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STANDARD OPERATING PROCEDURE			

U.S. FISH AND WILDLIFE SERVICE REFINED RANGE MAPS FOR THREATENED AND ENDANGERED SPECIES

STANDARD OPERATING PROCEDURE**1.0 PURPOSE**

The U.S. Fish and Wildlife Service (Service) is considered the definitive source for species listed as threatened or endangered under the Federal Endangered Species Act (ESA). As such, the Service will provide the best representation of where each listed species is currently found (see Section 4.0 for the definition of current range). For species that are wide-ranging and have sufficient documented occurrence data and environmental covariates that affect their life histories, the Service will use species distribution models (SDMs) to create range maps. For narrow-range species or those with insufficient data, alternative models will be used.

The following procedures define the parameters for creating refined range maps for ESA-listed threatened and endangered species. To maintain transparency and accountability, all Service-owned data used to create ranges will be made publicly available, with a few exceptions (see Section 4.0 for details). Final maps of ranges will be available through the Environmental Conservation Online System (ECOSphere) for public viewing and download. This SOP is not a static document and will need to be updated as the procedures are developed and refined.

2.0 SCOPE

This SOP establishes the standards by which range maps for listed species will be developed and assessed as part of the Species Range Project for the Service. It also lays out guidelines for how range maps that do not explicitly follow these guidelines will be evaluated and accepted as official ranges. These standards were created by reviewing peer-reviewed published literature and using two recent reviews on species distribution models (Araujo et al. 2019; Sofaer et al. 2019).

There are two general methods that will be applied, depending on the quality and amount of occurrence, environmental data available, and the geographic size of the range. This SOP details these methods, as well as the processes required for using species distribution models (SDMs), such as:

- Obtaining and cleaning occurrence data
- Selecting environmental covariates
- Building a geographic region for range depiction
- Using that geographic region to select pseudoabsence/background points where required
- Constructing and assessing models
- Building an ensemble model for a species

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3.0 RESPONSIBILITIES

Creating a model, and ultimately a refined range map for any species, will require close collaboration between regional leads, species biologists/lead biologists, GIS specialists, the Headquarters (HQ) Species Range Project Team, and, when requested by the species lead biologist, species experts and partners outside the Service. The final map will be approved by the species lead biologist and other biologists familiar with the species, as well as the species lead biologist's supervisor and the lead region's ARD. Roles and responsibilities for individuals or teams are as follows:

Regional Leads

Because the overall process involves multiple individuals and teams, regional leads are instrumental in coordinating the overall range refinement process. Regional leads will work in concert with the HQ Species Range Project Team to coordinate species occurrence data acquisition, data validation, and collaboration with biologists and species lead biologists. Additionally, they should assist species lead biologists with exception request submissions (see Section 4.0 for more information).

Species Biologists/Lead Biologists

Species biologists/lead biologists from field offices, regional offices, or other species-specific programs will be engaged throughout the range map refinement process, as they are the subject-matter experts who can help guide the modelers with expert advice and information on the species being modeled. The Service has designated a lead office for each species, as well as a species lead biologist from the lead office. The species lead biologist will coordinate and work with biologists in other field offices and will make final decisions during range development. Species lead biologists and biologists will:

- Make available internally collected occurrence and absence data for species
- Validate and provide quality assurance/quality control (QA/QC) of species occurrence data from external sources (e.g., state/heritage programs and other federal collaborators)
- Provide guidance on potential environmental covariates critical to the species
- Participate in the model and map review/selection process
- Assist, as needed, in obtaining necessary approvals from the lead region's ARD

Species Range Project Team

The Species Range Project Team is an interdisciplinary team with experience spanning ecology, species distribution modeling, statistics, data science, spatial science, programming, computing, and infrastructure development. As such, the team will lead and conduct most of the tasks involved in modeling and map creation, including pre- and post-processing datasets and resulting maps.

In addition, the team will provide hands-on support to regional teams or individuals (including necessary R and SDM training) if they wish to model or map their own species for which they have datasets.

Finally, the team will assist species lead biologists and will be responsible for coordinating and facilitating communication with biologists for species that span multiple field office jurisdictions.

STANDARD OPERATING PROCEDURE**Assistant Regional Director (ARD) and Deputy Assistant Director**

Assistant Regional Directors and the Deputy Assistant Director are responsible for approving exceptions for single ranges (see Section 4.0). Additionally, ARDs have final authority to approve range maps before publication to ECOSphere.

4.0 PROCEDURE**Overview**

The definition of current range used for the development of procedures in this document is: “the geographic area where we know a species occurs or that it is reasonable to conclude that the species is expected to be present.”

In 2017, the Service decided to move to a single, unified range for most species. Therefore, updated current ranges will also serve as the species list area (SLA) range, formerly known as the area of influence (Aoi) range. The formal definition of SLA is: “the area within which a species will be included on species lists generated by the Information for Planning and Consultation (IPaC) platform for consultation purposes.” As the definition suggests, SLAs will be used for the generation of species lists from IPaC. There are 3 exceptions when a single representation of the range may not be sufficient, and separate current and species list area ranges will need to be created.

1. For species that are subject to collection or eradication pressure, an exception may be granted. For these species, highly refined ranges and occurrence data will be restricted with limited public access to prevent negative impacts. A more generalized current range will be created and available to the public, and the highly refined range will serve as the SLA and be restricted from public viewing.
2. For some species, there is a need to limit the SLA to geographic regions where only specific actions apply, i.e., incorporate conditional SLAs so the Service can provide conditional information for specific sites on the landscape where only specific actions or project timing trigger the need for consultation. The conditional species list area could be smaller or larger than the current range.
3. There may be a need to capture where a species is not present, but actions could lead to indirect impacts. In this case, the SLA will likely be larger than the current range to account for the identified indirect impacts.

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To receive one of these exceptions, the species lead biologist must submit an exception request form and obtain the approval of their ARD and the Deputy Assistant Director of Ecological Services. Upon approval, two separate ranges can be created.

Regardless of whether there is a single range or multiple ranges for a species, the following conditions must be met for any range updated on ECOSphere: (1) the range is delineated based on natural, biologically relevant features (ranges created from geopolitical boundaries or quad maps are not acceptable); (2) the range receives approval from the appropriate officials within the Service; (3) the output encompasses the complete range of the species (i.e., regional models will not be accepted unless they represent some form of seasonal life history characteristic); and (4) all data, metadata, and documentation, with some exceptions, are available in conformance with the 2019 Open Data Act (<https://www.congress.gov/bill/115th-congress/house-bill/1770/>).

The Species Range Project Team will consult biologists to determine the appropriate method for estimating a species range. For narrow-range species, delimiting polygons around occurrence data or a statistical model using latitude and longitude may be sufficient (see section entitled “Delineating Ranges for Narrow-Range Terrestrial Species” for more details). For widespread species with sufficient occurrence and environmental data, a species distribution modeling (SDM) approach may produce a better estimate of the range. The set of species distribution models that will be used to create an ensemble includes random forest (RF), boosted regression trees (BRT), and maximum entropy (MAXENT), presuming appropriate assumptions (e.g., data densities) are met for each. Other model forms may be added to the ensemble, assuming they meet the conditions described in this SOP.

Depending on the taxonomic group being modeled, additional considerations may need to be made. For migratory species, especially birds, if sufficient occurrence data are available, seasonal (i.e., winter, migration, and summer) ranges may be created separately. Similarly, for anadromous species, separate models will be produced for marine and freshwater environments.

Obtaining and Cleaning Species Occurrence Data for Models

Acquire occurrence data from publicly available databases, including GBIF (www.gbif.org), eBird (www.ebird.org), BISON (bison.usgs.gov), iNaturalist (www.inaturalist.org), Berkeley Ecoinformatics (ecoengine.berkeley.edu), VertNet (vertnet.org), iDigBio (www.idigbio.org), OBIS (obis.org), as well as other appropriate taxon-specific databases. These include voucher museum records, as well as records from verified citizen science databases.

All threatened and endangered species on iNaturalist have their geographic coordinates obscured by default. Obscured data from iNaturalist will not be used for models. Additionally, only research-grade (i.e., verified by a photo or sound and another user) observations will be used for models.

If possible, additional data from within the Service, state natural heritage programs, and partner agencies and organizations should also be included. To be included in models, the data must be

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considered “research” quality, where either a biologist with significant knowledge of the species made the original identification or it has been verified by an independent expert.

To meet the requirements of the Open Data Act of 2019, all occurrence records owned by the Service and used to create ranges will need to be made publicly available at the end of the process. However, there may be cases when spatial coordinate data may be withheld or fuzzed to protect sensitive species localities. The appropriate exception will need to be requested and approved to withhold occurrence data (see Section 4.0).

Data will be acquired using the valid taxonomic name, as well as any species synonyms, according to the Integrated Taxonomic Information System (ITIS) database (<https://www.itis.gov/>). In some cases, additional data for a species may be available but listed under another valid and related species. This can occur when one species is split into two or more species, based on newly published taxonomic guidance. In many cases, data for the previous species will not have been transferred to the newly recognized species. Therefore, it may be important to research each species to determine previous taxonomic names to see whether additional data can be obtained and included. All taxonomic entries that have been used to obtain occurrence data will be documented.

Including data from previous taxonomic names and synonyms could lead to the inclusion of erroneous records. Additionally, vagrancy—when an individual occurs well outside its accepted range—can happen in some taxonomic groups. To address these issues, the records will first be obtained for the valid taxonomic name and, depending on species characteristics, an alpha convex hull will be created around the occurrence data. The selected geometry will be buffered 10 km to create a mask. The distance of this buffer may be modified depending on the traits of the individual species. This mask will then be used to identify erroneous and vagrancy records, which will be removed.

The approach above will not work for listed Distinct Population Segments. In this case, the ECOSphere range or another defined geographic region suggested by biologists will be used to select the occurrence data.

Records without an observation/collection year will be removed because it is unknown when the observation occurred. For species that require multiple seasonal ranges (e.g., migratory species), a full date will be necessary.

Historical records will be removed prior to any model development. The cutoff date used to divide occurrence data into current and historical categories will be determined for each species independently after consulting with biologists.

Factors to consider when choosing a cutoff date include how much sampling effort has occurred within the known range of the species, the rate of known species’ range decline or expansion, land cover change within the range, and the dispersal ability and generation time of the species.

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Many occurrence records from public databases are incorrectly georeferenced because of observer error or incorrect interpretation of field notes. Therefore, any records that contain geographic coordinates with suspicious values or those with fewer than two decimals for both latitude and longitude should be removed. Suspicious values include the following: 0, 0.25, 0.33 (with additional digits of 3), 0.5, 0.66 (with additional digits of 6 or 7), 0.67, 0.75, or 1. Coordinates that match the centroid of counties will also be removed. These are removed because they are likely not georeferenced correctly, if at all.

Remove duplicate records (i.e., records with the same coordinates). This process will yield only one record for a specific geographic location. Duplicate records would contain the same environmental information during the modeling process, thereby leading to pseudo-replication.

Many of the same records are included in more than one database, and the number of decimals for the same record differs among the databases (i.e., rounding occurs in some databases). Therefore, it will be necessary to identify the database with the fewest decimals and round the data from the others to match before duplicates are removed. Note: for most species, four decimal places appear to be the fewest number used across all public databases, so all records will be rounded to the fourth decimal place before duplication removal occurs.

In some cases, occurrence data may take the form of polygons instead of points, as is the case with data from many natural heritage programs. When the area of a polygon is less than or equal to the resolution of the model, an occurrence point will be created for the medial axis of the polygon. For larger polygons, additional information, such as field notes, may be used to assign an occurrence point(s), or the polygon may be removed.

The issue of uncertainty in georeferenced occurrence points will be addressed by having biologists vet and approve the data before modeling can occur. Before vetting the data, biologists will be informed of the model output resolution so an appropriate accuracy level can be used to remove records. Manual removal of occurrence data was chosen because many occurrence data do not have uncertainties; therefore, removing occurrence data that contain uncertainty information could create an inconsistent dataset.

After the review process by biologists, occurrence data will also be spatially thinned to reduce spatial autocorrelation. The appropriate distance will be selected based on the model resolution.

To proceed with a standard species distribution model, there need to be at least 30 grid cells with occurrence records (Guisan et al. 2017). If a species has fewer than 30, but at least 10, an alternative modeling approach may be considered, as described in Breiner et al. (2015). This alternative approach builds a suite of model iterations, with one predictor for each model iteration, that are averaged to create an ensemble model.

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Selection of Environmental Covariates/Data

For each species or subspecies, a standardized list of covariates will be made available, but selection of appropriate covariates for models will be left to biologists. Biologists can also suggest additional environmental covariates not included in the list, based on Service documents or expert knowledge. If possible, suggested covariates will either be found or created and included in models.

Biologists will select no more than one environmental covariate for each set of 10 occurrence points (Harrell et al. 1996). For example, if a species has 40 occurrence points, four covariates may be selected.

Multicollinearity between covariates will be assessed by computing variance inflation factor scores for covariates (Dormann et al. 2012). Covariates with scores higher than 5.0 will be candidates for removal. The highest-performing covariates will be retained, and the one with the lowest importance among those with high variance inflation factor scores will be removed. The process will run again iteratively until all remaining covariates have a score less than 5.0.

Relative importance will be computed using a permutation method in which a full-model prediction was compared to predictions made after randomizing one covariate at a time. The importance score will be calculated as $1 - \text{correlation}$, such that larger scores indicate greater contribution to model performance.

Environmental covariates will initially be created at 1 km resolution. If, after consultation with biologists, a higher resolution is needed, either 100 m or 30 m will be used instead, contingent upon available environmental covariates at the chosen resolution and the accuracy of occurrence data.

When large changes in grid size are needed, resampling will need to take place in stages to limit the introduction of mathematical artifacts. For example, when downscaling 800 m data to 30 m, it will need to be downscaled successively from 800 m to 600 m to 400 m to 300 m to 100 m and then down to 30 m. The number and size of the steps will vary depending on the dataset and change in resolution; however, all steps will be documented in the metadata for the final environmental layers.

Creating the Background Region and Selecting Pseudoabsences/Background Points

The geographic background, or the region for selecting pseudoabsences/background points, will be created by building a minimum convex polygon around all vetted occurrence data (Rodda et al. 2011).

For some species, a different background may need to be selected. Ideally, the background region should include the range of the species, as well as the region that the species can disperse to over “relevant” periods of time (Barve et al. 2011). In these cases, the region will be delineated in consultation with biologists.

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When peer-reviewed research demonstrates that a species occurs in different environmental spaces throughout its range, more than one background will need to be created, and the occurrence and pseudoabsence/background data subsetting by those regions (Mainali et al. 2015). Species distribution models will then be run for each region individually, and the resulting outputs combined. This approach presumes that sufficient data densities exist for regional models.

For all pseudoabsence/background point selection, the set-seed function should be set in R, so the pseudoabsence/background geographic locations can be replicated if needed.

Pseudoabsences or background points will be drawn spatially by one of two methods: randomly from the background, or with the same bias/intensity as the occurrence data. The second approach can be achieved by using a target-group background methodology (Phillips et al. 2009), which uses occurrence data from closely related species occurring in the same geographic space for pseudoabsences/background points. This second approach is especially important in cases where occurrence records are systematically biased—e.g., toward easily accessed areas.

If requested, biologists will also be provided an opportunity to vet pseudoabsence/background data. To support binary classification, 10,000 pseudoabsence points will be sampled from the modeling extent after removing all pixels containing an occurrence. Sampling will be performed without replacement. Additionally, pseudoabsence/background points will not be selected from within grid cells that contain occurrence data.

If true absence data are available for the species within the background region, these data will be used in place of, or supplemented with, pseudoabsences if necessary to meet the quota for regression models.

Presence and pseudoabsence records will be weighted equally in all models (i.e., prevalence = 0.5; Barbet-Massin et al. 2012).

Occurrence data will be combined with pseudoabsence/background data. This resulting dataset will be intersected with the selected environmental layers and run through three different modeling algorithms.

Building Individual and Ensemble Models

The biomod2 platform will be used to train three modeling algorithms: Gradient Boosting Machine (GBM), Random Forest (RF), and Maximum Entropy (MAX). All models will be implemented using the “bigboss” optimization strategy. These models are selected because they have been shown to perform well in several peer-reviewed studies (Drake et al. 2006; Elith et al. 2006; Elith and Graham 2009).

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Based on the characteristics of the datasets, the modeling team will tune the parameters for each model to achieve the best performance. The parameters for the best-performing models will be recorded and stored with the model for future reference.

Spatial block cross-validation will be used to evaluate model performance. Each algorithm will be run in four spatial blocks. These cross-validation runs will generate the evaluation metrics summarized in the section below. For final predictions and output maps, full models (i.e., models trained on all available occurrences) will be used.

The True Skill Statistic (TSS), Area Under the Curve (AUC), and the Boyce Index (Boyce et al. 2002) will serve as the primary evaluation metrics for species distribution models. TSS will measure each model's ability to correctly distinguish presences from absences after applying a threshold, with higher values indicating stronger discriminatory power. AUC will provide a threshold-independent measure of how well the model ranks presence locations above background or pseudoabsence locations. The Boyce Index, also threshold-independent, will assess how consistently each model assigns higher suitability values to known presence locations compared with the landscape in general. Together, these metrics will provide complementary perspectives on model accuracy and ecological reliability.

Each model will be projected onto the background region used for pseudoabsence/background point selection. Additional projection regions may be considered in consultation with species biologists.

Two weighted ensemble models will be generated using the full-model predictions from the GBM, RF, and MAX algorithms. For the Boyce-weighted ensemble, each algorithm's cross-validation Boyce score will be calculated, normalized so the values sum to one, and then applied as weights to produce a continuous ensemble prediction. A binary version of this ensemble will be generated by calculating the weighted mean of the algorithm-specific Boyce thresholds. A second ensemble will be produced using the same procedure but substituting TSS scores and TSS thresholds, resulting in a TSS-weighted ensemble. For both continuous ensembles, an additional occurrence-anchored threshold will be applied by identifying the lowest predicted suitability value that still contains at least one confirmed occurrence point; this value will serve as a conservative, presence-based cutoff for generating alternative binary maps.

Inter-algorithm uncertainty will be quantified as the standard deviation across the three full-model predictions. Higher values will indicate regions where algorithmic predictions diverge more strongly.

To ensure quality and guarantee that confirmed presences are retained in the final maps, a binary raster will be created across the modeling extent in which cells containing an occurrence are assigned a value of 1 and all others 0. The TSS and Boyce binary ensembles will then be combined with the binary occurrence raster using a pixel-wise maximum operation. This step will guarantee that all occurrence cells receive a final value of 1.

All output maps, including threshold outputs and ensemble models, will be sent to biologists for review. After reviewing the maps, biologists may request updates, including the addition of new occurrence data or environmental covariates. At the end of the model review and update process, the biologists will select a single threshold to serve as the official range.

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If output maps cannot be corrected through model adjustments, biologists may manually add locations where the species is known to be present, but the model does not predict it. This is likely to apply to critical habitat. If the model does not predict a species occurrence within critical habitat, that location will be appended to the output. Conversely, if the model inaccurately predicts the species within block-clearance areas (i.e., regions of confirmed absence), those predictions will be removed. Additional adjustments may be required for some species, such as the removal of predictions in urban areas. Any modification to model outputs will be documented in the associated metadata.

Delineating Ranges for Narrow Range Species

If a species has a very small range, it may be more appropriate to delineate the range by using a statistical model with latitude and longitude as covariates, by delineating polygons, or by using another modeling method.

Polygons will be delineated based on Service documents, taxonomic websites (e.g., amphibiaweb.org), and peer-reviewed literature. All sources that were used to delineate ranges need to be recorded and cited.

For “rule-based” models, covariates and associated thresholds will be chosen based on recommendations by biologists and examination of occurrence data.

5.0 FILE LOGISTICS/ATTRIBUTES

The following data standards shall be met for each geospatial file:

File Format

ESRI shapefiles shall serve as the common storage format for all data. A shapefile is a collection of files:

- .shp – the shapefile feature data
- .dbf – attribute table
- .shx – shape index file
- .prj – projection file
- .xml – metadata file (see below for additional information)

Each shapefile must contain features and attributes for only one species.

File Naming Convention

All shapefiles must comply with the following shapefile naming convention. This naming convention applies to the prefix of all components of the shapefile, including the metadata record.

<ScientificName><ENTITYID><EXT>

ScientificName: scientific name, capitalizing genus and species

ENTITYID: unique entity code

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EXT: indicates whether the shapefile is a current range <CURR>, species list area range <SLA>, or one range <ONE> (i.e., both current and SLA)

Example:

Shapefile prefix for the Marbled Murrelet:

ScientificName = BrachyramphusMarmoratus

Entity ID = 143

Shapefile prefix = BrachyramphusMarmoratus_143_CURR

Coordinate Format

All coordinates shall be in NAD 83 (EPSG: 4269).

Attributes for Range Shapefiles

Name of attribute: 'Status'

Description: The 'Status' attribute indicates whether the polygon was created from a "model" or reflects specific editing: "added" or "edited." Polygons created directly from model output should be designated as "model." For polygons that were manually created or edited, the user will be able to change the text value to "added" or "edited."

Type: Text

Name of attribute: 'Contact'

Description: The individual requesting the change (i.e., addition or edits) should be recorded. This field will automatically be left blank; however, biologists can modify it if "added" or "edited" is selected in the 'Status' attribute.

Type: Text

Name of attribute: 'Reason'

Description: If the polygon was "added" or "edited," a reason should be provided, along with any supporting documentation. This field will automatically be left blank; however, biologists can modify it if "added" or "edited" is selected in the 'Status' field.

Type: Text

Shapefile Metadata

All submitted shapefiles are required to have FGDC-compliant metadata records. The metadata records can be created using the ESRI ArcGIS metadata tools or other FGDC-compliant metadata creation tools. Please refer to the FGDC Metadata website at <http://www.fgdc.gov/metadata/> for detailed information on metadata standards, minimal metadata record requirements, and metadata document creation tools.

The naming convention for metadata files is the same as for other shapefile components. See the "File Naming Convention" section of this document for guidance.

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Final Range Map in ECOSphere

The Species Range Project Team will ensure that final range maps are posted to ECOSphere and made publicly available.

If the final range map was produced outside of the SRP, the species lead biologist must verify that all minimum criteria are met (see Section 4.0 of this SOP) and provide all appropriate shapefiles and metadata, as well as documentation of data sources.

6.0 LITERATURE CITED

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