

-- Readme --

NYDensiPOPd Version 2

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Overview

We assessed the population scale impacts of lead (Pb) toxicosis in bald eagles (*Haliaeetus leucocephalus*) in New York State, USA from 1990-2018 under high- and low-density scenarios. The NYDensiPOPd v2 repeats the comparison of Pb and non-Pb in DensiPOPd (<https://doi.org/10.7298/6yb8-5c25>), but with a geographic area specific to New York State. The comparisons include the early (low-density; 1990-2006) and later (high-density; 2002-2018) windows of population recovery.

The NYDensiPOPd v2 app allows the user to compare demographic properties between the time windows (early and late), between the sexes (male or female), or both. Comparisons include three scenarios: (1) current (leaded) scenario (“Actual”), (2) a hypothetical scenario with the removal of Pb poisoning (“Pb-reduced”), and (3) a hypothetical scenario with the removal of Pb exposure (“Pb-free”). 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, and (25) Maximum attenuation.

Unlike similar demographic apps, these apps do not contain information on each of the demographic properties. Similarly, these apps do not contain bias statements regarding algorithm performance for each demographic property. Should you like to know more about each of the 25 demographic properties, or review bias statements for each property, please explore the EaglePOPd software (<https://doi.org/10.7298/q4m1-se95>) and the CounterPOPd software (<https://doi.org/10.7298/0v1k-wq39.2>).

The summarized time series data appear in this packet. The raw data may be obtained by contacting the Wildlife Health Unit at the New York State Department of Environmental Conservation [wildlife@dec.ny.gov or (518) 478-2203].

User tutorial

We will describe the process to prepare and run the script for males in the early time period, but the processes to run males in the late time period or females in either time period are similar.

Step 0: Download R onto your machine. Go to <https://cran.r-project.org/bin/windows/base/old/4.2.1/>. Click R-4.2.1-win.exe to download the .exe file, then click on the file itself. Follow the instructions to download R onto your computer. [This will amount to clicking “Next” several times to accept all the defaults.]

Step 1: Open R and verify that you are running a version of the R Software (R Core Team 2020), that is at least 4.2.1 (2022-06-23 ucrt) -- "Funny-Looking Kid" Copyright (C) 2022 The R Foundation for Statistical Computing Platform: x86_64-w64-mingw32/x64 (64-bit).

Step 2: Install the `renv` package in R. Go to the top menu ribbon, click “Packages”, then click “Install package(s)”, select a CRAN mirror (any will do), scroll to “renv”, then click “OK”.

Step 3: Create a folder on your computer that will function as your working directory.

3-a: Create a new folder on your desktop, then name that folder in accordance with your project. This folder will be your working directory.

3-b: Set the path to the working directory in R by clicking the R Console, clicking “File”, clicking “Change dir...”, then navigating through the file paths to your working directory. Click “OK.”

3-c: Verify that R has the correct path to your working directory by clicking the R console, typing “`getwd()`”, and hitting enter.

Step 4: Prepare the NYDensiPOPd V2 materials to run on your machine.

4-a: Download, unzip, and save the contents of the NYDensiPOPd V2/EarlyMale subfolder to your working directory. Also unzip the folder named `renv` in the Download folder, and move it to your working directory. Your working directory should contain the contents of the Males subfolder and the folder named `renv`.

4-b: Double check that the contents of the EarlyMale folder is in your working directory: click the R console, type “`dir()`”, and hit enter. The file names of the EarlyMale folder should print in the R console. The file names include five .R files, three data files, and many results (pre-run) .txt files.

The five R files are named:

1_NY_Algorithm_Male_Early_Pb_Exposure.R,
1_NY_Algorithm_Male_Early_Pb_Poisoning.R,
1_NY_Algorithm_Male_Early_Pb.R,
2_NY_MaleDensiPOPdV2_Functions.R, and
3_NY_MaleEarlyDensiPOPdV2.R.

The three data files are named:

TIMESERIES_NY_COUNTER_FACTUAL_PB_EXPOSURE_MALES.txt,
TIMESERIES_NY_COUNTER_FACTUAL_PB_POISONING_MALES.txt, and
TIMESERIES_NY.txt.

And the results (pre-run) .txt files are named:

BestAlgorithmPredictedModelsCOUNTERFACTUAL_PAIN_A.txt,
BestAlgorithmPredictedModelsCOUNTERFACTUAL_PAIN_C.txt,
BestAlgorithmPredictedModelsNY.txt, EigenA.txt, EigenAM.txt,
EigenC.txt, EigenCM.txt, EigenNY.txt, EigenNYM.txt,
elastA.txt, elastAR.txt, elastC.txt, elastCR.txt,
elastNY.txt, elastNYR.txt, ETNY.txt, ETSA.txt, ETSC.txt,
hhsBOOTA.txt, hhsBOOTC.txt, hhsBOOTNY.txt,
NEW_AA_COUNTERFACTUAL_PAIN_A.txt,
NEW_AA_COUNTERFACTUAL_PAIN_C.txt, NEW_AA_NY.txt,
NEW_Adults_January_COUNTERFACTUAL_PAIN_A.txt,
NEW_Adults_January_COUNTERFACTUAL_PAIN_C.txt,
NEW_Adults_January_NY.txt,
NEW_Adults_June_COUNTERFACTUAL_PAIN_A.txt,
NEW_Adults_June_COUNTERFACTUAL_PAIN_C.txt,
NEW_Adults_June_NY.txt,
NEW_AdultsAbsorbPercent_COUNTERFACTUAL_PAIN_A.txt,
NEW_AdultsAbsorbPercent_COUNTERFACTUAL_PAIN_C.txt,
NEW_AdultsAbsorbPercent_NY.txt,
NEW_AdultsPurgePercent_COUNTERFACTUAL_PAIN_A.txt,
NEW_AdultsPurgePercent_COUNTERFACTUAL_PAIN_C.txt,
NEW_AdultsPurgePercent_NY.txt,
NEW_Juveniles_June_COUNTERFACTUAL_PAIN_A.txt,
NEW_Juveniles_June_COUNTERFACTUAL_PAIN_C.txt,
NEW_Juveniles_June_NY.txt,

NEW_PA_COUNTERFACTUAL_PAIN_A.txt,
 NEW_PA_COUNTERFACTUAL_PAIN_C.txt, NEW_PA_NY.txt,
 NEW_PS_COUNTERFACTUAL_PAIN_A.txt,
 NEW_PS_COUNTERFACTUAL_PAIN_C.txt, NEW_PS_NY.txt,
 NEW_SA_COUNTERFACTUAL_PAIN_A.txt,
 NEW_SA_COUNTERFACTUAL_PAIN_C.txt, NEW_SA_NY.txt,
 NEW_Subadults_January_COUNTERFACTUAL_PAIN_A.txt,
 NEW_Subadults_January_COUNTERFACTUAL_PAIN_C.txt,
 NEW_Subadults_January_NY.txt,
 NEW_Subadults_June_COUNTERFACTUAL_PAIN_A.txt,
 NEW_Subadults_June_COUNTERFACTUAL_PAIN_C.txt,
 NEW_Subadults_June_NY.txt,
 NEW_SubadultsPurgePercent_COUNTERFACTUAL_PAIN_A.txt,
 NEW_SubadultsPurgePercent_COUNTERFACTUAL_PAIN_C.txt,
 NEW_SubadultsPurgePercent_NY.txt,
 NEW_SubadultsAbsorbPercent_COUNTERFACTUAL_PAIN_A.txt,
 NEW_SubadultsAbsorbPercent_COUNTERFACTUAL_PAIN_C.txt,
 NEW_SubadultsAbsorbPercent_NY.txt,
 NEW_TIMESERIES_COUNTERFACTUAL_PAIN_A.txt,
 NEW_TIMESERIES_COUNTERFACTUAL_PAIN_C.txt,
 NEW_TIMESERIES_NY.txt, Probl.txt, ProblA.txt, ProblC.txt,
 proportionsA.txt, proportionsAB.txt, proportionsC.txt,
 proportionsCB.txt, proportionsNY.txt, proportionsNYB.txt,
 REACTA.txt, REACTC.txt, REACTM.txt, REACTMA.txt,
 REACTMC.txt, REACTNY.txt, rovalueA.txt, rovalueAB.txt,
 rovalueC.txt, rovalueCB.txt, rovalueNY.txt, rovalueNYB.txt,
 survivalA.txt, survivalC.txt, and survivalNY.txt.

Step 5: Run the 3_NY_MaleEarlyDensiPOPdV2.R.

5-a. Open the 3_NY_MaleEarlyDensiPOPdV2.R file in R Gui (64-bit). [Note: The directions that follow will not make sense in RStudio or RVisual]. To open the script, go to the top menu ribbon in R Gui (64-bit), click “File”, “Open script..”, then navigate to 3_NY_MaleEarlyDensiPOPdV2.R and click “Open”.

5-b: Click on the box containing the 3_NY_MaleEarlyDensiPOPdV2.R command codes. Under the top information box of command codes, you will find a series of commands to remove extant libraries. Run each of these lines in series:

```

remove.packages('shinydashboard')
remove.packages('shiny')
remove.packages('popdemo')
remove.packages('FSA')
remove.packages('shinycssloaders')
  
```

To run a line, right-click on the line and click “Run line or selection”. Note: These lines of code are meant to clean any extant versions of these packages off your computer so the environment of your current computer cannot interfere with the new

environment needed for this script. If a package does not already exist, then running this code will produce an error stating “Error in find.package(pkgs, lib): there is no packages called XXX”. This is ideal, as there is no package that could interfere. If a package does already exist, then running this code will produce a message stating “Removing package from XXX”. This is also ideal, in that it removed the package that could interfere.

5-c: Click on the box containing the `3_NY_MaleEarlyDensiPOPdV2.R` command codes. Hand-enter a “#” to the left of each line, producing this code:

```
#remove.packages('shinydashboard')
#remove.packages('shiny')
#remove.packages('popdemo')
#remove.packages('FSA')
#remove.packages('shinycssloaders')
```

5-d: Click on the box containing the `3_NY_MaleEarlyDensiPOPdV2.R` command codes. Right click on the command line that says:

```
library(renv)
and then click “run line or selection”.
```

5-e: Click on the box containing the `3_NY_MaleEarlyDensiPOPdV2.R` command codes. Right-click on the command line that says:

```
Sys.setenv(RENV_DOWNLOAD_METHOD = "wininet")
and then click “run line or selection”.
```

5-f: Click on the box containing the `3_NY_MaleEarlyDensiPOPdV2.R` command codes. Right click on the command line that says:

```
renv::restore()
and then click “run line or selection”. A prompt will appear in the console that asks “Would you like to activate this project before restore [Y/n]?” Type Y in the console and hit enter. A second prompt will appear in the console that asks “Do you want to proceed? [y/N]”. Type y in the console and hit enter. Wait until the console prints > on the bottom line, indicating that it is ready to execute additional commands. [Note: These questions might be in reverse order, depending on your machine.]
```

5-g: Comment out the previous three lines of code by hand. Directly in the script type “#” to the left of `library(renv)` so the new command line reads

```
#library(renv) . Similarly, type “#” to the left of
Sys.setenv(RENV_DOWNLOAD_METHOD = "wininet") so the new line reads
#Sys.setenv(RENV_DOWNLOAD_METHOD = "wininet"). Finally, type “#” to
the left of renv::restore() so the new command line reads
#renv::restore() .
```

5-h: In the upper ribbon menu of R, click “Edit”, then click “Run all”.

Step 6: The User Interface (UI) should open in a new window. You can interact with the software by clicking on options in the menu on the lefthand side of the screen. Once done interacting with the UI, close the tab depicting the UI, stop the R code by going to “Misc” in the upper ribbon menu of R and clicking on “Stop all computations”. Close the R program.

[NOTE: The six steps depicted above described the processes to prepare and run the script for males in the early time period. The processes to prepare and run the scripts for males in the late time period, females in the early time period, or females in the late time period are similar.]

Running a new analysis from scratch

The instructions provided in the **User tutorial** section guide the operator through the use of previously-generated .txt files to run the NYDensiPOPd V2 software application. If that is all you want to do, then stop there. However, we have included the algorithms (1_NY_Algorithm_Male_Early_Pb_Exposure.R, 1_NY_Algorithm_Male_Early_Pb_Poisoning.R, 1_NY_Algorithm_Male_Early_Pb.R,) and summary code (2_NY_Functions_Male_Early.R) used to generate these pre-saved files so that you can follow the analysis from start to finish, or you may start-from-scratch to run an entirely new analysis using different time series.

Start-from-scratch Step 1: Complete Steps 1-4 (above).

Start-from-scratch Step 2. Open the 1_NY_Algorithm_Male_Early_Pb_Exposure.R file in R Gui (64-bit). [Note: The directions that follow will not make sense in RStudio or RVisual]. To open the script, go to the top menu ribbon in R Gui (64-bit), click “File”, “Open script...”, then navigate to 1_NY_Algorithm_Male_Early_Pb_Exposure.R and click “Open”.

Start-from-scratch Step 3. In the upper ribbon menu of R, click “Edit”, then click “Run all”. Wait for the algorithm to complete [*may take up to 24 hours, depending on your machine*].

Start-from-scratch Step 4. Open the 1_NY_Algorithm_Male_Early_Pb_Poisoning.R file in R Gui (64-bit). [Note: The directions that follow will not make sense in RStudio or RVisual]. To open the script, go to the top menu ribbon in R Gui (64-bit), click “File”, “Open script...”, then navigate to 1_NY_Algorithm_Male_Early_Pb_Poisoning.R and click “Open”.

Start-from-scratch Step 5. In the upper ribbon menu of R, click “Edit”, then click “Run all”. Wait for the algorithm to complete [*may take up to 24 hours, depending on your machine*].

Start-from-scratch Step 6. Open the `1_NY_Algorithm_Male_Early_Pb.R` file in R Gui (64-bit). [Note: The directions that follow will not make sense in RStudio or RVisual]. To open the script, go to the top menu ribbon in R Gui (64-bit), click “File”, “Open script...”, then navigate to `1_NY_Algorithm_Male_Early_Pb.R` and click “Open”.

Start-from-scratch Step 7. In the upper ribbon menu of R, click “Edit”, then click “Run all”. Wait for the algorithm to complete [*may take up to 24 hours, depending on your machine*].

Start-from-scratch Step 8. Open the `2_NY_Functions_Male_Early.R` file in R Gui (64-bit). [Note: The directions that follow will not make sense in RStudio or RVisual]. To open the script, go to the top menu ribbon in R Gui (64-bit), click “File”, “Open script...”, then navigate to `2_NY_Functions_Male_Early.R` and click “Open”.

Start-from-scratch Step 9. In the upper ribbon menu of R, click “Edit”, then click “Run all”. Wait for the algorithm to complete [*may take up to an hour, depending on your machine*]. *Note: You may have to install the package `popdemo` in order to run this script.*

Start-from-scratch Step 10. Complete Steps 5-6 (above).

Technical details

The packet includes the environment in which the code was written, as packaged through the `renv` package version 0.16.0 (Ushey 2022). The `renv` folder, all its contents as well as the `renv.lock` file contain a list and versions of all the dependencies of this code.

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Citation for re-use

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Changes since the original version

The original version of this software is at <https://doi.org/10.7298/z3ym-1357>.

Version 2 Software published 2023-03-16.

Changes since the original version include:

1. Omitted the validation packet.
2. Changed NY to Actual, C to Pb-free, and A to Pb-reduced.
3. Edited the time series for New York State to remove the error in the data.
4. Altered the aesthetics of the user interface.
5. Added new intermediate files autosaved by the functions file.
6. Modularized the redundant functions to allow the app to run faster. Added the R script named `2_NY_MaleDensiPOPdV2_Functions.R`.
7. Altered the Readme to reflect all the changes described by this list.
8. Added the `renv` environment commands to the scripts as well as the environment itself to the package.