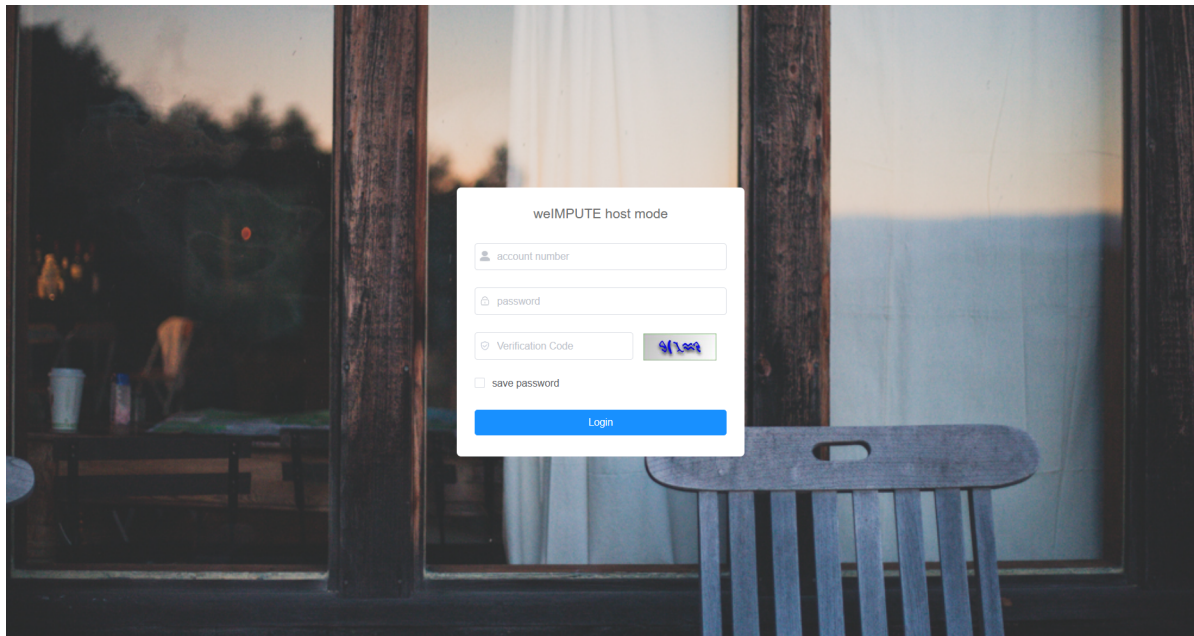# Data Preparation

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.

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.

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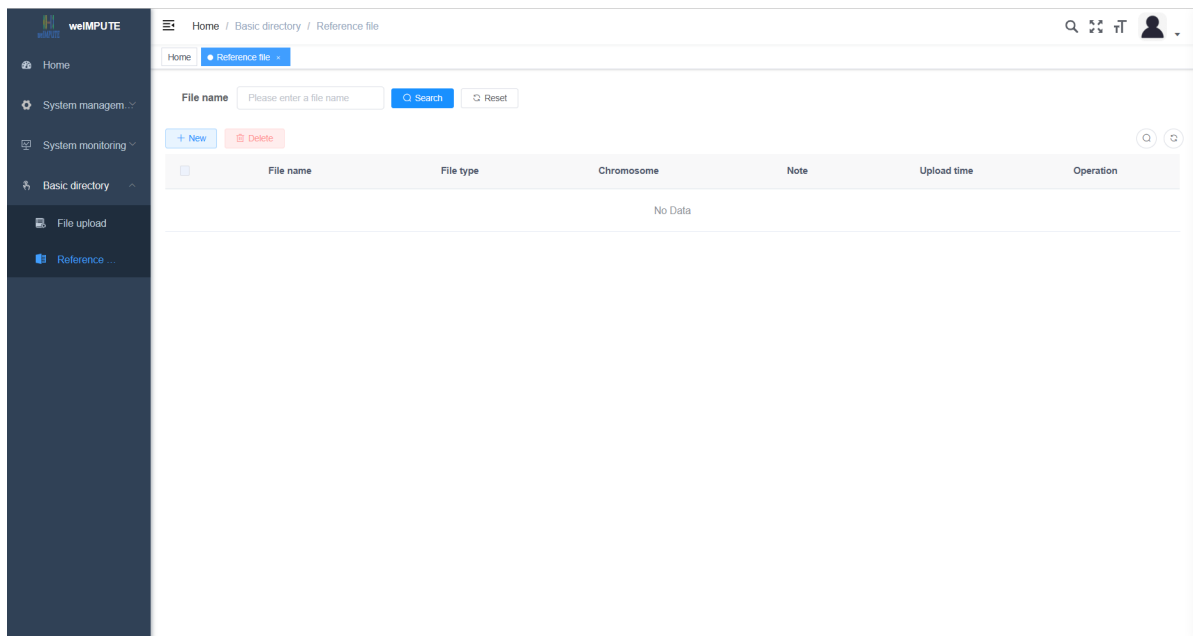
Click on the **_"Reference file"_** tab and the **_"New"_** tab , fill in relevant information. You have to choose the correct format from .vcf.gz, .m3vcf.gz (Minimac 4), or .zip (Shapeit).

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.

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.

View Uploaded Files ×

	Data Name	File Name	File Address	Public or not Public	Remark	Operate
☐	hg19ToHg38.over.chain.gz	hg19ToHg38.over.chain.gz	/upload/2022/1…	Public	undefined	🗑 Delete
☐	hg38ToHg19.over.chain.gz	hg38ToHg19.over.chain(1).gz	/upload/2022/1…	Not Public	hg38ToHg19.o…	🗑 Delete
☐	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.

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.