# Data Elements for the QTL Viewer

The QTL Viewer utilizes R and several different libraries in order to calculate the data for various types of QTL projects. The following sections will explain each element in detail.

Please note that some data element must be pre-computed.

## RData Environment Overview

The following elements should be contained within the RData file.

ensembl.version – the numerical version of Ensembl

genoprobs – the genotype probabilities

K – the kinship matric

map – list of one element per chromosome, with the genomic position of each marker

markers – marker names and positions

The following element is a special element and there must be at least one per RData file.

dataset.\* - where \* should be a very short, unique and informative name. This element will contain most of the data and will be detailed in the section below.

Exact case of element and variable names is very important.

Other meta data can be included in the RData file as long as there are no conflicting names.

## Elements

### ensembl.version

This specifies the genome release version for the genomic marker positions and for annotations attached to molecular phenotypes IF any, i.e. mRNA. Please see the documentation at Ensembl (<http://www.ensembl.org>) for build and version information.

**R data type:** numeric

### genoprobs

This is the genotype probabilities and must be supplied by the user. This is a list with one element per chromosome of **N** \* **K** \* **Mj** arrays, where:

**N** represents the number of mice

**K** represents the number of founders

**Mj**represents the number of markers on chromosome **j**

rownames(genoprobs) are the same value of the mouse.id column in the samples element

colnames(genoprobs) are the founder strain symbol (A,B,C,D,E,F,G,H)

dimnames(genoprobs[[j]]) are marker names on chromosome j

**R data type:** list, calc\_genoprobs

*May be produced by qtl2convert::probs\_doqtl\_to\_qtl2. Please see the documentation of R/qtl2geno.*

### K

A list of kinship matrices, with one element per chromosome of **N** \* **N** matrices, where:

**N** represents the number of mice

rownames(K) are the same value of the mouse.id column in the samples element

colnames(K) are the same value of the mouse.id column in the samples element

**R data type:** list

*May be produced by qtl2geno::calc\_kinship(genoprobs, type=”loco”). Please see the documentation of R/qtl2geno.*

## map

This is a list with one element per chromosome of named numeric vector. Elements of the vector are positions along the chromosome in Mb units. Element names are marker names and must match the dimnames of genoprobs.

Users can download maps for MUGA platforms or for 69k pseudomarker grid.

**R data type:** list

*May be produced by qtl2convert::map\_df\_to\_list. Please see the documentation of R/qtl2geno.*

### markers

Marker information containing the following information:

marker.id – character string, unique name of the marker

chr – character string, the chromosome

pos – numeric, position in Mbp

**R data type:** tibble

## The dataset.\* Element

The environment must contain at least one object of this type, multiple are allowed. The **\*** should be a very short, unique and informative name. It is for internal use only and will not appear in the QTL Viewer interface.

The main purpose of the dataset.\* element is to store multiple datasets per RData file with informative information regarding the data.

The dataset.\* element is a list that should contain the following named elements:

annot.**datatype**– annotations, where datatype is one of **mrna**, **protein**, or **phenotype**

annot.samples– annotation data for the samples

covar.matrix – a matrix of covariate data, samples (rows) x covariates (columns)

covar.info – information describing the covariates

data – either a matrix containing data or a list containing several kinds of data

datatype – one of **mrna**, **protein**, or **phenotype**

display.name – name of the dataset, for QTL Viewer display purposes

lod.peaks – a list of LOD peaks over a certain threshold

### annot.datatype

The annot.***datatype*** element will have different data and column names depending on whether this is a **mrna**, **protein**, or **phenotype** dataset.

For **mrna**,the following fields are required:

gene.id – character string, Ensembl gene id

symbol – character string, Symbol of the gene

chr – character string, chromosome

start – numeric, position in Mbp

end – numeric, position in Mbp

nearest.marker.id – character string, id of the marker in the marker element

For **protein**, all **mrna** fields *PLUS* the following field:

protein.id – character string, Ensembl protein id

For **phenotype**, the following fields are required:

data.name – character string, phenotype id

short.name – character string, short descriptive name

R.name – character string, name used by R

description – character string, phenotype description

units – character string, measureing units

category – character string, category if any

R.category – character string, category used by R

is.id – logical, should only be 1 TRUE

is.numeric – logical, is this a numeric field

is.date – logical, does this contain a date

is.factor – logical, is this a factor

factor.levels – character string, “:” separated values

is.covar – logical, is this a covariate

is.pheno – logical, is this an actual phenotype

is.derived – logical, is this phenotype derived

omit – logical, T to omit, F to include

use.covar – character string, Ensembl gene id

**R data type:** tibble

*Extra information in the tibble will be ignored by the QTL Viewer.*

### annot.samples

Annotations for the samples in this dataset. The unique identifying column is **mouse.id**. There should be a unique value for **mouse.id** in every row.

For the purpose of doing certain scans, there will need to be other columns that match the information stored in the covar.info element.

**R data type:** tibble

### covar.info

This element controls how we scan and interact with the RData object. The following columns must be present:

sample.column

name of the column in the annot.sample element

covar.column

name of the column in covar.matrix

display.name

QTL Viewer uses this to display a nice name

interactive

TRUE for an interactive covariate, must also set lod.peaks if TRUE. If FALSE, lod.peaks value should be NA. This controls whether or not interactive scans are performed for a particular covariate.

primary

which covariate to display preselected in the Effect Plot

lod.peaks

named tibble in the lod.peaks element

**R data type:** tibble

### covar.matrix

Covariates data, samples (rows) x covariates (columns) as produced by model.matrix.

**R data type:** matrix

### data

This element is either a matrix or a list.

If it is a matrix, there is one and only set of data for this dataset.

If it is a list, each named element in the list should be a matrix with the following controlled vocabulary for the names:

**rz**

**norm**

**raw**

**log**

**transformed**

Each matrix will contain numerical data with samples (rows) by annotations (columns).

**R data type:** matrix or list

### datatype

This will be used to identify the type of dataset. This is a controlled vocabulary consisting of the following values:

**mrna**

**protein**

**phenotype**

Based upon the value of this element, the QTL Viewer will treat the data as accordingly.

**R data type:** character

### display.name

This will be used to display the name of the dataset to the user in the QTL Viewer. This will be used in a dropdown menu to switch among the datasets.

**R data type:** character

### lod.peaks

This is a list with each value in the list being either **additive** (the default) or one of the interactive covariates (if set in covar.info). The **additive** values should always be present.

The covar.info element should have values with interactive set to TRUE and lod.peaks set to the name of the element in this list.

Depending on the value of datatype (**mrna**, **protein**, **phenotype**), the annotation column identifier will match to the appropriate column in the anot.dataype element.

The following shows the required fields in each tibble.

If datatype is **mrna**, the following fields are required:

gene.id

the Ensembl gene identifier in the annot.mrna element

marker.id

the marker identifier in the markers element

lod

the lod score

If datatype is **protein**, the following fields are required:

protein.id

the Ensembl protein id in the annot.protein element

marker.id

the marker identifier in the markers element

lod

the lod score

If datatype is **phenotype**, the following fields are required:

data.name

the unique identifier in the annot.pheno element

marker.id

the marker identifier in the markers element

lod

the lod score

**R data type:** list