PML Tutorial

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Introduction

The analyses in the *Population Management Library - (PML)* can be accessed through a command-line program. This program uses a script language to set data filters and to invoke analyses. These commands can be used interactively or are passed on the command-line as a script file with multiple commands in plain ASCII text (see e.g. animal.pml). The various script commands are described in the PML manual (stand-alone PDF or integrated as html).

The first time you use PML, it will create the folder (=directory) **pml** with the subfolders *projects*, *report*, *scripts* and *studbooks* in your home directory e.g. *C:\Users\your_name* (Windows) or */Users/your_name* (Linux, macOS and Unix). The symbol ~ is used to represent the home folder.

Projects

PML works with projects that link to a studbook. Multiple projects can be created using the same studbook but with different (permanent) data filters e.g. subspecies or regional population.

Project example *animal*

The Population Management Library (PML) includes the tutorial project *animal*. This project uses a studbook that is based on a real SPARKS data-set. The original data have been modified by removing early history data, changing studbook ID's, shifting month and year in dates of births and deaths and re-assigning locations randomly from the SPARKS institution list. This modified studbook is stored in a SQLite3 database. The tables and field names are the same as in the original dBase format.

Follow the procedures below to install the example project *animal*.

1. Start PML. macOS users: Dialog boxes to select a project and a script file, respectively, are shown when projects have already been created. Select and .

2. Enter the following command at the PML dot prompt:

```
pml > create project 'animal'
pml > save project
pml > exit
```

3. Unzip the file *example.zip* in a folder of choice. This will create the subfolder *example*. Copy the following files:

```
animal.studbook => ~/pml/studbook/animal.studbook        # SQLite3 studbook
animal.pml      => ~/pml/scripts/animal.pml              # Script command file
animal.biology  => ~/pml/projects/animal/animal.biology  # Species related data
animal.project  => ~/pml/projects/animal/animal.project  # Project information
animal.stages   => ~/pml/projects/animal/animal.stages   # Stages based on age ranges
```

Running PML

The PML "engine" has been developed as a terminal or console application that accepts (a few) parameters from the command-line. The macOS version includes a small wrapper that allows to select an existing project and/or a script file. The Windows version starts directly in interactive mode.

```
pml > set project to "animal"
pml > load project current
pml > load studbook
```

Commands to set view filters and run analyses can be entered directly at the PML prompt. For example:

```
pml > compute generation      # Calculates generation number
pml > compute inbreeding      # Calculates inbreeding coefficients
pml > init location view      # De-selects all locations
pml > set population to 'Europe'
pml > compute litter season   # Birth season (litters) in Europe
pml > set sex to female       # Restrict analyses to females
pml > compute fecundity       # Compute age-specific fecundity
```

Read the PML Script Manual for available analyses and view filters. The example file *animal.pml* is also a good source to become acquainted with script commands.

Reports

Reports are stored in XML format in the folder *~/pml/projects/animal/reports*. These files contain layout information and can be displayed in a web browser. A main menu to view reports is available by entering the command *reports* in PML or by selecting the file "index.html" in the folder ~/pml/report. The latter option may not work in all browsers, in which case reports have to be selected individually.

studbookR

The PML program exports both raw (filtered) studbook data and analyses results as tab-delimited ASCII files. These files can be imported by the R package **studbookR** for further statistical analyses and/or production of graphics (in various formats). See the information that is part of the *studbookR* package (including tutorial).

Import SPARKS studbooks

The PML program can import studbook data that are stored in SQLite3 databases which have the same table structures as SPARKS. The conversion from dBase to SQL format can be carried out within PML.

SPARKS studbooks are expected to be stored as subfolder under the folder *C:/ISISdosbox/SPARKS* on Windows (note that PML expects forslashes) or in the user folder *~/ISISdosbox/SPARKS* on macOS, by default. This path can be changed within PML.

Start PML in interactive mode to import (convert) a SPARKS database.

```
set sparks path to "<path-to-sparks>" # when path differs from default
import sparks "<name>"                # Converts SPARKS studbook <name> to database
                                      # <name>.studbook
```

The next step is to create a project for the newly imported studbook :

```
create project "<project-name>"
set studbook database to "<name>.studbook"
save project
load studbook

# Add species specific data (a selection):
set common name to "<common name>"
set latin name to "<scientific name>"
set gestation length to 99.0 days # format 999.9
set reproductive system to viviparous
save biology
```

Script files

Script files can be executed in interactive mode with the command *run*:

```
pml > run "animal.pml"
```

The macOS version provides an option to select a script file before the actual PML program is started. Note that the program will end after the last command has been executed.