

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

NYClosedDensiPOPd

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Software Information

Overview of the NYClosedDensiPOPd software application

This software was used to investigate whether population dynamics of bald eagle populations would have differed between low and high densities had New York State been closed to dispersal. The NYClosedDensiPOPd software integrates veterinary data with a population matrix model to compare the real and hypothetical impacts of lead on the density dependence mechanisms in the early and later windows of recovery when the system was hypothetically closed. The early window of recovery is defined as the period between 1990-2006, while the later window of recovery is defined as the period from 2002-2018. The NYClosedDensiPOPd app allows the user to compare demographic properties between the time windows, between the sexes, or between both.

Comparisons include three scenarios: (1) current (leaded) scenarios (“NY”), (2) a hypothetical scenario with the removal of Pb poisoning (“A”), and (3) a hypothetical scenario with the removal of Pb exposure (“C”). Comparative properties include:

- 1) Life table
- 2) Predicted annual abundances
- 3) Predicted bi-annual abundances
- 4) Predicted bi-annual hatchling abundances
- 5) Predicted bi-annual immature and non-breeding adult abundances
- 6) Predicted bi-annual breeding adult abundances
- 7) Predicted abundances during the breeding period
- 8) Predicted abundances during the non-breeding period
- 9) Migration and dispersal
- 10) Asymptotic growth rates
- 11) Survival rates
- 12) Stable stage distribution
- 13) Reproductive value
- 14) Sensitivities
- 15) Elasticities
- 16) Damping ratio and convergence time
- 17) Cumulative growth
- 18) Stochastic growth rate
- 19) Transient growth rate
- 20) Harmonic vs. arithmetic mean abundances
- 21) Loss of genetic diversity
- 22) Population inertia
- 23) Reactivity
- 24) Maximum amplification
- 25) Maximum attenuation

Interactive NYClosedDensiPOPd Software User Tutorial

Preparing and running the software for the early time period (1990-2006)

Step 1: Download the “NYClosedDensiPOPd for Females” folder, then select the “ClosedEarlyPOPd” subfolder.

Step 2: Inside the folder, you will find four .R files:

“NY_FemaleClosedEarlyPOPd”,

“NY_First 17 year – Algorithm Hypothetical Trajectory A”,

“NY_First 17 year – Algorithm Hypothetical Trajectory C”,

and

“NY_First 17 year – Algorithm”,

and several pre-saved .txt files:

“BestAlgorithmPredictedModelsNY”,

“BestAlgorithmPredictedModelsCOUNTERFACTUAL_PAIN_A”,

“BestAlgorithmPredictedModelsCOUNTERFACTUAL_PAIN_C”,

“NEW_AA_NY”,

“NEW_AA_COUNTERFACTUAL_PAIN_A”,

“NEW_AA_COUNTERFACTUAL_PAIN_C”,

“NEW_PA_NY”,

“NEW_PA_COUNTERFACTUAL_PAIN_A”,

“NEW_PA_COUNTERFACTUAL_PAIN_C”,
“NEW_SA_NY”,
“NEW_SA_COUNTERFACTUAL_PAIN_A”,
“NEW_SA_COUNTERFACTUAL_PAIN_C”,
“NEW_PS_NY”,
“NEW_PS_COUNTERFACTUAL_PAIN_A”,
“NEW_PS_COUNTERFACTUAL_PAIN_C”,
“NEW_Adults_January_NY”,
“NEW_Adults_January_COUNTERFACTUAL_PAIN_A”,
“NEW_Adults_January_COUNTERFACTUAL_PAIN_C”,
“NEW_Adults_June_NY”,
“NEW_Adults_June_COUNTERFACTUAL_PAIN_A”,
“NEW_Adults_June_COUNTERFACTUAL_PAIN_C”,
“NEW_Subadults_January_NY”,
“NEW_Subadults_January_COUNTERFACTUAL_PAIN_A”,
“NEW_Subadults_January_COUNTERFACTUAL_PAIN_C”,
“NEW_Subadults_June_NY”,
“NEW_Subadults_June_COUNTERFACTUAL_PAIN_A”,
“NEW_Subadults_June_COUNTERFACTUAL_PAIN_C”,
“NEW_Juveniles_June_NY”,
“NEW_Juveniles_June_COUNTERFACTUAL_PAIN_A”,
“NEW_Juveniles_June_COUNTERFACTUAL_PAIN_C”,
“NEW_AdultsAbsorbPercent_NY”,
“NEW_AdultsAbsorbPercent_COUNTERFACTUAL_PAIN_A”,
“NEW_AdultsAbsorbPercent_COUNTERFACTUAL_PAIN_C”,
“NEW_AdultsPurgePercent_NY”,
“NEW_AdultsPurgePercent_COUNTERFACTUAL_PAIN_A”,
“NEW_AdultsPurgePercent_COUNTERFACTUAL_PAIN_C”,
“NEW_SubadultsAbsorbPercent_NY”,
“NEW_SubadultsAbsorbPercent_COUNTERFACTUAL_PAIN_A”,
“NEW_SubadultsAbsorbPercent_COUNTERFACTUAL_PAIN_C”,
“NEW_SubadultsPurgePercent_NY”,
“NEW_SubadultsPurgePercent_COUNTERFACTUAL_PAIN_A”,
“NEW_SubadultsPurgePercent_COUNTERFACTUAL_PAIN_C”,
“NEW_TIMESERIES_NY”,
“NEW_TIMESERIES_COUNTERFACTUAL_PAIN_A”,
“NEW_TIMESERIES_COUNTERFACTUAL_PAIN_C”,

Step 3: Save these text files in a specific location on your computer.

Step 4: Open R Studio.

Step 5: In R Studio, install six packages: “shinyBS”, “popdemo”, “shiny”, “rgl”, “FSA”, and “rmarkdown”. To install a package, type `install.packages(“shinyBS”)` into your R console and run the line. Repeat this command with the other packages.

Step 6: Open the `NY_FemaleClosedEarlyPOPd.R` file in R studio and set the working directory to the location where you saved the .txt files.

Step 7: Click “Run All”.

Step 8: Begin interacting with the `NY_FemaleClosedEarlyPOPd` software application.

NOTE: The above 8-step process requires the use of all the pre-saved files that are listed in Step 2. However, you may generate the .txt files yourself using the three algorithm files. The "...NY.txt" files are generated using "NY_First 17 year - Algorithm.R", the "...COUNTERFACTUAL_PAIN_A.txt" are generated using "NY_First 17 year - Algorithm Hypothetical Trajectory A.R" and the "...COUNTERFACTUAL_PAIN_C.txt" files are generated using the "NY_First 17 year - Algorithm Hypothetical Trajectory C.R" file. If you wish to modify and run the altered algorithms on your own machine (to overwrite the .txt files with new versions):

Step i. Conduct Step 2-3 (above),

Step ii. Open the appropriate "NY_First 17 year - Algorithm...R" in R.

Step iii. Set the working directory to the folder in Step i.

Step iv. Select "Run all". ***Beware, the runtime of the unmodified algorithms is a minimum of 6 hours, so ensure your computer is plugged in and will not go to sleep, and then turn off your screen to save the backlight from burnout.*** The algorithm will run and automatically save the new .txt files into the folder that you specified in Step iii.

The process for running the app with male bald eagles when abundances are low is the same as that listed above, using the "NYClosedDensiPOPd for Males" folder (in Step 1) instead of the "NYClosedDensiPOPd for Females" folder.

The process for running the app when abundances are high is the same as that listed above, using the "ClosedLatePOPd" folder (in Step 1) instead of the "ClosedEarlyPOPd" folder.

Overview of the NYClosedDensiPOPd validation script

This validation bundle includes software to verify the use of the algorithm when the system is assumed to have low (early) or high (late) abundances and is closed to incoming or outgoing dispersal. The computer selects a randomly generated configuration of matrix elements, then projects an adult time series using those elements. The algorithm then uses that time series to estimate all the underlying parameters. The software then overlays the algorithm predictions onto the "true" underlying random parameters. If the algorithm catches the true value of the parameter within its range, it is said to have "successful predictive performance."

Preparing and running the NYClosedDensiPOPd software

Step 1: Decide whether to verify the predictions of the algorithm in systems with low abundances or in systems with high abundances.

Step 2: Download the "NY_ClosedDensiPOPd_Validation_Early.R" software (for low abundances) or the "NY_ClosedDensiPOPd_Validation_Late.R" software (for high abundances).

Step 3: Install the package "popdemo". To install a package, type `install.packages("popdemo")` into your console and run the line.

Step 4: Click "Run All". The software will automatically overlay the algorithm predictions for each of the demographic parameters found in NYClosedDensiPOPd.

Note: One can check different random trajectories by selecting a different starting seed, or by modifying the values of the “true parameters” in the first section of the code.

Technical details

The NYClosedDensiPOPd software was written under R Studio Version 3.5.3 (2019-03-11) – “Great Truth” © 2019 RStudio, Inc. requires six R Shiny packages: “shinyBS”, “shiny”, “rgl”, “FSA”, “popdemo”, and “rmarkdown”. The NYClosedDensiPOPd validation software was written under R Studio Version 1.1.463 – © 2009-2018 RStudio, Inc., and requires one package: “popdemo”.

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Citations

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