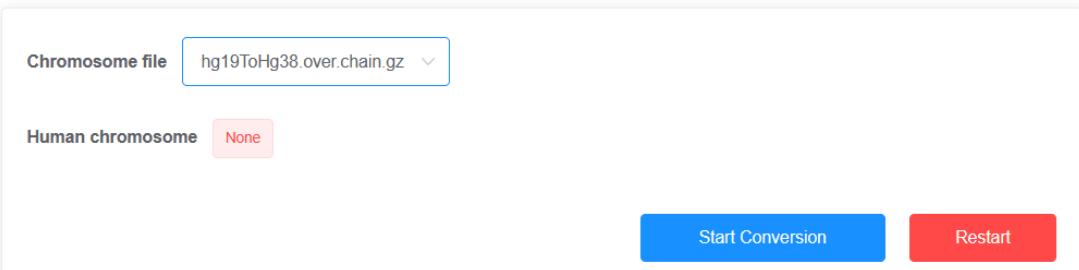
Choose the right transformation file uploaded.

③ Transform by LiftOver

Chromosome file hg19ToHg38.over.chain.gz

Human chromosome None

**Start Conversion** **Restart**



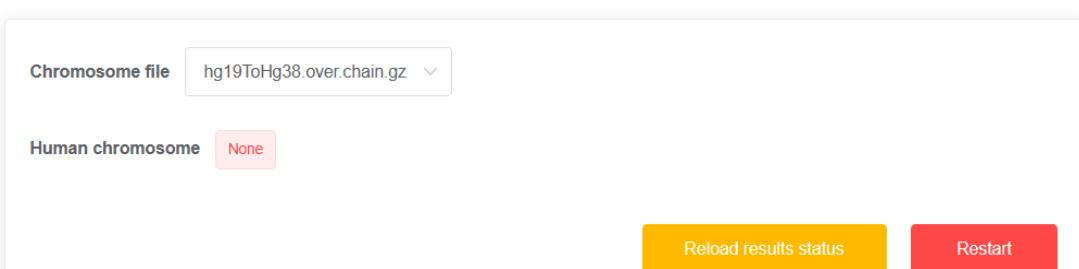
Click on the **Start Conversion** tab to transform by LiftOver.

③ Transform by LiftOver

Chromosome file hg19ToHg38.over.chain.gz

Human chromosome None

**Reload results status** **Restart**



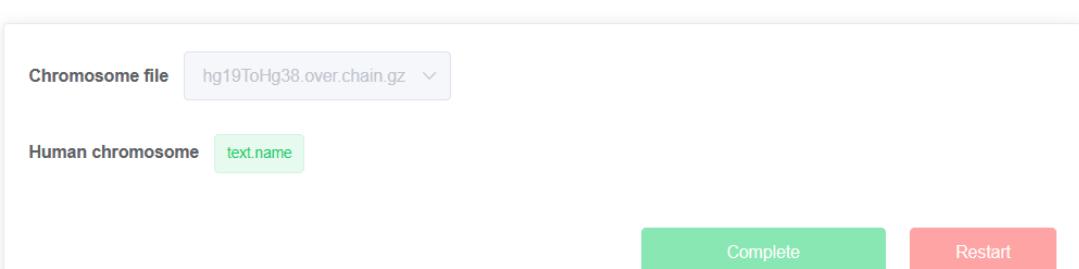
Wait a while, click on the **Reload results status** tab until the screen shows "**Complete**".

④ Transform by LiftOver

Chromosome file hg19ToHg38.over.chain.gz

Human chromosome text.name

**Complete** **Restart**



## Haplotype Phasing Program

[back to top](#)

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

### segment chromosomes

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

- Quality Control before Genotype Imputation
- Haplotype Phasing Program
- Genotype Imputation Program
- Quality Control after Genotype Imputation

## Haplotype Phasing Program

## ① Segment chromosomes

Split file

File name

Chromosomes

Operate

Add

No Data

Next

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

## Add split file

X

The segmented name

chr2

 List 1

0/0

 Please enter the chrom

No data

 List 2

0/1

 Please enter the chrom 2

OK

Cancel

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

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

## Haplotype Phasing Program

## ① Segment chromosomes

Split file

File name

Chromosomes

Operate

Add

chr2

2

Delete

Next

## 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 "Result file" table with one row. The columns are: Result file ..., Chromoso..., Phasing, Start time, End time, Gene start, Gene end, and Download. The row data is: chr\_chr2\_..., 2, Phasing, 2023-03-..., (empty), 10180, 33378. Below the table are two buttons: "Results status update" (blue) and "Next" (green).

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.

Phasing results could be obtained via the Result button.

The screenshot shows a "Result file" table with one row. The columns are: Result file ..., Chromoso..., Phasing, Start time, End time, Gene start, Gene end, and Download. The row data is: chr\_chr2\_..., 2, Filled, 2023-03-..., 2023-03-..., 10180, 33378. Below the table are two buttons: "Results status update" (blue) and "Next" (green).

## Genotype Imputation Program

[back to top](#)

### 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. The table displays 'No Data'. 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 has a 'Result file:' table with one row: 'beagle\_chr...' (File name after imputation), 'Imputing' (Imputing), '2023-03-04...' (Start time), 'Unimputed' (Imputation result), and 'Download' (with 'Log' and 'Result' links). At the top right is a 'Results status update' button. At the bottom right 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.

Imputation results could be obtained via the Result button.

## Quality Control after Genotype Imputation

[back to top](#)

### 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 four tabs: "Quality Control before Genotype Imputation", "Haplotype Phasing Program", "Genotype Imputation Program", and "Quality Control after Genotype Imputation". The fourth tab is highlighted with a blue border. The main panel shows a title "Quality Control after Genotype Imputation" and a sub-section "① Quality Control". It contains a "Close job after running is done" toggle switch (which is turned on), a "Detailed imputation results" section with a "Shown in detail" button, a "Threshold" input field set to "0.8", and two buttons: "Start quality control" and "Reload QC results". Below these is a "Quality control results" table with columns: File name, Chromoso..., Imputation ..., QC status, Results, and Download. One row is listed: "beagle\_chr..." under "File name", "2" under "Chromoso...", "Beagle" under "Imputation ...", "No QC" under "QC status", and two download links under "Results". 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 structure are the same, but the "Quality control results" table shows a different row: "beagle\_chr..." under "File name", "2" under "Chromoso...", "Completed" under "QC status", and "10000,400" under "Results". The "Download" column still contains two download links. The "Next" button at the bottom right is visible.

This result (10,000;400) means: Based on the thresholds entered by the user, 400 out of a total of 10,000 entries passed the quality inspection.

You can download the quality control results.

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

## Job Management

---

[back to top](#)

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

The screenshot shows a web-based application for managing operation records. On the left, there's a sidebar with two tabs: 'Operation Configuration' (disabled) and 'Operation Records' (selected). 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 columns: Start time, Operation name, Create by, Status, Completion time, Remark, and Operate. There are four rows of data:

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

---

[back to top](#)

## Log management

### Operation log

Administrators can access information like **Operator**, **Type**, **Status**, **Operation time**, and other Operation Records on this page.

The screenshot shows the 'Operation log' section of the weIMPUTE web interface. The left sidebar includes links for Home, System management, Log management, and Login Log. The main content area has search filters for Operator, Type, Status, and Operation time, along with buttons for Delete, Empty, and Export. A table lists 10 operation entries, each with columns for Log number, Operation type, Operator, Operation address, Operation location, Operation Data, and Operation status (Success or Failed). Each entry also has a 'Detailed' link.

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

## Login Log

Administrators can access information such as the **Login address**, **User name**, **State**, **Login time**, and other login records on this page.

The screenshot shows the 'Login Log' section of the weIMPUTE web interface. The left sidebar includes links for Home, System management, Log management, and Login Log. The main content area has search filters for Login address, User name, State, and Login time, along with buttons for Delete, Empty, and Export. A table lists 8 login attempts, each with columns for Access number, User name, Login address, Browser, Operating system, Login status, and Login date. One entry shows a 'Fail' status.

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

## System monitoring

### Online users

Administrators can see who is online and other relevant information from this page.

## 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