**Species Distribution Models**

In order to address Element 1 of Arizona’s State Wildlife Action Plan (SWAP), species distribution models were created for all of the Species of Greatest Conservation Need (SGCN). These species distribution models were modeled to represent the historic, present, and potential distribution for an individual species. A specific set of parameters was used for each species distribution model, including vegetation, elevation and slope associations, and known occurrences.

There were several base data layers that were used for a majority of the predictive distribution models. The USGS’s SWReGAP land cover layer, as modified above, was used to map vegetation associations for individual SGCN species. A digital elevation model (DEM) for Arizona was used to map elevational and slope associations for individual SGCN species. Hydrologic Unit Code (HUC) boundaries at the 10-digit level created by the Natural Resources Conservation Service (NRCS), along with species occurrence data were used to identify watersheds associations for individual SGCN species.

After the SGCN species distribution models were created, the parameters that went into each model were entered into the database. This created a straightforward way to access the model parameters via queries and tables. The species distribution parameters database is fully linked to the SWAP database, so future updates to the SWAP database (e.g., taxonomic or legal status changes) will be reflected in the species parameters database.

Methods for species distribution models were generally consistent within higher taxonomic levels (e.g., invertebrates, amphibians, birds, etc.), but occasionally species specific parameters were employed (see discussions below). However, all of the data sources discussed above were used in compiling the distribution models for the SGCN, and were further refined through expert opinion and through validation with the Heritage Data Management System (HDMS) element occurrence data (if those data were available). For most species, validation with HDMS data has not yet occurred. We are continuing to refine models as time permits.

Regardless of methods, there are assumptions inherent in all of the models:

1. Most of the models are built using SWReGAP Land Cover as a base layer and have a base pixel size of 30 m. However, the models, as is the Land Cover database, are meant to be used for landscape level analysis at a scale of 1,000 ha or greater (Boykin et al. 2007).

2. Each model represents a *predicted* range distribution for a species. Species are expected to occur within that range, but are not assumed to be present at every point within the geographic range. Also, the models do not provide information on species abundance or on habitat quality within the predicted range.

All of the SGCN species distribution models were reviewed by Department biologists before they became finalized. The SGCN species distribution models were created using the best available data at the time, and will be updated as data become available in the future.
**Invertebrates**

The species distribution models for the SGCN invertebrate species were created using several approaches. Aspect, slope, elevational and vegetation associations for individual species were identified by Department staff. The aspect, slope, and elevational associations were extracted from a 30 m DEM of Arizona, and the vegetation associations were extracted from SWReGAP vegetation layer. Occurrence data from the HDMS were used to identify watersheds in which each species occurs at the HUC 10-digit level. The identified watershed range was used to restrict the vegetation association layer down to only those watersheds in which the individual species occurs. Then the aspect, slope, and elevational association layers were used to further restrict the updated vegetation association layer.

In some cases, the watershed distributions identified by HDMS occurrence data were used to locate water springs that are within the selected watersheds. When the water springs were used in the invertebrate species distribution models, a spatial buffer (in meters) was used around each spring to ensure that the springs are present in the final version of each distribution model.

**Fish**

The species distribution models for the SGCN fish species were created using the same methods, in which three hydrological data layers were used to create the species distribution models. Two hydrologic data layers with stream features created by the Department were used to extract intermittent and perennial stream features. A hydrologic data layer with lake features created by the Arizona Department of Environmental Quality (ADEQ) was used to extract lake features for species that have an association with lakes.

Watersheds at the HUC 10-digit level were identified by Department staff using information from the LCRB Aquatic GAP Analysis Project. The identified watershed range was used to restrict hydrological features to only those watersheds in which the individual fish species was known to occur. The hydrological features were merged together to create a final distribution model for each SGCN fish species.

**Amphibians**

The species distribution models for amphibian species were created using several approaches. Elevation and vegetation associations for individual species were identified by Department staff, and those associations were extracted from a DEM of Arizona and the SWReGAP vegetation layer, respectively. Occurrence data from the primary literature, the Riparian Herpetofauna Database, HDMS and other Department sources (e.g., internal reports) were used to identify watersheds in which each species occurs at the HUC 10-digit level. The identified watershed range was used to restrict the vegetation association layer to only those watersheds in which the individual species was known to occur. Then the elevation association layer was used to further restrict the updated vegetation association layer. This method created predictive species distribution models that assumed that if a species was known to occur in a portion of a watershed within a specific elevational range and within specific vegetation types, then it should occur in other areas of the watershed that have the associated vegetation types and fall within that elevational range.
In some cases species distributions were inferred from distribution maps in field guides (e.g., Brennan and Holycross, 2007) or species accounts in the Catalogue of American Amphibians and Reptiles (published by the Society for the Study of Amphibians and Reptiles). This information was coupled with staff knowledge and literature reviews of habitat types and elevational ranges. Furthermore, species distribution models created by the SWReGAP project were used to map a few amphibian species distributions for the SWAP. When Arizona-specific species information was available, such as elevational range, vegetation associations, and occurrence information, the SWReGAP species distribution models were modified to incorporate those data.

**Reptiles**
The species distribution models for SGCN reptile species were created using a similar approach to that for amphibians. Elevation and vegetation associations for individual species were identified by Department staff, and those associations were extracted from a DEM of Arizona and the SWReGAP vegetation layer, respectively. Occurrence data from the primary literature, the Riparian Herpetofauna Database, Desert Tortoise Database, HDMS and other Department sources (e.g., internal reports) were used to identify watersheds in which each species occurs at the HUC 10-digit level. The identified watershed range was used to restrict the vegetation association layer to only those watersheds in which the individual species was known to occur. Then the elevation association layer was used to further restrict the updated vegetation association layer. This method created predictive species distribution models that assumed that if a species was known to occur in a portion of a watershed within a specific elevational range and within specific vegetation types, then it should occur in other areas of the watershed that have the associated vegetation types and fall within that elevational range.

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**Birds**
The species distribution models for SGCN bird species were created using the same methods. Elevational and vegetation associations for individual species were identified by Department staff, and those associations were extracted from a DEM of Arizona and the SWReGAP vegetation layer respectively. Occurrence data from the Arizona Breeding Bird Atlas (ABBA) were used to identify watersheds in which each species occurs at the HUC 10-digit level. The identified watershed range was used to restrict the vegetation association layer down to only those watersheds in which the individual species was known to occur, and then the elevational association layer was used to further restrict the updated vegetation association layer. This method created predictive species distribution models that assumed that if a species was known to occur in a portion of a watershed within a specific elevational range and within specific
vegetation types, then it should occur in other areas of the watershed that have the associated vegetation types and fall within that elevational range.

**Mammals**
The species distribution models for SGCN mammal species were created using a combination of new modeling and reuse of the distribution models created for the SWReGAP project. Elevational and vegetation associations for individual species were identified by Department staff and those associations were extracted from a DEM of Arizona and the SWReGAP vegetation layer respectively. Occurrence data from a variety of sources such as the HDMS were used to identify watersheds in which each species occurs at the HUC 10-digit level. The identified watershed range was used to restrict the vegetation association layer down to only those watersheds in which the individual species occurs, and then the elevational association layer was used to further restrict the updated vegetation association layer. This method created predictive species distribution models that assumed that if a species was known to occur in a portion of a watershed within a specific elevational range and within specific vegetation types, then it should occur in other areas of the watershed that have the associated vegetation types and fall within that elevational range.

In some cases species distributions models created for the SWReGAP project were used as the species distribution models for the SWAP. If Arizona specific species information was available the SWReGAP species distribution models were modified to incorporate the refined data such as elevational range, vegetation associations, and occurrence information.