Package 'qtlbook'

July 22, 2025

Version 0.20

Date 2025-05-12

Title Datasets for the R/qtl Book

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Description Datasets for the book, A Guide to QTL Mapping with R/qtl.
Broman and Sen (2009) <doi:10.1007/978-0-387-92125-9>.

Depends R (>= 2.10.1)

Suggests qtl

License GPL-3

URL https://rqtl.org/book/, https://github.com/kbroman/qtlbook

BugReports https://github.com/kbroman/qtlbook/issues

Encoding UTF-8

RoxygenNote 7.2.3

LazyData true

NeedsCompilation no

Repository CRAN

Date/Publication 2025-05-12 12:50:02 UTC

Contents

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ch3a *Data with a phenotype error*

Description

Anonymous data with a phenotype error and a pair of individuals with very similar phenotypes.

Usage

```
ch3a
```

Format

An object of class `cross`. See `qtl::read.cross()` for details.

Details

A backcross with 234 individuals, each with five phenotypes and typed at 166 markers.

Source

Karl W Broman, <broman@wisc.edu>

References

Broman, K. W. and Sen, S. (2009) *A Guide to QTL Mapping with R/qtl.* Springer, New York.

See Also

`ch3b`, `ch3c`

Examples

```
data(ch3a)

# phenotype problem
pairs(ch3a$pheno)
ch3a$pheno[ch3a$pheno[,4]==0,] # individual 159

# individuals with similar genotypes
library(qtl)
cg <- comparegeno(ch3a)
hist(cg, breaks=200)
max(cg[cg < 1])
which(cg == max(cg[cg < 1]), arr.ind=TRUE)
```

ch3b *Data with bad markers*

Description

Anonymous data with markers showing severe segregation distortion.

Usage

```
ch3b
```

Format

An object of class `cross`. See `qtl::read.cross()` for details.

Details

An intercross with 144 individuals, each with one phenotype and typed at 145 markers.

Source

Karl W Broman, <broman@wisc.edu>

References

Broman, K. W. and Sen, S. (2009) *A Guide to QTL Mapping with R/qtl.* Springer, New York.

See Also

ch3a, ch3c

Examples

```
data(ch3b)

library(qtl)
thetab <- geno.table(ch3b)
plot(-log10(thetab[,ncol(thetab)]), ylab=expression(-log[10](P)))
thetab[thetab[,ncol(thetab)] < 1e-6,]
```

ch3c *Data with misplaced markers*

Description

Anonymous data with markers out of place.

Usage

```
ch3c
```

Format

An object of class `cross`. See `qtl::read.cross()` for details.

Details

An intercross with 100 individuals, each with one real phenotype and typed at 108 markers.

Source

Karl W Broman, <broman@wisc.edu>

References

Broman, K. W. and Sen, S. (2009) *A Guide to QTL Mapping with R/qtl.* Springer, New York.

See Also

`ch3a`, `ch3b`

Examples

```
data(ch3c)

library(qtl)
ch3c <- est.rf(ch3c)
plotRF(ch3c, chr=c(1,7,12,13,15))
```

gutlength *Gut length intercross data*

Description

Data from a mouse intercross experiment on gut length, including both sexes. All individuals carry the $Sox10^{Dom}$ mutation.

Usage

```
gutlength
```

Format

An object of class `cross`. See `qtl::read.cross()` for details.

Details

A mouse intercross between C3HeBFeJ (C3) and C57BL/6J (B6), with one F1 parent carrying the $Sox10^{Dom}$ mutation. There are 1068 mice from reciprocal intercrosses. Over 2000 mice were generated, but only those individuals heterozygous at $Sox10^{Dom}$ were genotyped and included in the data set. $Sox10$ is on chromosome 15, and so that chromosome exhibits an unusual segregation pattern. Some mice received the mutation from their mother and some from their father.

The primary phenotype here is gut length (in cm). The phenotype `cross` indicates the cross used to generate an animal.

Source

E. Michelle Southard-Smith, Division of Genetic Medicine, Department of Medicine, Vanderbilt University School of Medicine, <michelle.southard-smith@vanderbilt.edu>

References

Owens, S. E., Broman, K. W., Wiltshire, T., Elmore, J. B., Bradley, K. M., Smith, J. R. and Southard-Smith, E. M. (2005) Genome-wide linkage identifies novel modifier loci of aganglionosis in the $Sox10^{Dom}$ model of Hirschsprung disease. *Hum. Mol. Genet.* **14**, 1549–1558.

Broman, K. W., Sen, \'S, Owens, S. E., Manichaikul, A., Southard-Smith, E. M. and Churchill G. A. (2006) The X chromosome in quantitative trait locus mapping. *Genetics* **174**, 2151–2158.

See Also

`iron`, `myocard`, `nf1`, `ovar`, `trout`

Examples

```
data(gutlength)
library(qtl)
plot(gutlength)
```

`iron` *Iron levels intercross data*

Description

Data from a mouse intercross experiment (using the C57BL/6J/Ola and SWR/Ola strains) on basal iron levels in the liver and spleen.

Usage

```
iron
```

Format

An object of class `cross`. See `qtl::read.cross()` for details.

Details

An intercross with 284 individuals (including both sexes and both cross directions), each with measures of iron (in $\mu g/g$) in the liver and spleen.

Source

Andrew G. Smith, MRC Toxicology Unit, <ags5@le.ac.uk>

References

Grant, G. G., Robinson, S. W., Edwards, R. E., Clothier, B., Davies, R., Judah, D. J., Broman, K. W. and Smith, A. G. (2006) Multiple polymorphic loci determine basal hepatic and splenic iron status in mice. *Hepatology* **44**, 174–185.

See Also

`link{gutlength}`, `link{myocard}`, `link{nf1}`, `link{ovar}`, `link{trout}`

Examples

```
data(iron)
library(qtl)
plot(iron)
```

`myocard` *Myocarditis intercross data*

Description

Data from a mouse intercross experiment on myocarditis.

Usage

```
myocard
```

Format

An object of class `cross`. See `qtl::read.cross()` for details.

Details

An intercross between the H-2s congenic mice A.SW and B10.S, with 296 individuals (including both sexes). The mice were injected with purified murine cardiac myosin, and the area of infiltrated myocardium in heart sections was measured. The phenotype is the percent myocarditis.

Source

Noel R. Rose, Department of Pathology, Johns Hopkins University, <nrrose@biostat.wisc.edu>

References

Guler, M. L, Ligons, D. L., Wang, Y., Bianco, M., Broman, K. W. and Rose, N. R. (2005) Two autoimmune diabetes loci influencing T cell apoptosis control susceptibility to experimental autoimmune myocarditis. *J. Immunol.* **174**: 2167–2173.

See Also

`link{gutlength}`, `link{iron}`, `link{nf1}` `link{ovar}`, `link{trout}`

Examples

```
data(myocard)
library(qtl)
plot(myocard)
```

nf1 *Neurofibromatosis type 1 backcross data*

Description

Data from a backcross experiment on neurofibromatosis type I. All individuals carry the *NPcis* mutation, received either from their mother or from their father.

Usage

```
nf1
```

Format

An object of class `cross`. See `qtl::read.cross()` for details.

Details

Backcrosses (C57BL/6J x A/J) x C57BL/6J and C57BL/6J x (A/J x C57BL/6J) with a total of 254 individuals. Individuals received the *NPcis* mutation from either their mother or their father (indicated by the phenotype `from.mom`. The major phenotype, `affected` indicates whether the mice were affected (1) or unaffected (0) with neurofibromatosis type 1.

References

Reilly, K. M., Broman, K. W., Bronson, R. T., Tsang, S., Loisel, D. A., Christy, E. S., Sun, Z., Diehl, J., Munroe, D. J. and Tuskan, R. G. (2006) An imprinted locus epistatically influences *Nstr1* and *Nstr2* to control resistance to nerve sheath tumors in a neurofibromatosis type 1 mouse model. *Cancer Research* **66**, 62–68. #' @source Karlyne Reilly, Mouse Cancer Genetics Program, National Cancer Institute at Frederick, <kreilly@ncifcrf.gov>

See Also

`link{gutlength}` `link{iron}`, `link{myocard}`, `link{ovar}`, `link{trout}`

Examples

```
data(nf1)
library(qtl)
plot(nf1)
```

ovar *Interspecific backcross in Drosophila*

Description

Data on ovariole number in a backcross between *D. simulans* and *D. sechellia*; the majority of individuals were selected to be recombinant in the region of a putative QTL on chromosome 3.

Usage

```
ovar
```

Format

An object of class `cross`. See `qtl::read.cross()` for details.

Details

The data come from an interspecific Drosophila backcross. *D. simulans* was crossed to *D. sechellia*, and the F_1 hybrid was crossed back to *D. simulans*.

The phenotype of interest was ovariole number in females (a measure of fitness). Phenotypes `on1` and `on2` are the ovariole counts in the left and right gonads. The phenotype `onm` is the average of the two counts; for many individuals, the ovariole count for one of two gonads was missing, and so `onm` is missing.

In an initial cross of 402 individuals, 383 had complete phenotype data. Initial genotyping focused on 94 individuals with extreme phenotype.

To increase the resolution of a major QTL identified on chromosome 3, a second cross of approximately 7000 flies was performed, though only 1050 individuals showing a recombination event between two morphological markers, *st* (bright red eyes) and *e* (dark brown body), were phenotyped and genotyped; 1038 had complete phenotype data. The aim was to oversample recombinants of the region of the QTL.

There are genotype data for 24 markers on 3 chromosomes. (The fourth chromosome had one marker, but showed no effect and is not included in these data.)

The phenotype `cross` indicates whether an individual came from the first or second cross.

Alleles `"I"` and `"E"` refer to *D. simulans* and *D. sechellia*, respectively.

Source

Virginie Orgogozo, Department of Ecology and Evolutionary Biology, Princeton University, `<virginie.orgogozo@normale`

References

Orgogozo, V., Broman, K. W. and Stern, D. L. (2006) High-resolution QTL mapping reveals sign epistasis controlling ovariole number between two Drosophila species. *Genetics* **173**, 197–205.

See Also

link{gutlength}, link{iron}, link{myocard}, link{nf1}, link{trout}

Examples

```
data(ovar)
library(qtl)
plot(ovar)
```

---

trout *Rainbow trout doubled haploid data*

Description

Data from doubled haploid individuals derived from a cross between Oregon State University (OSU) and Clearwater (CW) River rainbow trout clonal lines.

Usage

```
trout
```

Format

An object of class `cross`. See `qtl::read.cross()` for details.

Details

Doubled haploid individuals were produced from a cross between Oregon State University (OSU) and Clearwater (CW) river rainbow trout (*Oncorhynchus mykiss*) clonal lines. Eggs from one of eight outbred females, two from Troutlodge (TL) and six from Spokane (SP), were irradiated to destroy maternal nuclear DNA and fertilized with sperm from a single F_1 male. The first embryonic cleavage was blocked by heat shock to restore diploidy. There are a total of 554 individuals, with between 8 and 168 individuals from each of the eight females.

The primary phenotype is time to hatch (`tth`). An additional "phenotype", `female`, indicates maternal cytoplasmic environment (the source of the egg).

There are genotype data on 171 markers on 28 linkage groups. The linkage groups are named as in Nichols et al. (2002), though a pair of markers are assigned to linkage group "un", as they don't connect to any of the linkage groups in Nichols et al. (2002).

Note that the data have cross type `"dh"` (for doubled haploids); in R/qtl they are treated just like a backcross, except that genotypes are referred to as the homozygotes.

Source

Krista M. Nichols, Department of Biological Sciences, Purdue University, <kmnichol@purdue.edu>

References

Nichols, K. M., Broman, K. W., Sundin, K., Young, J. M., Wheeler, P. A. and Thorgaard, G. H. (2007) Quantitative trait loci by maternal cytoplasmic environment interaction for development rate in *Oncorhynchus mykiss*. *Genetics* **175**, 335–347.

Nichols, K. M., Young, W. P., Danzmann, R. G., Robison, B. D., Rexroad, C., Noakes, M., Phillips, R. B., Bentzen, P., Spies, I., Knudsen, K., Allendorf, F. W., Cunningham, B. M., Brunelli, J., Zhang, H., Ristow, S., Drew, R., Brown, K. H., Wheeler, P. A. and Thrgaard, G. H. (2002) A consolidated linkage map for rainbow trout (*Oncorhynchus mykiss*). *Animal Genetics* **34**, 102–115.

See Also

`link{gutlength}`, `link{iron}`, `link{myocard}`, `link{nf1}`, `link{ovar}`

Examples

```
data(trout)
library(qtl)
plot(trout)
```

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