Package ‘qtlbook’

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**Description**

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

**Usage**

data(ch3a)

**Format**

An object of class `cross`. See `read.cross` for details.

**Details**

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

**Source**

Karl W Broman, <kbroman@biostat.wisc.edu>

**References**


**See Also**

`ch3b`, `ch3c`

**Examples**

data(ch3a)

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

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

Description

Anonymous data with markers showing severe segregation distortion.

Usage

data(ch3b)

Format

An object of class cross. See read.cross for details.

Details

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

Source

Karl W Broman, <kbroman@biostat.wisc.edu>

References


See Also

ch3a, ch3c

Examples

data(ch3b)

thetab <- geno.table(ch3b)
plot(-log10(thetab[, ncol(thetab)]), ylab=expression(-log[10](P)))
thetab[thetab[, ncol(thetab)] < 1e-6,
Data with misplaced markers

Description
Anonymous data with markers out of place.

Usage
data(ch3c)

Format
An object of class cross. See read.cross for details.

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

Source
Karl W Broman, <kbroman@biostat.wisc.edu>

References

See Also
ch3a, ch3b

Examples
data(ch3c)

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

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

Usage

data(gutlength)

Format

An object of class \textit{cross}. See \texttt{read.cross} for details.

Details

A mouse intercross between C3HeBFeJ (C3) and C57BL/6J (B6), with one F1 parent carrying the \textit{Sox10}^{Dom} mutation. There are 1068 mice from reciprocal intercrosses. Over 2000 mice were generated, but only those individuals heterozygous at \textit{Sox10}^{Dom} were genotyped and included in the data set. \textit{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 \textit{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, \texttt{michelle.southard-smith@vanderbilt.edu}

References


See Also

\texttt{iron, myocard, nfl, ovar, trout}

Examples

data(gutlength)
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

data(iron)

Format

An object of class cross. See 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


See Also

`gutlength, myocard, nf1, ovar, trout`

Examples

data(iron)
plot(iron)
myocard

Description

Data from a mouse intercross experiment on myocarditis.

Usage

data(myocard)

Format

An object of class cross. See 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


See Also

gutlength, iron, nf1 ovar, trout

Examples

data(myocard)
plot(myocard)
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
data(nf1)

Format
An object of class cross. See 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.

Source
Karlyne Reilly, Mouse Cancer Genetics Program, National Cancer Institute at Frederick, <kreilly@ncifcrf.gov>

References

See Also
gutlength iron, myocard, ovar, trout

Examples
data(nf1)
plot(nf1)
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

data(ovar)

Format

An object of class `cross`. See `read.cross` for details.

Details

The data come from an interspecific Drosophila backcross. *D. simulans* was crossed to *D. sechellia*, and the F1 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 omn is the average of the two counts; for many individuals, the ovariole count for one of two gonads was missing, and so omn 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@normalesup.org>

References

trout

See Also
gutlength, iron, myocard, nf1, trout

Examples
data(ovar)
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
data(trout)

Format
An object of class cross. See 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


See Also
gutlength, iron, myocard, nf1, ovar

Examples
data(trout)
plot(trout)
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