

-----Readme file -----

MooseCounterPOPd Web Interactive: Software to investigate the population scale impact of Brain Worm and Liver Fluke in Moose in New York, USA from 2015-2019

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Overview of the software application

We used the annual counts of calf, young adult, and mature adult moose in the Adirondack region of New York, USA between 2015 and 2019 understand the population scale influences of lethal parasites on native moose populations. We investigated 17 demographic properties:

- 1) Life table
- 2) Predicted annual abundances
- 3) Predicted bi-annual calf abundances
- 4) Predicted bi-annual young adult abundances
- 5) Predicted bi-annual mature adult abundances
- 6) Asymptotic growth rates
- 7) Survival rates
- 8) Stable stage distribution
- 9) Reproductive value
- 10) Sensitivities
- 11) Elasticities
- 12) Damping ratio
- 13) Cumulative growth
- 14) Transient growth rate
- 15) Harmonic vs. arithmetic mean abundances
- 16) Loss of genetic diversity
- 17) Reactivity

Interactive Software User Tutorial

Preparing and running the software:

Step 1: Download the “MooseCounterPOPd.R” software code.

Step 2: Select the “Females” folder.

Step 3: Download each of the .txt files and save them in a specific location on your computer. The files include:

“FemaleMooseCounterPOPd.R”,

“Algorithm New York – Females.R”,
“BestAlgorithmPredictedModelsNortheast.txt”,
“NEW_Adults_January_Northeast.txt”,
“NEW_Adults_June_Northeast.txt”,
“NEW_Subadults_January_Northeast.txt”,
“NEW_Subadults_June_Northeast.txt”,
“NEW_Juveniles_January_Northeast.txt”,
“NEW_Juveniles_June_Northeast.txt”,
“TIMESERIES_NORTHEASTa.txt”,
“TIMESERIES_NORTHEASTc.txt”,
“TIMESERIES_NORTHEASTs.txt”,

“Algorithm Liver Fluke – Females.R”,
“BestAlgorithmPredictedModelsLIVERFLUKE.txt”,
“NEW_Adults_January_LIVERFLUKE.txt”,
“NEW_Adults_June_LIVERFLUKE.txt”,
“NEW_Subadults_January_LIVERFLUKE.txt”,
“NEW_Subadults_June_LIVERFLUKE”,
“NEW_Juveniles_January_LIVERFLUKE.txt”,
“NEW_Juveniles_June_LIVERFLUKE.txt”,
“TIMESERIES_NORTHEASTaLF.txt”,
“TIMESERIES_NORTHEASTcLF.txt”,
“TIMESERIES_NORTHEASTsLF.txt”,

“Algorithm Brain Worm – Females.R”,
“BestAlgorithmPredictedModelsBRAINWORM.txt”,
“NEW_Adults_January_BRAINWORM.txt”,
“NEW_Adults_June_BRAINWORM.txt”,
“NEW_Subadults_January_BRAINWORM.txt”,
“NEW_Subadults_June_BRAINWORM.txt”,
“NEW_Juveniles_January_BRAINWORM.txt”,
“NEW_Juveniles_June_BRAINWORM.txt”,
“TIMESERIES_NORTHEASTaV.txt”,
“TIMESERIES_NORTHEASTcV.txt”,
“TIMESERIES_NORTHEASTsV.txt”,

Step 4: Install five packages: “shinyBS”, “shiny”, “rgl”, “popdemo”, and “rmarkdown”. To install a package, type `install.packages(“shinyBS”)` into your console and run the line. Repeat with the other packages.

Step 5: Open the FemaleMooseCounterPOPd.R file in R studio and set the working directory to the location where you saved the .txt files.

Step 6: Click “Run All”. Begin interacting with the software application.

The FemaleMooseCounterPOPd.R code automatically draws upon the information in these pre-saved files to display the algorithm-predicted results for each of the demographic properties. Accordingly, each of the .txt files were generated using a combinatorial optimization algorithm (Algorithm New York – Females; Algorithm Liver Fluke – Females.R; Algorithm Brain Worm – Females.R). The algorithm settings (and subsequent .txt files) may be altered to calculate demographic parameters using differing time series data by modifying the algorithmic parameters per the directions that appear in the code.

Steps 1-6 may be repeated for Males.

The **validation packet** contains software to assess the performance of the algorithm with cow and bull moose using a randomly generated mock time series. The pre-saved .txt files illustrate the results from one run of the validation code, but they may be replaced by rerunning the validation using a different starting seed. Further details of validation code are described in Hanley et al. 2019: (<https://doi.org/10.1002/ecs2.2963>).

Technical details

This app was written under R Studio Version 1.1.463 – © 2009-2018 RStudio, Inc., and requires five R Shiny packages: “shinyBS”, “shiny”, “rgl”, “popdemo”, and “rmarkdown”.

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