

PHENOTYPIC DATA

🔍 Hover here for details

Step 1: Select if file contains column names

- ☒ yes
☐ no

Step 2: Is the file comma separated

- ☐ yes
☒ no

Step 3: Code for missing value

Step 4: Select phenotypic file

Select File

or enter file name (including full path)

/tmp/phenoex.dat

Step 5: Upload file



Loading Phenotype file ...

Summary of Phenotype File

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File name: /tmp/phenoex.dat

Number of individuals: 800

Number of columns: 4

First 5 rows of the phenotype file are

|           |   |       |          |
|-----------|---|-------|----------|
| 0.4175858 | M | OBT40 | 44.43333 |
| 0.6184936 | M | OBT40 | 38.93333 |
| 0.2972836 | M | OBT40 | 37.40000 |
| 0.7123469 | M | OBT40 | 41.20000 |
| 1.4439608 | M | OBT40 | 50.93333 |

Column classes are

Bioch.HDL numeric

Sex character

Batch character

Weight.Average numeric

The phenotype file has been loaded.

## MAP DATA

🔍 Hover here for details

Step 1: Select if file contains column names

- ☒ yes  
☐ no

Step 2: Is the file comma separated

- ☐ yes  
☒ no

Step 3: Select map file

Select File

or enter file name (including full path)

/tmp/mapex.dat

Step 4: Upload file



Loading map file ...

### Summary of Map File

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File name: /tmp/mapex.dat

Number of marker loci: 70484

Number of columns: 3

Number of chromosomes: 19

First 5 markers of the map file are

M1C1	1	5151352
M6C1	1	5168874
M11C1	1	5181919
M16C1	1	5197376
M21C1	1	5213830

The map file has been loaded.