Package 'qtl.outbred'

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Type Package

Title Interface for Genotype Probabilities from Outbred Intercross

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Description The package calculates and imports genotype probabilities from outbred intercross designs into an R object. This allows fast scans for main effect QTL and two way interactions.

License Unlimited

LazyLoad yes

Depends qtl

R topics documented:

```
qtl.outbred-package
```
Interface for Genotype Probabilities of Outbred Intercross

Description

The package calculates and imports genotype probabilities from outbred intercross designs into an R object. This allows fast scans for main effect QTL and two way interactions. Using this interface, most functions in package `qtl` can be used for outbred designs.

Details

1

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License:	Unlimited
LazyLoad:	yes
Depends:	qtl

Author(s)

Ronnie Nelson and Xia Shen

Maintainer: Xia Shen <xia.shen@lcb.uu.se>

See Also

impo.prob, calc.prob

Examples

```
## Not run:
# ----- impo.prob example
file <- paste(R.home(), '/library/qtl.outbred/example_data.csv', sep = '')
data <- read.cross('csv', file = file, genotypes = c('AA', 'AB', 'BB'))
outbred.data <- impo.prob(cross.data = data, stepsize = 5,
                          path = paste(R.home(), '/library/qtl.outbred/', sep = ''))

# ----- QTL scan using Haley-Knott regression and plotting
hk.model <- scanone(outbred.data, method = 'hk', pheno.col = 2)
plot_outbred(hk.model, data)

## End(Not run)
```

---

calc.prob	*Calculate genotype probabilities for outbred intercrosses using cnF2freq*

Description

The function calculates genotype probabilities from outbred intercross data using published software 'cnF2freq'. This software is C++ based and might require re-compiling for different platforms.

Usage

```
calc.prob(os = 'unix', stepsize = 1,
marker.info.file = 'mi.txt', pedigree.file = 'mp.txt',
genotype.file = 'mg.txt', output.file = 'cnout')
```

Arguments

`os`	A string specifying the operating system, typically 'unix' or 'windows'.
`stepsize`	An integer giving the distance that the two consecutive test loci are spaced in centi-morgan.
`marker.info.file`	
	A marker information file required by `cnF2freq`, see Details.
`pedigree.file`	
	A pedigree information file required by `cnF2freq`, see Details.
`genotype.file`	
	A genotype data file required by `cnF2freq`, see Details.
`output.file`	An output file name required by `cnF2freq`, see Details.

Details

Three files are required for the calculating of genotype probabilities. All the files are tab-delimited. The marker information files provides information on the number of chromosomes, the total number of markers, followed by the number of per chromosomes and the name of each. Finally the space between each marker for each chromosome is provided. Note that the first column of each row should be filled with a '1' followed by the position data (each chromosome in a single row). The genotype file provide the genotypic information for each individual. The individuals IDs are indicated in the first column of each row. The following columns are filled with integer values indicating the genotype at each locus. Each column corresponds one marker and are arranged sequentially as indicated in the marker file. The marker pedigree file are arranged in fullsib families. For each family the the number of F2 individuals within the family are provided. This is followed wit the individual ID's in the first column (starting with the F0 generation, then the F1s and then the F2s). For each individual his/her parent's ID's are provided in the next two columns followed by it's sex. Note for the F0 generation their parents are indicated with a '0' while an additional column with their line origins are provided.

Three example files with the required format described above are provided in the package installation folder. 'mp.txt', 'mi.txt', and 'mg.txt' are the pedigree information file, marker information file, and the marker genotype file, respectively.

Note that Perl is required for some of the functions in the package `qtl.outbred`.

Value

The function generates a file named by `output.file` for each chromosome containing genotype probabilities that can be thereafter imported using `impo.prob`.

Author(s)

Ronnie Nelson and Xia Shen

See Also

`impo.prob`, `qtl.outbred-package`

Examples

```
# ----- calc.prob example
# ----- calculating the genotype probabilities from the files 'mi.txt',
# 'mp.txt' and 'mg.txt' at 5 cM intervals and produce the files
```

```
# 'p_chrom_A.txt' (where A indicates the chromosome number for each chromosome).

## Not run:

setwd(paste(R.home(), '/library/qtl.outbred/', sep = ''))
calc.prob(stepsize = 5)

## End(Not run)
```

---

impo.prob   *Import genotype probabilities into an existing cross object*

Description

The function imports genotype probabilities into an existing qtl object.

Usage

```
impo.prob(cross.data, path = NULL, stepsize = 1, Grid = FALSE)
```

Arguments

cross.data   A cross object typically read in via `read.cross` in package `qtl`.

path   The directory path where the genotype probabilities input files are located.

stepsize   An integer giving the distance that the two consecutive test loci are spaced in
             centi-morgan.

Grid   If the genotype probabilities are saved from a GridQTL coefficient file it can be
             imported directly if TRUE.

Details

The data in the object of class `cross` is used to create a new object of the same class, while
importing the genotype probabilities from a set of files. It is necessary to import create the original
object prior to using the impo.prob function (see `read.cross` for more information).

The genotype probabilities are imported from a file for each chromosome separately. In this for-
mat first column indicates the individual id. The next three columns are the genotype probabilities
of being homozygous, heterozygous and homozygous for the other alleles respectively (i.e. AA,
AB and BB). A separate row for each centi-morgan interval per individual is provided. The rows
are arranged to have the probabilities per individual together (i.e. from position 1 to end of chro-
mosome for individual 1 followed by position 1 to end of chromosome for individual 2 etc.). It
is important to note that the filenames should be for each chromosome as follows (where A indi-
cates the chromosome number): 'p_output_chrom_A.txt'. This is also the file output created by
`calc.prob`.

A set of example files with the required format described above are provided in the package instal-
lation folder. 'p_output_chrom_1.txt' and 'p_output_chrom_2.txt' contains the genotype probabil-
ities for the two chromosomes to be imported. 'example_data.csv' is an F2 intercross file that can
be read by `read.cross` function in package `qtl`.

Alternatively, the genotype probabilities can be imported directly from the coefficient file generated
by GridQTL. This file will contain the genotype probabilities for all the chromosomes specified
when the job is submitted to the GridQTL server (see installation folder for an example file). It is

important to note that the filename for this file should be 'Gout.coe', and should be located in the working directory.

Note that Perl is required for some of the functions in the package `qtl.outbred`.

Value

The new cross object `cross.data` is returned, with the genotype probabilities imported.

Author(s)

Ronnie Nelson and Xia Shen

See Also

`calc.prob`, `qtl.outbred-package`, `read.cross`

Examples

```
## Not run:

# ----- impo.prob example
file <- paste(R.home(), '/library/qtl.outbred/example_data.csv', sep = '')
data <- read.cross('csv', file = file, genotypes = c('AA', 'AB', 'BB'))
outbred.data <- impo.prob(cross.data = data, stepsize = 5,
                          path = paste(R.home(), '/library/qtl.outbred/', sep = ''))

# ----- impo.prob example for GridQTL output
file <- paste(R.home(), '/library/qtl.outbred/example_data.csv', sep = '')
data <- read.cross('csv', file = file, genotypes = c('AA', 'AB', 'BB'))
outbred.data <- impo.prob(cross.data = data, stepsize = 5,
                          path = paste(R.home(), '/library/qtl.outbred/', sep = ''),
                          Grid = TRUE)

# ----- QTL scan using Haley-Knott regression and plotting
hk.model <- scanone(outbred.data, method = 'hk', pheno.col = 2)
plot_outbred(hk.model, data)

## End(Not run)
```

---

  plot_outbred   *Plot LOD curves for outbred data*

Description

Plot the LOD curve including the markers for a genome scan with the single-QTL model.

Usage

```
plot_outbred(model, old.data, dimension = '1D', chr = -1, gap = 25, ...)
```

Arguments

`model`	An object of class scanone, as output by [scanone](#).
`old.data`	An object of class cross. See [read.cross](#) for details.
`dimension`	A string giving the dimension of the QTL scan to be plotted, and the current version allows '1D' or '2D'.
`chr`	Optional vector indicating the chromosomes to plot.
`gap`	Gap separating chromosomes (in cM).
`...`	Other arguments. See package qtl for details.

Details

This function allow the user to plot the results produced by scanone. The LOD scores for single or multiple chromosomes are plotted with the markers indicated.

See also [plot.scanone](#) for plotting the scan results but with the probabilities on the marker positions.

Value

None

Author(s)

Ronnie Nelson and Xia Shen

See Also

[impo.prob](#), [qtl.outbred-package](#), [plot.scanone](#),

Examples

```
## Not run:

# ----- impo.prob example
file <- paste(R.home(), '/library/qtl.outbred/example_data.csv', sep = '')
data <- read.cross('csv', file = file, genotypes = c('AA', 'AB', 'BB'))
outbred.data <- impo.prob(cross.data = data, stepsize = 5)

# ----- QTL scan using Haley-Knott regression and plotting
hk.model <- scanone(outbred.data, method = 'hk', pheno.col = 2)
plot_outbred(hk.model, data)

## End(Not run)
```

Index