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## **Regional Wildlife Disease Positives Software**

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### **Overview of the Regional Wildlife Disease Positives Software**

The *Regional Wildlife Disease Positives Software* allows the user to track the occurrence, persistence, or spread of chronic wasting disease (CWD) in free ranging white-tailed deer (*Odocoileus virginianus*) in select states and provinces in the eastern United States (US) and Canada (CAN). The *Regional Wildlife Disease Positives Software* was adapted from the *Wildlife Disease Positives Software* (Mitchell et al. 2021) to display pooled data and results up to the continental scale. The R scripts of the *Regional Wildlife Disease Positives Software* contain a sequential network of commands that format the geospatial files and surveillance (testing) data, then launch the user interface (UI) of the interactive software to depict pooled results at the continental scale. The *Regional Wildlife Disease Positives Software* packet includes (redacted) disease testing data from a select assortment of United States wildlife agencies: Alabama, Arkansas, Connecticut, Florida, Georgia, Indiana, Iowa, Kentucky, Louisiana, Maryland, Michigan, Minnesota, Mississippi, New Hampshire, New York, North Carolina, Ohio, Pennsylvania, Rhode Island, Tennessee, Virginia, and Wisconsin and Canadian provincial agencies: Ontario. While the *Regional Wildlife Disease Positives Software* was designed for use

by state and provincial agencies to track chronic wasting disease (CWD) in white-tailed deer from 2013-2025, the software is easily adaptable to other wildlife diseases in other states or provinces, in different years, and/or in differing wildlife species.

The *Regional Wildlife Disease Positives Software* contains four types of R scripts:

- "0\_Regional\_Positives\_Pre\_Processing.R" script,
- "1\_Regional\_Positives\_Data\_Prep.R" script,
- "2\_Regional\_Positives\_App.R" script,
- "3\_Regional\_Positives\_Command\_Center.R" script.

The 0\_Regional\_Positives\_Pre\_Processing.R script of the *Regional Wildlife Disease Positives* creates the geospatial and related files containing administrative boundaries for all included states and provinces in the structural format needed for immediate upload into upload into the 2\_Regional\_Positives\_App.R of the *Regional Wildlife Disease Positives Software*.

The 1\_Regional\_Positives\_Data\_Prep.R script of the *Regional Wildlife Disease Positives Software* converts CWD surveillance (disease testing) data from Mitchell et al. (2021) into the structural format needed for immediate upload into the 2\_Regional\_Positives\_App.R script of the *Regional Wildlife Disease Positives Software*.

The 2\_Regional\_Positives\_App.R script of the *Regional Wildlife Disease Positives Software* intakes the autosaved geospatial files from the execution of the 0\_Regional\_Positives\_Pre\_Processing.R script and the autosaved data from the execution of the 1\_Regional\_Positives\_Data\_Prep.R script, and launches the interactive user interface from which the user may explore a mapped version of the data and summaries. Thus, the 0\_Regional\_Positives\_Pre\_Processing.R, 1\_Regional\_Positives\_Data\_Prep.R, and 2\_Regional\_Positives\_App.R scripts of the *Regional Wildlife Disease Positives Software* must run in sequence.

With one click, the 3\_Regional\_Positives\_Command\_Center.R script of the *Regional Wildlife Disease Positives Software* runs the appropriate sequence and set of scripts of the *Regional Wildlife Disease Positives Software*:

- 0\_Regional\_Positives\_Pre\_Processing.R,
- 1\_Regional\_Positives\_Data\_Prep.R, and
- 2\_Regional\_Positives\_App.R scripts.

Any data available for any state or province in North America may be included in the interface. Missing data do not hinder the ability to run the software. Please see the **Instructions to add data to the *Regional Wildlife Disease Positives Software*** section below.

## Inputs Needed to Run the Regional Wildlife Disease Positives Software

Data inputs necessary to run the `0_Regional_Positives_Pre_Processing.R` script of the *Regional Wildlife Disease Positives Software* include:

- 0-i.** Raw geospatial files containing administrative boundaries for the US and Canada.  
*Note: The Cartographic Boundary and TIGER line files (US Census Bureau 2019; 2020) necessary to create the appropriate files for the US states are procured using command lines directly in the script. The files necessary for Canada (Statistics Canada 2019), however, require additional steps to procure from an outside source. See **Steps 5-6** in the Regional Wildlife Disease Positives Software User Tutorial section (below).*
- 0-ii.** A csv file containing a list of all participating state and province names in a single column (for more details see **Step 7** below):  
`"All_States.csv"`  
*Note: This script will automatically create a single set of geospatial files and related files consisting of all states and provinces included in "All\_States.csv" and should only be run once, unless additional states are added to "All\_States.csv" after the initial run.*

Data necessary to run the `1_Regional_Positives_Data_Prep.R` script of the *Regional Wildlife Disease Positives Software* include:

- 1-i.** Pre-processed surveillance (testing) data summaries of (1) all samples and (2) confirmed CWD positives by county (or other administrative area) and age/sex segment generated for years ("XX") 2013-2025 for all participating states and provinces (created for each state and province in Mitchell et al. 2021):  
`"All_(state name)CountySummary20XX.txt"`  
`"(state name)CountySummary20XX.txt"`
- 1-ii.** A csv file containing a list of all participating state and province names in a single column (for more details see **Step 7** below):  
`"All_states.csv"`

The surveillance data (**1-i**) are not included in this *Regional Wildlife Disease Positives Software* packet. Data summaries can be created for states (or provinces) with Mitchell et al. (2021), alternatively, templates can be modified to include real data by replacing "999999" in all templates.

Data inputs necessary to run the `2_Regional_Positives_App.R` script of the *Regional Wildlife Disease Positives Software* include:

- 2-i.** Geospatial files *autosaved* during the execution of the `0_Regional_Positives_Pre_Processing.R` script containing the county (or other administrative area) boundaries of all participating states and provinces:  
`"All_counties.dbf"`  
`"All_counties.prj"`

"All\_counties.shp"

"All\_counties.shx"

**2-ii.** Text files *autosaved* during the execution of the

0\_Regional\_Positives\_Pre\_Processing.R script containing the geographic center of the region of interest:

"All\_Latitude.txt"

"All\_Longitude.txt"

**2-iii.** A csv file containing a list of all participating state and province names in a single column (for more details see **Step 7** below):

"All\_states.csv"

**2-iv.** Data file outputs *autosaved* during the execution of the

1\_Regional\_Positives\_Data\_Prep.R script generated for years ("XX") 2013-2025:

"AllPositives20XX.txt"

"AllTesting20XX.txt"

"Table20XX.txt"

"TableAll.txt"

Data inputs necessary to run the 3\_Regional\_Positives\_Command\_Center.R script of the *Regional Wildlife Disease Positives Software* include:

**3-i.** Raw geospatial files containing administrative boundaries for the US and Canada.

*Note: The Cartographic Boundary and TIGER line files (US Census Bureau 2019; 2020) necessary to create the appropriate files for the US states are procured using command lines directly in the script. The files necessary for Canada (Statistics Canada 2019), however, require additional steps to procure from an outside source. See Steps 5-6 in the Regional Wildlife Disease Positives Software User Tutorial section (below).*

**3-ii.** A csv file containing a list of all participating state and province names in a single column (for more details see **Step 7** below):

"All\_states.csv"

**3-iii.** Pre-processed surveillance (testing) data summaries of (1) all samples and (2) confirmed CWD positives by county (or other administrative area) and age/sex segment generated for years ("XX") 2013-2025 for all participating states and provinces (created for each state and province in Mitchell et al. 2021):

"All\_(state name)CountySummary20XX.txt"

"(state name)CountySummary20XX.txt"

The surveillance data (**1-i**) are not included in this *Regional Wildlife Disease Positives Software* packet. Data summaries can be created for states (or provinces) with Mitchell et al. (2021), alternatively, templates can be modified to include real data by replacing "999999" in all templates.

## ***Regional Wildlife Disease Positives Software user tutorial***

### ***Preparing and running the Regional Wildlife Disease Positives Software***

**Step 1:** Open R and verify that you are running the appropriate version of the R Software (R Core Team 2020). The appropriate version is 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].

**Step 2:** Install the appropriate versions of the dependencies (R packages) in R. Packages include:

- (1) "devtools" version 2.3.2
- (2) "dplyr" version 1.0.2
- (3) "leaflet" version 2.0.3
- (4) "leaflet.extras" version 1.0.0
- (5) "leafletpop" version 0.0.6
- (6) "RColorBrewer" version 1.1-2
- (7) "rgdal" version 1.5-18
- (8) "rgeos" version 0.5-5
- (9) "rgl" version 0.100.54
- (10) "raster" version 3.4-5
- (11) "rmapshaper" version 0.4.4
- (12) "maptools" version 1.5-2
- (13) "shiny" version 1.5.0
- (14) "shinyBS" version 0.61
- (15) "shinycssloaders" version 1.0.0
- (16) "shinydashboard" version 0.7.1
- (17) "sf" version 0.9-6
- (18) "sp" version 1.4-4
- (19) "stringr" version 1.4.0
- (20) "tidyr" version 1.1.2
- (21) "tigris" version 1.0

To install a particular version of an R package, run the code:

```
library(devtools)
devtools::install_version("package name", version =
"#.#.#").
```

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

**3-a:** Create a folder, then name it 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 "dir()", and hitting enter. The file names of the contents of your working directory will print in the R console.

**Step 4:** Prepare the *Regional Wildlife Disease Positive Software* on your machine.

**4-a:** Download, unzip, and save the *Regional Wildlife Disease Positive Software* contents in your working directory.

**4-b:** To double check all contents are in your working directory, click the R console, type "dir()", and hit enter. The file names of the contents of your working directory will print in the console.

**Step 5.** Download and prepare the census division units shapefiles from Statistics Canada.

**5-a.** Go to [www12.statcan.gc.ca/census-recensement/2011/geo/bound-limit/bound-limit-2016-eng.cfm](http://www12.statcan.gc.ca/census-recensement/2011/geo/bound-limit/bound-limit-2016-eng.cfm).

**5-b.** Select the following options: Language: "English"; Format: "ArcGIS"; Boundary files: "Census division" under "Cartographic Boundary File"; then click "Continue" to be directed to the download page.

**5-c.** Download the zipped folder (lcd\_000b16a\_e.zip).

**5-d.** Unzip the downloaded folder into the working directory.

**Step 6.** Download and prepare the geographic attribute file for the 2016 census year for Canada.

**6-a.** Go to [www12.statcan.gc.ca/census-recensement/2011/geo/ref/att-eng.cfm](http://www12.statcan.gc.ca/census-recensement/2011/geo/ref/att-eng.cfm).

**6-b.** Select the following options: Census year: 2016; Format: "Comma-separated values (.csv)"; then click "Continue" to be directed to the download page.

**6-c.** Download the zipped folder (2016\_92-151\_XBB\_csv.zip).

**6-d.** Unzip the downloaded folder into the working directory.

**Step 7.** Open the file titled "All\_States" and verify the list of all regional state and province names in the single column named "All\_States". This list is used by the *Regional Wildlife Disease Positives Software* to create the geospatial files necessary to run the application as well as read in and collate the surveillance (testing) data for each participating state and province listed.

*Note: This file must contain a list of all entities to be displayed in the Regional Wildlife Disease Positives Software. To add a state (or province), please see*

**Instructions to add data to the Regional Wildlife Disease Positives Software (below).**

*States or provinces with spaces, such as “New York” should be written with the space. Do not include the country in the name. For example, type “New York” as “New York”, not as “New York, USA”. States and provinces should be listed in ascending alphabetical order (from A at top to Z at bottom).*

**Step 8:** Open in R the file named “3\_Regional\_Positives\_Command\_Center.R”.

**Step 9:** Hit “Run all”.

*Note: From this moment, your script will automatically call the appropriate libraries, then begin running the series of scripts of the Regional Wildlife Disease Positives Software. Several lines of code will be executed without any further interaction from you. Your script will automatically load the geospatial files, initiate projections, crunch data, and sort data. This computational process is normal. All files are autosaved to your working directory. Finally, the script will open the interactive app.*

**Step 10:** Once done interacting with the UI, close the tab depicting the UI, stop the R code, and close the R program.

### **Instructions to add an additional state (or province) to the Regional Wildlife Disease Positives Software**

The *Regional Wildlife Disease Positives Software* was initially developed to accommodate the needs of a consortium of state and provincial wildlife agencies that opted to participate in the Surveillance Optimization Project for Chronic Wasting Disease (SOP4CWD; CHWL 2021). Accordingly, the list of states and provinces included in this packet reflect a selection of partnering agencies, but other states and provinces are welcome to join.

In the event additional states or provinces join, this software can accommodate their inclusion with ease. To add a state or province to the *Regional Wildlife Disease Positives Software*:

**Step i:** Open the “All\_States.csv” file.

**i-a:** Enter the name of the new state (or province) in the alphabetically appropriate row.

*Note: States or provinces with spaces, such as “New York” should be written with the space. Do not include the country in the name. For example, type “New York” as “New York”, not as “New York, USA”. States and provinces should be listed in ascending alphabetical order (from A at top to Z at bottom).*

**i-b.** Save the updated “All\_States.csv” file to your working directory.

**Step ii.** Reference Mitchell et al. (2021) to create the surveillance (testing) data summaries of (1) all samples and (2) confirmed CWD positives by county (or other administrative area) and age/sex segment for years (“XX”) 2013-2025 for the new state (or province):

```
"All_(new state name)CountySummary20XX.txt"
```

```
"(new state name)CountySummary20XX.txt"
```

**Step iii:** Complete **Steps 1-9** above.

*Note: If you previously completed **Steps 2-6** for another state (or province) (i.e., installed the appropriate packages, setup your working directory, prepared the Regional Wildlife Disease Positives Software, and downloaded and added the Canadian provincial boundary shapefiles, census division units shapefiles, and geographic attribute file to your working directory), you may skip **Steps 2-6**.*

## Technical details

0\_Regional\_Positive\_Pre\_Processing.R script of the *Regional Wildlife Disease Positives Software* was written under 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) and requires the packages: (1) “devtools” version 2.3.2 (Wickman et al. 2020), (2) “rgdal” version 1.5-18 (Bivand et al. 2020), (3) “tigris” version 1.0 (Walker 2020), (4) “stringr” version 1.4.0 (Wickman 2019), (5) “mapproj” version 1.0-2 (Bivand and Lewin-Koh 2021), (6) “raster” version 3.4-5 (Hijmans 2020), (7) “dplyr” version 1.0.2 (Wickman et al. 2021), (8) “rmapshaper” version 0.4.4 (Teucher and Russell 2020), and (9) “rgeos” version 0.5-5 (Bivand and Rundel 2020).

1\_Regional\_Positives\_Data\_Prep.R script of the *Regional Wildlife Disease Positives Software* was written under 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) and requires the packages: (1) “devtools” version 2.3.2 (Wickman et al. 2020), (2) “raster” version 3.4-5 (Hijmans 2020), (3) “rmapshaper” version 0.4.4 (Teucher and Russell 2020), and (4) “stringr” version 1.4.0 (Wickman 2019).

2\_Regional\_Positives\_App.R script of the *Regional Wildlife Disease Positives Software* was written under 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) and requires the packages: (1) “devtools” version 2.3.2 (Wickman et al. 2020), (2) “shinydashboard” version 0.7.1 (Chang and Borges Ribeiro 2018), (3) “shiny” version 1.5.0 (Chang et al. 2020), (4) “leaflet” version 2.0.3 (Cheng et al. 2019), (5) “dplyr” version 1.0.2 (Wickman et al. 2021), (6) “leaflet.extras” version 1.0.0 (Karambelkar and Schloerke 2018), (7) “rgl” version 0.100.54 (Adler et al. 2020), (8) “shinyBS” version 0.61 (Bailey 2015), (9) “RColorBrewer”



version 1.1-2 (Neuwirth 2014), (10) “sp” version 1.4-4 (Pebesma and Bivand 2005; Bivand et al. 2013), (11) “sf” version 0.9-6 (Pebesma 2018), (12) “rgdal” version 1.5-18 (Bivand et al. 2020), (13) “leaflet” version 0.0.6 (Appelhans and Detsch 2020), (14) “tidyr” version 1.1.2 (Wickman 2020), (15) “rgeos” version 0.5-5 (Bivand and Rundel 2020), (16) “raster” version 3.4-5 (Hijmans 2020), (17) “shinycssloaders” version 1.0.0 (Sali and Attali 2020), and (18) “rmapshaper” version 0.4.4 (Teucher and Russell 2020).

3\_Regional\_Positives\_Command\_Center.R script of the *Regional Wildlife Disease Positives Software* was written under 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) and requires all the packages listed for the other scripts.

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*Chronic Wasting Disease: Streamlining a Web Application for Disease Visualization and Data-Driven Decisions* (2021).

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