

Data Preparation

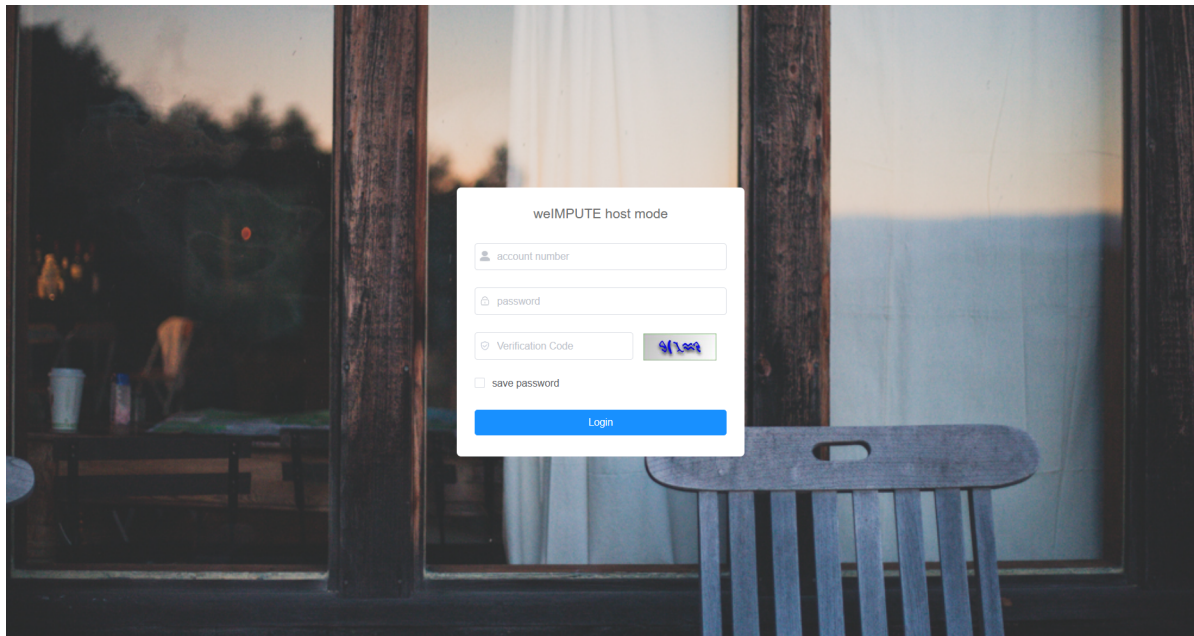
File requirements

If your team wants to use other genotype files for the filling service, you need to prepare the following files in advance:

- MAP file
- Reference Panel files
- LiftOver files
- Input files

Administrator Back-end Upload

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

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.

- Home
- System management
- System monitoring
- Basic directory
- File upload**
- Reference ...

Home / Basic directory / File upload

Software name

Please select

Map id

Please enter Map id

Search

Reset

New

Delete

Export

	Map id	Map name	Software name	File name	File Path	Remarks	Operation
<input type="checkbox"/>	g38.txt	g38.txt	Impute2	g38.txt	/upload/2022/11/18/6ed7...	g38.txt	Delete
<input type="checkbox"/>	g38_chr2.txt	g38_chr2.txt	Shapeit	g38_chr2.txt	/upload/2022/11/18/52eb...	g38_chr2.txt	Delete
<input type="checkbox"/>	plink_chr2_GRCh38.map	plink_chr2_GRCh38.map	Beagle	plink_chr2_GRCh38.map	/upload/2022/11/18/ec06...	plink_chr2_GRCh38.map	Delete
<input type="checkbox"/>	genetic_map_hg38_withX.txt.gz	genetic_map_hg38_withX.txt.gz	eagle	genetic_map_hg38_withX.txt.gz	/upload/2022/11/18/b770...	genetic_map_hg38_withX.txt.gz	Delete
<input type="checkbox"/>	genetic_map_hg38_withX.txt	genetic_map_hg38_withX.txt	Minimac4	genetic_map_hg38_withX.txt	/upload/2022/11/18/ac6e...	genetic_map_hg38_withX.txt	Delete

Total 5

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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

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

Select File

genetic_map_hg38_withX.txt.gz

Chromosome number

x

Note

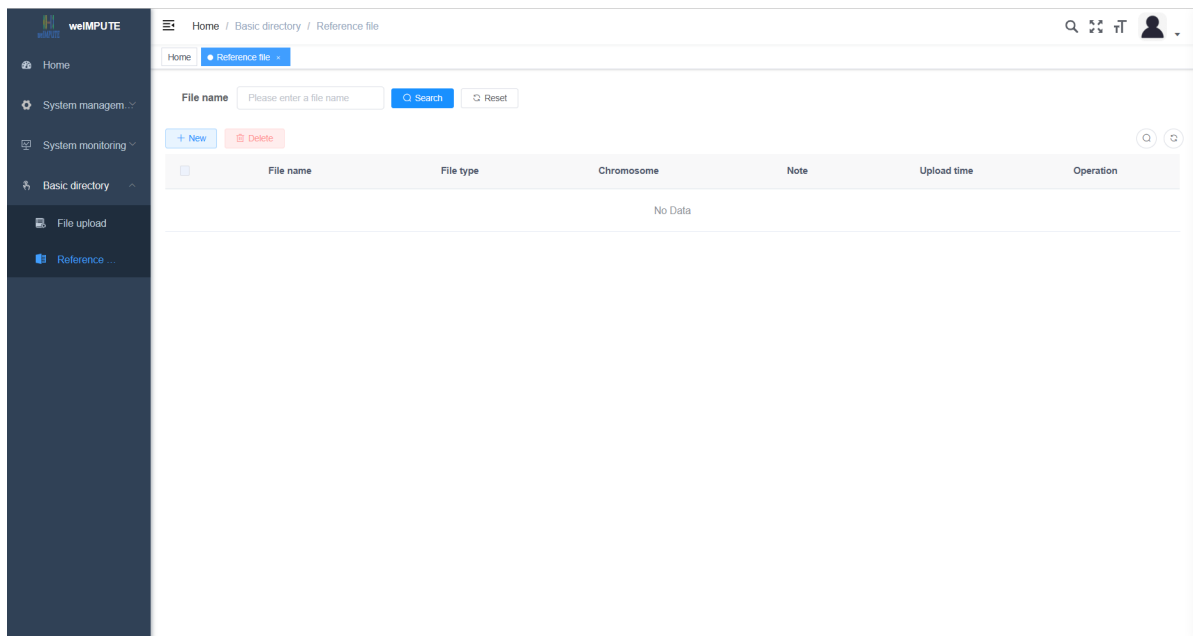
genetic_map_hg38_withX.txt.gz

OK

Close

Reference genotype data

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 planform 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 operating system.



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

File type

vcf.gz ▼

File path

Pick File

refile.vcf.gz

Chromosome

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.

Front-end Usage

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.

1

Reference panel files

Upload files

File upload

View uploaded files

Done

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

×

Data Name

Please enter the data name

Public or not Public

Please choose

▼

File

switchType

Select a file

Remark

Please enter the data name

↩

OK

Cancel

<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

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Go to

1

Cancel

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

Input files

All the genotype files for imputation must be a separated vcf.gz file for each chromosome.

Variations must be sorted by genomic position.