Package ‘dartR.data’

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Title Auxiliary Data Package for Our Main Package 'dartR'

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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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Contents

`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`

`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

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`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

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`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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