# Package 'popgenr'

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**Type** Package

**Title** Accompaniment to the Book Population Genetics with R: An Introduction for Life Scientists

**Version** 0.1

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**Description** Provides several data sets and a linkage disequilibrium function to accompany the book ``Population Genetics with R: An Introduction for Life Scientists''.

**License** CC0

**Encoding** UTF-8

**LazyData** true

**NeedsCompilation** no

**Depends** R (>= 3.5.0)

**Repository** CRAN

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## R topics documented:

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## `Dcalc` *Calculate and visualize LD*

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### Description

Calculates the degree of linkage disequilibirum between two biallelic diploid loci and plots the results.

### Usage

```
Dcalc(AABB, AaBB, aaBB, AABb, AaBb, aaBb, AAbb, Aabb, aabb)
```

### Arguments

| | |
|---|---|
| `AABB` | Count of A and B double homozygotes. |
| `AaBB` | Count of A heterozygotes, B homozygotes. |
| `aaBB` | Count of a and B double homozygotes. |
| `AABb` | Count of A homozygotes, B heterozygotes. |
| `AaBb` | Count of double heterozygotes. |
| `aaBb` | Count of a homozygotes, B heterozygote. |
| `AAbb` | Count of A and b double homozygotes. |
| `Aabb` | Count of A heterozygotes, b homozygotes. |
| `aabb` | Count of a and b double homozygotes. |

### Examples

```
#assign genotype counts
AABB=2
AaBB=0
aaBB=0
AABb=0
AaBb=1
aaBb=0
AAbb=1
Aabb=0
aabb=0

#run function
Dcalc(AABB, AaBB, aaBB, AABb, AaBb, aaBb, AAbb, Aabb, aabb)
```

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## `fly` *Drosphila melanogaster bw75 data*

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### Description

A matrix of observed allele counts from Buri (1956). Each row contains observations starting at generation 1 in the first row, across 107 replicates of the number of bw75 allele.

### Usage

```
fly
```

### Source

Buri, P. (1956). "Gene frequency in small populations of mutant Drosophila" <doi:10.1111/j.1558-5646.1956.tb02864.x>

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## `genotypes` *Genotype data from Aleppo Pines*

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### Description

Multiple sampled alleles from Aleppo Pine (Pinus halepensis) in the Eastern Mediterranean. Adapted from Gershberg et al. 2016.

### Usage

```
genotypes
```

### Source

Gershberg, A., Ne'eman, G., Ben-Shlomo, R. (2016) "Genetic structure of a naturally regenerating post-fire seedling population: Pinus halepensis as a case study" <doi:10.3389/fpls.2016.00549>

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## `moth` *Temporal allele frequency shifts*

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### Description

Change in allele frequency over eight generations in the scarlet tiger moth (Callimorpha dominula).

### Usage

```
moth
```

### Source

Fisher, R.A. and E.B. Ford (1947) "The Spread of a Gene in Natural Conditions in a Colony of the Moth Panaxia dominula" <doi:10.1038/hdy.1947.11>

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## `snp` *SNP information for 25 loci*

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### Description

Single Nucleotide Polymorphism data for 25 loci from the 1,000 Genomes Project (http://www.internationalgenome.org). Includes information on allele frequency, homozygosity, heterozygosity, chromosome location, and functional location of SNP.

### Usage

```
snp
```

### Source

Auton, A., Abecasis, G., Altshuler, D. et al. (2015) "A global reference for human genetic variation" <doi:10.1038/nature15393>

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`thirteen` *Genotypes across 13 CODIS loci*

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## Description

Genotypes of 1,036 individuals across 13 core CODIS (Combined DNA Index System) loci, collected in the USA.

## Usage

```
thirteen
```

## Source

Hill, C.R., Duewer, D.L., Kline, M.C., Coble, M.D., Butler, J.M. (2013) "U.S. population data for 29 autosomal STR loci" <doi:10.1016/j.fsigen.2012.12.004>

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`whale` *Genotypes of 246 South Pacific Blue Whales*

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## Description

Data frame of genotypes collected from 264 individual blue whales (Balaenoptera musculus) across seven distinct loci. Adapted from Attard et al. 2012.

## Usage

```
whale
```

## Source

Attard, C. R., Beheregaray, L. B., Jenner, K. C. S., Gill, P. C., Jenner, M. N., Morrice, M. G., Robertson, K.M. & Moller, L. M. (2012) "Hybridization of Southern Hemisphere blue whale subspecies and a sympatric area off Antarctica: impacts of whaling or climate change?"<doi:10.1111/mec.12025>

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