**File Descriptions for: GitHub – MimsLabVT > National –Fishes-Vulnerability-Assessment-Project**

**R-code**

1. **GBIF data filtering and AOO estimation\_11\_13\_2018**
   * **Downloads data from GBIF and renames file to reflect the species name associated with the file. Take the renamed GBIF files through a loop to clean missing values in longitude, latitude, and year. Removes point occurrence data falling outside of the lower 48 contiguous US. Removes species for which there are less than 50 records. Takes filtered data through a loop to clip by estuary (i.e. locations within estuaries are removed) and Nature Serve shape files (removes locations outside of NatureServe shapefiles that reflect known nativ distributions, thereby removing non-native occurrences). These are the Final location data**
   * **Calculates area of occupancies for fish in final species list using 7 different range metrics: HUC8 and HUC12 watersheds, point buffers with radii of either 1, 5, 10, 20km, minimum convex polygon.**
   * **Creates maps of occurrence points and AOOs for each species**
2. **nature serve area\_11\_13\_2018.R**
   * **This code calculates area of occupancy for each species based on their known distribution reflected in digital distribution maps downloaded form NatureServe at the following URL: http://www.natureserve.org/conservation-tools/data-maps-tools/digital-distribution-native-us-fishes-watershed**
3. **AOO ranking and RCS Code\_JAS\_11\_13\_2018.R**
   * **ONE: ranks area of occupancies (AOOs) in order of size (1=smallest, 128=largest) for each of the 7 range size metrics used to estimate AOOs, and for the AOOs based on the NatureServe maps (downloaded from http://www.natureserve.org/conservation-tools/data-maps-tools/digital-distribution-native-us-fishes-watershed) For each of the 8 sets of AOO rankings (for the 7 range metrics plus NatureServe), the code then scales the values between 0 and 1**
   * **The code then calculates mean and standard deviations for the ranks across the 7 range metrics for each species.**
   * **The code then calculates logarithms(base 10) of AOOs for all 7 range metrics AND AOO based on NatureServe maps (downloaded from http://www.natureserve.org/conservation-tools/data-maps-tools/digital-distribution-native-us-fishes-watershed)**
   * **TWO: calculates Relative Climate Sensitivity index (RCS) for each species (for HUC8, HUC12, 1km and 10km buffer scales). RCS combines areas of occupancies and standard deviations of climatic variables experienced by each species (calculated using PRISM data – see below).**
4. **PRISM extraction and processing from HUCs\_11\_13\_2018**
   * **Downloads PRISM data via Package PRISM, extracts PRISM data to HUCs, creates 30-year moving window matrix for each climate variable for each species, creates a occupied/unoccupied matrix highlighting occupancy of each HUC for each year, multiplies PRISM matrix by occupancy matrix. Takes final matrix and calculates standard deviation across values for each climate variable.**
   * **Standard deviations are used to calculate relative climate sensitivity indices"**
5. **PRISM data extraction from buffers\_11\_13\_2018**
   * Downloads PRISM data via Package PRISM and extracts PRISM data to buffers
6. **Post extraction PRISM processing\_pointbuffers\_11\_13\_2018.R**
   * Takes PRISM data extracted to buffers and performs a 30-yr moving window analysis   
     for each variable per species. Creates an occupied/unoccupied matrix for each species   
     highlighting occupancy of each buffer on a yearly basis. Multiples PRISM data by   
     occupancy matrix. Calculates standard deviation across values for each climate variable.  
     Standard deviations are used to calculate relative climate sensitivity indices
7. **species\_fishtraits\_11\_13\_2018.R**
   * Takes fishtraits from the FishTraits database and extracts data for the species represented in the final species list
8. **fish trait availability\_11\_13\_2018.R**
   * Takes species represented in the final species list (n=128) and provides a summary of the % of traits available for each species, and the the % of species represented by each trait