

studbookR: Introduction

Frank PG Princee

Draft 2016-12-29

Introduction

The **studbookR** package contains a large number of demographic and genetic analyses for studbook-like data. These analyses can be grouped in the following categories:

1. Natural history
2. Census
3. Life tables
4. Population projection
5. Survival analysis
6. Inbreeding depression
7. Quantitative genetics

Vignettes for each of these categories are available.

Studbook projects

The data for **studbookR** analyses are organised per studbook project. In this documentation it is assumed that these data are created by the *Population Management Library (PML)* software.

The analyses in this package are not restricted to data generated by PML. Vignette “9. Data files” provides information on data fields required for each analysis.

Quick start

Load the **studbookR** package, and select an existing studbook project from a menu list:

```
library(studbookR)
studbook()
```

A numbered list with available studbook projects will be displayed for selection. For example:

```
Select project number (0=cancel):
```

```
1: ailurus          2: cephalophus      3: damaliscus      4: ursus
```

The project name can also be entered directly:

```
studbook("ursus")
```

Explore studbookR

The *studbookR* package includes data from a real-time studbook named **animal** that can be used to explore the various (statistical) analyses when no PML projects are available.

```
tutorial()  
studbook("animal")
```

The vignettes included in this R package introduce the various analyses with basic (default) settings. The help pages of *studbookR* provide more detailed information on each analysis.

Re-set the analysis mode from tutorial to studbooks with the following command:

```
pml()
```