PML Script Language

1.0.2

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Contents

Chapter 1

PML script

The PML script is used to set parameters and run demographic and genetic analyses in the command-line interface of the Population Management Library (**PML**).

Commands can be entered interactively on the command-line or passed as a script file. The latter option allows to run the shell as an 'engine' which can be invoked from, for example, a graphical shell.

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Command list

Chapter 2

Project Folders

The main folder **pml** is stored in the home directory (symbol ∼).

e.g. project `animal`

```
Home directory
 |
 +--[pml]
    |
    +--[projects]
    |   | projects.xml
    |   |
    |   +--[animal]
    |       | reports.xml
    |       |
    |       +--[export]
    |       |  age-20140519-male.csv
    |       +--[graphics]
    |       +--[reports]
    |       |  age-20140519-male.xml
    |       +--[views]
    |          animal.view
    |          southern_europe.fed
    |       animal.biology
    |       animal.project
    |
    +--[report]
    |   |index.html
    |   |pml.js
    |   |
    |   +--[xsl]
    |      age.xsl
    |      projects.xsl
    +--[scripts]
    |   animal.pml
    |
    +--[studbooks]
        animal.sparks
```

Results of PML analyses are stored in **XML** files in the project folder (= directory) **reports** and/or as tab delimited text files in **export** .

Command list

Chapter 3

Version history

Version

1.0.2

Since

30 January 2017

- Added command `run` to run file scripts while in interactive mode

15 December 2016

- Added commands to create SQLite3 database from SPARKS studbook
- Changed command `compute viability` to `compute lethal` (equivalents)

Version

1.0.0

Since

08 November 2014

- Version used for analyses in Exploring studbooks for Wildlife Management and Conservation.
- Added commands set/get left truncation and set/get right censored

29 October 2014

- Removed command `run R`; R is intended to be launched in the background from a GUI program.

21 October 2014

- Added commands load location, list location view and list views.
- Changed command list view to list active view
- Added parameter RISK and BIRTH to compute fecundity

Version

0.4

Since

23 May 2014
  - Adapted code to C++11 standards
  - Added commands export fecundity and survival (Kaplan Meier estimator)

01 June 2012
  - Added command export pedigree as TAB delimited csv

02 May 2011
  - Added command compute first breeding

04 November 2010
  - Added command to run R with package studbookR in background

28 October 2010
  - Added commond set/get rearing

06 July 2010
  - The generation function applies 4 methods in one computation
  - Added rule to compute & save all genetics that refer to individuals (e.g. inbreeding, lineage)

10 April 2010
  - Added option to compute maternal and average generation

27 January 2010
  - Added parameter regarding offspring viability to birth season

09 December 2009
  - Added command: compute growth rate

17 November 2009
  - Added commands: set/get origin
  - Added command : set location to 'level' 'deme'
  - Added commands: set population to 'regions', get population

05 June 2009
  - Added function to export inbreeding coefficient/longevity

25 May 2009
  - Added commmands handle subspecies

18 April 2009
  - Added 'set' commands to enter integer representations of enumerations
  - Added handle sex in case of unknowns

02 April 2008
  - Added command gene drop

12 March 2008
  - Added command to list founders

16 January 2008
  - Added command message to display text on console

03 January 2008
  - Added command to list and save life history (biology) data

05 November 2007
  - Implemented new field classes for data filters
  - Extend studbook listings to select active view
  - Added set/get for contraception views

Version

0.3

Since

20 July 2007

- Added get functions for all parameters that are set

17 July 2007

- Changed command *help index* to *help contents* (which calls contents.html)

24 April 2007

- Implemented new date and date format settings

20 April 2007

- Adapted accuracy levels to new names, and implemented hours in 'lifespan' data
- Removed all, neutered and contracepted male/female options from setsex()
- Removed selection of SQLite version 2 ad database system

06 April 2007

- Changed lifespan settings to double values

Version

0.2

Since

29 August 2005

- Changed commands to lowercase (and created case-sensitive lexer)

19 August 2005

- Adapted to change in name from PAM to PML

Version

0.1

Date

11 March 2005

Author

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Command list

Chapter 4

About PML

The Population Management Library (PML) can be used to analyse demographic and genetic trends in studbook-like populations. Management strategies can be based on the results of these analyses.

Although studbooks traditionally refer to management of domestic livestock and zoo populations, the PML library is by no means restricted to these *captive* populations. More and more data on individuals in *wild* populations, through long-term behavioural-ecological studies and conservation studies on endangered species, are available. In this sense, there is no difference in analyses between captive and wild populations.

The PML libraries find their origin in the analysis package of the Zooresearch Studbook Management - ZRBOOK (Princée,1989) and the genetic simulation models GeneFlow and ChromoFlow (Princée, 1985,1988, 1998). However, all demographic and genetic analyses have been redesigned and programmed from scratch in C++11.

Statistical analyses, including bootstrap techniques - have been added to the various demographic and genetic analyses.

PML exports data that are extracted from studbooks in tab delimited format for more extensive statistical analysis by the R package *studbookR* (Princée 2014).

Command list

Chapter 5

Analyses overview

The following demographic and genetic analyses are included in the PML libraries:

- Life-history analyses: longevity, reproductive life-span, inter-birth interval, litter/clutch size, seasonality
- Crude demographic analyses: census at given date, birth rate,death rate and migration rate
- Life table analyses: age distribution, age specific mortality, age specific fecundity, Kaplan-Meier estimator for surival and first offspring, life table analyses and Leslie's matrix
- Genetic analyses: generation number,inbreeding coefficients, founder representation, mean kinship, lethal equivalents, blood lineages, gene drop.

Command list

Chapter 6

Command syntax

PML commands can be entered interactively on the command-line or in script files. These commands are described in this manual.

Command parameters are presented with a dollar **$** sign. Text parameters are embedded in single quotes e.g. '$user_data'.

Single line commands can be included in **C++** style double forslashes // and the **Perl** style hash **#**. The C style / ∗ .... ∗ / is used to embed comments that span multiple lines.

Command list

6.1 add taxon

syntax: `add taxon '$name'`

Add taxon (subspecies) '$name' to list in the case a studbook includes subspecies

See also

list taxa

Command list

6.2 clear screen

syntax: `clear screen`

Clear the [console] screen. This command calls the system function to clear the screen.

Command list

6.3 clear studbook

syntax: `clear studbook`

Clears studbook data from memory

See also

load studbook

Command list

6.4 clear location

syntax: `clear location view`

Clears the view on locations (demes), which means that demes are selected.

See also

set population

Command list

6.5 clear taxon view

syntax: `clear taxon view`

Clears taxon filter

See also

set taxon, add taxon

Command list

6.6 clear view

syntax: `clear view`

Clear population view, and set to default settings

See also

load view

Command list

6.7 compute age distribution

syntax: `compute age distribution`

Compute age distribution at monitor date for different sexes. The default class width is one year and can be changed to intervals that are more appropiate for the longevity of the taxon involved.

Results are written to files with the basename "age-[YYYY-MM-DD]-[sex]"

See also

compute longevity, compute mortality

Command list

6.8 compute births

syntax: `compute births`

Compute number of births during specified date intervals.

Results are written to files with the basename "births-[sex]"

See also

set begin date, set end date, set census interval

Command list

6.9 compute census

syntax: `compute census`

Compute number of living animals at census dates during the period as set between start and end dates, and interval. Default the census date is 31 December and the census is carried annually

Results are written to files with the basename "census-[sex]"

See also

set begin date, set end date, set census interval

Command list

6.10 compute deaths

syntax: `compute deaths`

Compute number of deaths during specified date intervals from `start` to `end` date.

Results are written to files with the basename "births-[sex]".

See also

set begin date, set end date, set census interval

Command list

6.11 compute emigration

syntax: `compute emigration [to] (all|release|'$name')`

Computes animals leaving the selected population per census interval. Animals which are lost-to-follow-up (LTF) are not included in this view.

Results are written to files with the basename "immigration-[origin]-[sex]"

See also

compute immigration, set begin date, set end date, set census interval

Command list

6.12 compute fecundity

syntax: `compute fecundity`

Compute age specific fecundity rates between `start` and `end`. The default "class width" is set default to 1 year.

Results are written to files with the basename "fecundity-[sex]"; bootstrap results are stored compressed in file "bootstrap-Mx-[sex].csv.gz".

See also

compute reproductive life set begin date set end date set class width, compute first breeding, compute reproductive life

Command list

6.13 compute first breeding

syntax: `compute first breeding`

Compute mean and median first age at reproduction

Results are written to files with the basename "firstbreeding-[sex]".

See also

compute reproductive life, compute fecundity

Command list

6.14 compute founder representation

syntax: `compute founder (group|individual)`

Compute founder representation in group (population) or in individuals.

Results are written to files with the basename "founders-group-all" and "founders-indiv-all".

See also

compute lineage

Command list

6.15 compute generation

syntax: `compute generation`

Compute generation number of all individuals in the pedigree since population was founded. The generation number of founders is 0. The generation number of offspring is computed for the following methods:

- cites : add 1 to the generation number of the parent with the lowest generation number; rule used by CITES authorities
- genetic : add 1 to the generation number of the parent with the highest generation number (Princée,1988).
- maternal: add 1 to the generation number of the dam (Schwitzer and Kaumans,2009)
- average : add 1 to the average of average generation number of sire and dam (SPARKS, 1989)

Note

The generation number of offspring of `wildborn x F1` is F1 following CITES rules.

Command list

6.16 compute genetics

`compute` `genetics`

Compute genetic parameters such as inbreeding, generation for each individual and stores these in table genetics (SQLite databases only)

See also

compute inbreeding, compute founder representation, compute generation, compute lineage

Command list

6.17 compute growth rate

`syntax:` `compute growth rate`

Computes the fractional growth rate (**lambda**) from census data for the selected sex group

Note

Lambda is the **annual** growth rate when the census interval is set to 1 year.

Command list

6.18 compute immigration

`syntax:` `compute immigration [from] (all|captive|unknown|wild)`

Computes number of animals entering the selected population view per census interval. The option 'all' includes also animals which directly were imported from the source (which is/are generally wild) populations(s). 'wild' refers to individuals from the source (wild) population

Results are written to files with the basename "immigration-[origin]-[sex]"

See also

compute emigration

Command list

6.19 compute inbreeding

`syntax:` `compute inbreeding`

Compute inbreeding coefficients of all individuals in the pedigree. Individuals with both `WILD` parents are considered as unrelated to each other.

Note

Note Individuals with the same `WILDxx` parents, `UNKxx` or `MULTxx` are considered (full) siblings.

Command list

6.20 compute interbirth interval

syntax: `compute interbirth interval`

Compute interbirth interval. If the range in litter date has been set, the interval is computed from last date of the previous litter/clutch to first date of the litter/clutch

Results are written to files with the basename "birth_interval-female"

See also

set litter daterange

Command list

6.21 compute leslie matrix

syntax: `compute leslie matrix [for] $number`

Carry out future projections using Leslie's matrix. The projections are carried out for the sex as selected in view settings. This analysis requires that age distribution, fecundity and mortality rates have been computed. The used class width must be the same in these analyses.

$number refers to the number of time intervals that need to be computed. The time interval equals the class width as used in age distribution. For example, 25 means a future projection of 25 years if the class width is one year.

Results are written to files with the basename "leslie-[sex]"

See also

compute age distribution, compute fecundity, compute mortality

Command list

6.22 compute lifetable

syntax: `compute lifetable`

Compute reproductive values, life expentacy, growth rates and generation time from life tables. This analysis requires that fecundity and mortality rates for the sex as selected in view settings have been computed

Results are written to files with the basename "lifetable-[sex]".

See also

compute fecundity, compute mortality, compute leslie matrix

Command list

6.23 compute lineage

syntax: `compute (lineage|line)`

Compute blood lineages. Each founding individual is assigned an unique character-code. The number of characters in the code depends on the number of potential founders.

Results are written to file "lineages.xml"

See also

compute founder representation

Command list

6.24 compute littersize

syntax: `compute littersize`

Compute distribution of littersizes

Results are written to file "littersize.ml"

See also

compute fecundity, compute reproductive life

Command list

6.25 compute longevity

syntax: `compute longevity`

Compute lifespan and longevity

Results are written to files with the basename "lifespan-[sex]"

See also

compute mortality

Command list

6.26 compute mean kinship

syntax: `compute kinship`

Computes mean kinship and kinship value (if demographics data) are available for each individual in the population

Results are written to files with the basename "mean_kinship.csv" and "mating_table.csv".

See also

compute inbreeding, compute founder representation

Command list

6.27 compute mortality

syntax: `compute mortality`

Compute age-specific mortality rates between `begin` and `end` dates. The default width of age classes is one year.

Results are written to files with the basename "mortality-[sex]"; bootstrap results are stored compressed in file "bootstrap-Qx-[sex].csv.gz".

See also

compute longevity, set begin date, set end date

Command list

6.28 compute neonatal deaths

syntax: `compute neonatal deaths`

Compute fraction of new-born that died the end of the neonatal phase for each interval between census dates during between `start` and `end` dates.

Results are written to files with the basename "neonatal-[sex]".

See also

compute deaths, compute mortality, set begin date, set end date

Command list

6.29 compute reproductive life

`syntax:` `compute reproductive life`

Compute reproductive life-span: average age and lowest & highest range

Results are written to files with the basename "lifespan-[sex]".

See also

compute fecundity, compute first breeding

Command list

6.30 compute birth season

`syntax:` `compute birth season (all|stillbirth|nonviable|neonate|viable)`

Compute seasonality in births. The following filter criteria regarding survival of offspring can be set:

- `all` Include all births
- `stillbirth` Only stillbirths (death at age 0)
- `nonviable` All births between day 1 and end of neonatal age
- `neonate` All births between 0 and end of neonatal age
- `viable` All births of offsping surviving beyond the neonatal age

The data are grouped per month. The Raleigh test is used to test for a significant season

Results are written to files with the basename "birth_season-[sex]".

See also

compute litter season, set neonatal age

Command list

6.31 compute litter season

`syntax:` `compute litter season`

Compute seasonality in births but grouped as litters.

The data are grouped per month. The Raleigh test is used to test for a significant season

Results are written to files with the basename "litter_season-all".

See also

compute_birth_season, set_neonatal_age

Command list

6.32 compute death season

syntax: `compute death season`

Compute seasonality in deaths. The data are grouped per month. The Raleigh test is used to test for a significant season

Results are written to files with the basename "birth_season-[sex]". "litter_season-all" and "death_season-[sex]".

Command list

6.33 compute lethal

syntax: `compute lethal $days (both|inbred|single|none)`

Compute lethal equivalents from regression between inbreeding coefficient and survival rate until age $days (which can be a fraction).(default: 30.0 days) Lethal equivalents are computed for offspring of parents which are:

- both: both parents are inbred
- inbred: at least one of the parents is inbred
- single: only on the parents is inbred
- sire: sire is inbred, dam is not inbred
- dam: dam is inbred, sire is not inbred
- none: parents are both non-inbred

Results are written to files with the basename "lethaleqv-[parents]-[sex]".

See also

compute inbreeding, compute longevity

Command list

6.34 create project

syntax: `create project '$name'`

Create new project with `$name`, and load parameters.

See also

load project

Command list

6.35 edit a text file

syntax: `edit '$file'`

Invoke text editor as set by system and load `$file`

Command list

6.36 exclude neonates

syntax: `exclude neonates`

Exclude neonates in analyses.

See also

include_neonate

Command list

6.37 exclude stillbirths

syntax: `include stillbirths`

Exclude stillbirths i.e. all that died at day of birth in analyses.

See also

include_stillbirth

Command list

6.38 exit

syntax: `exit`

Exit command-line program or script processing.

Command list

6.39 export fields

syntax: `export fields`

Export fields of individual animal records that match the view filter to CSV format. The following fields are exported:

- inbreeding coefficient
- generation number
- age at death (blank if alive)

These data are stored in the file: "∼/pml/project/[project_name]/export/animal_data.csv"

Command list

6.40 export fecundity

syntax: `export (survival|fecundity) (stillbirth|alive)`

Creates censored fecundity age list to be used with external Kaplan-Meier estimator analysis.

Data are are exported to "kmfecundity-[sex].csv".

See also

export_survival

Command list

6.41 export pedigree

syntax: `export pedigree`

Export fields ID, SIRE, DAM, SEX ,BIRTHSITE, BIRTHDATE, DEATHDATE, STATUS, F, G,TAXON and BREEDER to `tab` delimited text file.

Wild and unknown parents are replaced with NA (not applicable) as used by various pedigree packages in R (e.g. MCMCglmm)

Data are exported to "pedigree.csv"."

Command list

6.42 export poplib

syntax: `export poplib`

Export master and transfer data to POPLIB format (to be used with DOS ChromoFlow version)

These data exportyed to the files: "STUDBOOK.DAT" and "STUDBOOK.TRF"

Command list

6.43 export survival

syntax: `export survival (stillbirth|alive)`

Creates censored survivorship list to be used with external Kaplan-Meier estimator analysis and/or Cox Proportional Hazard Regression. Select stillbirth to include individuals which died at birth in survival analysis. Select alive to exclude stillbirths.

Data are are exported to "kmmortality-[sex].csv".

See also

export_fecundity

Command list

6.44 flag breeders

syntax: `flag breeders`

Flags all individuals that have reproduced.

Command list

6.45 gene drop

syntax: `gene drop $runs`

Run gene drop simulation model with `$runs` of iterations

- etc. This version is experimental.

Command list

6.46 get begin date

syntax: `get begin date`

Display begin date of data included in analyses

See also

set begin date

Command list

6.47 get bootstrap

syntax: `get bootstrap`

Display use of bootstrap status

See also

set bootstrap, set resamples, get resamples

Command list

6.48 get date accuracy

syntax: `get accuracy`

Display date accuracy used for births, deaths and other events e.g. dispersal

See also

set date accuracy

Todo fix multiple lines

Command list

6.49 get census day

syntax: `get census day`

Display day of the month of repeated census

See also

set census day, get census month, get census interval

Command list

6.50 get census interval

syntax: `get census interval`

Display number of days between census dates, or length of census interval

See also

set census interval, get census day, get census month,

Command list

6.51 get census month

syntax: `get census month`

Display month of repeated census

See also

set census month, get census day, get census interval

Command list

6.52 get class width

syntax: `get class width`

Display class width (in number of days)

See also

set class width

Command list

6.53 get common name

syntax: `get common name`

Display common name of taxon

See also

set common name

Command list

6.54 get configuration

syntax: `get configuration of '$option'`

Display configuration [of] $option

See also

set configuration, list configuration

Command list

6.55 get contraception

syntax: `get contraception`

Display method of contraception in view settings

See also

set contraception

Command list

6.56 get date format

syntax: `get date (format|separator)`

Display date format or separator between days, months and years

See also

set date format, set date separator

Command list

6.57 get period

syntax: `get period`

Display begin and end date of period in viewdate format or separator between days, months and years.

See also

get end date, get begin date

Command list

6.58 get den emerge

syntax: `get den emerge`

Get time in days when animals emerge from the den

Command list

6.59 get end date

syntax: `get end date`

Display end date of data included in analyses

See also

set end date

Command list

6.60 get generations

syntax: `get generations`

Display generation groups that are included in analyses

See also

set generation

Command list

6.61 get gestation

syntax: `get gestation length`

Display gestation length in days

See also

set gestation length

Command list

6.62 get handle parent

syntax: `get handle [unknown] parent`

Display method to handle births with unknown parent(s) in fecundity analyses

See also

set handle parent

Command list

6.63 get handle sex

syntax: `get handle [unknown] sex`

Display method to handle individuals of unknown sex in analyses

See also

set handle sex

Command list

6.64 get inbreeding

syntax: `get inbreeding`

Display range of inbreeding coefficient which is included in analyses

See also

set inbreeding

Command list

6.65 get implantation

syntax: `get implantation`

Get delayed implantation period as number of days before birth

See also

set implantation

Command list

6.66 get latin name

syntax: `get latin name`

Display scientific (latin) name of taxon

See also

set latin name

Command list

6.67 get left truncated

syntax: `get left truncated`

Display left truncated status

See also

set left truncated, get right censored

Command list

6.68 get litter

syntax: `get litter (daterange|size)`

Display range in dates of birth/egglaying to be considered as same litter/clutch or average litter/clutch size

See also

set litter daterange, set litter size

Command list

6.69 get location

syntax: `get location view`

Display location(s) selected for analyses

See also

set location, set population

Command list

6.70 get longevity

syntax: `get longevity`

Display average longevity (as set by user) in days

See also

set longevity

Command list

6.71 get max class

syntax: `get max classes`

Display maximum number of classes to used in life-tables

See also

set max class

Command list

6.72 get monitor date

syntax: `get monitor date`

Display date of census monitoring

See also

set monitor date

Command list

6.73 get month format

syntax: `get month format`

Display format of month

See also

set month format

Command list

6.74 get neonatal age

syntax: `get neonatal age`

Display neonatal age in days

See also

set neonatal age

Command list

6.75 get origin

syntax: `get origin status`

Get origin as selected for analyses

See also

set origin

Command list

6.76 get project

syntax: `get project (name|'$option')`

Display name of project or settings of project parameter $option.

See also

set project name, set project

Command list

6.77 get prorating

syntax: `get prorating`

Display prorating status

See also

set prorating

Command list

6.78 get rearing

syntax: `get rearing`

Get type of rearing as selected for analyses

See also

set rearing

Command list

6.79 get reproductive

syntax: `get reproductive (lifespan|season|system)`

Display reproductive lifespan or type of reproduction

See also

set reproductive lifespan, set reproductive system

Command list

6.80 get resamples

syntax: `get resamples`

Get number of bootstrap resamples

See also

set resamples, set bootstrap and get bootstrap

Command list

6.81 get right censored

syntax: `get right censored`

Display right censored status

See also

set right censored, get left truncated

Command list

6.82 get same sex

syntax: `get same sex`

Display status of sex of offspring included in fecundity

See also

set same sex

Command list

6.83 get scientific name

syntax: `get scientific name`

Display scientific (latin) name of taxon

Note

This command is equals to 'get latin name'

See also

set latin name

Command list

6.84 get sex

syntax: `get sex`

Display sex group(s) included in analyses

See also

set sex

Command list

6.85 get update

syntax: `get update`

Display date when dataset was updated

See also

set update

Command list

6.86 get use emerge

syntax: `get use emerge`

Get status of use of day of emerging from den

See also

get_den_emerge

Command list

6.87 get verbose

syntax: `get verbose`

Display verbose status

See also

set verbose

Command list

6.88 help on command

syntax: `help '$keyword'`

Displays correct syntax for provided command or group of commands.

See also

manual

Command list

6.89 import sparks

syntax: `import sparks '$name'`

Create SQLite3 database with SPARKS (© ISIS) studbook `$name` tables

A database base with the extension ".studbook" is created in the path: ∼/pml/studbooks.

Command list

6.90 include animal

syntax: `include animal '$id'`

Include animal with studbook `$id` in analyses.

Command list

6.91 include neonates

syntax: `include neonates`

Include neonates in analyses.

See also

exclude_neonate

Command list

6.92 include stillbirths

syntax: `include stillbirths`

Include stillbirths i.e. all that died at day of birth in analyses.

See also

exclude_stillbirth

Command list

6.93 init location

syntax: `init location view`

Initialises location view by unselecting all locations.

See also

set population

Command list

6.94 list active view

syntax: `list active view`

List active view settings.

Command list

6.95 list animal

syntax: `list animal '$id'`

List data of animal with studbook `$id` on console screen.

See also

list studbook

Command list

6.96 list life history data

syntax: `list biology`

Load life history data of the selected studbook species from file.

See also

save life history

Command list

6.97 list configuration

syntax: `list configuration`

List configuration data to console.

See also

load project

Command list

6.98 list founders

syntax: `list founders`

List founders with 'blood' lineages in metapopulation.

Command list

6.99 list living

syntax: `list living`

List living animals at date of monitoring and other criteria being set in the active view

See also

list studbook set monitor date

Command list

6.100 list location view

syntax: `list location views`

List available location views for active project

See also

load location

Command list

6.101 list metapopulation

syntax: `list metapopulation`

List metapopulation data (populations, subpopulations and social groups) on screen.

Command list

6.102 list offspring

syntax: `list offspring '$id'`

List of offspring of animal `id`.

See also

list animal,list_pedigree,list_studbook,

Command list

6.103 list pedigree

syntax: `list pedigree '$id'`

List of pedigree of animal `$id`.

See also

list animal,list_offspring,list_studbook,

Command list

6.104 list project

syntax: `list project`

List parameters of active project on screen.

See also

load project

Command list

6.105 list studbook

syntax: `list studbook (all|view)`

List studbook data on screen console. Select view to apply filter settings

See also

list animal

Command list

6.106 list taxa

syntax: `list taxa`

See also

add taxon

Command list

6.107 list available views

syntax: `list views`

List avaiable views for active project

Command list

6.108 load configuration

syntax: `load configuration`

Re-load the configuration parameters. The initial settings - including project date - are loaded, unless the configuration was saved before re-loading

See also

save configuration, load project

Command list

6.109 load location

syntax: `load location [from] '$file' [to] '$level'`

Load locations that are stored in `$file` and organise them under the provided `$level` e.g. load from 'northern' to 'SUBREGION'.

Locations are stored as one per line. Comment lines start with # and are not not read. Do not write a comment character after a location name.

See also

load view

Command list

6.110 load project

syntax: `load project (current|'$name')`

Re-load current project parameters, or open project with `$name`.

See also

create project

Command list

6.111 load studbook

syntax: `load studbook`

Load studbook data into the memory. The studbook as defined in the project configuration is used.

See also

load project

Command list

6.112 load view

syntax: `load view [from] '$file'`

Load view settings that are stored in `$file`.

See also

load project

Command list

6.113 manual

syntax: `manual`

Start on-line manual in browser.

See also

help

Command list

6.114 message

syntax: `message '$text'`

Displays message whenever verbose is on.

See also

set verbose, get verbose

Command list

6.115 more

syntax: `more`

Displays xx lines and waits until the user presses a key to continue or `ESC` to quit. This command can be use in scripts.

Command list

6.116 quit

syntax: `quit`

Quit command-line program or script processing. Same as exit.

Command list

6.117 remove project

syntax: `remove project`

Removes active project. All data will be erased from disk

Warning

All data will be erased from disk

See also

create project

Command list

6.118 reports

syntax: `reports`

View PML reports per project in webbrowser.

Command list

6.119 run PML script

syntax: `run "$name"`

Run script file in interactive (console) mode. The directory path of scripts is fixed to `~/pml/scripts`. Therefore only the basename of the file needs to be provided e.g. "test.pml"."

Command list

6.120 scan studbook

syntax: `scan studbook`

Raw scan to compute basic statistics on studbook data (without view)

Command list

6.121 save life history

syntax: `save biology`

Save life history data of selected (studbook) species

See also

list life history data

Command list

6.122 save configuration

syntax: `save configuration`

Save configuration parameters.

See also

load configuration

Command list

6.123 save project

syntax: `save project`

Save parameters of active project.

See also

load project

Command list

6.124 save view

`syntax:` `save view [as] '$name'`

Save view settings to `$name` in XML format.

The view settings will be saved in ∼/pml/[project]/views

See also

load project, clear view

Command list

6.125 set age group

`syntax:` `set age group ([to] all|[from] $low [to] $high) (hours|days|weeks|months|years)`

Set age group (`$low` to `$high`) in the selected unit i.e. days, weeks (= 7 days), months (=30.6 days) or years (=365.25 days).

set age [to] all resets

Command list

6.126 set begin date

`syntax:` `set begin date [to] (init|$user_date)`

Set the begin date for data to be included in analyses. The option `init` refers to the first date of birth or import date as registered, or enter a `$user_date` according the 'system'.

See also

set end date

Command list

6.127 set bootstrap

`syntax:` `set bootstrap (on|off)`

Set use of bootstrap in life table analyses on/off

See also

get bootstrap, set resamples and get resamples

Command list

6.128 set census day

syntax: `set census day [to] $number [1..31]`

Set day of month (as number between 1..31).

See also

get census day, set census month, set census interval

Command list

6.129 set census interval

syntax: `set census interval [to] day|week|month|quarter|biannual|annual|biennial|fiveyear`

Set interval between monitoring dates from one day to five years.

- `day`
- `week`
- `month`
- `quarter`
- `biannual`
- `annual`
- `biennial`
- `fiveyear`

See also

get census interval, set census day, set census month, compute census

Command list

6.130 set census month

syntax: `set census month [to] $number`

Set census month as number between 1..12.

See also

get census month, set census day, set census interval

Command list

6.131 set class width

syntax: `set class width [to] $number (days|weeks|months|years ).`

Set the width of age classes as used in life-table analyses. The value `$number` is a real value that contains the class width in the selected unit i.e. (parts of) days, weeks, months or years. A year is 365.25 days to compensate for leap years (month = 30.6; week = 7.0 days).

See also

compute age distribution, compute fecundity, compute mortality

Command list

6.132 set common name

syntax: `set common name [to] '$name'`

Set common name of taxon in analyses.

See also

set latin name

Command list

6.133 set configuration

syntax: `set configuration '$option' [to] '$setting'`

Set configuration `$option` to `$setting`

Command list

6.134 set contraception

syntax: `set contraception [to] (none|intact|neutered|vasectomy|contracepted|reversed|$numb`

Set contraception method:

- none: no specific selection i.e. include all
- intact: animals which have not been treated
- neutered: animals which have been neutered (castrated)
- vasectomy: animals which have been vasectomized
- contracepted: animals which are temporarily contracepted e.g. anti-conception pill
- reversed: animals of which contraception has been reversed
- $number: enumeration value of contraception method (none=0)

See also

get contraception

Command list

6.135 set date accuracy

syntax: `set date accuracy (all|birth|death|event) [to] (accurate|day|week|month|year|none|$`

Set the level of date accuracy for births, deaths or events to be included in analyses. Select `ALL` to set the date accuracy for all categories. The following levels of accuracy are recognized:

- `accurate` : only accurate dates are included
- `day` : date estimates at the level of 1 day are also included
- `week` : date estimates at the level of 7 days are also included
- `month` : date estimates at the level of 30 days are also included
- `year` : date estimates at the level of 365 days are also included
- `none` : no accuracy setting; all dates are included
- `$number` : enumeration value

Command list

6.136 set date format

syntax: `set date format [to] (american|european|iso8601)`

Set date format for input and output to:

- `american` (mm/dd/yyyy HH:MM:SS)
- `european` (dd-mm-yyyy HH:MM:SS)
- `ISO8601` (yyyy-mm-dd HH:MM:SS)

See also

set date separator, set month format

Command list

6.137 set date separator

syntax: `set date separator [to] (dot|hyphen|forslash|space|none)`

Set date separator between day, month and year

See also

set date format, set month format

Command list

6.138 set end date

syntax: `set end date [to] (last|today|$user_date)`

Set the end date for data to be included in analyses. Select `last` for the last registered birth, death or transfer, enter `today` for the todays's date or enter a `$user_date` in the 'system' date format.

See also

set begin date

Command list

6.139 set den emerge

syntax: `set den emerge [to] $number`

Set time in $number of days (and fraction thereof) when individuals emerge from the den

Command list

6.140 set generation

syntax: `set generation ([to] (all|$number) | [from] $low [to] ($high|max) )`

Select `all` to include all generations.

See also

compute generation

Command list

6.141 set gestation length

syntax: `set gestation length [to] $number (days|weeks|months ).`

Set gestation length `$number` in the selected unit i.e. hours or part of days, weeks (= 7 days) or months (= 30.5 days).

Command list

6.142 set handle parent

syntax: `set handle [unknown] parent[to] ( ignore|equal|ratio|$number).`

Set method to handle births to unknown parent(s):

- ignore: ignore births
- equal: equal distribution of births with unknown parent
- ratio: distribute births according observed sex-ratio
- $number: enumeration value

This method is used in handling unknown parents in fecundity rates

Command list

6.143 set handle sex

syntax: `set handle sex [to] ( ignore|equal|ratio|$number).`

Set method to handle individuals of unknown sex:

- ignore: ignore individuals of unknown sex
- equal: assume equal sex-ratio
- ratio: distribute according observed sex-ratio
- $number: enumeration value

Command list

6.144 set inbreeding

syntax: `set inbreeding [to] (all|inbred|noninbred|fullsib|$number|) ([from] $low [to] ($high|max) )`

Set the inbreeding coefficients to be included in analyses. Enter a real value for `number` to limit to one value or select a range from `$low` to `$high`. The value for `max` is set to 1.0. Select `all` to include all individuals, `inbred` and `noninbred` to include only inbred and non-inbred individuals, `fullsib` to restrict to full siblings respectively.

Command list

6.145 set implantation

syntax: `set implantation to $number`

Set delayed implantation period as $number of days (and fractions thereof) before birth.

See also

get implantation

Command list

6.146 set latin name

syntax: `set (latin | scientific) name [to] '$name'`

Set latin (scientific) $name of taxon in analyses.

See also

set_common

Command list

6.147 set left truncated

syntax: `set left truncated (on|off)`

Set left truncation of life table data on/off

See also

get left truncated, set right censored

Command list

6.148 set location

syntax: `set location [to] '$level' '$deme'`

Select location ($deme) in given $level. For example 'REGION' 'AFRICA' will select the African region in SPARKS studbooks. This is equivalent to `set population to 'Africa'`.

Use init location view to initialize a location view before adding locations to a view.

See also

init location set population

Command list

6.149 set longevity

syntax: `set longevity [to] $number ( days |weeks|months|years)`

Set the average longevity. The value `$number` is a real number that contains the age according the selected unit i.e. days, weeks (= 7.0 days), months (= 30.6 days) or years (= 365.25 days).

See also

compute longevity

Command list

6.150 set litter daterange

syntax: `set litter daterange [to] $number`

Set the range in $number of days of dates of birth of same litter.

Command list

6.151 set litter size

syntax: `set litter size [to] $number`

Set maximal litter size `$number` as has been observed in taxon.

Command list

6.152 set max class

syntax: `set max classes [to] $number`

Set maximum `$number` of classes to be included in life table analyses. Set $number to 0 in order to include all observed age classes.

See also

compute age distribution, compute fecundity, compute mortality

Command list

6.153 set monitor date

`syntax:` `set monitor date [to] last | today | $user_date`

Set the last date to be included in analyses. Select `last` for the last registered birth, death or transfer, enter `today` for the todays's date or enter a `$user_date` in the 'system' date format.

The monitor date is used in the age distribution

See also

set begin date, set end date, compute age distribution

Command list

6.154 set month format

`syntax:` `set month format [to] (number|short|long)`

Set the format of months in output of dates. Select `number` for numerical representation of month i.e. 01 to 12, `short` for three character names e.g. Jan to Dec, or `long` for full (english month name).

See also

set date format

Command list

6.155 set neonatal age

`syntax:` `set neonatal age [to] $number ( days|weeks|months|years)`

Set the end of the neonatal age. The value `$number` is a real number that contains the age according the selected unit i.e. days, weeks (= 7 days), months (=30.6 days) or years (=365.25 days).

See also

compute neonatal deaths

Command list

6.156 set origin

syntax: `set origin [to] (wild,captive,unknown,all)`

Set the origin of individuals to be included in the view. The following settings are possible:

- wild : include animals born in the wild (*in-situ* population)
- captive : include animals born in the captive (*ex-situ* population)
- unknown : include animals of unknown origin
- all : not criteria i.e. includes animals of unknown origin.

Deprecated Origin is a specific data field for SPARKS studbooks. Metapopulations may include multiple wild populations with known individuals which are included in the studbook. It means that the meaning of the term 'wild' becomes vague.

Command list

6.157 set population

syntax: `set population to '$region'`

Set location views to regional (zoo) populations. This command is only valid for SPARKS-based studbooks.

Valid region names (enter within quotes) are:

- Africa
- Asia
- Australasia
- Central America
- Europe
- Middle East
- North America
- Oceania
- South America
- World

Note that the view `Asia` excludes North Asia - which are the Baltic States and former USSR - and are, therefore, included as part of Europe. South West Asia is the region Middle East.

The option `World` excludes locations named UNKNOWN and WILD. Initialize a view before using it the first time.

Use set location to add (group of) locations at any level

See also

init location set location, get location

Command list

6.158 set project name

syntax: `set project name [to] '$name'`

Set project to `$name` and load parameters

See also

create project, load project

Command list

6.159 set project

syntax: `set project '$option' [to] '$setting'`

Set project `$option` to required $setting (value)

Command list

6.160 set prorating

syntax: `set prorating (on|off)`

Set prorating of individuals at risk in life table data on/off

See also

set left truncated, set right censored

Command list

6.161 set rearing

syntax: `set rearing [to] (parent|hand|foster|colony|supplemental|peer|none|unknown|all)`

Set report to type of rearing

See also

get rearing

Command list

6.162 set reproductive lifespan

syntax: `Set reproductive lifespan [from] $low [to] $high (days|weeks|months|years)`

Set the reproductive life-span (`$low` to `$high`) for the selected unit i.e. days, weeks (= 7 days), months (=30.6 days) or years (=365.25 days). These values refer to the sex group that has been selected.

set sex

Command list

6.163 set reproductive season

syntax: `set reproductive season [to] (flow|pulse|$number)`

Set the reproductive season:

- flow : birth-flow, births all around the year
- pulse: birth-pulse, specific birth season
- `$number`**:** enumeration value

See also

get reproductive

Command list

6.164 set reproductive system

syntax: `set reproductive system [to] (viviparous|ovoviviparous|oviparous|$number)`

Set the reproductive system:

- viviparous: give birth to live young
- ovoviviparous: young hatched within body of parent
- ovivparous: young hatched after eggs have been laid
- `$number`**:** enumeration value

See also

get reproductive

Command list

6.165 set resamples

syntax: `set resamples [to] $number`

Set `$number` of resamples in bootstrap.

See also

get resamples, set bootstrap and get bootstrap

Command list

6.166 set right censored

syntax: `set right censored (on|off)`

Set right censoring of life table data on/off

See also

get right censored, set left truncated

Command list

6.167 set same sex

syntax: `set same sex (on|off)`

Include only offspring of same sex as parent in fecundity

Command list

6.168 set sex

syntax: `set sex [to] (female|male|unknown|hermaphrodite|abnormal|all|$number)`

Select sex group. The option `$number` refers to the enumeration value.

Command list

6.169 set sparks path

syntax: `set sparks path [to] '$db_path'`

Set the full path to main SPARKS directory (folder). The default settings are:

- `Mac` OS X : ~/ISISdosbox/SPARKS
- `Windows` : C:/ISISdosbox/SPARKS

Command list

6.170 set studbook database

syntax: `set studbook database [to] '$name'`

Set name of database with studbook data. Add the extension `.studbook` for SQLite3 databases.

See also

set studbook path

Command list

6.171 set studbook format

syntax: `set studbook format [to] (pml|sparks)`

The following studbook formats are (currently)supported:

- `pml` : PML's internal format
- `SPARKS` : Sqlite3 version of SPARKS (©ISIS, Eagan, MN, USA) is a studbook program that uses dBase III+ compatible tables.

See also

set studbook path

Command list

6.172 set studbook path

syntax: `set studbook path [to] '$db_path'`

Set the full path for non-server based SQLite3 studbook database. Default studbook databases are stored in `~/pml/studbooks`

Command list

6.173 set taxon

syntax: `set taxon [to] '$name'`

Add taxon `$name` to view.

See also

clear taxon view, add taxon, list taxa

Command list

6.174 set update

syntax: `set update [to] $user_date`

Set the date (`$user_date`) when population data were last updated. in the 'system' date format.

See also

set end date

Command list

6.175 set use merge

syntax: `set use emerge (on|off)`

Switch status of using date when offspring emerged from den

See also

get use emerge

Command list

6.176 set verbose

syntax: `set verbose (on|off)`

Set verbose on/off. This command overrides initial settings

See also

get verbose

Command list

6.177 shell

syntax: `shell '$command'`

Execute shell command `$command`

Command list

6.178 sort

`syntax:` `sort [by] (birth|death|key|id|sire|dam|moves)`

Sort population data using the following options:

- `birth` : date of birth
- `death` : date of death
- `key` : primary key in order of birth(unique)
- `id` : studbook id (unique)
- `sire` : studbook id of sire
- `dam` : studbook id of dam
- `moves` : move data are sorted on date of event

See also

set begin date

Command list

6.179 test module

`syntax:` `test`

Allows developer to run function doTest()

Command list

6.180 trace possible parents

`syntax:` `trace parents`

Trace possible parents of individuals with unknown parents. The results are stored in the file `parents.xml`.

Command list

6.181 set gis location

`syntax:` `set gis location $name [to] $longitude $latitude`

Update location `name` with longitude and latitude in decimal degree format i.e. ddd.mmmmm

Command list

6.182 version

syntax: `version`

Display version and extended program information.

Command list

6.183 wait

syntax: `wait`

Wait (pause) until the user presses a key. This command can be use in scripts.

Command list

Chapter 7

Script example

```
###
# Example of PML project
#

/*
There is no ’rule’ which comment style to use:
+ Commands or text after a hash (#) or double slashes (//) on a single line are
ignored.
+ C-style comment blocks are useful for comments that span multiple lines or to
disable a block of command lines.
*/

set verbose on                         // Display messages, progress bar etc.

###
# Load project configuration (which includes name and format of studbook).
# This procedure can be skipped if the project name is passed to as
# command-line parameter
#
load project "example"                 // Load project configuration
load studbook                          // Load studbook data associated with project

###
#  Date settings
#
set date format to iso8601             // Set date to YYYY-MM-DD
set begin date to 1977-01-01           // Begin of time window (default:first date)
set end date to 2012-12-31             // End of time window (default: last date)
set monitor date to 2012-06-30         // Last date of monitoring
set census day to  30                  // Set census day to 30
set census month to 6                  // Set (annual) census month to June
set census interval to annual          // Annual census
set date accuracy all to day           // Accuracy by day for birth, death and moves

###
# Compute generation and inbreeding
#
compute generation                     // Compute (captive-born) generation numbers
compute inbreeding                     // Compute inbreeding coefficients

set neonatal age to 30.0 days          // Set end of neonatal period
include neonates                       // Include neonates in analyses

export pedigree                        // Export pedigree for use in R

###
# Set location view
#

# Both these commands are required before setting a location view!
clear location view                    // Clear location list
init location view                     // Initialise list


# Geographic regions in northern hemisphere
set population to ’Europe’             // includes Russia and Baltic states
set population to ’North America’
set population to ’Asia’


/* Disable
```

```
# Geographic regions in southern hemisphere
set population to 'Australasia'
set population to 'South America'

# Locations in file <southern_africa.fed> (fed extension for compatibility with SPARKS)
load location 'southern_africa' 'SUBREGION' // Store locations in 'SUBREGION'

*/

###
# Natural history data
#
set sex to all                        // Repeat for male, female and unknown
compute longevity                     // Longevity and median age at death
compute birth season stillbirth       // Seasonality in births including stillbirths (zero age)
compute litter season                 // Seasonality in births grouped per litter
compute death season                  // Seasonality in death
export survival alive                 // Export data for Kaplan-Meier/Cox survival analyses
                                      // Stillbirths are excluded

set sex to male                       // Repeat for female
compute first breeding
compute reproductive life


###
# Crude demographic analyses
#
set sex to all                        // Repeat for male, female and unknown
set date accuracy all to month        // Allow estimates by month
compute births                        // Births in census interval
compute census                        // Living at census date
compute deaths                        // Deaths in census interval
compute neonatal deaths               // Neonatal deaths in census interval
compute immigration all               // Immigration (import) in census interval
compute immigration wild              // Import from wild in census interval


###
# Demographics
#
set date accuracy all to day
set class width to 1.0 years          // Class width is 1 year (365.25 days)
set max classes to 20                 // Pool individuals >= 20 classes (years)

//Remove comment to change active settings for mortality/fecundity
/*
set bootstrap off                     // default: on
set resamples 1999                    // default: 999
set left truncated off                // default: on
set right censored off                // default: on
set prorating on                      // default: off
set handle unknown to ignore          // default: equal
set handle parent to ignore           // default: ratio
*/

set sex to male                       // Repeat for female and unknown
compute age distribution              // Age distribution at monitoring date
compute mortality                     // Age-specific mortality

set sex to male                       // Repeat for female
compute fecundity                     // Age-specific fecundity
compute lifetable                     // Combine mortality and fecundity

###
# Data export for external Kaplan-Meier or Cox proportional hazard regression
#
set sex to male                       // Repeat for female
export survival alive                 // Survival data excluding stillbirths
export fecundity                      // Export age at birth

set sex to female
set rearing to parent                 // Only include parent-reared offspring
exclude neonates                      // Exclude neonates
set origin to all                     // Set origin to all groups

compute interbirth interval           // Interbirth interval

# reset
set origin to captive                 // Set origin top captive-born
set rearing to all                    // Set rearing to all types
include neonates                      // Include neonates

compute littersize                    // Compute litter size

set sex to all
```

```
compute founder group                 // Compute founder representation in group
compute mean kinship                  // Compute mean kinship


###
# Lethal equivalents
#
set sex to all                        // Repeat for male, female and unknown offspring
compute lethal 180.0 inbred           // Survival to 180 days; single/both parents inbred
compute lethal 180.0 noninbred        // both parents noninbred
compute lethal 180.0 dam              // dam inbred
compute lethal 180.0 single           // dam or sire inbred
compute lethal 180.0 sire             // sire inbred
compute lethal 180.0 both             // both parents inbred



# THE END
```

Command list

Chapter 8

Command list

A | C | E | F | G | H | I | L | M | Q | R | S | T | V | W |

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clear taxon view

clear view

compute age distribution

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compute births

compute census

compute death season

compute deaths

compute emigration

compute fecundity

compute first breeding

compute founder representation

compute generation

compute genetics

compute growth rate

compute immigration

compute inbreeding

compute interbirth interval

compute mean kinship

compute leslie matrix

compute lethal

compute lifetable

compute lineage

compute litter season

compute littersize

compute longevity

compute mortality

compute neonatal deaths

compute reproductive life

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exclude stillbirths

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export pedigree

export poplib

export survival

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get origin

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get prorating

get rearing

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get same sex

get scientific name

get sex

get update

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include stillbirths

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set gestation length

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8.15 W

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Chapter 9

Todo List

Page Command syntax

fix multiple lines

Chapter 10

Deprecated List

Page Command syntax

Origin is a specific data field for SPARKS studbooks. Metapopulations may include multiple wild populations with known individuals which are included in the studbook. It means that the meaning of the term 'wild' becomes vague.