

# Package ‘popgenr’

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**Type** Package

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

**Version** 0.2

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**Description** Provides several data sets and functions to accompany the book ``Population Genetics with R: An Introduction for Life Scientists'' (2021, ISBN:9780198829546).

**License** CC0

**Encoding** UTF-8

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coal	<i>Simulate and visualize a coalescent process</i>
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### Description

A function that provides a simple starting off point to simulate a coalescent process.

### Usage

```
coal(length, number, muscale, reps, prnt)
```

### Arguments

length	Length of sequence to simulate.
number	Number of starting lineages.
muscale	Mutation rate, scaled by 4Neu.
reps	Number of replicates to run.
prnt	Whether to print calculation output to the terminal (prnt=1), or not (prnt=0).

### Examples

```
#assign genotype counts
length=250

number=8

muscale=6.25 # theta = 4Neu = 25, theta/4 = 6.25

reps=100

prnt=0

#run function
coal(length, number, muscale, reps, prnt)
```

Dcalc	<i>Calculate and visualize LD</i>
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### Description

Calculates the degree of linkage disequilibrium 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*Drosophila 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. Evolution, 10, 367-402.

genotypes

*Genotype data from Aleppo Pines***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. *Frontiers in Plant Science* 7: 549.

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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*. *Heredity* 1: 143-174.

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snp *SNP information for 25 loci*

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### Description

Single Nucleotide Polymorphism data for 25 loci. Includes information on allele frequency, homozygosity, heterozygosity, chromosome location, and functional location of SNP.

### Usage

snp

### Source

1,000 Genomes Project (<http://www.internationalgenome.org>)

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thirteen *Genotypes across 13 CODIS loci*

---

### 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., and Butler, J.M. (2013) U.S. population data for 29 autosomal STR loci. *Forensic Sci. Int. Genet.* 7: e82-e83. Accessed from: <https://strbase.nist.gov/fbicore.htm>

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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. and Moller, L. M. (2012). Hybridization of Southern Hemisphere blue whale subspecies and a sympatric area off Antarctica: impacts of whaling or climate change? *Molecular Ecology*, 21(23), 5715-5727.

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