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## **Chronic Wasting Disease Surveillance Optimization Software**

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### **Overview of the Chronic Wasting Disease Surveillance Optimization Software**

The *Chronic Wasting Disease Surveillance Optimization Software* computes sampling strategy recommendations for state-wise use of surveillance funds by a state wildlife management agency when the goal of the disease surveillance program is to detect chronic wasting disease (CWD) in white-tailed deer (*Odocoileus virginianus*). Driven by a combinatorial optimization algorithm (Korte and Vygen 2018), the *Chronic Wasting Disease Surveillance Optimization Software* pinpoints the combination of samples that should be tested in each population segment of deer (adult male, adult female, yearling male, yearling female, fawn male, fawn female), in each collection category of deer (hunter harvested, non-hunter harvested), and in each county (or other

administrative area) of the state to maximize the return-on-investment, while keeping the overall cost of the surveillance program within the predetermined budget.

Inputs to the combinatorial optimization algorithm in the *Chronic Wasting Disease Surveillance Optimization Software* broadly include the *Optimization Matrix* and the *Historical Data*. The *Optimization Matrix* includes information such as the costs, benefits, and starting prevalence of CWD for each population segment, collection category, and county or other administrative unit. The *Historical Data* considers the previously enacted sampling strategy in each county (or other administrative area), then uses that data as comparison to the algorithmic recommendations.

Agencies may further parameterize their algorithm to achieve specific management objectives, including monitoring known infections, searching for new infections, and providing detailed information to the public.

The *Chronic Wasting Disease Optimization 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; CWHL 2021). However, the current release of the *Chronic Wasting Disease Optimization Software* is designed for use by US state wildlife agencies, and the list of states included in this packet reflect the current list of US partnering agencies. Thus, the *Chronic Wasting Disease Surveillance Optimization Software* includes (redacted) *Optimization Matrices* and (redacted) *Historical Data* from 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, US, but the software may be adapted for use in other states and provinces.

## The scripts of the software

The *Chronic Wasting Disease Surveillance Optimization Software* contains the R scripts:

```
_0a_ (state name)_Optimization_Spatial_Prep.R script,  
_0b_ (state name)_Optimization_Cost_Prep.R script,  
_0c_ (state name)_Optimization_Habitat_Variable_Prep.R script,  
_0d_ (state name)_Optimization_Monitoring_Prep.R script,  
_0e_ (state name)_Optimization_Early_Detect_Prep.R script,  
_0f_ (state name)_Optimization_Prevalence_Prep.R script,  
_0g_ (state name)_Optimization_Weights_Prep.R script,  
_0h_ (state name)_Optimization_Matrix_Prep.R script,  
_0i_ (state name)_Optimization_INIT_File_Prep.R script,  
_1_ (state name)_Optimization_Data_Prep.R script,  
_2_ (state name)_Optimization_User_Interface.R script,  
_3_ (state name)_Optimization_Algorithm_Twelve_Categories.R script,  
_4_ (state name)_Optimization_Command_Center.R script.
```

*Note: The (state name) in all file names is a placeholder to depict the geographical entity of interest, regardless of whether the entity is a state, province, or otherwise.*

The `_0a_(state name)_Optimization_Spatial_Prep.R` script creates the geospatial files containing administrative boundaries, as well as related files necessary for executing the user interface for the state of interest. The outputs of the `_0a_(state name)_Optimization_Spatial_Prep.R` script include the geospatial files and related files autosaved in the structural format needed for immediate upload into the remaining scripts.

The `_0b_(state name)_Optimization_Cost_Prep.R` script converts distance and diagnostic fee information into estimated cost per deer for each county. The script calculates the distance (miles) from the centroid of each county to the nearest National Animal Health Laboratory Network (NAHLN; APHIS 2021) laboratory that conducts CWD testing, then multiplies the distance by the 2021 Standard Mileage Rate (IRS 2021). The script then adds to the total distance costs, the per deer diagnostic cost to determine CWD status (APHIS 2021), then saves the data in the format needed for immediate upload into the remaining scripts.

The `_0c_(state name)_Habitat_Variable_Prep.R` script extracts and calculates habitat variables from pre-processed raster layers (created in Mitchell et al. 2021) into county (or other administrative area) summaries, then saves the data in the format needed for immediate upload into the remaining scripts.

The `_0d_(state name)_Optimization_Monitoring_Prep.R` script converts spatial, regulatory, testing, and other variables (Hanley et al. unpublished data) into the benefits for Monitoring, then saves the data in the format needed for immediate upload into the remaining scripts.

The `_0e_(state name)_Optimization_Early_Detect_Prep.R` script converts spatial, regulatory, testing, and other variables (Hanley et al. unpublished data) into the benefits for Early Detection, then saves the data in the format needed for immediate upload into the remaining scripts.

The `_0f_(state name)_Optimization_Prevalence_Prep.R` script converts testing summaries (created in Mitchell et al. 2022) into the standardized prevalence for each population segment based on white-tailed deer vital rates and sex ratios (Chitwood et al 2015; Verme and Ozoga 1981), then saves the data in the format needed for immediate upload into the remaining scripts.

The `_0g_(state name)_Optimization_Weights_Prep.R` script converts surveillance weights (Jennelle et al. 2018) into the format needed for immediate upload into the remaining scripts.

The `_0h_(state name)_Optimization_Matrix_Prep.R` script converts the data from scripts 0a-0g into the format needed for immediate upload into the remaining scripts. The output from this script is the *Optimization Matrix*.

The `_0i_(state name)_Optimization_INIT_File_Prep.R` script creates the user interface start-up files (that contain placeholder information needed to initiate the user interface).

The `_1_(state name)_Optimization_Data_Prep.R` script converts the *Optimization Matrix* into the format necessary for display in the user interface in the `_2_(state name)_Optimization_User_Interface.R` script. The script further determines which counties are eligible for Early Detection, Monitoring, and Public Communications, then saves the outputs in the format needed in the next script. Scripts `0a`, `0b`, `0c`, `0d`, `0e`, `0f`, `0g`, `0h`, `0i`, and `1` prepare the data, and must be run in sequence.

The `_2_(state name)_Optimization_User_Interface.R` script converts the *Historical Data* into the format necessary for display in the user interface, intakes the autosaved geospatial and optimization files, and launches the user interface of the algorithm. From this interface the user will enter their algorithmic settings assuming either a non-homogenous distribution of disease (Belsare et al. 2021) or a homogenous distribution of disease (Walsh and Miller 2010) and initiate the algorithm to run behind the scenes. Scripts `0a`, `0b`, `0c`, `0d`, `0e`, `0f`, `0g`, `0h`, `0i`, and `1` prepare the data and must be run in sequence before script `2` is loaded.

The `_3_(state name)_Optimization_Algorithm_Twelve_Categories.R` script contains the algorithm programmed with commands that reflect the names of the counties (or other administrative areas) for the state of interest. This script is tailored to reflect the state's mathematical dimensions, and the dimensions of vectors in the algorithm are specified by the number of counties (or other administrative areas) that partition the state. The `_3_(state name)_Optimization_Algorithm_Twelve_Categories.R` script is called by the `_2_(state name)_Optimization_User_Interface.R` script once the user enters their settings into the algorithm. Thus, the `_3_(state name)_Optimization_Algorithm_Twelve_Categories.R` script should not be directly opened nor run by the user.

With one click, the `_4_(state name)_Optimization_Command_Center.R` script of the *Chronic Wasting Disease Optimization Software* runs the appropriate sequence of scripts:

```
_0a_(state name)_Optimization_Spatial_Prep.R,  
_0b_(state name)_Optimization_Cost_Prep.R,  
_0c_(state name)_Optimization_Habitat_Variable_Prep.R,  
_0d_(state name)_Optimization_Monitoring_Prep.R,  
_0e_(state name)_Optimization_Early_Detect_Prep.R,  
_0f_(state name)_Optimization_Prevalence_Prep.R,  
_0g_(state name)_Optimization_Weights_Prep.R,  
_0h_(state name)_Optimization_Matrix_Prep.R,  
_0i_(state name)_Optimization_INIT_file_Prep.R,  
_1_(state name)_Optimization_Data_Prep.R,  
_2_(state name)_Optimization_User_Interface.R, and  
_3_(state name)_Optimization_Algorithm_Twelve_Categories.R  
scripts.
```

## Data inputs needed to run the software

The *Chronic Wasting Disease Optimization Software* contained in this packet will not run until real data are entered into the *Optimization Matrix* and *Historical Data* templates.

Data inputs necessary to run the `(state name)_Optimization_Spatial_Prep.R` script include:

**0a-i.** Raw geospatial files containing administrative boundaries for the US.

*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.*

Autosaved outputs from this script include:

**0a-ii.** US shapefiles and zipped folders (for US states only):

`"tl_2020_us_county"`  
`"cb_2019_us_county_500k"`

**0a-iii.** The geospatial files for the state of interest:

`"(state name)_counties.dbf"`  
`"(state name)_counties.prj"`  
`"(state name)_counties.shp"`  
`"(state name)_counties.shx"`

**0a-iv.** Text files containing the geographic center of the state of interest:

`"(state name)_Latitude.txt"`  
`"(state name)_Longitude.txt"`

*Do not modify the names of these files, as they are used as is in later scripts.*

Data inputs necessary to run the `(state name)_Optimization_Cost_Prep.R` script include:

**0b-i.** Geospatial files autosaved during the execution of the 0a script.

**0b-ii.** The latitude and longitude coordinates (WGS84) of the nearest laboratory in the National Animal Health Laboratory Network (NAHLN; APHIS 2021) that conducts CWD testing. This data is pre-entered for all states in this packet.

**0b-iii.** The CONUS cost per mile (IRS 2021). This 2021 cost is pre-entered for all states in this packet.

**0b-vi.** The cost per deer to test for CWD at the nearest laboratory in the National Animal Health Laboratory Network (NAHLN; APHIS 2021) that conducts CWD testing. The current cost as of December 2021 is pre-entered for all states in this packet.

Autosaved outputs from this script include:

**0b-v.** The data files (csv and txt) which contain the estimated cost to sample a single individual deer from each county (or other administrative area) in the state of interest:

`"Cost_Per_Deer_(state name).csv"`  
`"Cost_Per_Deer_(state name).txt"`

**0b-vi.** The data files (csv and txt) which contain the  $n \times 12$  *Cost Matrix* to sample a single individual from each county (or other administrative area) in the state of

interest, where  $n$  is the number of counties and 12 is the number of age/sex segments:

"Cost\_Matrix\_(state name).csv"

"Cost\_Matrix\_(state name).txt"

*Do not modify the names of these files, as they are used as is in later scripts.*

Data inputs necessary to run the `_0c_(state name)_Habitat_Variable_Prep.R` script include:

**0c-i.** Geospatial files autosaved during the execution of the 0a script.

**0c-ii.** Pre-processed raster layers representing distance to streams and percent clay created from publicly available datasets in Mitchell et al. (2021):

"Streams\_NHDstrahler4plus\_distance\_(state code)\_(SPCS).tif"

"Soils\_gNATSGO\_30m\_(state code)\_(SPCS).tif"

**0c-iii.** A  $n \times 11$  data frame named "EDC\_(state name).csv" containing data for each of the  $n$  counties (or other administrative areas) in the state of interest. The 11 variables (column names) in the EDC file include:

State, County, CountyFIPS, Taxidermists, Streams,  
ClayPercent, DistanceToInfection,  
BreedingFacilities, UrineLures, CWDCaptivePrevious,  
CWDCaptiveCounty

State is the official two-letter postal code for the state of interest. This data is provided for the states included in this packet.

County is the current name of the county along with the associated legal/statistical area description and should match the NAMELSAD attribute of the geospatial file for the state of interest. This data is provided for states included in this packet.

CountyFIPS represents the unique Federal Information Processing Series (FIPS) code of the county. FIPS codes corresponding to counties in the US are found at:

[https://www.nrcs.usda.gov/wps/portal/nrcs/detail/national/home/?cid=nrcs143\\_013697](https://www.nrcs.usda.gov/wps/portal/nrcs/detail/national/home/?cid=nrcs143_013697).

Taxidermists represents the number of taxidermists that exist in the county.

Streams represents the average distance in the county to the nearest medium-large streams and rivers. This data will be calculated with this script if any county is missing data for this category (represented by 9999 or NA).

ClayPercent represents the average percentage of clay in the upper 50 cm of soil in each county. This data will be calculated with this script if any county is missing data for this category (represented by 9999 or NA).

DistanceToInfection represents the distance (km) from the county (or other administrative area) centroid to the centroid of the nearest county with a confirmed CWD sample.

BreedingFacilities represents the number of cervid breeding facilities that exist in the county.

UrineLures represents whether urine baits are prohibited (0), restricted/controlled (0.5), or allowed (1) in the county.

CWDCaptivePrevious represents whether the county had a CWD-positive case in a captive herd before CWD was detected in wild deer in the county (yes=1, no=0).

CWDCaptiveCounty represents whether CWD has been detected in a captive herd in the county at any point in time (yes=1, no=0).

*Missing values should take on a value of 0.*

*Note: The real data do not appear in the EDC file for any state in this packet. However, the templates are included. A user must modify the "EDC\_(state name).csv" template to replace the 9999 with real data before this script will run (see **Step 6** below).*

Autosaved outputs from this script include:

**0c-iv.** The "EDC\_(state name).csv" file with Streams and ClayPercent calculated and filled in for each county (or other administrative area).

Data inputs necessary to run the \_0d\_(state name)\_Optimization\_Monitoring\_Prep.R script include:

**0d-i.** The "EDC\_(state name).csv" file described in **0c-iii**.

**0d-ii.** The coefficient values from the Monitoring regression in Hanley et al. (unpublished data). These values have been pre-entered for all the states in this packet.

Autosaved outputs from this script include:

**0d-iii.** The data files (csv and txt) which contain the estimated values of benefits for monitoring for each county (or other administrative area) in the state of interest:

"Benefits\_Monitoring\_(state name)\_Mean.csv"

"Benefits\_Monitoring\_(state name)\_Mean.txt"

"Benefits\_Monitoring\_(state name)\_Upper.csv"

"Benefits\_Monitoring\_(state name)\_Upper.txt"

"Benefits\_Monitoring\_(state name)\_Lower.csv"

"Benefits\_Monitoring\_(state name)\_Lower.txt"

**0d-iv.** The data files (csv and txt) which contain the  $n \times 12$  benefits for monitoring for each county (or other administrative area) in the state of interest, where  $n$  is the number of counties and 12 is the number of age/sex segments:

"Benefits\_Monitoring\_Matrix\_Mean\_(state name).csv"

"Benefits\_Monitoring\_Matrix\_Mean\_(state name).txt"

"Benefits\_Monitoring\_Matrix\_Upper\_(state name).csv"

"Benefits\_Monitoring\_Matrix\_Upper\_(state name).txt"

"Benefits\_Monitoring\_Matrix\_Lower\_(state name).csv"

"Benefits\_Monitoring\_Matrix\_Lower\_(state name).txt"

*Do not modify the names of these files, as they are used as is in later scripts.*

Data inputs necessary to run the \_0e\_(state name)\_Optimization\_Early\_Detect\_Prep.R script include:

**0e-i.** The "EDC\_(state name).csv" file described in **0c-iii**.

**0e-ii.** The coefficient values from the Early Detection regression in Hanley et al. (unpublished data). These values have been pre-entered for all the states in this packet.

Autosaved outputs from this script include:

**0e-iii.** The data files (csv and txt) which contain the estimated values of benefits for early detection for each county (or other administrative area) in the state of interest:

```
"Benefits_Early_Detection_(state name)_Mean.csv"  
"Benefits_Early_Detection_(state name)_Mean.txt"  
"Benefits_Early_Detection_(state name)_Upper.csv"  
"Benefits_Early_Detection_(state name)_Upper.txt"  
"Benefits_Early_Detection_(state name)_Lower.csv"  
"Benefits_Early_Detection_(state name)_Lower.txt"
```

**0e-iv.** The data files (csv and txt) which contain the  $n \times 12$  benefits for early detection for each county (or other administrative area) in the state of interest, where  $n$  is the number of counties and 12 is the number of age/sex segments:

```
"Benefits_Early_Detection_Mean_Matrix_(state name).csv"  
"Benefits_Early_Detection_Mean_Matrix_(state name).txt"  
"Benefits_Early_Detection_Upper_Matrix_(state name).csv"  
"Benefits_Early_Detection_Upper_Matrix_(state name).txt"  
"Benefits_Early_Detection_Lower_Matrix_(state name).csv"  
"Benefits_Early_Detection_Lower_Matrix_(state name).txt"
```

*Do not modify the names of these files, as they are used as is in later scripts.*

Data inputs necessary to run the `_of_(state name)_Optimization_Prevalence_Prep.R` script include:

**0f-i.** Pre-processed surveillance (testing) data summaries of confirmed CWD-positives by county (or other administrative area) and age/sex segment generated for years 2013-2021, as produced in Mitchell et al. (2022):

```
"(state name)CountySummary2013.txt"  
"(state name)CountySummary2014.txt"  
"(state name)CountySummary2015.txt"  
"(state name)CountySummary2016.txt"  
"(state name)CountySummary2017.txt"  
"(state name)CountySummary2018.txt"  
"(state name)CountySummary2019.txt"  
"(state name)CountySummary2020.txt"  
"(state name)CountySummary2021.txt"
```

**0f-ii.** Pre-processed surveillance (testing) data summaries of all samples by county (or other administrative area) and age/sex segment generated for years 2013-2021, as produced in Mitchell et al. (2022):

```
"All_(state name)CountySummary2013.txt"  
"All_(state name)CountySummary2014.txt"  
"All_(state name)CountySummary2015.txt"  
"All_(state name)CountySummary2016.txt"  
"All_(state name)CountySummary2017.txt"  
"All_(state name)CountySummary2018.txt"  
"All_(state name)CountySummary2019.txt"  
"All_(state name)CountySummary2020.txt"  
"All_(state name)CountySummary2021.txt"
```

*Note: The real data do not appear in this packet for any state. See Mitchell et al. 2022 to create data outputs or templates.*

Autosaved outputs from this script include:

**0f-iii.** The data files (csv and txt) which contain the  $n \times 6$  data array of maximum apparent prevalence from 2013-2021 for each age/sex segment in each county. Where  $n$  is the number of counties and 6 is the number of age/sex segments (adult male, adult female, yearling male, yearling female, fawn male, fawn female).  
"Prevalence\_(state name).csv"  
"Prevalence\_(state name).txt"

**0f-iv.** The data files (csv and txt) which contain the  $n \times 12$  prevalence for each county (or other administrative area) in the state of interest, where  $n$  is the number of counties and 12 is the number of age/sex segments.  
"Prevalence\_Matrix\_(state name).csv"  
"Prevalence\_Matrix\_(state name).txt"

*Do not modify the names of these files, as they are used as is in later scripts.*

Data inputs necessary to run the `_0g_(state name)_Optimization_Weights_Prep.R` script include:

**0g-i.** The surveillance weights as computed for Wisconsin using Jennelle et al. (2018). These values have been pre-entered for all the states in this packet using the proxy values in Jennelle et al. (2018) but may be modified in this script when other state-specific data to estimate weights become available.

**0g-ii.** The exact autosaved outputs from the previous scripts:  
"Cost\_Per\_Deer\_(state name).txt"

Autosaved outputs from this script include:

**0g-iii.** The data files (csv and txt) which contain the  $12 \times 1$  data array of weights, where the 12 weights represent hunter-harvested deer (adult male, adult female, yearling male, yearling female, fawn male, fawn female), followed by non-hunter harvested deer (adult male, adult female, yearling male, yearling female, fawn male, fawn female).  
"Weights\_(state name).csv"  
"Weights\_(state name).txt"

**0g-iv.** The data files (csv and txt) which contain the  $n \times 12$  sampling weights, where  $n$  is the number of counties and 12 is the number of age/sex segments.  
"Weights\_Matrix\_(state name).csv"  
"Weights\_Matrix\_(state name).txt"

*Do not modify the names of these files, as they are used as is in later scripts.*

Data inputs necessary to run the `_0h_(state name)_Optimization_Matrix_Prep.R` script include:

**0h-i.** The exact autosaved outputs from the previous scripts:  
"Cost\_Matrix\_(state name).txt"  
"Benefits\_Monitoring\_Matrix\_Mean\_(state name).txt"  
"Benefits\_Early\_Detection\_Matrix\_Mean\_Matrix\_(state name).txt"

```
"Prevalence_Matrix_(state name).txt"  
"Weights_Matrix_(state name).txt"
```

Autosaved outputs from this script include:

**0h-ii.** The data files (csv and txt) which contain the  $n \times 72$  optimization matrix with the costs, benefits (Monitoring, Early Detection, and Public Communication), prevalence, and weights for all age/sex segments in each of the  $n$  counties.

*NOTE: The rows represent the  $n$  counties (or other administrative areas) of the state of interest.*

```
"OptimizationMatrix(state name).csv"  
"OptimizationMatrix(state name).txt"
```

*The column headers are:*

```
cost_male_adult_hunter,  
cost_female_adult_hunter,  
cost_male_yearling_hunter,  
cost_female_yearling_hunter,  
cost_male_fawn_hunter,  
cost_female_fawn_hunter,  
cost_male_adult_other,  
cost_female_adult_other,  
cost_male_yearling_other,  
cost_female_yearling_other,  
cost_male_fawn_other,  
cost_female_fawn_other,  
benefit_delta_p_male_adult_hunter,  
benefit_delta_p_female_adult_hunter,  
benefit_delta_p_male_yearling_hunter,  
benefit_delta_p_female_yearling_hunter,  
benefit_delta_p_male_fawn_hunter,  
benefit_delta_p_female_fawn_hunter,  
benefit_delta_p_male_adult_other,  
benefit_delta_p_female_adult_other,  
benefit_delta_p_male_yearling_other,  
benefit_delta_p_female_yearling_other,  
benefit_delta_p_male_fawn_other,  
benefit_delta_p_female_fawn_other,  
benefit_detection_male_adult_hunter,  
benefit_detection_female_adult_hunter,  
benefit_detection_male_yearling_hunter,  
benefit_detection_female_yearling_hunter,  
benefit_detection_male_fawn_hunter,  
benefit_detection_female_fawn_hunter,  
benefit_detection_male_adult_other,  
benefit_detection_female_adult_other,
```

benefit\_detection\_male\_yearling\_other,  
benefit\_detection\_female\_yearling\_other,  
benefit\_detection\_male\_fawn\_other,  
benefit\_detection\_female\_fawn\_other,  
benefit\_communication\_male\_adult\_hunter,  
benefit\_communication\_female\_adult\_hunter,  
benefit\_communication\_male\_yearling\_hunter,  
benefit\_communication\_female\_yearling\_hunter,  
benefit\_communication\_male\_fawn\_hunter,  
benefit\_communication\_female\_fawn\_hunter,  
benefit\_communication\_male\_adult\_other,  
benefit\_communication\_female\_adult\_other,  
benefit\_communication\_male\_yearling\_other,  
benefit\_communication\_female\_yearling\_other,  
benefit\_communication\_male\_fawn\_other,  
benefit\_communication\_female\_fawn\_other,  
starting\_p\_male\_adult\_hunter,  
starting\_p\_female\_adult\_hunter,  
starting\_p\_male\_yearling\_hunter,  
starting\_p\_female\_yearling\_hunter,  
starting\_p\_male\_fawn\_hunter,  
starting\_p\_female\_fawn\_hunter,  
starting\_p\_male\_adult\_other,  
starting\_p\_female\_adult\_other,  
starting\_p\_male\_yearling\_other,  
starting\_p\_female\_yearling\_other,  
starting\_p\_male\_fawn\_other,  
starting\_p\_female\_fawn\_other,  
weight\_male\_adult\_hunter,  
weight\_female\_adult\_hunter,  
weight\_male\_yearling\_hunter,  
weight\_female\_yearling\_hunter,  
weight\_male\_fawn\_hunter,  
weight\_female\_fawn\_hunter,  
weight\_male\_adult\_other,  
weight\_female\_adult\_other,  
weight\_male\_yearling\_other,  
weight\_female\_yearling\_other,  
weight\_male\_fawn\_other,  
weight\_female\_fawn\_other

*Note: The real data do not appear in this packet for any state.*

*Do not modify the names of these files, as they are used as is in later scripts.*

Data inputs necessary to run the `_0i_(state name)_Optimization_INIT_Prep.R` script include:

**0i-i.** The `"EDC_(state name).csv"` file described in **0c-iii**.

Autosaved outputs from this script include:

**0i-ii.** User interface start-up files (that contain only placeholder information needed to initiate the user interface):

```
"OptimalAdjustedCostINIT.txt"  
"OptimalAdjustedDesiredChangePrevalenceRecipeINIT.txt"  
"OptimalAdjustedFreedomFromDiseaseINIT.txt"  
"OptimalAdjustedRecommendationsINIT.txt"  
"OptimalAdjustedRecommendationsMachineReadableINIT.txt"  
"OptimalStrategyChangeInPrevalenceBenefitINIT.txt"  
"OptimalStrategyChangeInPrevalenceCostINIT.txt"  
"OptimalStrategyChangeInPrevalenceRecipeINIT.txt"  
"OptimalStrategyPresenceAbsenceBenefitINIT.txt"  
"OptimalStrategyPresenceAbsenceCostINIT.txt"  
"OptimalStrategyPresenceAbsenceRecipeINIT.txt"  
"OptimalStrategyPublicCommunicationsBenefitINIT.txt"  
"OptimalStrategyPublicCommunicationsCostINIT.txt"  
"OptimalStrategyPublicCommunicationsRecipeINIT.txt"  
"StartingVectorChangeInPrevalenceINIT.txt"  
"StartingVectorPresenceAbsenceINIT.txt"  
"StartingVectorPublicCommunicationINIT.txt"
```

Data inputs necessary to run the `_1_(state name)_Optimization_Data_Prep.R` include:

**1-i.** Geospatial files autosaved during the execution of the 0a script.

**1-ii.** An  $n \times 18$  data frame named `"HistoricData(state name).csv"` containing historical surveillance sampling data for each of the  $n$  counties (or other administrative areas) in the state of interest. The names of the counties are listed down the rows in alphabetical order. The 18 variables (column names) listed from left to right include:

```
County, Latitude, Longitude, Male_adult_hunter,  
Female_adult_hunter, Male_yearling_hunter,  
Female_yearling_hunter, Male_fawn_hunter,  
Female_fawn_hunter, Male_adult_other,  
Female_adult_other, Male_yearling_other,  
Female_yearling_other, Male_fawn_other,  
Female_fawn_other, Total_Hunter, Total_Other, Total  
Note: Use these exact header names, capitalization scheme, and order.
```

`County` is the current name of the county along with the associated legal/statistical area description and should match the NAMELSAD attribute of the geospatial file for the state of interest. This data is provided for states included in this packet.

Latitude and Longitude represent the latitude and longitude coordinates of the center of each county (or other administrative area).

Male\_adult\_hunter, Female\_adult\_hunter, Male\_yearling\_hunter, Female\_yearling\_hunter, Male\_fawn\_hunter, and Female\_fawn\_hunter represent the historic number of samples harvested by hunters from deer in the corresponding age/sex segment in each county for the user specified time period.

Male\_adult\_other, Female\_adult\_other, Male\_yearling\_other, Female\_yearling\_other, Male\_fawn\_other, and Female\_fawn\_other represent the historic number of samples from deer in the corresponding age/sex segment that were removed from the population via non-hunting mechanisms, such as targeted culling or other actions overseen by the agency, in each county for the user specified time period.

Total\_Hunter represents the total number of samples from all age/sex segments of hunter harvested deer for each county for the user specified time period.

Total\_Other represents the total number of samples from all age/sex segments of deer removed from the population via non-hunting mechanisms for each county for the user specified time period.

Total represents the total number of samples from hunter harvested and other (non-hunting mechanisms) deer for each county for the user specified time period.

*Note: The real data do not appear in the Historical Data for any state in this packet. However, the templates are included. A user must modify the "HistoricData(state name).csv" template to replace the 9999 with real data before this script will run (see **Step 5** below).*

**1-iii.** The Optimization Matrix data file autosaved during the execution of the 0h script:  
OptimizationMatrix(state name).txt

Autosaved outputs from this script include:

**1-iv.** Parameter files:

```
"Benefit_To_Optimize_Comm.txt"  
"Benefit_To_Optimize_Early.txt"  
"Benefit_To_Optimize_Monitoring.txt"  
"ChangePrevalenceBenefitVector.txt"  
"column_names.txt"  
"Cost.txt"  
"Cost_To_Optimize_Comm.txt"  
"Cost_To_Optimize_Early.txt"  
"Cost_To_Optimize_Monitoring.txt"  
"names_row.txt"  
"PresenceAbsenceBenefitVector.txt"  
"Prevalence_To_Optimize_Comm.txt"  
"Prevalence_To_Optimize_Early.txt"
```

```
"Prevalence_To_Optimize_Monitoring.txt"  
"PublicCommBenefitVector.txt"  
"StartingPrevalence.txt"  
"Vector_To_Optimize_Comm.txt"  
"Vector_To_Optimize_Early.txt"  
"Vector_To_Optimize_Monitoring.txt"  
"Weights.txt"
```

*Do not modify the names of these files, as they are used as is in later scripts.*

Data inputs necessary to run the `_2_(state name)_Optimization_User_Interface.R` script include:

- 2-i.** Geospatial files autosaved during the execution of the `0a` script.
- 2-ii.** Autosaved files generated during the execution of scripts `0b-0i`.
- 2-iii.** The pre-saved coordinates to inform the progress arrow in the user interface, which displays the user's progression through the steps necessary for use of the algorithm:  
    `"progresscoordinates.csv"`
- 2-iv.** Historical data, titled `"HistoricData(state name).csv"` described in 1-ii.
- 2-v.** The `_1_(state name)_Optimization_Data_Prep.R` script.
- 2-vi.** The `_3_(state name)_Optimization_Algorithm_Twelve_Categories.R` script.

Autosaved outputs from opening this script include:

- 2-vii.** Placeholder files:
  - `"OptimalAdjustedCostSELECTED.txt"`
  - `"OptimalAdjustedDesiredChangePrevalenceRecipeSELECTED.txt"`
  - `"OptimalAdjustedFreedomFromDiseaseSELECTED.txt"`
  - `"OptimalAdjustedRecommendationsMachineReadableSELECTED.txt"`
  - `"OptimalAdjustedRecommendationsSELECTED.txt"`
  - `"OptimalStrategyChangeInPrevalenceBenefitSELECTED.txt"`
  - `"OptimalStrategyChangeInPrevalenceCostSELECTED.txt"`
  - `"OptimalStrategyChangeInPrevalenceRecipeSELECTED.txt"`
  - `"OptimalStrategyPresenceAbsenceBenefitSELECTED.txt"`
  - `"OptimalStrategyPresenceAbsenceCostSELECTED.txt"`
  - `"OptimalStrategyPresenceAbsenceRecipeSELECTED.txt"`
  - `"OptimalStrategyPublicCommunicationsBenefitSELECTED.txt"`
  - `"OptimalStrategyPublicCommunicationsCostSELECTED.txt"`
  - `"OptimalStrategyPublicCommunicationsRecipeSELECTED.txt"`
  - `"StartingVectorChangeInPrevalenceSELECTED.txt"`
  - `"StartingVectorPresenceAbsenceSELECTED.txt"`
  - `"StartingVectorPublicCommunicationSELECTED.txt"`
- 2-viii.** Parameter files:
  - `"Alpha.txt"`
  - `"Confidence.txt"`
  - `"DESIRED_CHANGE.txt"`
  - `"f.tst"`
  - `"freedom.from.diseaseBelsare.txt"`

```
"freedom.from.diseaseMiller.txt"
```

*Do not modify the names of these files, as they are used as is in the interface.*

Autosaved outputs from initializing the algorithm internal to the script include:

**2-vix.** Additional parameter files:

```
"freedomfromdisease.txt"
```

```
"Parameters.txt"
```

```
"slider.txt"
```

```
"sliderM.txt"
```

```
"sliderND.txt"
```

```
"TESTS.txt"
```

**2-x.** Output files, including all the sampling strategies (too many to list).

*Do not modify the names of these files, as they are used as is in the interface.*

The `_3_(state name)_Optimization_Algorithm_Twelve_Categories.R` script is called directly from the user interface and should not be directly opened nor run by the user. Data inputs necessary to run the `_3_(state name)_Optimization_Algorithm_Twelve_Categories.R` script include the parameter file outputs created in scripts 1 and 2.

The `_4_(state name)_Optimization_Command_Center.R` script runs the appropriate sequence and set of scripts for each state with one click. The data inputs necessary to run the `_4_(state name)_Optimization_Command_Center.R` script include all inputs and autosaved outputs from all previous scripts detailed above.

## **Chronic Wasting Disease Surveillance Optimization Software user tutorial**

### **Preparing and running the command code**

**Step 1:** Open R and verify that you are running the appropriate version of the R Software (R Core Team 2020), which 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:

- (1) "devtools" version 2.3.2
- (2) "dplyr" version 1.0.2
- (3) "exactextractr" version 0.7.2
- (4) "geodist" version 0.0.7
- (5) "GISTools" version 0.7-4
- (6) "leaflet" version 2.0.3
- (7) "leaflet.extras" version 1.0.0
- (8) "leafpop" version 0.0.6

- (9) "maptools" version 1.5-2
- (10) "raster" version 3.4-5
- (11) "Rcpp" version 1.0.7
- (12) "RColorBrewer" version 1.1-2
- (13) "rgdal" version 1.5-18
- (14) "rgeos" version 0.5-5
- (15) "rmapshaper" version 0.4.4
- (16) "sf" version 0.9-6
- (17) "shiny" version 1.5.0
- (18) "shinycssloaders" version 1.0.0
- (19) "shinydashboard" version 0.7.1
- (20) "sp" version 1.4-4
- (21) "stringr" version 1.4.0
- (22) "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 *Chronic Wasting Disease Surveillance Optimization Software* materials to run on your machine.

**4-a:** Download, unzip, and save the *Chronic Wasting Disease Surveillance Optimization 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:** Enter the real surveillance sampling data into the "HistoricData(state name) .csv" template.

*Note: You can define your historic sampling data in any way you please so long as it represents a sampling effort that has occurred in the past. For example, your historic data can represent the sampling data from the previous year, the average sampling data from several previous years, the maximum sampling data from several previous years, etc.*

- 5-a.** Open the "HistoricData(state name).csv" template for the state of interest or, if creating a file for a new state not included in this packet, update the County column with a comprehensive list of counties (or other administrative areas) in the new state of interest.
- 5-b.** Enter the latitude of the center of each county (or other administrative area) in the column labeled Latitude.  
*Note: Latitude should be entered as a decimal numeric value.*
- 5-c.** Enter the longitude of the center of each county (or other administrative area) in the column labeled Longitude.  
*Note: Longitude should be entered as a decimal numeric value that includes (if necessary) the negative sign.*
- 5-d.** Enter the historic number of samples from adult male deer harvested by hunters in each county (or other administrative area) for the user specified time period in the column labeled Male\_adult\_hunter.  
*Note: Male\_adult\_hunter should be entered as a numeric, non-negative integer value ( $0 \leq x$ ).*
- 5-e.** Enter the historic number of samples from adult female deer harvested by hunters in each county (or other administrative area) for the user specified time period in the column labeled Female\_adult\_hunter.  
*Note: Female\_adult\_hunter should be entered as a numeric, non-negative integer value ( $0 \leq x$ ).*
- 5-f.** Enter the historic number of samples from yearling male deer harvested by hunters in each county (or other administrative area) for the user specified time period in the column labeled Male\_yearling\_hunter.  
*Note: Male\_yearling\_hunter should be entered as a numeric, non-negative integer value ( $0 \leq x$ ).*
- 5-g.** Enter the historic number of samples from yearling female deer harvested by hunters in each county (or other administrative area) for the user specified time period in the column labeled Female\_yearling\_hunter.  
*Note: Female\_yearling\_hunter should be entered as a numeric, non-negative integer value ( $0 \leq x$ ).*
- 5-h.** Enter the historic number of samples from fawn male deer harvested by hunters in each county (or other administrative area) for the user specified time period in the column labeled Male\_fawn\_hunter.  
*Note: Male\_fawn\_hunter should be entered as a numeric, non-negative integer value ( $0 \leq x$ ).*
- 5-i.** Enter the historic number of samples from fawn female deer harvested by hunters in each county (or other administrative area) for the user specified time period in the column labeled Female\_fawn\_hunter.  
*Note: Female\_fawn\_hunter should be entered as a numeric, non-negative integer value ( $0 \leq x$ ).*
- 5-j.** Enter the historic number of samples from adult male deer removed from the population via non-hunting mechanisms, such as targeted culling or other actions overseen by the agency, in each county (or other administrative area) for the user specified time period in the column labeled Male\_adult\_other.

*Note: Male\_adult\_other should be entered as a numeric, non-negative integer value ( $0 \leq x$ ).*

- 5-k.** Enter the historic number of samples from adult female deer removed from the population via non-hunting mechanisms, such as targeted culling or other actions overseen by the agency, in each county (or other administrative area) for the user specified time period in the column labeled Female\_adult\_other.

*Note: Female\_adult\_other should be entered as a numeric, non-negative integer value ( $0 \leq x$ ).*

- 5-l.** Enter the historic number of samples from yearling male deer removed from the population via non-hunting mechanisms, such as targeted culling or other actions overseen by the agency, in each county (or other administrative area) for the user specified time period in the column labeled Male\_yearling\_other.

*Note: Male\_yearling\_other should be entered as a numeric, non-negative integer value ( $0 \leq x$ ).*

- 5-m.** Enter the historic number of samples from yearling female deer removed from the population via non-hunting mechanisms, such as targeted culling or other actions overseen by the agency, in the county (or other administrative area) for the user specified time period in the column labeled Female\_yearling\_other.

*Note: Female\_yearling\_other should be entered as a numeric, non-negative integer value ( $0 \leq x$ ).*

- 5-n.** Enter the historic number of samples from fawn male deer removed from the population via non-hunting mechanisms, such as targeted culling or other actions overseen by the agency, in each county (or other administrative area) for the user specified time period in the column labeled Male\_fawn\_other.

*Note: Male\_fawn\_other should be entered as a numeric, non-negative integer value ( $0 \leq x$ ).*

- 5-o.** Enter the historic number of samples from fawn female deer removed from the population via non-hunting mechanisms, such as targeted culling or other actions overseen by the agency, in each county (or other administrative area) for the user specified time period in the column labeled Female\_fawn\_other.

*Note: Female\_fawn\_other should be entered as a numeric, non-negative integer value ( $0 \leq x$ ).*

- 5-p.** Sum the samples from hunter harvested deer for each county (or other administrative area) for the user specified time period and enter that value into the Total\_Hunter column.

*Note: Total\_Hunter should be entered as a numeric, non-negative integer value ( $0 \leq x$ ).*

- 5-q.** Sum the samples from other deer (non-hunting) for each county (or other administrative area) for the user specified time period and enter that value into the Total\_Other column.

*Note: Total\_Other should be entered as a numeric, non-negative integer value ( $0 \leq x$ ).*

- 5-r.** Sum the samples from hunter harvested and other deer for each county (or other administrative area) for the user specified time period and enter that value into the Total column.

*Note: Total should be entered as a numeric, non-negative integer value ( $0 \leq x$ ).*

**5-s.** Save the "HistoricData (state name) .csv" to your working directory.

**Step 6:** Enter the real data into "EDC\_ (state name) .csv" template.

**6-a.** Open the "EDC\_ (state name) .csv" template for the state of interest or, if creating a file for a new state not included in this packet, update the State column with the official two-letter postal code for the state of interest, the County column with a comprehensive list of counties (or other administrative areas) in the new state of interest, and the CountyFIPS column with the unique Federal Information Processing Series (FIPS) code of the county.

**6-b.** Enter the Taxidermists by county.

*Note: Taxidermists should be entered as a numeric, non-negative integer value. Enter zero if the data is unknown.*

**6-c.** Retain 9999 values for the Streams by county column. This data will be automatically calculated by the \_0c\_ (state name) \_Habitat\_Variable\_Prep.R script.

*Note: The pre-processed raster layer created in Mitchell et al. 2021 representing distance to streams in the state of interest must be in the working directory.*

*The resulting Streams value should be a numeric, non-negative decimal value ( $0 \leq xx$ ), where xx represents the average distance (m) to the nearest medium-large streams and rivers in each county.*

**6-d.** Retain 9999 values for the ClayPercent by county column. This data will be automatically calculated by the \_0c\_ (state name) \_Habitat\_Variable\_Prep.R script.

*Note: The pre-processed raster layer created in Mitchell et al. 2021 representing percentage of clay in the state of interest must be in the working directory. The resulting ClayPercent value should be a numeric, non-negative decimal value ( $0 \leq x \leq 1$ ), where xx represents the average percentage of clay in the top 50 cm of soil in each county.*

**6-e.** Enter the DistanceToInfection by county.

*Note: DistanceToInfection should be entered as a numeric, non-negative value ( $0 \leq xx$ ), where xx represents the distance (in km) from the county centroid to the centroid of the nearest county with a confirmed CWD-positive sample.*

**6-f.** Enter the BreedingFacilities by county.

*Note: BreedingFacilities should be entered as a numeric, non-negative integer value representing the number of cervid breeding facilities that exist in the county.*

**6-g.** Enter the UrineLures by county.

*Note: UrineLures should be entered as 0 (if urine baits are prohibited), 0.5 (if urine baits are restricted/controlled), or 1 (if urine baits are allowed) in the county.*

**6-h.** Enter the CWDPreviousCounty by county.

*Note: CWDPPreviousCounty represents whether the county had a CWD-positive case in a captive herd before CWD was detected in wild deer in the county (yes = 1, no = 0). Missing values should take on a value of 0.*

**6-i.** Enter the CWDCaptiveCounty by county.

*Note: CWDCaptiveCounty represents whether CWD has been detected in a captive herd in the county at any point in time (yes = 1, no = 0). Missing values should take on a value of 0.*

**6-j.** Save the "EDC\_(state name).csv" to your working directory.

**Step 7:** For the state of interest, run the *Chronic Wasting Disease Surveillance Optimization Software*.

**7-a.** Open the file named

`_4_(state name)_Optimization_Command_Center.R`.

**7-b:** Hit "Run all".

*Note: From this moment, your script will automatically call the appropriate libraries, then begin running the series of scripts of the Chronic Wasting Disease Surveillance Optimization Software. Several lines of code will be executed without any further interaction from you. Your script will automatically create the shapefiles, initiate projections, load the data, convert the data, then open the user interface (UI). The algorithm will not run until the user then interacts with the interface.*

**Step 8:** Once the UI opens, follow the directions on the landing page to interact with the app.

**Step 9:** Once done interacting with the UI, close the tab depicting the UI, stop the R code, and close the R program.

## Technical details

Modification of data templates to include real data, as instructed in **Steps 5 and 6** require Microsoft® Excel® for Microsoft 365 MSO (16.0.14326.20384) 64-bit. The R scripts will not run until real data is entered into these templates.

The `_0a_(state name)_Optimization_Spatial_Prep.R` script of the *Chronic Wasting Disease Surveillance Optimization 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) "maptools" 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), and (8) "rgeos" version 0.5-5 (Bivand and Rundel 2020).

The `_0b_(state name)_Optimization_Cost_Prep.R` script of the *Chronic Wasting Disease Surveillance Optimization 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) "GISTools" version 0.7-4 (Brunsdon and Chen 2014), and (4) "geodist" version 0.0.7 (Padgham and Sumner 2021).

The `_0c_(state name)_Optimization_Habitat_Variable_Prep.R` script of the *Chronic Wasting Disease Surveillance Optimization 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) "raster" version 3.4-5 (Hijmans 2020), (4) "sf" version 0.9.8 (Pebesma 2018), (5) "exactextractr" version 0.7.2 (Baston 2021), and (6) "Rcpp" version 1.0.7 (Eddelbuettel and Francois 2011; Eddelbuettel 2013; Eddelbuettel and Balamuta 2018).

The `_0d_(state name)_Optimization_Monitoring_Prep.R` script of the *Chronic Wasting Disease Surveillance Optimization 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 does not require packages.

The `_0e_(state name)_Optimization_Early_Detect_Prep.R` script of the *Chronic Wasting Disease Surveillance Optimization 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 does not require packages.

The `_0f_(state name)_Optimization_Prevalence_Prep.R` script of the *Chronic Wasting Disease Surveillance Optimization 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 does not require packages.

The `_0g_(state name)_Optimization_Weights_Prep.R` script of the *Chronic Wasting Disease Surveillance Optimization 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 does not require packages.

The `_0h_(state name)_Optimization_Matrix_Prep.R` script of the *Chronic Wasting Disease Surveillance Optimization 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 does not require packages.

The `_0i_(state name)_Optimization_INIT_File_Prep.R` script of the *Chronic Wasting Disease Surveillance Optimization 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 does not require packages.

The `_1_(state name)_Optimization_Data_Prep.R` script of the *Chronic Wasting Disease Surveillance Optimization 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) and (2) "rgdal" version 1.5-18 (Bivand et al. 2020).

The `_2_(state name)_Optimization_User_Interface.R` script of the *Chronic Wasting Disease Surveillance Optimization 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) "RColorBrewer" version 1.1-2 (Neuwirth 2014), (8) "sp" version 1.4-4 (Pebesma and Bivand 2005; Bivand et al. 2013), (9) "sf" version 0.9-6 (Pebesma 2018), (10) "rgdal" version 1.5-18 (Bivand et al. 2020), (11) "leafpop" version 0.0.6 (Appelhans and Detsch 2020), (12) "shinycssloaders" version 1.0.0 (Sali and Attali 2020), and (13) "rmapshaper" version 0.4.4 (Teucher and Russell 2020).

The `_3_(state name)_Optimization_Algorithm_Twelve_Categories.R` script of the *Chronic Wasting Disease Surveillance Optimization 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 does not require any packages.

The `_4_(state name)_Optimization_Command_Center.R` script of the *Chronic Wasting Disease Surveillance Optimization 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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