

# GenomicTools - Vignette

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## Introduction

The R-package GenomicTools is designed for the analysis of so-called omics data, and here especially on gene expression and SNP data. The focus is on performing an eQTL, a QTL or a Multifactor dimensionality reduction (MDR). Although MDR is not limited to the genomic field and all other kinds of categorical data can be used with it, the implementation is here tailored for genomic data and currently the generalization to other variables proves to be difficult. The package comes with a couple of example datasets, further datasets can be downloaded from the project page, links are given for that below. The following chapters explain in detail, how the package can be applied in different scenarios and how the output is to be interpreted.

## Installation of GenomicTools

The latest stable version of GenomicTools is located on Cran and can be installed via

```
install.packages("GenomicTools")
```

No special dependices are required and the dependencies should also be automatically installed by R.

The latest developer version, including the latest bugfixes is located at GitHub and can be installed like this:

```
library("devtools")  
install_github("fischiu/GenomicTools")
```

The GitHub page is located here

<https://github.com/fischiu/GenomicTools>

and bugfixes and comments can easily be handed in via that platform. The package has also an own webpage where additional information may be posted and is located here:

<http://genomictools.danielfischer.name/>

After this webpage is established, it will beside other things also provide a couple of other example datasets.

Once the package is installed, it can be loaded into the workspace by typing

```
library("GenomicTools")
```

## Included datasets and the import functions

An overview of the example datasets. Currently many of them are simulated, but they will be moved to real datasets gradually.

## Annotation files

### Simulated Example File

An example annotation track is the `annotTrack` object. It can be loaded to the workspace via

```
data("annotTrack")
```

and the first rows of it look like this

```
annotTrack
```

	V1	V2	V3	V4	V5	V6	V7	V8	gene_id
1:	1	havana	gene	11869	14409	.	+	.	ENSG00000223972
2:	1	havana	gene	14404	29570	.	-	.	ENSG00000227232
3:	1	mirbase	gene	17369	17436	.	-	.	ENSG00000278267
4:	1	ensembl_havana	gene	29554	31109	.	+	.	ENSG00000243485
5:	1	havana	gene	34554	36081	.	-	.	ENSG00000237613
---									
996:	1	ensembl_havana	gene	32013829	32060850	.	+	.	ENSG00000121774
997:	1	havana	gene	32052291	32073474	.	-	.	ENSG00000203325
998:	1	ensembl_havana	gene	32072031	32102866	.	+	.	ENSG00000121775
999:	1	mirbase	gene	32086949	32087007	.	+	.	ENSG00000266203
1000:	1	ensembl	gene	32087523	32087813	.	-	.	ENSG00000276493
		gene_name							gene_biotype
1:		DDX11L1	transcribed_unprocessed_pseudogene						
2:		WASH7P	unprocessed_pseudogene						
3:		MIR6859-1							miRNA;
4:		MIR1302-2							lincRNA
5:		FAM138A							lincRNA
---									
996:		KHDRBS1							protein_coding
997:		RP11-277A4.4							antisense
998:		TMEM39B							protein_coding
999:		MIR5585							miRNA;
1000:		Metazoa_SRP							misc_RNA;

### An own gtf file

GTF files are provided e.g. from Ensembl and can be downloaded from the corresponding webpage. For example the human annotation for Ensembl build 85 can be found here:

```
ftp://ftp.ensembl.org/pub/release-85/gtf/homo_sapiens/Homo_sapiens.GRCh38.85.gtf.gz
```

After downloading this file, it can be imported to R with

```
ensGTF <- importGTF(file="Homo_sapiens.GRCh38.85.gtf.gz")
```

## Genotype files

### Simulated Example File

An example annotation track is the `genotData` object. It can be loaded to the workspace via

```
data("genotData")
```

and the first rows of it look like this

```
genotData
```

First 6 rows and 6 columns of \$genotypes:

```
  SNP1 SNP2 SNP3 SNP4 SNP5 SNP6
1:  01   01   01   01   02   01
2:  01   01   01   01   03   01
3:  01   01   01   02   02   01
4:  01   01   02   01   02   02
5:  01   01   02   01   02   02
6:  01   01   01   02   02   03
... 44 rows and 49994 columns omitted
```

First 6 rows of \$fam:

```
  pedigree member father mother sex affected
sample1 sample1 sample1 <NA> <NA> 2       2
sample2 sample2 sample2 <NA> <NA> 1       2
sample3 sample3 sample3 <NA> <NA> 2       2
sample4 sample4 sample4 <NA> <NA> 2       2
sample5 sample5 sample5 <NA> <NA> 1       2
sample6 sample6 sample6 <NA> <NA> 2       2
... 44 rows omitted
```

First 6 rows of \$map:

```
  V1 snp.names V3  V4 allele.1 allele.2
1  1   SNP1   0   1         G   <NA>
2  1   SNP2   0  53         T   <NA>
3  1   SNP3   0 106         T     G
4  1   SNP4   0 158         A     G
5  1   SNP5   0 211         G     A
6  1   SNP6   0 263         G     C
... 49994 rows omitted
```

## An own ped/map filepair

An own filepair of ped/map files can be loaded, using the `importPED()` command:

```
ownGenotypes <- importPED(file="myGenotypes.ped", snps="myGenotypes.map")
```

Here, we assume that the filepair has the name `myGenotypes`.

## Gene expressions

### Simulated Example File

There is also a simulated example file on board. This can be loaded into the namespace by typing

```
data("geneEXP")
```

and the first rows of it look like this

```
geneEXP[1:5,1:4]
```

	ENSG00000223972	ENSG00000227232	ENSG00000278267	ENSG00000243485
sample1	-0.1409671	1.4785011	1.8348913	1.5911752
sample2	-0.4052411	0.4425597	1.7152213	0.4719993
sample3	2.7193846	1.0915978	0.7543625	-1.9447849
sample4	-1.1601908	0.3864105	1.1507785	-1.4717733
sample5	2.5717304	1.6234966	-0.5463051	1.1073764

This data is a basic data frame respective matrix and own datasets can be loaded with the common commands like e.g. `read.table()` or `read.csv()`.

## General background for eQTL/QTL analyses

There are two methods implemented to perform an (e)QTL that may be picked with the `method=` option in the `eQTL/QTL` function. The two options are `LM` and `directional`. In case of `LM` a classical linear model is fitted to the data and it is tested if the slope is zero or not. This is the same method that is practically implemented in all (e)QTL software tools. The second option `directional`, however, uses a directional test based on probabilistic indices as it was presented in (Fischer et al. 2014). For the directional test, there is still another parameter option. The p-values can be either determined using a permutation type test, or using asymptotic results. The options to set this are either `testType="permutation"` or `testType="asymptotic"`. Currently the required asymptotic test is not implemented in the used R-package `gMWT`, but this will happen during August 2016 and is then also available in `GenomicTools`.

## Perform an eQTL analysis

### Calculating the results

To run an eQTL first a couple of data objects have to be prepared. In the most simplest case there is only a single gene that should be tested against. We show here the use with the included example datasets, to apply the methods to own data they only need to be imported to R with the commands `importGTF` (annotation data), `importPED` (genotype data) and `read.table()` (gene expressions).

```
# Make the example data available
data("annotTrack") # Standard gtf file, imported with importGTF
data("geneEXP")    # Matrix with gene expression
data("genotData")  # A imported Ped/Map filepair, using importPED
```

The annotation is usually imported in gtf format. However, the function expects the data to be in bed format (With the first four columns being `Chr`, `Start`, `End`, `Gene`). The function `gtfToBed()` transforms a previous imported `gtf` object into the required format. This step is, however, only optional, as the functions also accept a `gtf` object and transform the object then internally. Especially if an own annotation it provided, it might be easier to do that directly in bed format, using the columns as above.

```
# Transform gtf to bed format (not necessarily required)
annot.bed <- gtfToBed(annotTrack)
```

Now run different cis-eQTLs with different options and input parameters:

```
# cis-eQTL
#####

# Most basic cis-eQTL runs:
EQTL1 <- eQTL(gex=geneEXP[,1:10], xAnnot = annotTrack, geno= genotData)
```

```

# Same run, if gtf has been transformed to bed previously
EQTL1.1 <- eQTL(gex=geneEXP[,1:10], xAnnot = annot.bed, geno= genotData)

# Same run, when the genotype data wasn't loaded and should be loaded
# here instead
EQTL1.2 <- eQTL(gex=geneEXP[,1:10], xAnnot = annotTrack,
+             geno= file.path("Datasets","genotypes.ped"))

# Full set of genes, this time filtered with column names
EQTL2 <- eQTL(gex=geneEXP, xAnnot = annot.bed, geno= genotData,
+           which = colnames(geneEXP)[1:20])

# Single vector of gene expression values, underlying gene is specified
# in the which option
EQTL3 <- eQTL(gex=as.vector(geneEXP[,1]), xAnnot = annot.bed,
+           geno= genotData, which="ENSG00000223972")

# Same call, but instead of the name the row number in the gtf/bed
# file is provided
EQTL3.2 <- eQTL(gex=geneEXP[,1], xAnnot = annot.bed, geno= genotData,
+           which=1)

# The same expression values are now assigned to three different genes
EQTL4 <- eQTL(gex=as.vector(geneEXP[,1]), xAnnot = annot.bed,
+           geno= genotData, which=1:3)

```

The typical (verbose) output of the eQTL run looks then like this

```

# Same call, but this time is the corresponding column not casted
EQTL3.1 <- eQTL(gex=geneEXP[,1] , xAnnot = annot.bed, geno= genotData,
+           which="ENSG00000223972")

```

```

## A vector of gene expression was provided. These expression values will be used for EACH gene in xAnnot
## We will transform the gene annotations into a list ... done (Wed Aug 17 08:27:30 2016)!
## We have for 100 % of the samples in the expression data the genotype information available.
## We have for 100 % of the samples in the genotype data the expression values available.
## We have for 100 % of the expression data the annotations.
## We will test for 1 genes possible eQTLs!
## -----
## We calculated eQTLs for ENSG00000223972 for 9,799 SNPs (Wed Aug 17 08:27:39 2016)

```

And the same for the trans-eQTL

```

# Trans-eQTL
#####

# Trans eQTL for the first and the last gene in our expression matrix
EQTL5 <- eQTL(gex=geneEXP[,c(1,1000)] , xAnnot = annot.bed,
+           geno= genotData, windowSize = NULL)

# Same call, this time distributed to 8 cores (only available on
# Linux computers)
EQTL5 <- eQTL(gex=geneEXP[,c(1,1000)] , xAnnot = annot.bed,
+           geno= genotData, windowSize = NULL, mc=8)

```

The output here is similar to the output from the cis-eQTL:

```

# Expression values from the first gene are used to test the 100st
# gene for trans-eQTL
EQTL6 <- eQTL(gex=as.vector(geneEXP[,1]) , xAnnot = annot.bed, geno= genotData, windowSize = NULL, wh

## Warning in eQTL(gex = as.vector(geneEXP[, 1]), xAnnot = annot.bed, geno = genotData, : You choose tr
##           all results, please set the 'IHaveSpace'-Option to TRUE.

## A vector of gene expression was provided. These expression values will be used for EACH gene in xAnno
## We will transform the gene annotations into a list ... done (Wed Aug 17 08:27:39 2016)!
## Expression values are unnamed. We assume same order in expression and genotype objects and match sampl
## We have for 100 % of the samples in the expression data the genotype information available.
## We have for 100 % of the samples in the genotype data the expression values available.
## We have for 100 % of the expression data the annotations.
## We will test for 1 genes possible eQTLs!
## -----
## We calculated eQTLs for ENSG00000169962 for 50,000 SNPs (Wed Aug 17 08:28:27 2016)

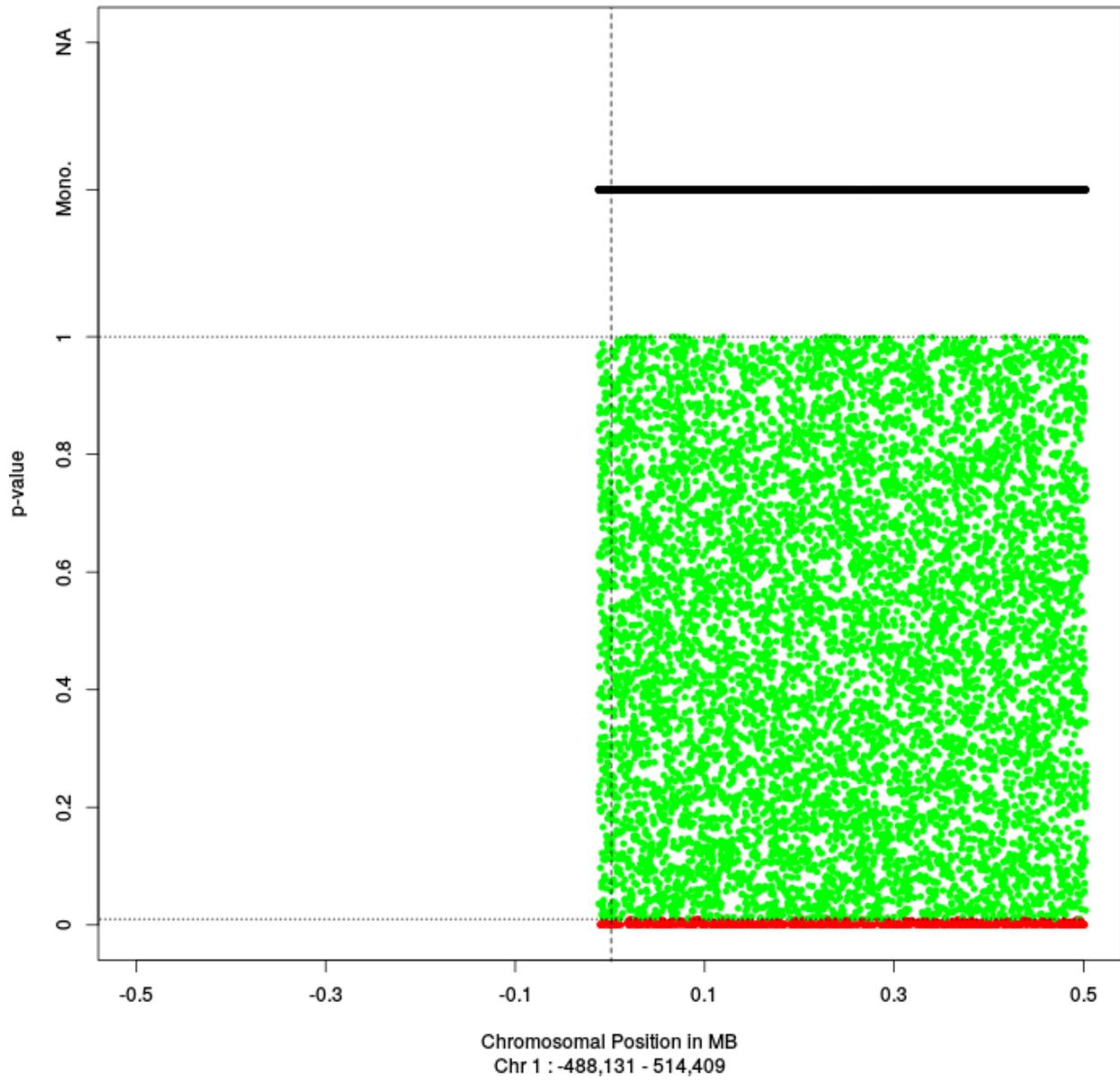
```

## Visualize the results

The easiest way to visualize the results is with the associated S3 method `plot`. For that, just the `eQTL` result has to be fed into the function

```
plot(EQTL3.1)
```

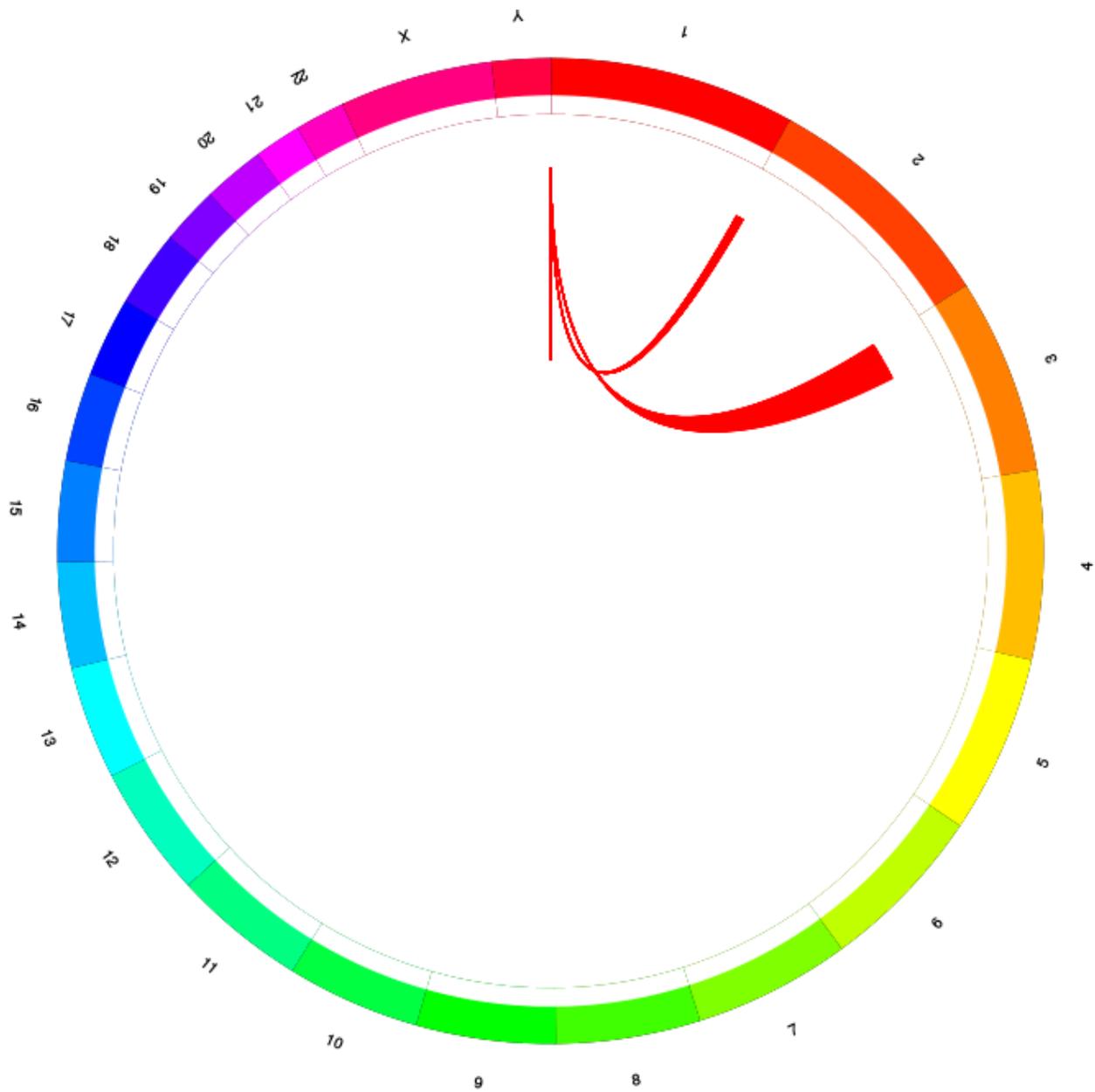
### ENSG00000223972 - 1



and the same for the trans-eQTL

```
plot(EQTL6)
```

```
## Warning in plot.eqtl(EQTL6): Warning!!! No genome information provided, use  
## the default (Ensembl Human, build 68).
```



## Perform an QTL

The QTL analysis is technically very similar to the eQTL analysis and an example workflow is as follows

### Calculate the QTLs

```
# Make the example data available
data("phenoData")
data("genotData")
```

```

qt11 <- QTL(pheno=phenoData[,2:3], geno=genotData)

## We have for 100 % of the samples in the phenotype data the genotype information available.
## We have for 100 % of the samples in the genotype data the phenotype values available.
## We will test for 2 phenotypes possible QTLs!
## -----
## We calculated QTLs for Pheno2 for 50,000 SNPs (Wed Aug 17 08:29:33 2016)
## We calculated QTLs for Pheno3 for 50,000 SNPs (Wed Aug 17 08:30:20 2016)

# The most basic approach
qt11 <- QTL(pheno=phenoData, geno=genotData)

# Use only a named subset of phenotypes
qt12 <- QTL(pheno=phenoData, geno=genotData, which = c("Pheno1", "Pheno4"))

# Use a numbers subset of genotypes, distributed to 3 cores
qt12.1 <- QTL(pheno=phenoData, geno=genotData, which = 3:4, mc=3)

# Use a single phenotype only
qt12.2 <- QTL(pheno=phenoData, geno=genotData, which = 7)

# Same thing, but filtering applied directly to the data
qt13 <- QTL(pheno=phenoData[,5], geno=genotData)

# Also a vector input instead of a matrix is possible
qt13.1 <- QTL(pheno=as.vector(phenoData[,5]), geno=genotData)

# The genotype data can be loaded in runtime, without previous step
qt14 <- QTL(pheno=phenoData[,5], geno=file.path("Datasets","genotypes.ped"))

```

## Visualize QTLs

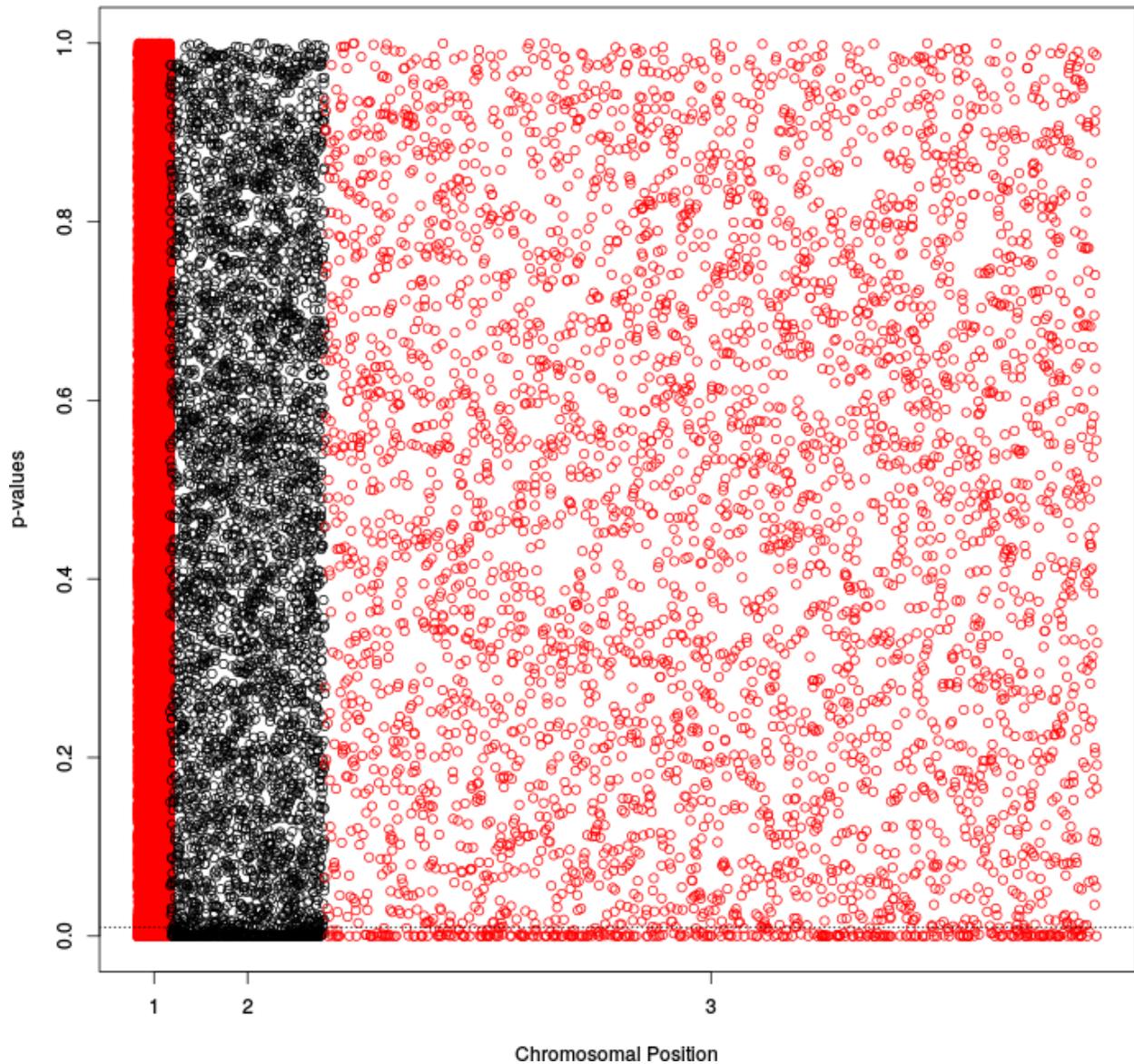
```

# Visualize e.g. the 1st phenotype from previous runs
plot(qt11, which=1)

## Warning in plot.qtlRes(qt11, which = 1): No genome information provided,
## we will visualize only the SNPs without further chromosomal length
## information!

```

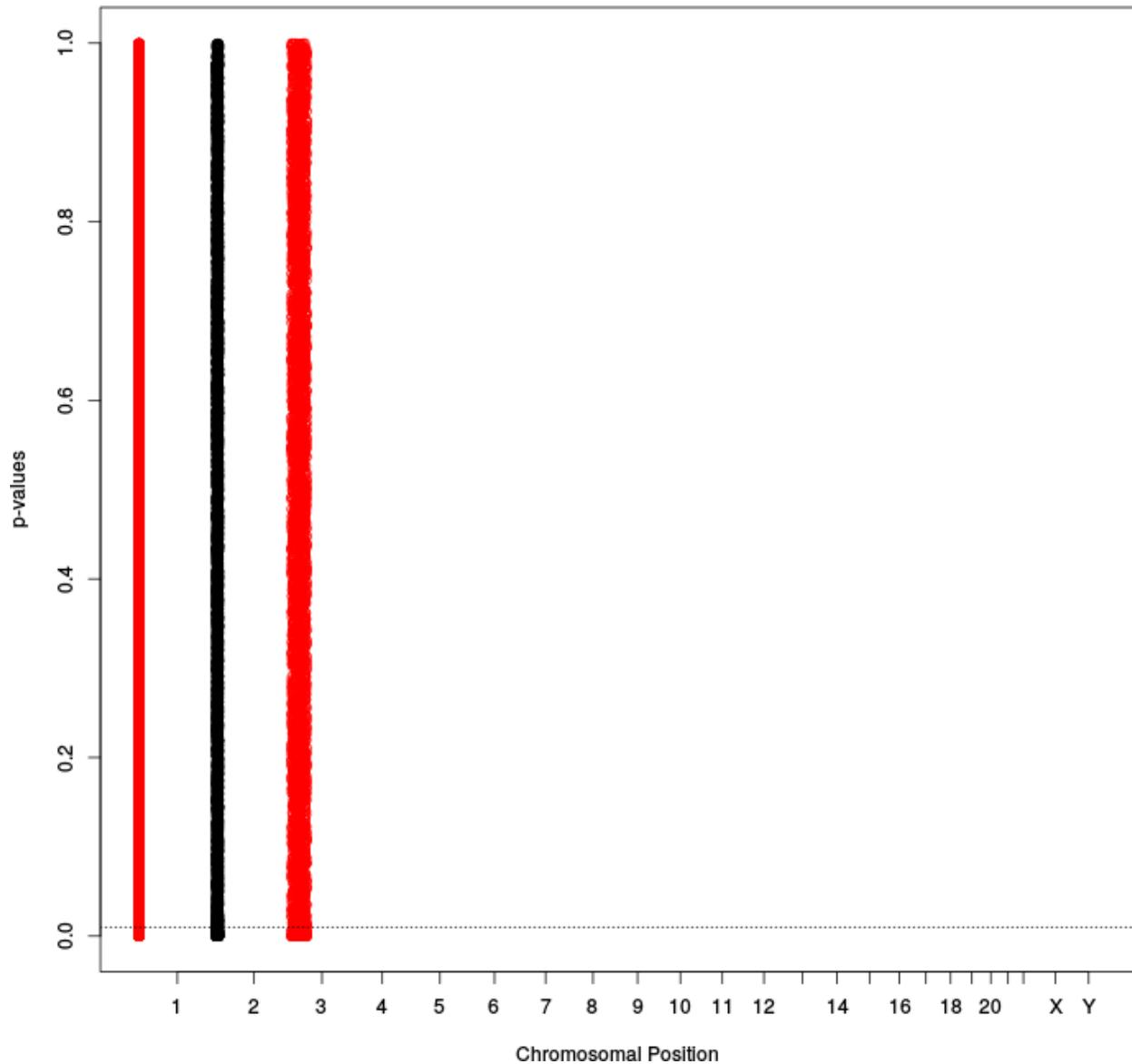
## Pheno2



If no genome information is provided, the function visualizes only the existing results. However, the user can either provide an own genome information as a data.frame with the two columns **Chr** and **length**, giving the lengths of each chromosome or use the default genome that comes with the package (Human Ensembl build 68). This can be made available with the `genome = "Human68"` option

```
# Visualize e.g. the 1st phenotype from previous runs  
plot(qt11, which=1, genome = "Human68")
```

## Pheno2



## Perform an MDR

### Calculate the accuracies

An MDR can be performed in the following manner. The SNP information is stored in a matrix, with 0,1,2 format, see e.g. `mdrExample`.

```
data(mdrExample)
mdrSNP <- mdrExample[,1:20]
fit.mdr <- mdr(mdrSNP, mdrExample$Class, fold=3, top=5)
fit.mdr
```

```
## NULL
```

```
fit.mdr <- mdr(mdrSNP, mdrExample$Class)
fit.mdr
```

```
## NULL
```

## Use the Ensemble classifier

To use this MDR run to start a MDR ensemble classification from it, just run

```
data(mdrExample)
mdrSNP.train <- mdrExample[1:350,1:20]
mdrSNP.test <- mdrExample[351:400,1:20]
fit.mdr <- mdr(mdrSNP.train, mdrExample$Class[1:350], fold=2, top=20)
ensResult <- mdrEnsemble(fit.mdr, data = mdrSNP.test)
table(ensResult, mdrExample[351:400,21])
```

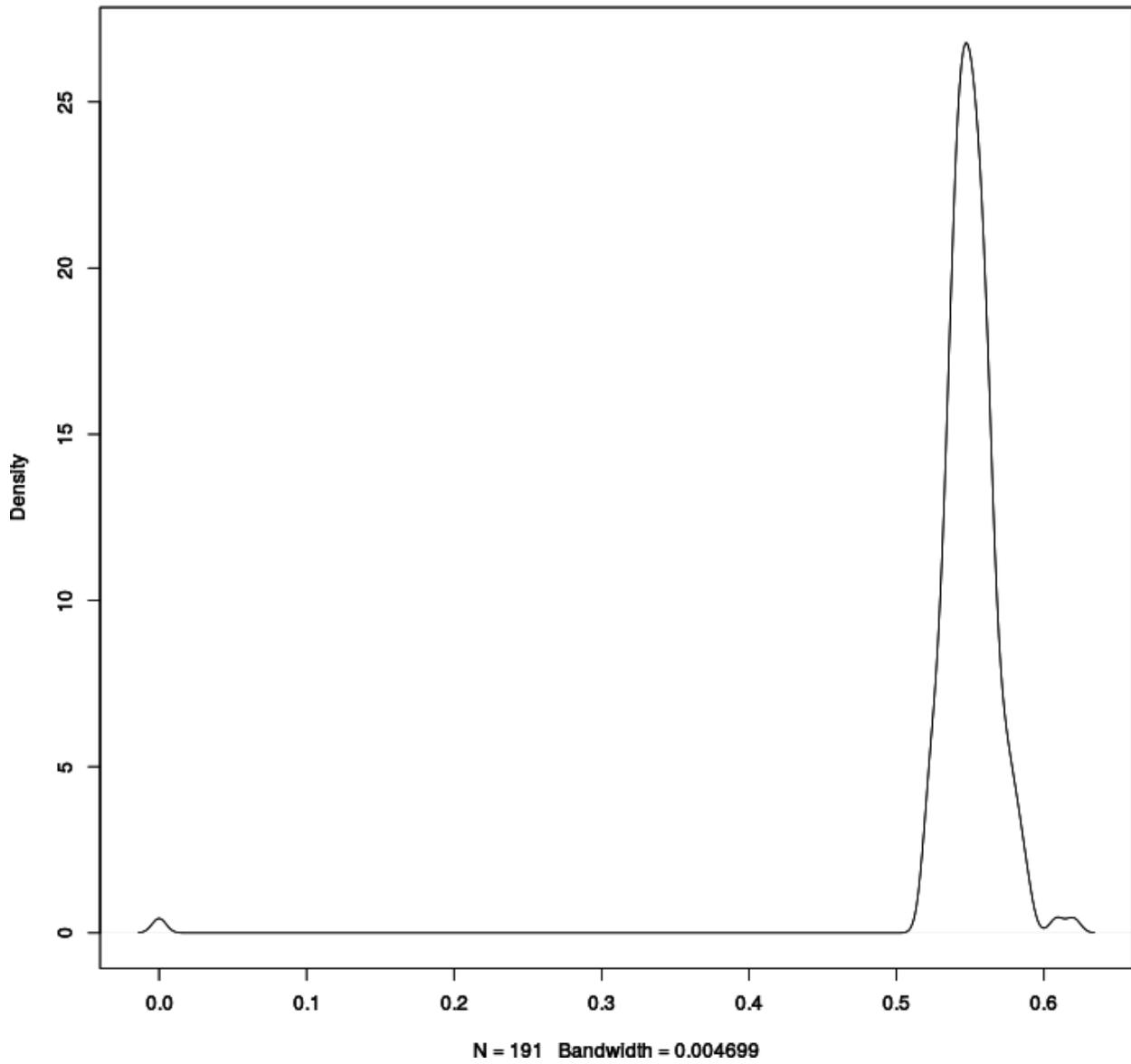
```
##
## ensResult  0  1
##           0 11  7
##           1 14 18
```

## Visualize the results

A density plot over all calculated accuracies can be plotted using again the S3method plot:

```
plot(fit.mdr)
```

### Precision Density Plot



### References

Fischer, Daniel, Hannu Oja, Johanna Schleutker, Pranab K. Sen, and Tiina Wahlfors. 2014. "Generalized Mann-Whitney Type Tests for Microarray Experiments." *Scandinavian Journal of Statistics* 41 (3): 672-92.