Methods for the Census of Agriculture Overlap Tool (V1.1)

Background

This document provides background information and the methods used to develop the Census of Agriculture Overlap Tool. This tool was developed to expedite the process for conducting an overlap analysis for federally listed endangered and threatened ("listed") species assessments. The purpose of the overlap analysis is to determine the percent overlap of the proposed labeled use sites and the listed species' ranges and designated critical habitats. The outputs from the Overlap Tool are conservative in nature and intended to maximize efficiency estimating potential overlap. This tool may be used along with the UDL Overlap tool, as both tools provide areas of refinement based on different principles. In cases when a more refined spatial analysis is required, a higher Tier analysis can be conducted.

This tool runs in Python editor and has a Graphical User Interface (GUI) for selecting the key inputs for analysis. Key features that the tool provides from a user perspective are the following:

- GIS analysis is not required for the user
- The GUI uses Individual Crop or Crop-Group nomenclature for ease-of-use site selection
- The GUI includes entering geographic restrictions
- The overlap is presented as cumulative and by the individual Use Site
- Buffering for offsite transport is included and presented in multiple formats
- In addition to the continental United States, data for Alaska, Hawaii, and Puerto Rico are included in the tool by crop. Island territories (*i.e.,* Guam, American Samoa, Virgin Islands of US, and Northern Mariana Islands) are included at the Total Agriculture level.
- The tool utilizes two years of USDA Census of Agriculture (CoA) data and reports the highest acreage value over the two reports. The current scope of the tool is for agricultural uses. Overlaps for non-agricultural uses, such as residential, rangeland, forestry, etc. are not included.

Conceptual Model

This section provides a brief overview of the conceptual model for the tool. Details of the method are further described in "General Data/Inputs" and "Methodology" sections below.

There are two inputs to the Overlap tool, the Census of Agriculture (CoA) county-level crop acreage values and the species range and designated critical habitat (CH) acreage in each county. For deriving the species acreage by county using ArcGIS spatial overlap analysis, the key process is the "intersect" of the designated CH and species range location with the U.S. County boundaries. Together, with the crop acreage inputs by county, these inputs are used to determine an upper-bound maximum potential percent overlap based on the number of acres of crop within the county. This is considered an "upper-bound percent overlap" as it is assumed that the species location (range or CH) county acres overlap with the crop acres.

For example, in **Figure 1,** the green shape represents the species range. This range can fall anywhere within a county and overlap with county borders. The crop acres are shown with the orange box but the exact location within the county is unknown and it may be distributed across the county with varying intensity. For the overlap analysis, these two areas (*i.e.,* species range or CH and the crop acreage) are assumed to coexist in space as shown in the overlap where the green shape overlaps with the orange box. This overlap may occur, or it may not occur in the landscape. The overlapping assumption is made to be certain any potential overlap of range and CH is accounted for in the percent overlap for a species.
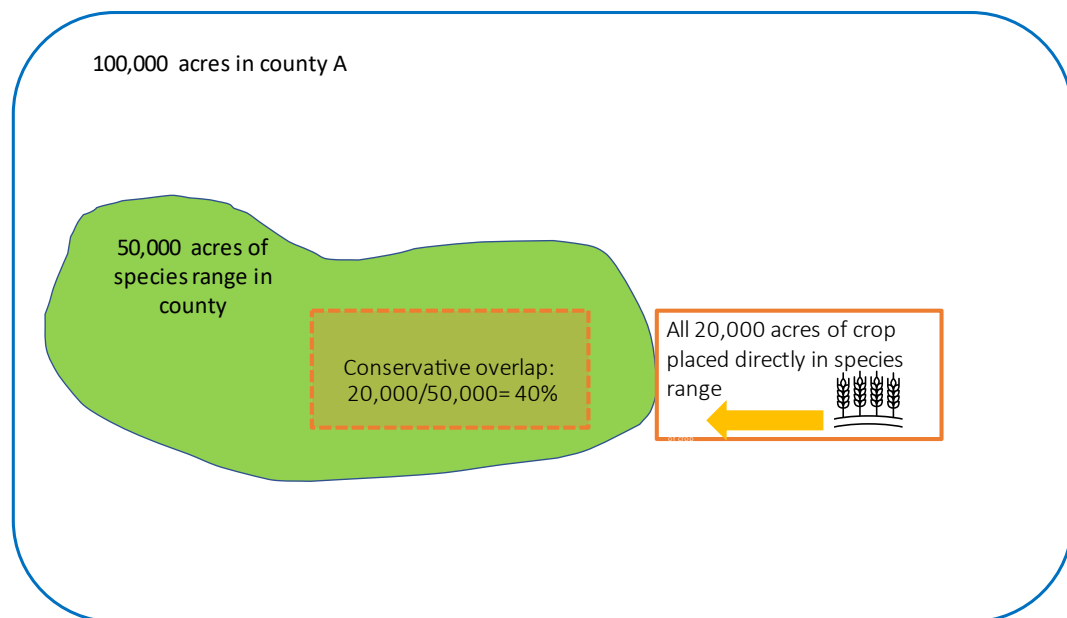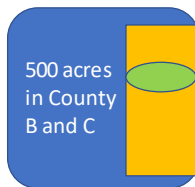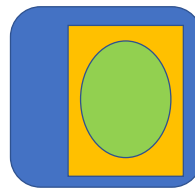

100,000 acres in county A

50,000 acres of species range in county

Conservative overlap: 20,000/50,000= 40%

All 20,000 acres of crop placed directly in species range

FIGURE 1. GENERAL EXAMPLE OF OVERLAP ASSUMPTION WITH SPECIES ACRES

A limitation of working with CoA data is that there is non-disclosed acreage for some crop-county combinations (*e.g.,* acreage is not reported to protect the confidentiality of the growers). For this reason, a conservative proxy is utilized to account for these non-disclosed acres and is described further in methodologies section (see non-disclosed acreage imputation). This is a preprocessing step.

To begin calculating the overlap, for each species, the county crop acres are summed but are capped (*i.e.,* cannot exceed) at the species range/CH for each individual county. For example, **Figure 2** shows a simple example of three counties and how the acreage may be capped if the crop acreage exceeds the species range. Counties B and C have crop acres (100 and 300 acres, respectively) that exceed the species range for the county, therefore, they are capped at the species range (20 and 200 acres, respectively). County A has less crop acres than the species range and does not require capping. After the crop acres are capped (if needed) at the county level the values for the crop acres and the species range are summed for the state level (**Figure 2**).

- 20 acres of the crop
- 50 acres of species range in county

Acres of Crop=
20+**20** (capped due to species range)+**200** (capped due to species range)=**240**

1000
Acres in
County A

50+20+200 = **270** total acres range

240/270=89% overlap for
crop rolled up to state level

500 acres
in County
B and C

- 100 acres of the crop
- 20 acres of species range

- 300 acres of crop
- 200 acres of species range

FIGURE 2. DEPICTION OF CAPPING USING SPECIES RANGE BY COUNTY

Figure 2 depicts a single crop, however, when there are multiple crops selected, a redundancy step may be used in cases where the sum of overlap from all potential use sites within a county exceeds the county species acreage. In such cases, an adjustment is applied that maintains the ratio of crop overlap areas while reducing the sum of the overlap areas to the total species area (described further in "Methodology" section below).

To check the potential overestimation of the earlier assumptions (*e.g.,* non-disclosed acre proxy, species acres distribution), the county crop acres, when rolled up (*e.g.*, added together) to the state and national level are compared to the state/national acreage for the individual crops and are capped if the sum of the county crop acres for a species exceeds the state or national crop value. The direct overlap value is then calculated by dividing the sum of the crop acres across all states by the total species range or CH acres. **Figure 3** depicts the national level for a species with a multi-state range, thus, as an example, the "rolled up values" depicted in **Figure 2** would fit into a single state (the blue boxes in **Figure 3**).

Acres that overlap are counted by county, state, and national (all states the species range is in)
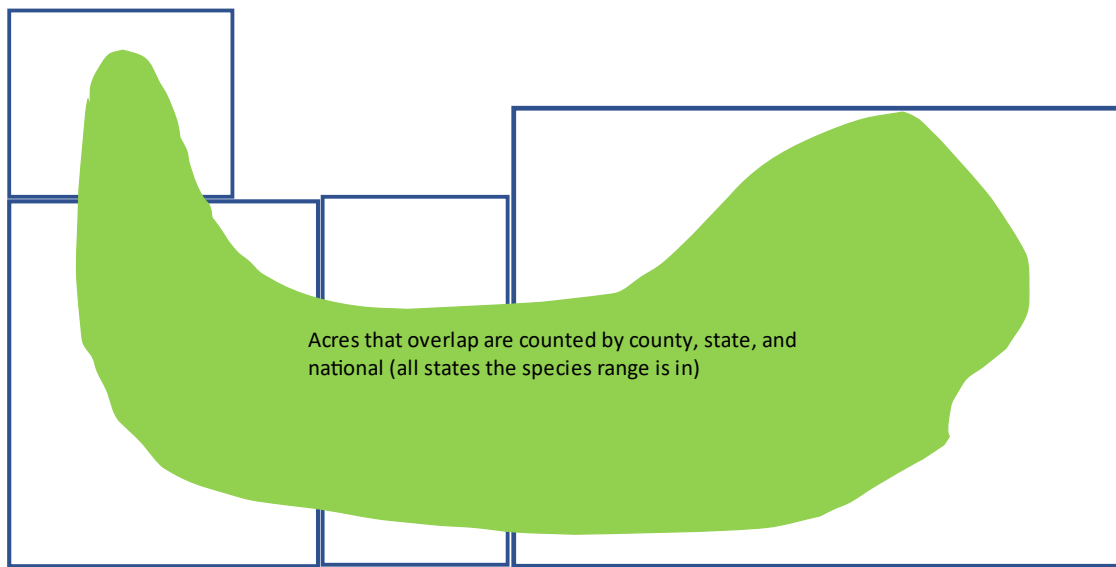
FIGURE 3 SPECIES RANGE- ACROSS MULTIPLE STATES

The overlap tool also accounts for offsite transport by buffering out the use area. To account for spray drift this is done by using 30 m increments, 305 m and 792m buffer distances (based on the AgDRIFT maximum/model limits for aerial and ground). To account for runoff, the tool includes a 1500m buffer for assessments that require maximum 'runoff' buffering (US EPA, 2022).

For the buffering, the method assumes that the acreage within a county is divided up into multiple fields. Because there can be differences in field size by crop, the crops from the CoA are binned into two size categories for the spray drift calculations. In general, the row crops such as corn, soybean, and wheat have larger field sizes and the specialty crops (e.g., strawberries, apples, cucumbers, etc.) have a smaller field size. Data are available from USDA Census of Agriculture (USDA, 2017- Tables 35-38) to inform on the breakdown of crop acres grown/harvested by field size. Based on a review of the available data, the specialty crops are assigned a field size of 25 acres and Row crops are assigned a field size of 500 acres. These field size acreages are used to adjust the spray drift by assuming that the crop acreage in the county is divided into multiple fields (i.e., divided by the field size of either 25 or 500 acres) and then the drift is calculated for each field before summing up.   Using this model, the buffer extends from all four sides of the modeled field to the various buffer distances (see Section 3; **Figure 6** for further details).

General Data /Inputs

- Census of Agriculture (2017 and 2012)- national, state and county acreage (preprocessed by BEAD[1])- The Census of Agriculture is a complete count of agricultural activity on U.S. farms and ranches. This analysis utilizes the crop acreage data. The CoA census is published every 5 years (2012 and 2017 being the most recent two surveys conducted) and the two most recent surveys are used to account for temporal variability in crop patterns and ensure conservatism. Data are available for all states.

- Census of Agriculture-2017[2]- For Puerto Rico and the Island Territories of Guam, American Samoa, Virgin Islands of US, and Northern Mariana Islands, data were not available in a preprocessed format. Data were extracted from the USDA NASS Quick Stats database. For Puerto Rico, the crop acres were extracted for the territory as a whole. For the other islands, the data resolution was at the total acres in agriculture level (i.e., not available by crop).

- Location files for listed species- (range and designated critical habitat) and the U.S. county boundary shapefile. All files were provided by EFED/EISB with the requisite data preparation. Originally, the source files of the species location files were provided by the Services. For EPA's endangered species biological evaluation, these source files were standardized and organized by taxonomic group in file geodatabases (referred to as species libraries)[3].

- Master Species List-Species subject to Section 7 under the Endangered Species Act are obtained from the US Fish and Wildlife Threatened and Endangered Species System (TESS[4]). The resulting table is filtered to include listing statuses[5] currently subject to Section 7 or potentially subject to Section 7 during the registration period. Information from TESS for species under the jurisdiction of the National Marine Fisheries Service (NMFS) is supplemented with information from the NMFS website[6], deferring to the NMFS website if conflicts exist between the sources. The master species list was *provided by EFED/EISB* (file version generated- 09_2022).

Methodology

There are three main sections for the methods descriptions:

1) Preprocessing the Census of Agriculture Data
2) ArcGIS Species Range and CH County Projection and Processing
3) Overlap Calculations

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[1] Census Acreage Data (USDA NASS 2012, 2017) Processed by BEAD- 2012 version 111/15/2018; 2017 version 1- 11-23-2020.
[2] USDA, NASS. 2017. Census of Agriculture for Outlying Areas
https://www.nass.usda.gov/Surveys/Guide_to_NASS_Surveys/Census_for_Outlying_Areas/index.php
https://www.nass.usda.gov/Surveys/Guide_to_NASS_Surveys/Census_for_Outlying_Areas/index.php
[3] More details about the location files preparation can be found in the EISB document titled "Tool Documentation – Processed GIS Data – Listed Species Spatial Files"-Updated 2020 Ver 1.2.
[4] https://ecos.fws.gov/ecp/
[5] Statuses included: Threatened, Endangered, Experimental Population Non-Essential, Proposed Threatened, Proposed Endangered, and Candidate
[6] https://www.fisheries.noaa.gov/national/endangered-species-conservation/esa-threatened-endangered-species

1. Preprocessing of Census of Agriculture Crop Acreage Data

Crop acreages at the county-, state-/territory-, and national- level are sourced from the Census of Agriculture (CoA). To account for temporal variability in crop patterns, crop acreage values from both the 2012 and 2017 CoA are used to generate the input values used in the overlap analysis. Due to the presence of non-disclosed acreage values (assigned as D values in CoA) for specific crop/location combinations in the two CoA datasets a preprocessing step is conducted prior to overlap analysis to fill missing values.

Non-Disclosed Acreage Imputation
The imputation method for missing acreage values requires that all crops have national-level acreage values. In limited cases where national-level acreage values are unavailable[7], estimates are obtained from other datasets (*i.e.*, alternate CoA years). Once a complete set of national-level crop acreage estimates are obtained the missing state acreage values are imputed. To generate the most conservative crop acreage estimates, each state/crop combination with a non-disclosed acreage value is filled with the difference between the national-level crop acreage values and the sum of available state acreage values. An example of this approach is described below.

Before Imputation:

State 1 Acres	State 2 Acres	State 3 Acres	State 4 Acres	State 5 Acres	National Acres
100	300	200	(D)	(D)	1000

D=acreage non-disclosed

After Imputation (Imputed values in Red):

State 1 Acres	State 2 Acres	State 3 Acres	State 4 Acres	State 5 Acres	National Acres
100	300	200	400	400	1000

In this example shown in the Before Imputation table there are 3 states (State 1, State 2, and State 3) with disclosed crop acreage values totaling 600 (100+300+200) acres, a national crop acreage value of 1000 acres, and 2 states with non-disclosed acreage values. Because the distribution of the non-disclosed acres is unknown, each state is assumed to have acreage equal to the difference (1000 acres – 600 acres = 400 acres), which represents the maximum possible acreage in each non-disclosed state given all known acreage values. This is shown in the After Imputation table (assumed acres shown in red).

Following the state-level non-disclosed acreage imputation, the county-level non-disclosed acreage values are imputed. This county-level imputation is performed using a similar approach to the state-level

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[7] Guar, jojoba, ginger root, birdsfoot trefoil-seed, miscanthus and sugarcane, sugar all were national "D" values in 2012. 2017 values were subbed as a proxy. Sugarcane had similar values in the 2007 and 2017 census.

imputation; each non-disclosed county/crop combo is filled with the difference between the state-level acreage total for the crop and the sum of disclosed county-level acreage values for that crop.

In addition to the non-disclosed acreage values (indicated by a "(D)" in the CoA tables), some crop/location combinations entries are labeled as "(Z)", which indicates that the value corresponds to half an acre or less of the crop in the location. Once the non-disclosed (D) values have been filled using the approach described above, all crop/location combinations with (Z) values in the CoA tables are filled with 0.5 acres (the maximum possible value). The filling of (Z)-values occurs after the imputation of (D) values to ensure that (D) maximum estimates [i.e. each (Z)-value reflects an acreage value between 0 and 0.5 acres, so the program first estimates (D) values assuming that (Z) values are 0 to obtain the highest possible acreage for both sets of unknown values].

Once the imputation steps are complete, tables of county- state- and national- level crop acreage values with numeric values for all crop/location combinations are available.

Merging multiple CoA Years

To capture the potential difference (e.g., crop rotation) in cropping overtime both the 2012 CoA and 2017 CoA values are used in the final crop acreage input table that is used for overlap calculations. Both CoA datasets are first processed using the imputation approach described in the previous section to fill missing values. Following the imputation steps, acreages from the two datasets for each location/crop combination are compared at the county, state, and national level. For each combination, if both or neither crop area was imputed (i.e., estimated because of a non-disclosed acreage entry in the raw CoA table), the maximum acreage value was selected from the two years. If one dataset contains an imputed value and the other contains a value that did not require imputation, however, the non-imputed value was retained in the final crop area table. This approach assumes that non-imputed values will introduce less uncertainty into the final overlap estimates compared with imputed values.

2   ArcGIS Overlap Analysis of Species Locations and U.S. Counties

This section provides information on how the ArcGIS analysis was done for the spatial overlap of listed species locations and the U.S. counties. The described overlap analysis was conducted in ArcMap/ArcGIS Pro and ArcGIS version of Python 2.7, with ArcPy and ArcPy.sa modules imported.

The goal of this spatial overlap analysis is to generate chemical-independent species acreage in each county of the United States. The output tables of this analysis are used as the inputs by the overlap tool (written in Python).

In this spatial analysis, the key process is the "intersect" of CH and range files of species with U.S. county boundaries. Intersect is a ArGIS intersect tool that calculates the geometric intersection of any number of feature classes and feature layers. Prior to this key step, all input files (i.e., species location files and U.S. county boundary files) were projected to the appropriate projection (i.e., Albers equal area conic) for the projected coordinate system (PCS). Following the intersect analysis, the acreage of species per county was calculated and, together with the other identifiers (i.e., entity ID, GEOID, state, etc),

exported to output tables. **Figure 4** illustrates the conceptual model of this spatial analysis. A more detailed explanation is described below.
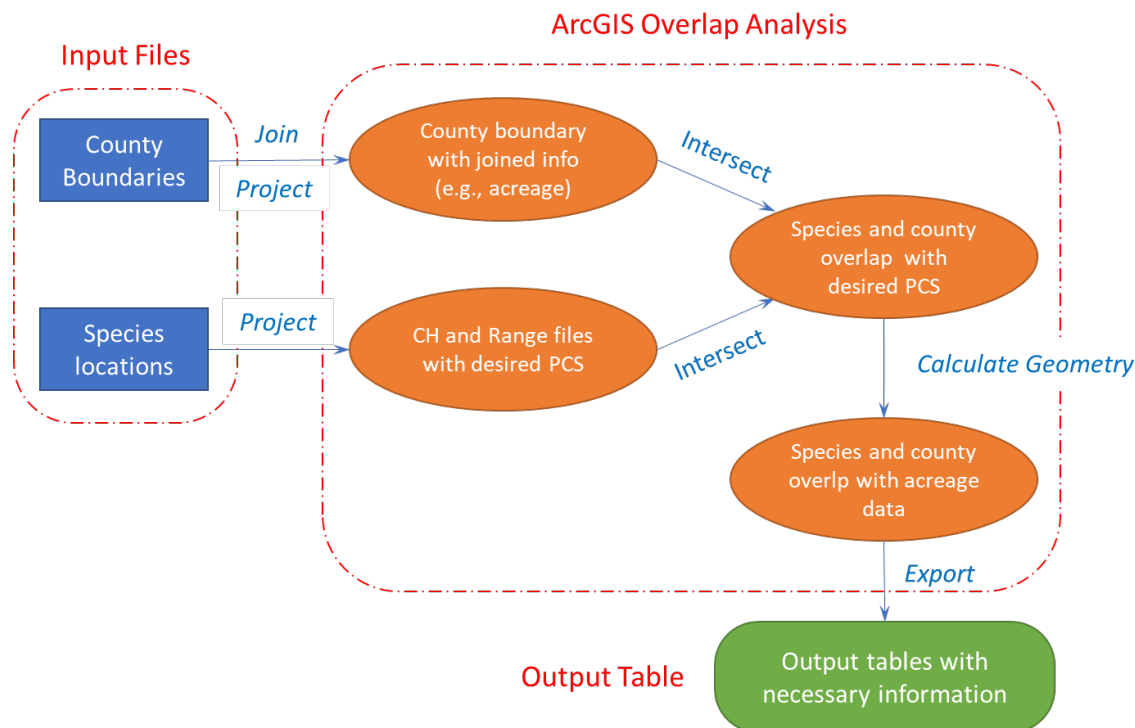

FIGURE 4. CONCEPTUAL MODEL OF THE SPATIAL OVERLAP ANALYSIS FOR THE LISTED SPECIES AND US COUNTIES

Input files
The input files of this overlap analysis included location files for list species (range and designated critical habitat) and U.S. County boundary shapefile. All these files were provided by EFED/EISB with the requisite data preparation. Originally, the source files of the species location files were provided by the Services. For EPA's endangered species biological evaluation, these source files were standardized and organized by taxonomic group in file geodatabases (referred to as species libraries). More details about the location file preparation can be found in the EISB document titled "Tool Documentation – Processed GIS Data – Listed Species Spatial Files" -Updated 2020 Ver 1.2.

Approach
Integrating county acreage info into county boundary shapefile
A set of county boundary shapefiles were provided by EISB containing slightly different aspects of information of the counties in each file. To integrate all essential information into one shapefile, especially the acreage of the counties, the 'join' tool in ArcGIS was used to combine attribute tables together and generate a new county boundary shapefile based on the "COUNTYNS" (a common attribute contained in each county shapefile). The newly generated county boundary shapefile contained all the essential information and was used as an input file of the overlap analysis.

Projecting species location and county boundary shapefiles

Prior to being used as inputs in the spatial overlap analysis, both species location and county boundary shapefiles were projected to the appropriate projected coordinate systems (PCS). For the 48 US CONUS states, the Albers Equal-area Conic projection was used because it is suitable for land masses that extend in an east-to-west orientation (e.g., the conterminous United States) to minimize the distortion of the shape and linear scale, therefore increasing the accuracy of the geometry calculation (e.g., areas and distance). For the states/regions outside the conterminous United States, the following selected PCSs were used in projecting species location and county boundary shapefiles (**Table 1**). Projecting analysis was conducted by using the "projection" tool in ArcGIS or "arcpy.Project_managment" function in ArcPy.

Table 1. Projected coordinate system used for U.S. regions.

Region	Projected Coordinate System
Conterminous United States (ConUS)	Albers_Conical_Equal_Area.prj.
Hawaii (HI)	NAD_1983_UTM_Zone_4N.prj
Alaska (AK)	WGS_1984_Albers.prj
Puerto Rico (PR)	Albers_Conical_Equal_Area.prj
United States Virgin Islands (VI)	WGS_1984_UTM_Zone_20N.prj
American Samoa (AS)	WGS_1984_UTM_Zone_2S.prj
Guam (GU	WGS_1984_UTM_Zone_55N.prj
Commonwealth of the Northern Mariana (CNMI)	WGS_1984_UTM_Zone_55N.prj

Intersection of species location and county shapefiles

As mentioned above, the "intersect" process was the key step of the overlap analysis. The "intersect" tool in ArcGIS or "arcpy.Intersect_analysis" function in ArcPy was used to calculate the geometric intersection of species locations and U.S. counties. The projected species spatial files (CH and range files) and county shapefile were used as input files in this step. The output features were species locations per county, only including the areas where a polygon from species critical habitat or range file intersected from the county boundary file. See **Figure 5** for an illustration of the result of intersecting two polygon feature classes.[8]

In the intersect analysis, the acreage of each intersected polygon in square meters was calculated using the intersect tool. This analysis used the default shape area from the attribute table and the units were confirmed as square meters. This information tells the acreage of a species in a specific county, i.e., species acreage per county, in square meters.

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[8] Figure 5 was cited from ArcGIS online help document (https://pro.arcgis.com/en/pro-app/latest/tool-reference/analysis/intersect.htm)
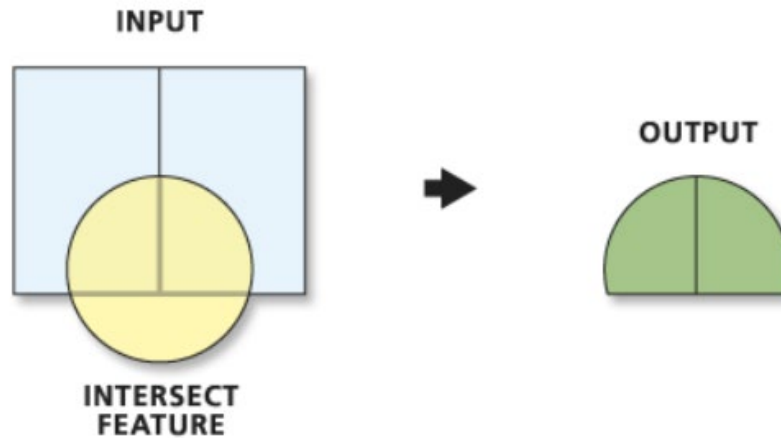
FIGURE 5. ILLUSTRATION OF INTERSECT OF POLYGONS

Exporting attribute table

Once the intersect was completed, the attribute table was exported as a .csv file. This was done by using the "table to table" tool in ArcGIS or "arcpy.TableToTable_conversion" function in ArcPy. The intersect output tables contained all the attributes from species location files and county boundary files. In addition, the intersect output table also included species by county acreage which was calculated in the intersect process. Once exported to the .csv files, all the intersect output tables were combined into two separate all-in-one tables (one for range and the other for critical habitat) and used as the input data for the overlap Python tool.

Use of Python and ArcPy

As mentioned above, the species location files were organized by taxonomic group in file geodatabases (referred to as species libraries). One location shapefile was designated for each individual species range and critical habitat. Each location file was processed following the same approach, i.e., projected to Albers project, intersected with the county boundary file, and exported the interest output attributes to a .csv file.

Due to the large number of location files and the same process for each file, Python scripts were developed to employ ArcPy functions to run files in a batch for each step described above where spatial files were involved.

The key ArcPy functions used in the Python scripts and their corresponding ArcGIS tools were listed in the **Table 2** and mentioned above in each step as well.

Table 12. Key ArcPy functions used and their corresponding ArcGIS tools

Process	ArcPy function	ArcGIS tool
Project	arcpy.Project_management	Project
Intersect feature classes	arcpy.Intersect_analysis	Intersect
Export attribute table	arcpy.TableToTable_conversion	Table to table

Output tables

The final output generated from this spatial overlap analysis includes two all-in-one tables with all species included in each table. One is for the species range, and the other is for designated critical habitat. Each row of the tables represents one species in one county, i.e., single species per county. The attributes/columns of the two tables are slightly different from each other depending on the attribute tables in the source files. However, both output tables contain the essential attributes (but not limited to) that are utilized in the overlap Python tool or further analysis. **Table 3** listed the essential attributes and the corresponding aspect that each attribute represents.

Table 23. Output Attribute Tables for Species' Ranges and Critical Habitats

Attribute	Note
EntityID	The unique integer value of the species entity within the database
STATEFP	State FIPS code – the unique two digits value for the state
GEOID	Geographic identifiers – the unique codes identify all administrative/legal and statistical geographic areas i.e., counties.
NAME	Common name of the species
State	The name of the state
Shape_Area	The acreage of the species in the county in square meters
Area*	The acreage of the county in square meters

Note: * This attribute was not used as a filter in the overlap tool but may be needed for other analysis.

3. Overlap Calculations

Direct Overlap

Calculations of direct overlap percentages begin with tables of county-level acreage values for both listed species and crops of interest. The analysis uses GEOIDs as unique identifiers for counties, allowing assessors to match up entries in the species and CoA input tables. For each county/crop/species combination, the minimum of the county/species area and county/crop area is extracted and stored in a table as an overlap area. For this calculation, it was assumed that each additional marginal unit of cropped area within a county will overlap any available species range/critical habitat within that county until 100% of the species area is overlapped. By taking the minima of the two area values it ensures that county-level overlap area cannot exceed the species acreage (i.e., overlap cannot exceed 100%).

Redundancy Adjustment

While individual crop overlap in each county is capped at 100% of the county species area, the initial overlap calculation described above may result in cases where the sum of overlap from all crops of interest within a county exceeds the county species acreage when multiple crops are considered. In such cases, a redundancy adjustment is applied that maintains the ratio of crop overlap areas while reducing the sum of the overlap areas to the total species area. An example of this redundancy adjustment is provided below:

Unadjusted Overlap Acreage:

Crop 1 Overlap Area (Acres)	Crop 2 Overlap Area (Acres)	Crop 3 Overlap Area (Acres)	Species Range in County (Acres)
30	20	50	50

Overlap Acreage after Redundancy Adjustment (Adjusted values in Red):

Crop 1 Overlap Area (Acres)	Crop 2 Overlap Area (Acres)	Crop 3 Overlap Area (Acres)	Species Range in County (Acres)
15	10	25	50

In the example, the first step is to calculate overlap areas for each crop independently and compares the sum of overlap areas with the species range area. Because the sum of overlap areas for the three crops in the example (100 acres) exceeds the species range (50 acres), each overlap area was multiplied by a factor that represents the species range divided by the sum of individual overlap areas (in this case the factor equals 1/2). The adjusted overlap areas are consequently reduced in such a way that they sum to the species range area but maintain their original proportions relative to one another.

State-Level Rollup/Capping

Once the redundancy adjustment factor to applicable county-level overlap values was applied, the process of rolling up county-level overlap values to obtain state-level overlap values begins. This process initially involves summing county-level overlap values from the same state for each crop/species combination. Once the initial sums have been obtained, the resulting state-level overlap areas was compared with the state-level crop acreage values from the CoA input tables. The minimum of these two values was then taken as the state-level overlap area. The primary function of this capping procedure is to correct for the highly conservative county-level crop acreage estimates introduced by the non-disclosed acreage imputation procedure. In the imputation all county-level non-disclosed acreage values were assigned with the difference between state acreage values and sum of disclosed county acreage values within that state. While this procedure produces maximum possible acreage estimates in each county (due to the uncertainty regarding the distribution of the acres), it has the potential to result in state-level overlap values that exceed the (known) maximum acreage of crop within the state. The capping procedure enforces this maximum value and corrects state-level overlap estimates downward where necessary.

National-Level Rollup/Capping
The rollup of state-level overlap acreages to national-level overlap acreage values follows a similar procedure to the county-to-state rollup. Rollup of state-level overlap areas to national-level overlap areas is accomplished by first taking the all state-level overlap areas for each crop/species combination and then taking the minimum of the sum and national-level CoA acreage value for that crop (like the state-level capping described in the previous section).

Conversion of National Overlap Areas to Percentages
Once national-level overlap areas have been obtained for each crop/species combination, the overlap areas are divided by the total area of range for the corresponding species to generate percentage

values. These final percentage values represent an estimate of the portion of species range or critical habitat that overlapped with each selected crop.

Overlap Calculations – Drift

The process for calculating drift overlap areas differs from direct overlap calculations in a few key aspects. As in the direct overlap procedure, we begin with tables of county-level acreage values for both species and crops of interest. For "all ag" estimates of drift overlap, we first take the sum of acreages for all crops of interest within each county (this allows for more straightforward subsequent calculations that do not require redundancy considerations). A list of buffer distances (i.e., distances from the original field over which we might expect drift to occur under different application scenarios) is also specified for drift calculations.

The area impacted by drift for each county/buffer distance combination is estimated by dividing the total crop area in a county into square 25-acre fields, and modeling the areas impacted by drift as the difference between the area of a square determined by extending each side of the original field by the buffer distance and the area of the original 25-acre field as shown in **Figure 6.**
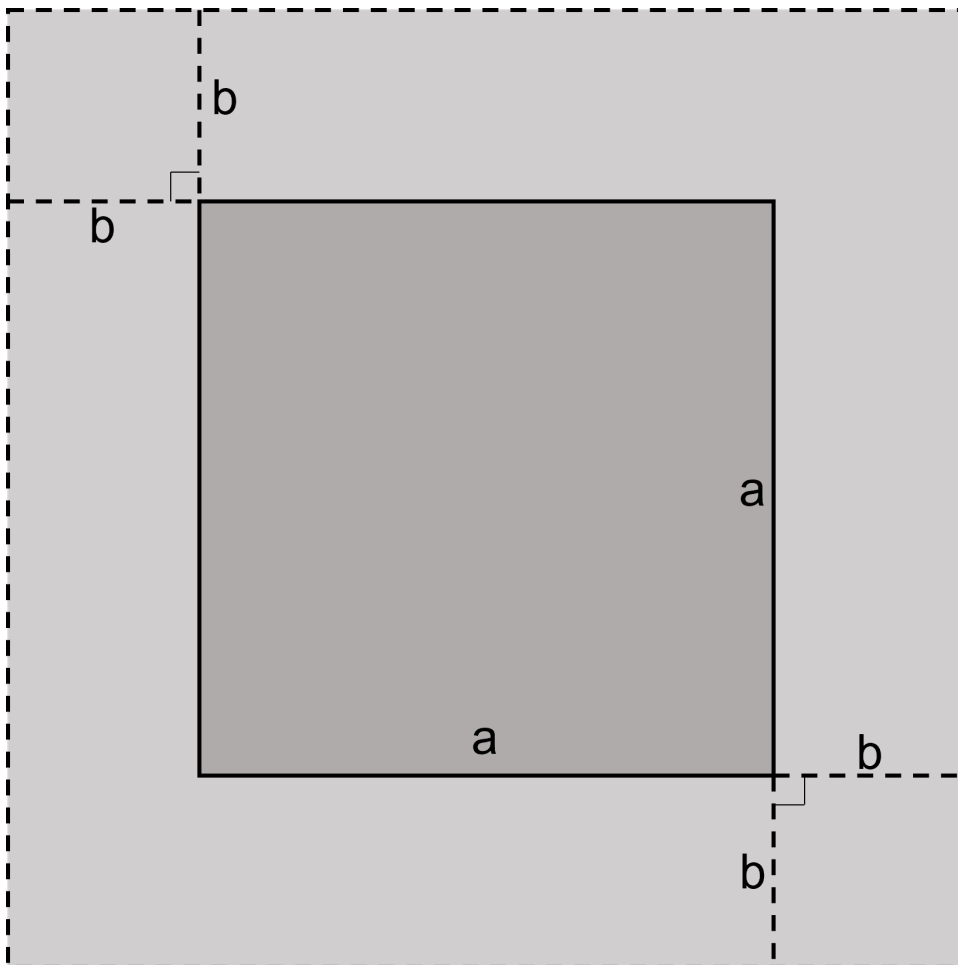
Each 25-acre field in a county has an "a" value of ~318 meters, with specified buffer distance "b" values. The calculation of drift for all crops within a county is shown in Equation 1:

$$DriftArea = \frac{Total\ Crop\ Area}{25\ Acres} \cdot \left(\left(\sqrt{25\ Acres} + 2 \cdot Buffer\ Distance\right)^2 - 25\ Acres\right)$$

Equation 1. Calculation of county-level drift area for all ag columns and specialty crops.

Estimates produced by Equation 1 thus reflect the conservative assumption that drift areas produced by different 25-acre fields do not overlap one another.

In the "all ag" calculation of drift for a given buffer distance, drift areas are first calculated using Equation 1 for each county/crop/species combination. Then the overlap area is capped so that the direct overlap of the crop area + drift zone cannot exceed the species range in the county. The drift overlap areas can be summed for each crop/state/species combination to roll up to state-level overlap or sum all drift overlap areas for a given crop/species combination to roll up to national-level overlap areas. Unlike in the direct overlap calculations, state- or national-level crop area caps do not apply to the estimated drift overlap areas. Once the national overlap areas have been obtained, the values are divided by the sums of range/critical habitat areas for the corresponding species to arrive at an overlap percentage.

The overlap tool output tables contain two types of "all ag" drift overlap columns. One group consists of total overlap percentages, which represent all overlap due to drift up to the specified buffer distances of 305 meters, 792 meters, and 1500 meters and these columns require no further calculations besides those already described. Another set of columns output marginal increases in percent overlap over a specified buffer interval (e.g., 60 meters to 90 meters). Marginal drift overlap increase values are obtained by subtracting the national percent overlap value at the start of the buffer interval from the national percent overlap value at the end of the interval. The overlap tool output provides these marginal drift values at 30-meter intervals over the range of 0 to 810 meters (810 selected to complete the last 30m interval). The 30-m increments are presented in the output individually and marginal increases to drift areas will become zero once the maximum number of available acres has been reached.

In addition to the "all ag" drift overlap columns, the tool also outputs a series of crop-specific overlap direct overlap and drift columns. These columns are generated on a per-crop basis by first applying a slightly modified version of Equation 1 to county-level crop acreage values using buffer distances of 0, 30, 305, 792 and 1500 meters to obtain drift areas. The crop-specific drift calculation differs slightly from the "all ag" drift calculations in that row crops (e.g. corn, soybean, etc.) are modeled as 500-acre fields while specialty crops (e.g. strawberries, apples, cucumbers, etc.) are modeled as 25-acre fields. Thus,

specialty crop calculations use Equation 1, while row crops calculations make use of Equation 2, as shown below:

$$Drift\ Area\ =\ \frac{Total\ Crop\ Area}{500\ Acres} \cdot \left(\left(\sqrt{500\ Acres}\ +\ 2\ \cdot\ Buffer\ Dis\tan ce\right)^{2}\ -\ 500\ Acres\right)$$

Equation 2. Calculation of county-level drift area for row crops.

Once the drift area calculation employing the appropriate field size has been performed, the original crop area is then added to the drift areas to obtain a total affected area for each county/crop/buffer distance combination. The minimum of county-level direct+drift areas and county-level species areas are then taken to produce an overlap area for each county/crop/buffer distance/species combination. County-level overlap values for each crop/buffer distance/species combination to produce a national overlap area value. The national overlap areas are then divided by national-level species areas and multiplied by 100 to produce overlap percentage values for each crop/buffer distance/species combination. In contrast with calculations described in previous sections, no redundancy factor or state/national-level crop-acreage caps are applied in the calculation of these overlap values.

Version Updates: This document accompanies the October 31, 2022, version update from V1.0 to V1.1. Changes to the tool in this version reflect the latest updates to the species range and critical habitat files (Master list-09_2022) as Inputs. This update incorporates new projection methods for regions outside of the conterminous United States. Additionally, this version also includes two additional output tabs [Overlap by Use (Direct and buffered) and Overlap by use in 30 m increments].

Tool Update Cycle: Crop Acreage Inputs may be updated on a 5 year cycle as inputs are available every 5 years from the Census of Agriculture. Species ranges and critical habitats are often updated more frequently, and updates will be scheduled depending on data availability from the Services.

References

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