Local Notes on Rarity BAP work

**PROCESS**

**qryRarityHuc.sql** – Summarizes Gap\_AnalyticDB data for species rarity analysis. Summary by Species, HUC12/L2ecorgion, and GAP Status. Utilizes all Huc12 polygons. Reassigns each Huc12 to the predominant L2 Ecoregion. Output is GAP\_AnalyticDB.qtblRarityHuc dB table.

Output: GAP\_AnalyticDB.qtblRarity

* huc12rng 12 digit identifier for GAP range delimiting polygons
* hucPix total pixel count for each HUC12 polygon
* na\_l2code Omernik L2 code
* na\_l2name Omernik L2 name
* ecoPix total pixel count for each L2 ecoregion polygon
* Taxa Single character representing species’ taxa
* Spp GAP species code
* gs1SppPix pixel count of GAP Status 1 for a species’ predicted habitat
* gs2SppPix pixel count of GAP Status 2 for a species’ predicted habitat
* gs3SppPix pixel count of GAP Status 3 for a species’ predicted habitat
* gs4SppPix pixel count of GAP Status 4 for a species’ predicted habitat
* totalSppPix pixel count of a species’ predicted habitat

**qryRarity.sql** – Summarizes Gap\_AnalyticDB data for species rarity analysis. Summary by Species, HUC12/L2ecorgion, and GAP Status. Utilizes all intersected polygons from Huc12 and Ecoregion datasets. No hucs are discarded. Output is GAP\_AnalyticDB.qtblRarity dB table. See above for format. Not used in analysis.

**qryRarityXLS.sql** - Summarizes Gap\_AnalyticDB data for species rarity analysis. Summary by Species, HUC12/L2ecorgion, and GAP Status. Specifically written to mimic the original XLS work done by Anne Davidson and Leah Dunn (50% hucs discard rule on L4 ecoregions). Output is GAP\_AnalyticDB.qtblRarityXLS dB table. See above for format. Not used in analysis.

**rarity\_IUCN.py** – Retrieves a table of IUCN data for all GAP species (1533) that match IUCN species’ concepts. The table IUCN\_Gap.csv is attached to the GAP Habitat Map Collection Item within ScienceBase. Updates to the IUCN status and trends are implemented from a separate script 20190311SW\_updateIUCN.py

Output: IUCN\_Gap.csv

* gapSppCode GAP Species Code
* gapSciName GAP scientific name
* gapComName GAP common name
* iucnID IUCN numeric id (NOTE: IUCN does not maintain this field)
* iucnSci IUCN scientific name
* iucnCom IUCN common name
* iucnCat IUCN vulnerability category
* iucnTnd IUCN population trend

**rarity\_GapAnalyticDB.py** – Retrieves data from GAP\_AnalyticDB.qtblRarity (summarized Species, Huc12/L2ecoregion, and GAP Status). This version uses all Huc12 polygons and applies L2 Ecoregion labels based on 50% rule.

**rarity\_GapAnalyticDBxls.py** – Retrieves data from GAP\_AnalyticDB.qtblRarityXLS (summarized Species, Huc12/L2ecoregion, and GAP Status). This version drops HUCS that have <50% within an ecoL2 polygon. This matches the analysis from the rarity paper under review. Note: Original work applied 50% rule to Level 4 polygons and then aggregated to Level 2. Not used in the analysis.

Rarity\_Analysis.py – Opens the AnalyticDB output and IUCN\_Gap tables and …