Package 'dartR.data'

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Title Auxiliary Data Package for Our Main Package 'dartR'

Version 1.2.7

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Revision Generous Gecko

Description Data package for 'dartR'. Provides data sets to run examples in 'dartR'.
This was necessary due to the size limit imposed by 'CRAN'. The data in 'dartR.data'
is needed to run the examples provided in the 'dartR' functions.
All available data sets are either based on actual data (but reduced in size)
and/or simulated data sets to allow the fast execution of examples and demonstration
of the functions.

Depends R (>= 3.5)

Imports methods, utils, crayon, adegenet (>= 2.0.0)

License GPL (>= 3)

LazyData true

LazyDataCompression xz

Encoding UTF-8

NeedsCompilation no

RoxygenNote 7.3.3

URL https://github.com/green-striped-gecko/dartR.data

BugReports https://groups.google.com/g/dartr?pli=1

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`bandicoot.gl` *A dartR object created via the read.dart functions*

Description

This a test data set to test the validity of functions within dartR and is based on a DArT SNP data set of simulated bandicoots across Australia. It contains 96 individuals and 1000 SNPs.

Usage

```
bandicoot.gl
```

Format

genlight object

Author(s)

Bernd Gruber (bugs? Post to https://groups.google.com/d/forum/dartr

EYR — *Eastern yellow robin (EYR) DArT data in a genlight object*

Description

Genetic data from EYR collected in VIC, Australia by researchers at Monash University. The data comes in the form of a genlight object ready to be used by dartR. The file contains data for 782 individuals from 4 populations and 1,000 binary SNPs. The dataset contains a mix of autosomal and sex-linked loci.

Usage

```
EYR
```

Format

genlight object

Author(s)

Custodian: Diana Robledo-Ruiz – Post to https://groups.google.com/d/forum/dartr

References

Robledo-Ruiz et al. (2023) Easy-to-use R functions to separate reduced-representation genomic datasets into sex-linked and autosomal loci, and conduct sex assignment. *Mol. Ecol. Res.* (doi:10.1111/17550998.13844)

LBP — *Laedbeater's possum (LBP) DArT data in a genlight object*

Description

Genetic data from LBP collected in VIC, Australia by researchers at Monash University. The data comes in the form of a genlight object ready to be used by dartR. The file contains data for 376 individuals from 2 populations and 1,000 binary SNPs. The dataset contains a mix of autosomal and sex-linked loci.

Usage

```
LBP
```

Format

genlight object

Author(s)

Custodian: Diana Robledo-Ruiz – Post to https://groups.google.com/d/forum/dartr

References

Robledo-Ruiz et al. (2023) Easy-to-use R functions to separate reduced-representation genomic datasets into sex-linked and autosomal loci, and conduct sex assignment. *Mol. Ecol. Res*. doi:10.1111/17550998.13844

`platy` *Example data set as text file to be imported into a genlight object*

Description

Check ?read.genetable in pacakge PopGenReport for details on the format.

Format

csv

Author(s)

Bernd Gruber (bugs? Post to https://groups.google.com/d/forum/dartr

Examples

```
## Not run:
library(PopGenReport)
fp <- file.path(system.file( package="dartR.data"),"extdata/platy.csv")
read.csv(fp)
platy <- read.genetable(fp, ind=1, pop=2, lat=3, long=4, other.min=5, other.max=6,
oneColPerAll=FALSE, sep='/')
platy.gl <- gi2gl(platy, parallel=FALSE)
df.loc <- data.frame(RepAvg = runif(nLoc(platy.gl)), CallRate = 1)
platy.gl@other$loc.metrics <- df.loc
gl.report.reproducibility(platy.gl)

## End(Not run)
```

platypus.gl *A genlight object created via the gl.read.dart function*

Description

This is a test data set on platypus with 81 individuals, 3 populations and 1,000 binary SNPs.

Usage

```
platypus.gl
```

Format

genlight object

Author(s)

Luis Mijangos (bugs? Post to https://groups.google.com/d/forum/dartr

possums.gl *A simulated dartR object created to run a landscape genetic example*

Description

This a test data set to run a landscape genetics example. It contains 10 populations of 30 individuals each and each individual has 300 loci. There are no covariates for individuals or loci.

Usage

```
possums.gl
```

Format

genlight object

Author(s)

Bernd Gruber (bugs? Post to https://groups.google.com/d/forum/dartr

testset.gl — *A genlight object created via the gl.read.dart function*

Description

This is a test data set on turtles. 250 individuals, 255 loci in >30 populations.

Usage

```
testset.gl
```

Format

genlight object

Author(s)

Custodian: Arthur Georges (bugs? Post to https://groups.google.com/d/forum/dartr

testset.gs — *A genlight object created via the gl.read.silicodart function*

Description

This is a test data set on turtles. 218 individuals, 255 loci in >30 populations.

Usage

```
testset.gs
```

Format

genlight object

Author(s)

Custodian: Arthur Georges (bugs? Post to https://groups.google.com/d/forum/dartr

testset2.gl — *A genlight object with a known-pedigree captive population, for kinship analyses*

Description

An augmented companion to testset.gl. 274 individuals, 755 loci in 31 populations. Extends testset.gl with a captive-bred population (EmmacCaptBred, n = 24) with known pedigree structure - parent-offspring, full-sib, half-sib and first-cousin pairs bred from six wild-caught founders drawn from six different populations - for testing kinship-based analyses. Pedigree truth (sire, dam, cohort) and COLONY-style offspring/mother/father flags are recorded in ind.metrics. 500 of the loci are simulated (CloneID prefix SIM) with intermediate allele frequencies and Balding-Nichols population structure so that kinship classes are statistically recoverable; the original 255 DArT loci and 250 wild individuals are unchanged from testset.gl.

Usage

```
testset2.gl
```

Format

genlight object

Author(s)

Custodian: Arthur Georges (bugs? Post to https://groups.google.com/d/forum/dartr

testset2.gs — *A genlight object (SilicoDArT) with a known-pedigree captive population*

Description

An augmented companion to testset.gs. 242 individuals, 755 loci in 30 populations. Companion to testset2.gl: includes the same captive-bred population (EmmacCaptBred, n = 24, same individual ids and pedigree - parent-offspring, full-sib, half-sib and first-cousin pairs) with pedigree truth (sire, dam, cohort) and COLONY-style offspring/mother/father flags in ind.metrics; founders re-selected where the testset2.gl founders are absent from this dataset (same one-founder-per-population design). 500 of the loci are simulated presence/absence markers (CloneID prefix SIM) with Balding-Nichols population structure; offspring bands follow Mendelian inheritance of latent presence alleles. The original 255 SilicoDArT loci and 218 wild individuals are unchanged from testset.gs.

Usage

```
testset2.gs
```

Format

genlight object

Author(s)

Custodian: Arthur Georges (bugs? Post to https://groups.google.com/d/forum/dartr

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testset_metadata *Metadata file. Can be integrated via the dart2genlight function.*

Description

Metadata file. Can be integrated via the dart2genlight function.

Format

csv

Author(s)

Custodian: Arthur Georges (bugs? Post to https://groups.google.com/d/forum/dartr

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testset_pop_recode *Recode file to be used with the function.*

Description

This test data set is provided to show a typical recode file format.

Format

csv

Author(s)

Custodian: Arthur Georges (bugs? Post to https://groups.google.com/d/forum/dartr

testset_SNPs_2Row *Testfile in DArT format (as provided by DArT)*

Description

This test data set is provided to show a typical DArT file format. Can be used to create a genlight object using the read.dart function.

Format

csv

Author(s)

Custodian: Arthur Georges (bugs? Post to https://groups.google.com/d/forum/dartr

YTH *Yellow-tufted honeyeater (YTH) DArT data in a genlight object*

Description

Genetic data from YTH collected in VIC, Australia by researchers at Monash University. The data comes in the form of a genlight object ready to be used by dartR. The file contains data for 641 individuals from 8 populations and 1,000 binary SNPs. The dataset contains a mix of autosomal and sex-linked loci.

Usage

```
YTH
```

Format

genlight object

Author(s)

Custodian: Diana Robledo-Ruiz – Post to https://groups.google.com/d/forum/dartr

References

Robledo-Ruiz et al. (2023) Easy-to-use R functions to separate reduced-representation genomic datasets into sex-linked and autosomal loci, and conduct sex assignment. *Mol. Ecol. Res.* (doi:10.1111/17550998.13844)

zzz *dartR.data Imports data for examples in dartR.base*

Description

dartR.data Imports data for examples in dartR.base

Usage

```
zzz
```

Format

An object of class `NULL` of length 0.

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