

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

## **StallPOPdV4 Web Interactive: Software to compute population control treatments of a subsidized predator**

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### **Overview of the *StallPOPdV4 Software***

Wildlife managers must stay abreast and act quickly when deleterious situations for sensitive wildlife prey emerge because of human subsidy of predators. The ***StallPOPdV4 Software*** leverages density independent and density dependent population matrix models (Caswell 2001) to identify population reduction strategies that may be used by managers to reset, slow, or halt subsidized population growth of a 3-stage species, such as the common raven (*Corvus corax*). Potential treatment strategies include the reduction in fertility or the culling of live individuals. The ***StallPOPdV4 Software*** is not limited to use with common ravens; it may be used to identify treatment strategies for any species depicted by a three-stage life history. This software is the fourth of its kind behind ***StallPOPd Software*** (Version 1.0; Shields et al. 2019b), ***StallPOPdV2 Software*** (Hanley et al. 2020a), and ***StallPOPdV3 Software*** (Hanley et al. 2020b).

### **Capabilities of the *StallPOPdV4 Software***

The *StallPOPdV4 Software* allows the user to:

1. Enter the deterministic elements of an annual, 3-stage, one-sex, density dependent or density independent Lefkovitch matrix model (Shields et al. 2019). Default values for common ravens are used from the demographic work of Kristan et al. (2005).
2. Enter the characteristics of the geographical areas of interest, including size (in square kilometers), current densities of the undesirable predator (in individuals per square kilometer), and the target densities of the undesirable predator (in individuals per square kilometer). Default values for common raven are used from the work of Coates et al. (2020).
3. Identify one-, two-, or three-treatment combinations that may be used to “reset” predator abundances to levels sustainable for coexistence with sympatric wildlife prey over the duration of one calendar year. Possible treatment combinations include all one-, two-, or three-way combinations of the (i.) reduction in fertility, (ii.) the culling of hatchlings, (iii.) the culling of non-breeders, and/or (iv.) the culling of breeders.
4. Identify one-, two-, or three-treatment combinations that may be used to maintain the growth rate of one in perpetuity. Possible treatment combinations include all one-, two-, or three-way combinations of the (i.) reduction in fertility, (ii.) the culling of hatchlings, (iii.) the culling of non-breeders, and/or (iv.) the culling of breeders.
5. Identify the magnitude of the growth rate under no treatments, partial levels of treatments (one-, two-, or three-way combinations), or under optimal levels of treatments (one-, two-, or three-way combinations).
6. Save (download) the results of the investigation.

### ***StallPOPdV4 Software user tutorial***

#### *Preparing and running the StallPOPdV4 Software on your machine*

**Step 1:** Open R and verify that you are running the appropriate version of R studio .

*Note: The correct version is 1.3.1093 © 2009–2020 R Studio, PBC  
“Apricot Nasturtium” (ae44535, 2020-09-17) for Windows.*

**Step 2:** Create a folder on your computer that will function as your working directory.

**2a:** Create a folder, then name it in accordance with your project.

*Note: This folder will be your working directory.*

**Step 3:** Prepare the *StallPOPdV4 Software* on your machine.

**3a:** Download, unzip, and save the contents of the *StallPOPdV4 Software* into the folder prepared in **2a** (your working directory).

**Step 4:** Click on the “StallPOPdV4.R” script.

*Note: The script should open directly in R Studio, and the program will automatically set the internal path to the working directory prepared in 2a.*

**Step 5.** Verify that all packages are installed.

**5a.** Upon execution of **Step 4.**, your R Studio will automatically peruse the “StallPOPdV4.R” commands to ascertain whether the script requires the installation and/or update of packages that are not already loaded into your machine. If R Studio gives you an option to install a package dependency, click “Install”. Packages include:

- (1) “devtools” (version 2.3.2),
- (2) “shiny” (version 1.5.0),
- (3) “shinyBS” (version 0.61),
- (4) “shinydashboard” (version 0.7.1),
- (5) “scatterplot3d” (version 0.3-41).

**Step 6:** Hit “Run App”.

*Notes: Many newer package versions can accommodate the commands written in earlier versions. However, if your machine automatically loads a newer version of a package and execution of **Step 6** throws an error, you can manipulate your machine to overwrite the newer versions of each package with the older ones. To install a particular version of an R package, close out R Studio completely, open R in an unrelated window [R version 4.0.2 (2020-06-22) -- "Taking Off Again" Copyright (C) 2020 The R Foundation for Statistical Computing Platform: x86\_64-w64-mingw32/x64 (64-bit)] then run:*

```
library(devtools)
devtools::install_version("shiny", version = "1.5.0").
```

*This command will remove the previously installed (presumably newer) version of the shiny package from your machine then replace it with the older (1.5.0) version of shiny. Rerun this command for all required packages. Once the exact versions are loaded onto your machine, close R and return to **Step 4**. We have further provided the workspace file (.RData) to aid in re-engineering the exact environment. After this process is complete, anytime you then open R Studio, it will automatically give you the option to update the versioning of any “older” packages. If you would like to undo what you just did (and reload the latest version) simply click “Update”.*

*Interacting with the user interface of the **StallPOPdV4 Software***

**Step 1:** Click the *Matrix Initiation* tab to initiate a matrix depicting the life history of the undesirable predator.

**Step 2:** Use the tabs to select a density dependent model or a density independent model.

*Note: A density independent model does not allow individuals in the non-breeding stage to remain in that stage for more than one year’s time. A density dependent model allows non-breeders to remain non-breeders indefinitely. See Caswell (2001).*

**Step 3:** Enter the numeric values of the matrix elements into your population matrix model.  
*Note: The top row of both matrices represent reproduction in the life history of the undesirable predator. All numeric entries in the top row must be equal to or greater than zero and may be defined as fertility (actual reproduction) or fecundity (maximum reproduction). Reproduction elements are in the units of per breeding female, per time period. The middle and bottom rows of both matrices represent survival (and transition) probabilities in the life history of the undesirable predator. All numeric entries in the middle or bottom rows must fall between zero and one. A transition that begins in one stage and ends in a different stage represents the average probability that a female will survive the time unit and transition to the latter stage. Alternatively, in the case of the middle ( $a_{22}$ ) and lower right elements ( $a_{33}$ ), individuals survive but do not exit their stage. For additional information, refer to Caswell 2001, pgs. 10 and 171.*

**Step 4:** Click on the *Geographical Area* tab.

**Step 5:** Enter the geographical characteristics of your study area.

**5a.** Enter the numeric size of the study area (in square kilometers). *Note: Default values reflect the size of an example critical habitat unit of the Mojave Desert, California (K. Holcomb, unpublished data).*

**5b.** Enter the numeric current density of the undesirable predators in the study area (in individuals per square kilometer). *Note: Default values reflect densities of common raven in an example critical habitat unit of the Mojave Desert, California (K. Holcomb, unpublished data).*

**5c.** Enter the numeric target density of the undesirable predators in the study area (in individuals per square kilometer). *Note: Default values reflect desirable densities of common raven from the work by Coates et al. (2020).*

**Step 6:** If you entered values into a density dependent matrix, click the *Density Dependent System* tab.

**Step 7:** If you entered values into a density independent matrix, click the *Density Independent System* tab.

**Step 8:** Interact with the results of your system.

*Note: The results tabs include “One-Time Reset”, “Long-Term Maintenance Overview” and “Long-Term Maintenance Details” results.*

**8a.** The “One-Time Reset” results. This result is defined as the number of individuals that must be removed from your system in one year’s time to align your system with target densities. The computations assume the population is in stable stage distribution (Caswell 2001) and that treatment can during that year on every possible vital rate. The one-time matrix is the target matrix of the population during intensive treatment. For example, if the breeder fertility is 0.19, then managers should aim to conduct any treatment that reduces breeder fertility to an average of 0.19 across the population for that year.

**8b.** The “Long-Term Maintenance Overview” results. This result is defined as the marginal or joint rates of removal (destruction of eggs and/or culling of live individuals)

necessary to constrain the overall population growth rate to one. Marginal rates of removal are depicted as a number, while 2- and 3-way joint rates are depicted as 2-D and 3-D graphs (respectively). In the graphs, every 2- or 3-way coordinate shown by a colored line constitute a solution that combined to produce a growth rate of one. For example, if a line goes through the coordinates (0.2, 0.5), then simultaneous reduction of average survival of the first stage listed to 0.2 and reduction in average survival of second stage listed to 0.5 will force the overall population to a growth rate of one.

**8c.** The “Long-Term Maintenance Details” results. These results depict the marginal and joint rates needed to halt (constrain the growth rate to one) or stall (reduce the current growth rate) growth. As well, these results allow the user to interim rates of treatment to view how the population trajectory of breeders may respond.

**Step 9:** Click on the *Download My Results* tab.

**Step 10:** Use the tabs to select a density dependent model or a density independent model.

**Step 11:** Click on the “Download the treatments” button to save the results to your machine.

**Step 12:** Once your investigation is complete, close R.

### **Changes between the *StallPOPdV3* and *StallPOPdV4* Software**

Alterations to the *StallPOPdV3* Software to formulate the *StallPOPdV4* Software were made per peer review requests at *Human Wildlife Interactions* on 24 August 2021 to 29 August 2021.

#### *Aesthetic changes*

1. Modified the color of the background.
2. Formatted to make bold, resize, or emphasize the titles, headers, and narratives.
3. Organized sets of inputs into boxes to better organize the look and flow of the user interface.
4. Highlighted in red the matrix elements that require user entry and better-defined inputs.
5. Cited the source of our example (initial) values.
6. Added an introduction page that contains a header, photo, and explanation of app intent.
7. Removed the foundational help button and placed the narrative in the introduction page.
8. Reworded “killing” to “destroying” (eggs) or “culling” (live individuals).
9. Highlighted in red the geographical areas that require user entry and better-defined inputs.

#### *Navigational changes*

1. Partitioned the “Matrix Initiation” tab into two sub panels: (1) a panel to initialize a density dependent matrix, and (2) a panel to initialize a density independent matrix.
2. Created a new tab to house the “Geographical area” inputs and moved those inputs from the original “Matrix initiation” tab to this new tab.
3. Added an introduction page to the app that contains a quick user tutorial.

4. Partitioned the “Download My Results” tab into two sub panels: (1) to download the results of the dependent matrix, and (2) to download the results of the density independent matrix.

### *Computational changes*

1. Nothing that would alter the results from the earlier versions. We renamed each matrix input value to differentiate density dependent vs. density independent matrices, then cascaded the new naming conventions into the old equations.

### **Technical details**

The *StallPOPdV4 Software* written under R studio version 1.3.1093 © 2009–2020 R Studio, PBC “Apricot Nasturtium” (aeee44535, 2020-09-17) for Windows and requires the packages: (1) “devtools” (version 2.3.2), (2) “shiny” (version 1.5.0), (3) “shinyBS” (version 0.61), (4) “shinydashboard” (version 0.7.1), and (5) “scatterplot3d” (version 0.3-41).

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The *StallPOPdV4 Software* is shared under a MIT License.

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## Suggested citation for the re-use of the *StallPOPdV4 Software*:

- Hanley, B., A. Currylow, K. Holcomb, T. Shields, S. Boland, W. Boarman, & M. Vaughn. 2021. StallPOPdV4 Web Interactive: Software to compute population control treatments of a subsidized predator [Software]. doi.org/10.7298/sk2e-0c38.4