USING SPATIAL INFORMATION TO SUPPORT DECISIONS ON SAFEGUARDS AND MULTIPLE BENEFITS FOR REDD+

# STEP-BY-STEP TUTORIAL V1.0: EXTRACTING AND PROCESSING IUCN RED LIST SPECIES DATA USING A RASTER METHOD USING ARCGIS 10.3

UN-REDD PROGRAMME

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The UN-REDD Programme is the United Nations Collaborative initiative on Reducing Emissions from Deforestation and forest Degradation (REDD) in developing countries. The Programme was launched in September 2008 to assist developing countries prepare and implement national REDD+ strategies, and builds on the convening power and expertise of the Food and Agriculture Organization of the United Nations (FAO), the United Nations Development Programme (UNDP) and UN Environment.

The UN Environment World Conservation Monitoring Centre (UNEP-WCMC) is the specialist biodiversity assessment centre of UN Environment, the world's foremost intergovernmental environmental organisation. The Centre has been in operation for over 35 years, combining scientific research with practical policy advice.

**Prepared by Corinna Ravilious and Simon Blyth**



We welcome comments on any errors or issues. Should readers wish to comment on this document, they are encouraged to get in touch via: ccb@unep-wcmc.org.

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**Acknowledgements:** With thanks to support provided by IUCN Species Programme.

These training materials have been produced from materials developed for working sessions held in various countries, to aid the production of maps using open-source GIS software to inform REDD+ planning and safeguards policies.

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# Contents

# 1. Introduction

## 1.1. About this tutorial

REDD+ is a voluntary climate change mitigation approach that has been developed by Parties to the UNFCCC. It aims to incentivize developing countries to reduce emissions from deforestation and forest degradation, conserve forest carbon stocks, sustainably manage forests and enhance forest carbon stocks. This will involve changing the ways in which forests are used and managed, and may require many different actions, such as protecting forests from fire or illegal logging, or rehabilitating degraded forest areas.

REDD+ has the potential to deliver multiple benefits beyond carbon. For example, it can promote biodiversity conservation and secure ecosystem services from forests such as water regulation, erosion control and non-timber forest products (NTFPs). Some of the potential benefits from REDD+, such as biodiversity conservation, can be enhanced through identifying areas where REDD+ actions might have the greatest impact using spatial analysis and other approaches. To understand this, it helps to know where species are likely to be present.

The purpose of this tutorial series is to help participants in technical working sessions, who are already skilled in GIS, to undertake analyses that are relevant to REDD+. The tutorials have been used to build capacity in a number of countries to produce datasets and maps relevant to their spatial planning for REDD+, and to develop such map products. Maps developed using these approaches appear in a number of publications whose aim is to support planning of strategy options that enhance biodiversity and ecosystem services as well as delivering climate change mitigation (see http://bit.ly/mbs-redd for country materials). There is of course no requirement for countries to use the approaches described in these tutorials.

Where countries have identified biodiversity conservation as a goal for REDD+, and to be consistent with the Cancun safeguards for REDD+ on protecting biodiversity, it is useful to identify areas where specific REDD+ actions are feasible and can protect threatened species. It may also be useful to identify areas outside forest where threatened species may be vulnerable to the displacement of land-use change pressures or to afforestation.

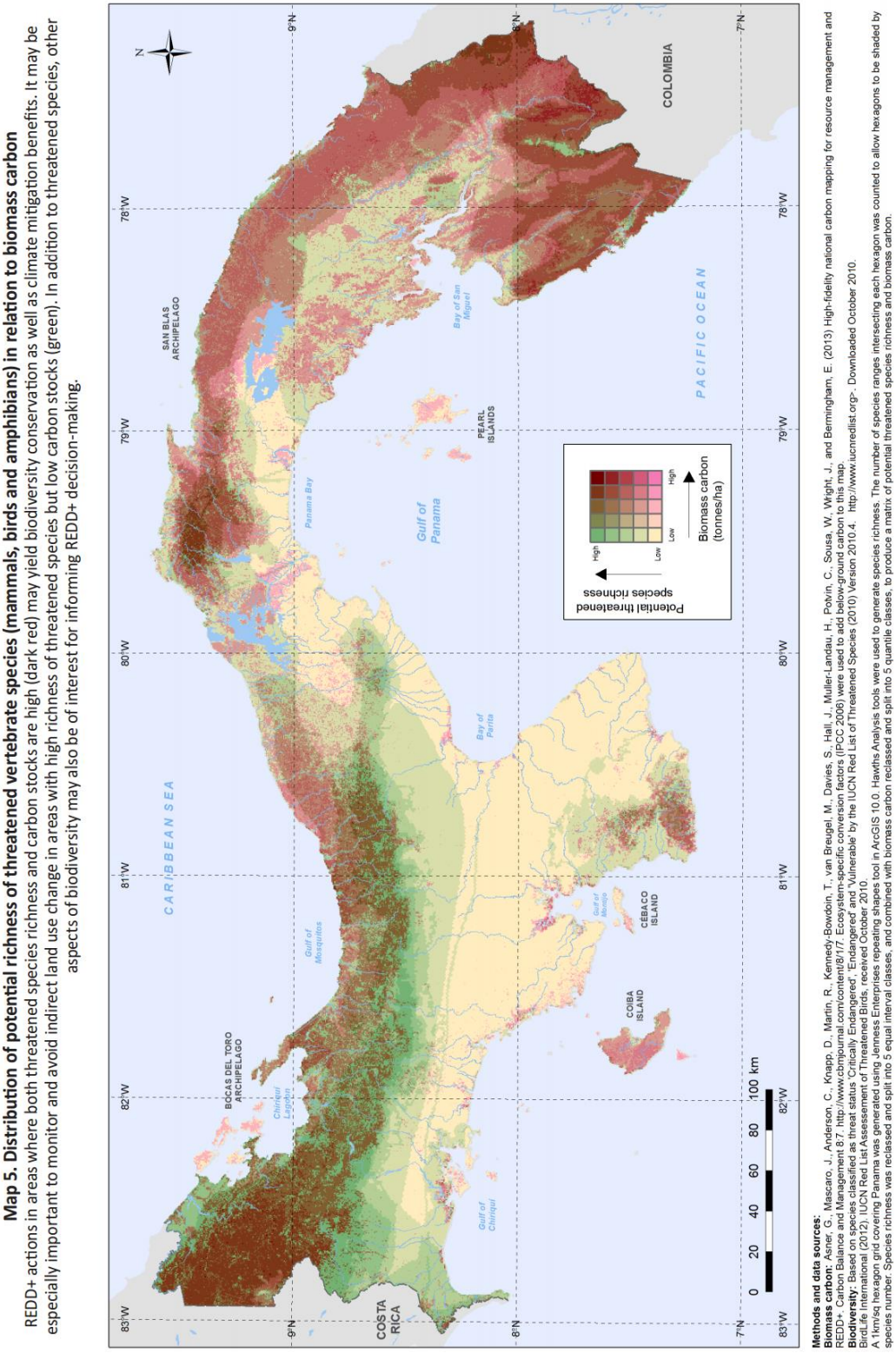
This tutorial demonstrates how a species richness grid can be created using species range data from the IUCN Red List (IUCN, 2013). It provides full instructions on how to select, analyze and export information from the non-spatial species data on the IUCN Red List website and how to further analyze the information along- side the IUCN spatial data using ArcGIS 10.x. A similar tutorial that uses QGIS as an open-source alternative platform is available from http://bit.ly/GIStools-redd:

> Ravilious, C. (2015) Using spatial information to support decisions on safeguards and multiple benefits for REDD+. Step-by-step tutorial v1.1: Extracting and processing IUCN Red List species data using a raster method in QGIS 2.8. Prepared on behalf of the UN-REDD Programme. UNEP World Conservation Monitoring Centre, Cambridge, UK.

Please note that the range data represent areas of occurrence rather than areas of occupancy. That is, there are areas within each range where the species is likely not to be present. For this and other reasons, protecting only a small part of the range may not be sufficient to ensure that a species is protected. Whilst this tutorial uses extent of occurrence data from the global IUCN dataset, the same methods can be used with other national-level data where it is available.

## 1.2. Example species richness maps from Panama and Kenya

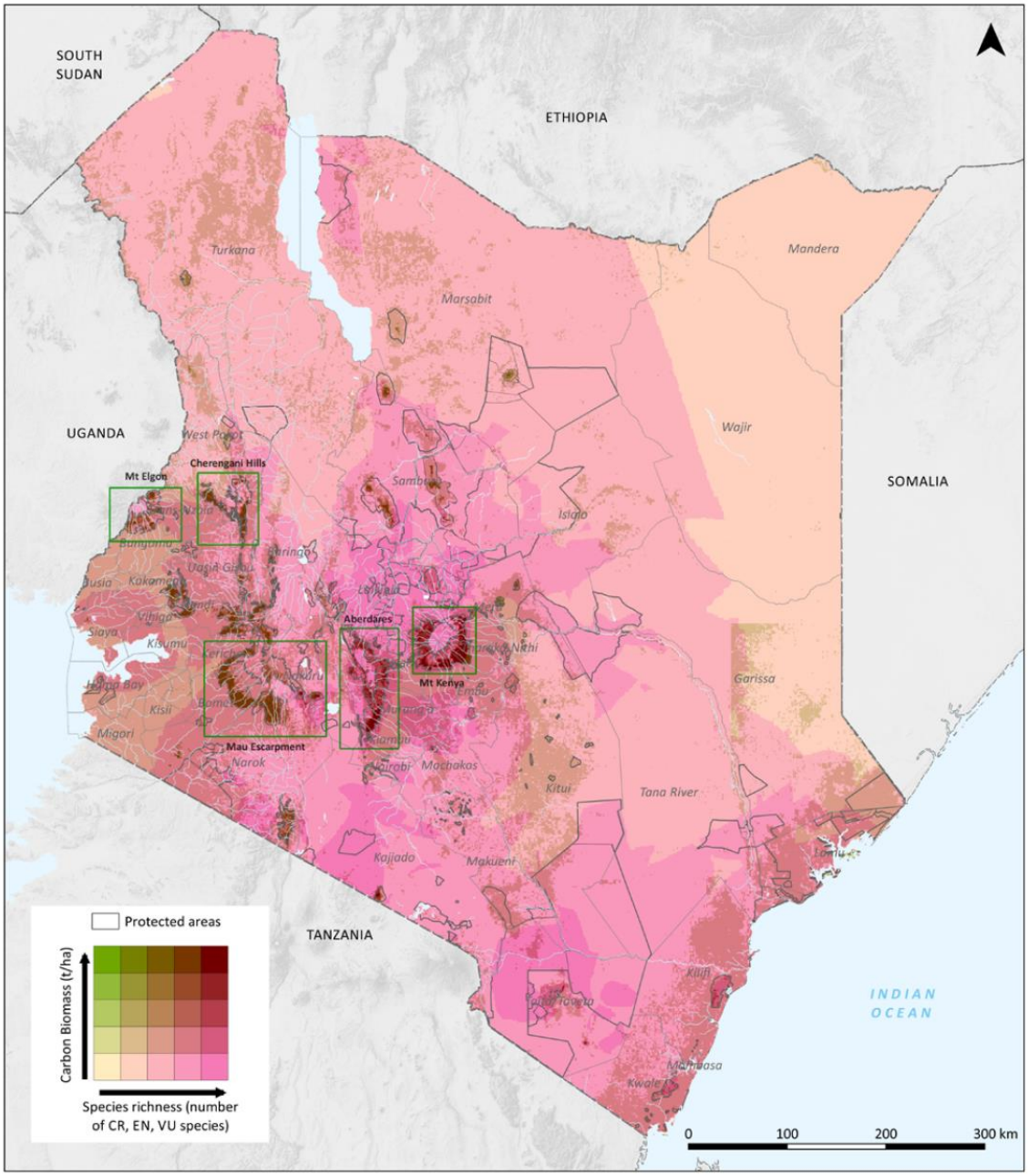
In both examples, biomass carbon is contrasted with species richness using a matrix legend. A matrix legend tutorial is also available at http://bit.ly/GIStools-redd.




Source: Kapos, V., Walcott, J., Thorley, J., Mariscal, E., Labbate, G., Ravilious, C., Miles, L., Narloch, N., Trumper, K. and Bertzky, M. (2015) Planning for REDD+ in Panama: securing social and environmental benefits. Cambridge, UK: UNEP-WCMC. http://bit.ly/panama-redd

**Map 6: How are biomass carbon stocks distributed in relation to the ranges of threatened species and protected areas?**

*This map shows the distribution of biomass carbon stocks and threatened species richness in Kenya. The dark red areas have the highest density of both biomass carbon and threatened species, notably the five water towers (see Map 10). Pink areas have high threatened species richness and low carbon stocks.*




**Methods and data sources:**

*Biomass carbon (left):* Baccini, A., Goetz, S., Walker, W., Laporte, N., Sun, M., Sulla-Menashe, D., Hackler, J., Beck, P., Dubayah, R., Friedl, M. (2012) Estimated carbon dioxide emissions from tropical deforestation improved by carbon-density maps. Nature Climate Change 2. 3:182-185. http://dx.doi.org/10.1038/NCLIMATE1354, The Woods Hole Research Center. National dataset of Aboveground Live Woody Biomass density at spatial resolution of circa 500m derived from field/LiDAR(GLAS)/MODIS. Ecosystem-specific conversion factors (IPCC 2006) were used to add below-ground biomass carbon to this map.

*Species richness:* Derived from the ranges of mammal, bird, reptile and amphibian species classified as 'Critically Endangered', 'Endangered', and 'Vulnerable' by the IUCN Red List of Threatened Species (2014) Version 2014.2 http://www.iucnredlist.org. Downloaded Nov 2014.

*Protected areas:* IUCN and UNEP-WCMC (2014), The World Database on Protected Areas (WDPA) [On-line]. Cambridge, UK: UNEP-WCMC. *Available at: www.protectedplanet.net Accessed 12/2014. Additional information from the Kenya Forest Service (KFS) was used to supplement this data. National parks and reserves are labeled on this map.*

Source: Maukonen, P., Runsten, L., Thorley, J., Gichu, A., Akombo, R. and Miles, L. (2016). Mapping to support land-use planning for REDD+ in Kenya: securing additional benefits. Prepared on behalf of the UN-REDD Programme, Cambridge, UK: UNEP-WCMC. http://bit.ly/kenya-redd

# 2. Using IUCN Red List species data and generating species richness maps

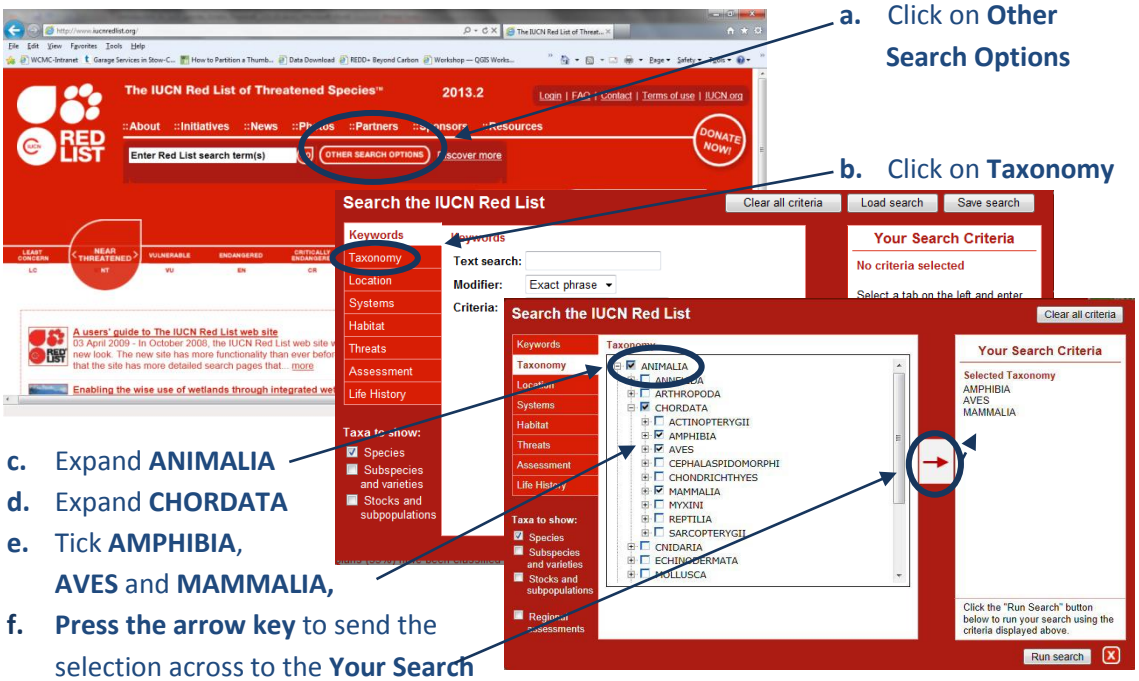
## 2.1. Selecting and downloading species data from the IUCN Red List website

The IUCN Red List of Threatened Species website allows users to search for and extract tabular information (in comma separated values (CSV) file format) on the status of threatened species. The website provides a user friendly interface and gives the user flexibility to customize searches based on a range of criteria. Users must register with the website to save and export customized searches.

### 2.1.1. Searching for non-spatial data

Open a web browser and go to the IUCN Red List website at http://www.iucnredlist.org/.

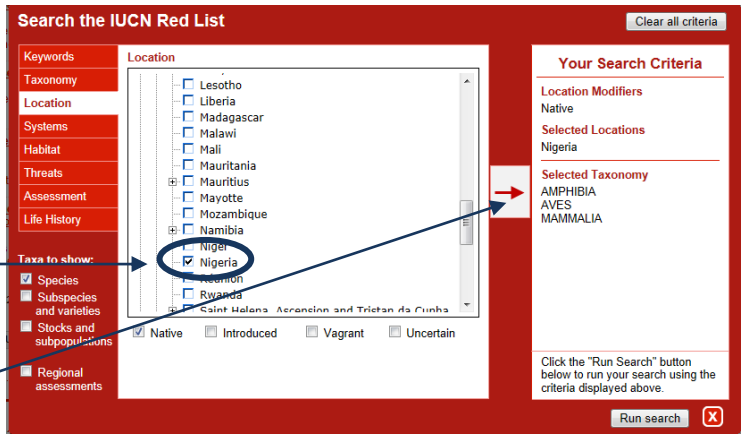
This search below is an EXAMPLE search for Mammals with threat status of Critically Endangered (CR) and Endangered (EN).




c. Expand **ANIMALIA**
d. Expand **CHORDATA**
e. Tick **AMPHIBIA**, **AVES** and **MAMMALIA,**
f. **Press the arrow key** to send the selection across to the **Your Search Criteria** panel

*You may want to limit the search to a single location e.g. a single country or group of locations only.*

g. Click on **Location,** expand **land regions,** expand and tick the **country of interest**
h. **Press the arrow key** to send the selection across to the **Your Search Criteria** panel

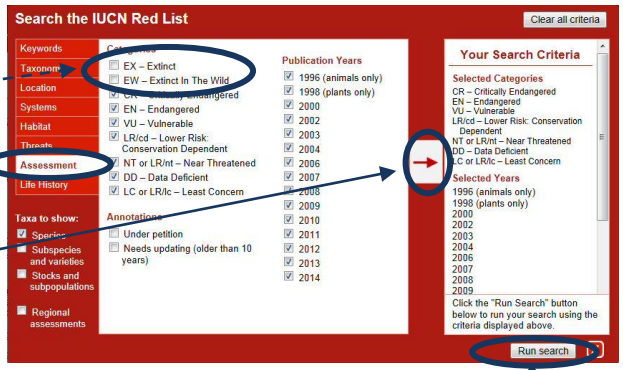


i. Next Click on **Assessment**

j. Untick categories not required i.e. in this example **unticking EX and EW** and keeping the rest.

k. **Press the arrow key** to send the selection across to the **Your Search Criteria** panel

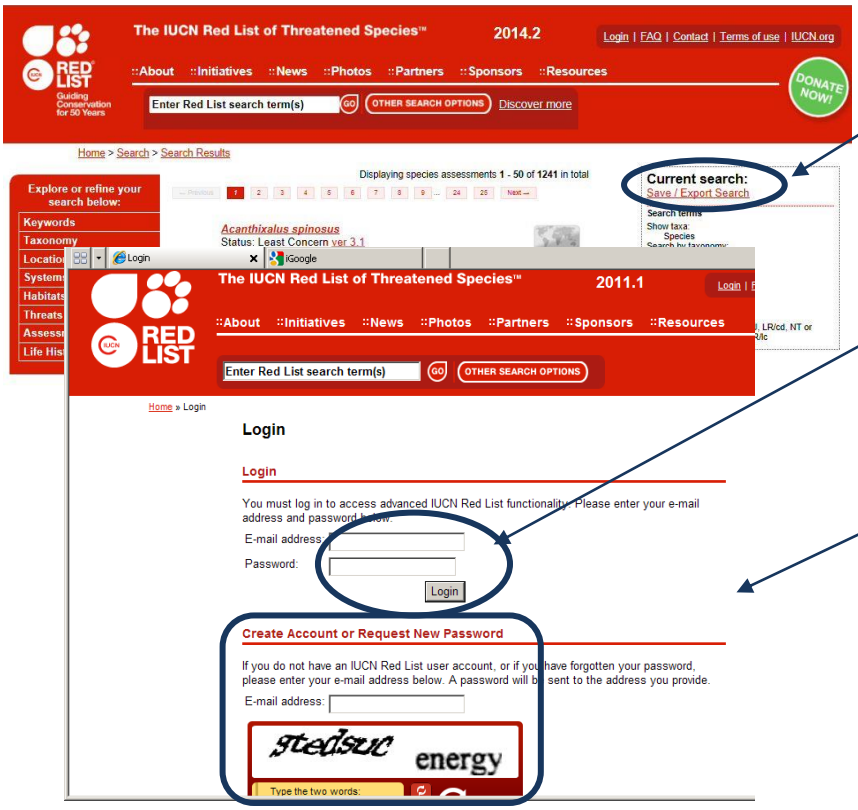
l. Click **Run search**




*This search will result in a list of species within the AMPHIBIA, AVES and MAMMALIA taxonomic groups that have critically endangered, Endangered, Vulnerable, Lower Risk: Conservation Dependent, Near Threatened, Data Deficient or Least Concern Red List status. The search will produce in a list of species containing and additional attribute data, including the threat status of each of the species.*

*There are other criteria that you may want to include. For example, to limit the search to species dependent upon a particular habitat type you would click on Habitat, expand and tick the relevant habitat type and send that across to the search criteria panel.*

### 2.1.2. Save the search and exporting to CSV format



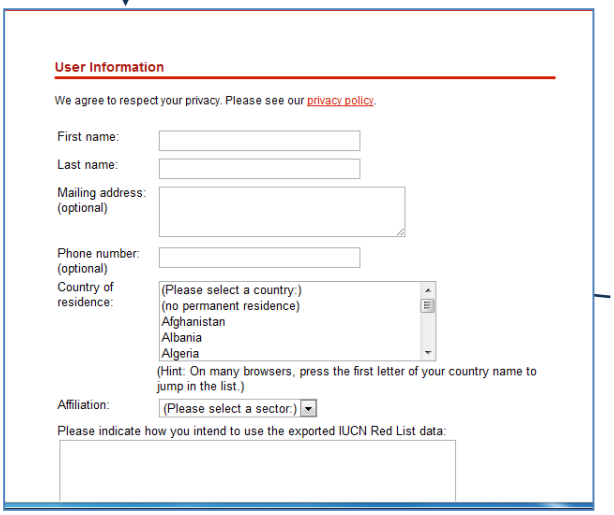

a. Click **Save/Export Search**

b. If already registered, **fill in your email address and password** and click **login**

c. If you have not yet registered, you need to **create an account (see box below)**

*An account is needed in order to save and export the search results.*

**d.** New users will be asked to fill out the details in the box below




The first time new users export a search, they are required to fill out some information about themselves and the intended use of the data

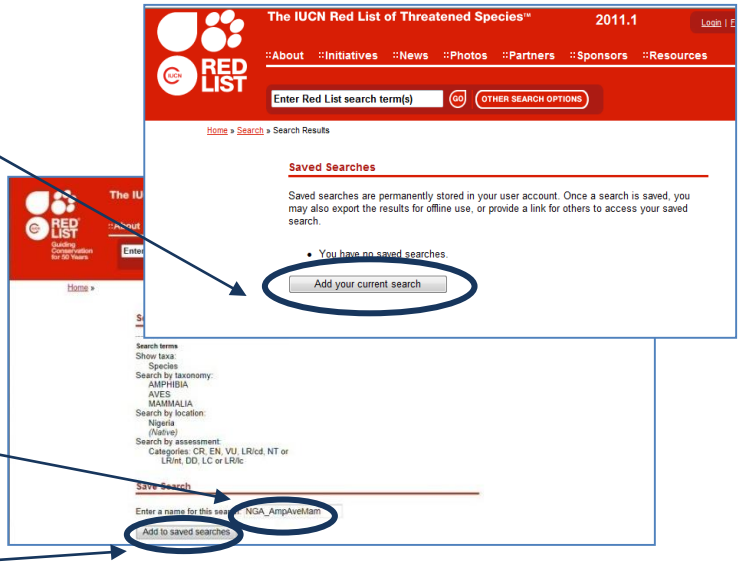
Click on **Supply your information** and fill in the requested details

Click on **Submit**

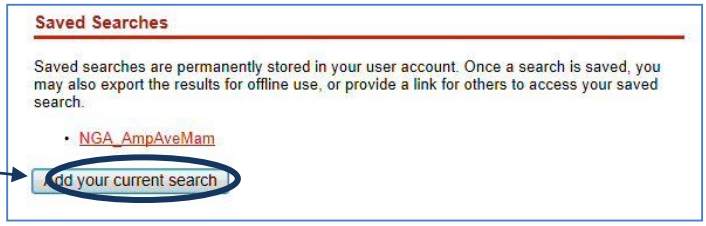
**e.** Once registered and/or logged in, Click on **Add your currentSearch**

**f.** Give the search a name e.g. **NGA_AmpAveMam** in this example

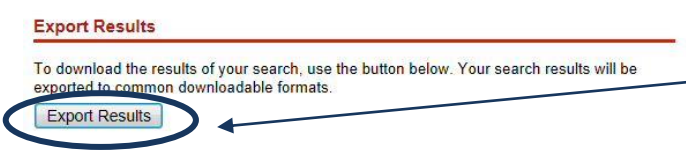
**g.** Click **add to saved searches**

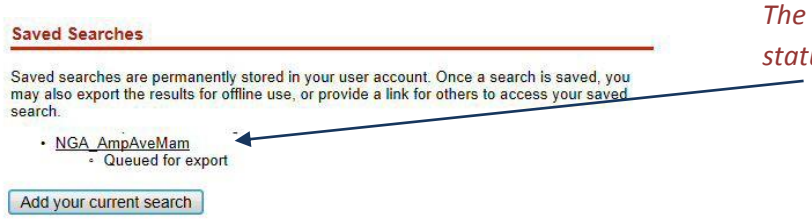



**h.** Click on the **saved search** e.g. **NGA_AmpAveMam** in this example

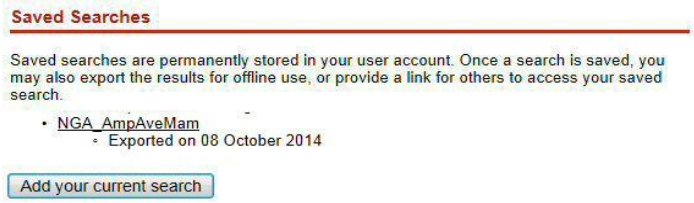



**i.** **Scroll down to Export results** and click on **Export results**






*The dataset will then give a status of Queued for export.*

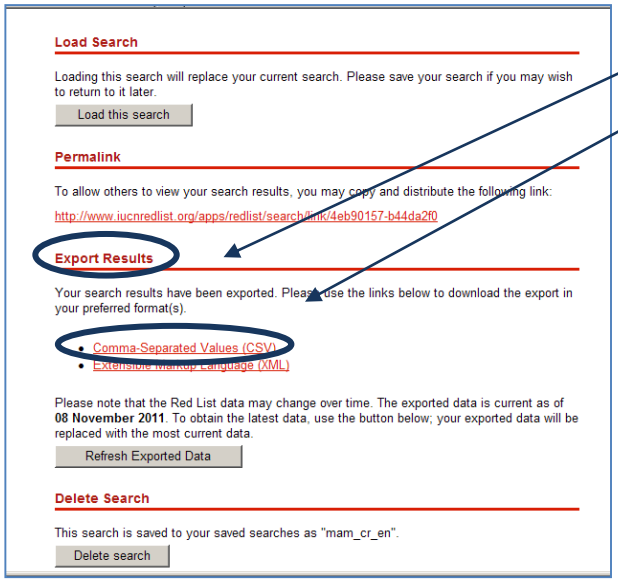



*An email will be sent to you once it has been exported. This is usually within minutes but may take hours for large searches).*

j. **Refresh the browser** to see the status change to show the export is complete or if it is taking a long time log out and once the **email has been received**, log back in to the Red List website and click on the **My Downloads** Tab to get back to your saved searches.



k. Click on the **exported search** e.g. **NGA_AmpAveMam** in this example




**NGA_AmpAveMam.csv** in this example

l. **Scroll down** to the **Export results**

m. Click on **Comma-Separated Values (CSV)** and the zip file will download

n. If the download has placed the file in a general download folder move the zip file to a more suitable location e.g. in a project folder

o. **Rename** the zip file to somthing sensible e.g. **NGA_AmpAveMam.zip** in this example

p. **Right click on zip folder**, extract the csv file

q. **Rename** the csv file e.g.

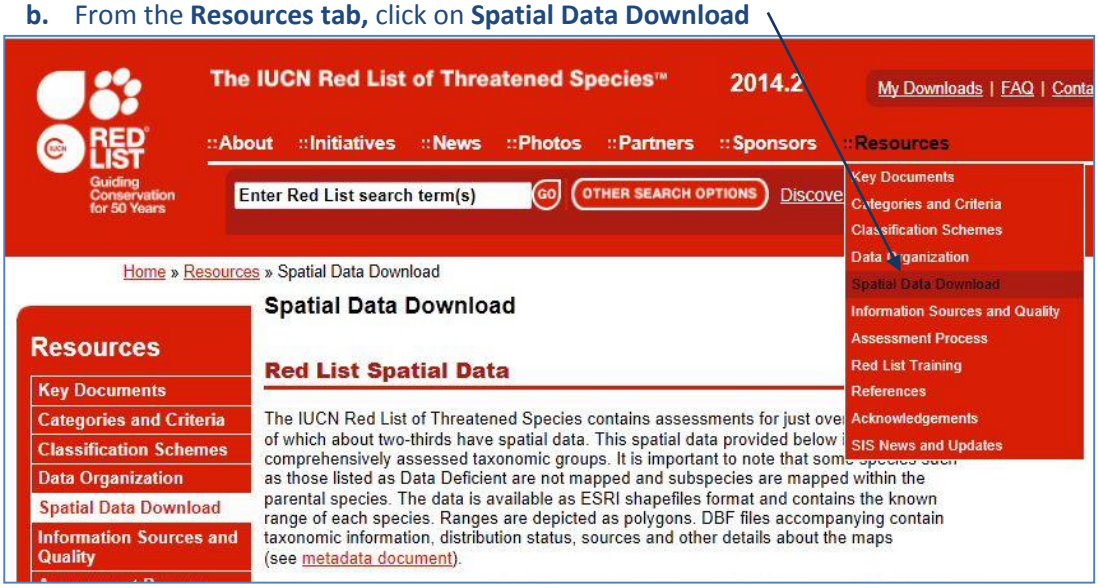
### 2.1.3. Download the IUCN Red List spatial data layers

*The next steps are for downloading spatial data. It is only possible to download the whole global dataset. It is not possible to filter by county prior to download. Please note that some of the spatial datasets are very large.*

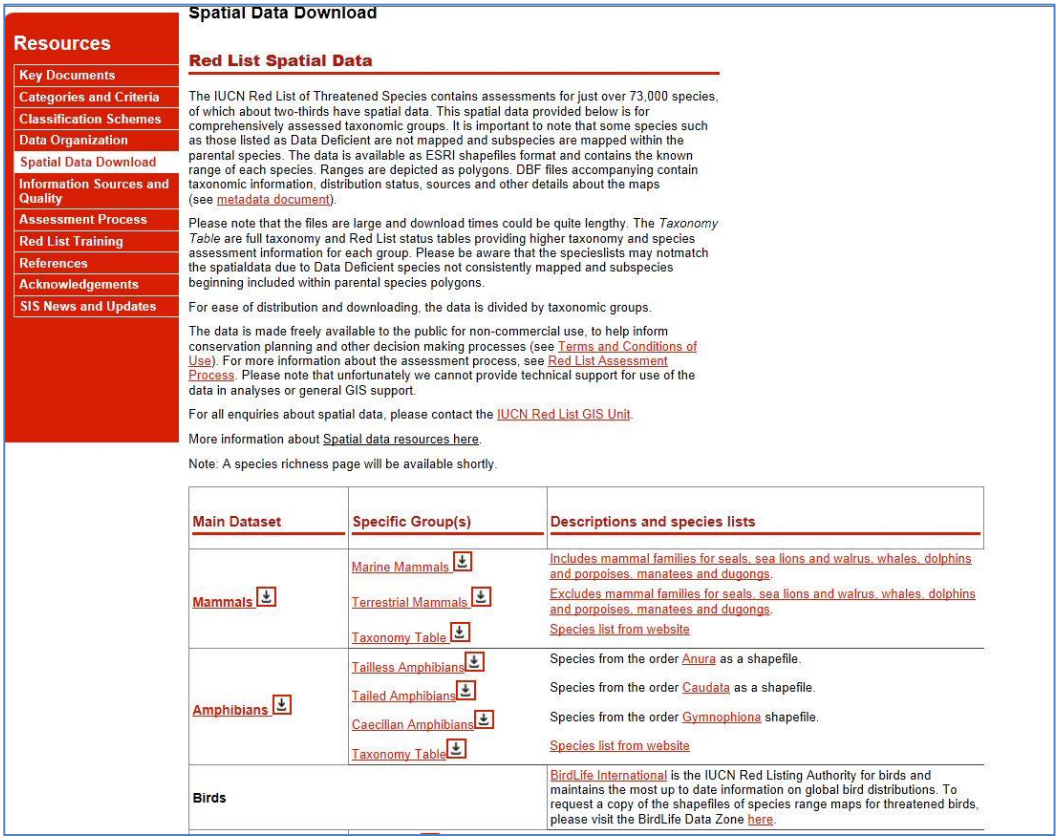
*If you have received the spatial data directly from IUCN you can skip this section.*

**a.** Open a web browser and go to the IUCN Red List website at
http://www.iucnredlist.org/

**b.** From the **Resources tab,** click on **Spatial Data Download**




**c.** **Scroll down** on the Spatial Data page to the **Datasets table**



**d.** **Click the links** to navigate to each dataset and download the following global datasets:

- Mammals
- Amphibians
- Birds (via the link to the BirdLife Data Zone)

(Leave Reptiles for now as assessment is not yet complete for all species)

*These files are all stored in geographic coordinate system (EPSG: 4326). Be aware these large files will take some time to download.*

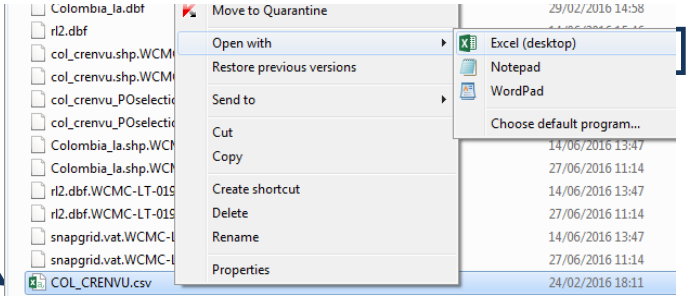
***Note: If you have received the spatial data directly from IUCN, this may be a single geodatabase containing all taxa in a single feature class rather than as separate files.***

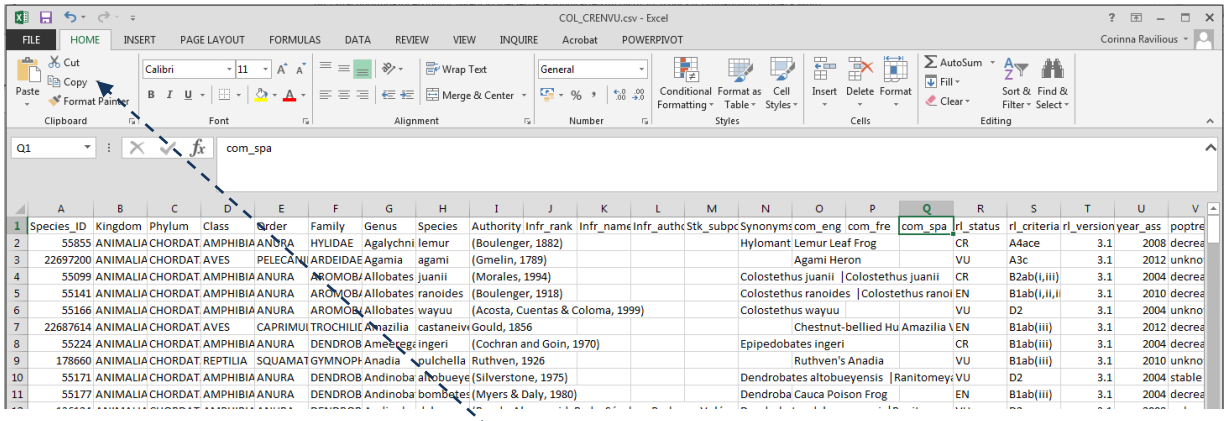
## 2.2. Vector spatial data selection and preparation

The next section we will use a CSV file extracted from the IUCN RedList web search for Critically Endangered, Endangered and Vulnerable birds, mammals, amphibians and reptiles in Colombia.

### 2.2.1. Format species CSV file in preparation for querying the spatial data

**a.** Open the 'exported search' results csv file (that was downloaded in section 2.3 step m) e.g. **COL_CRENVU.csv** in this example. **Open the file Excel.**





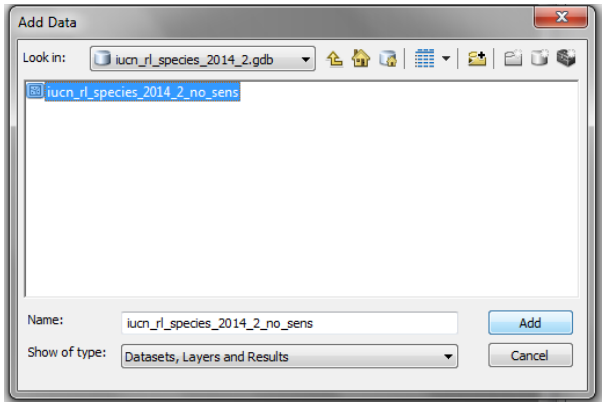

**b.** Scroll along the **column headings** of the table. Some will need to be changed as GIS software such as ArcGIS will not accept them. **Change the ones listed below in red**

| OLD Field Name | | New Field Name |
|---|---|---|
| Species ID | = | Species_ID |
| Kingdom | = | Kingdom |
| Phylum | = | Phylum |
| Class | = | Class |
| Order | = | Order |
| Family | = | Family |
| Genus | = | Genus |
| Species | = | Species |
| Binomial | = | Binomial |
| Authority | = | Authority |
| Infraspecific rank | = | Inf_rank |
| Infraspecific name | = | Inf_name |
| Infraspecific authority | = | inf_auth |
| Stock/subpopulation | = | stk_subpop |
| Synonyms | = | Synonyms |
| Common names (Eng) | = | com_eng |
| Common names (Fre) | = | com_fre |
| Common names (Spa) | = | com_spa |
| Red List status | = | rl_status |
| Red List criteria | = | rl_criteria |
| Red List criteria version | = | rl_version |
| Year assessed | = | year_ass |
| Population trend | = | poptrend |
| Petitioned | = | Petitioned |

**c.** Click **File>>Save** to save the file (save the file as a .xls.

## 2.3. Setting up a relate between the species table and the spatial dataset

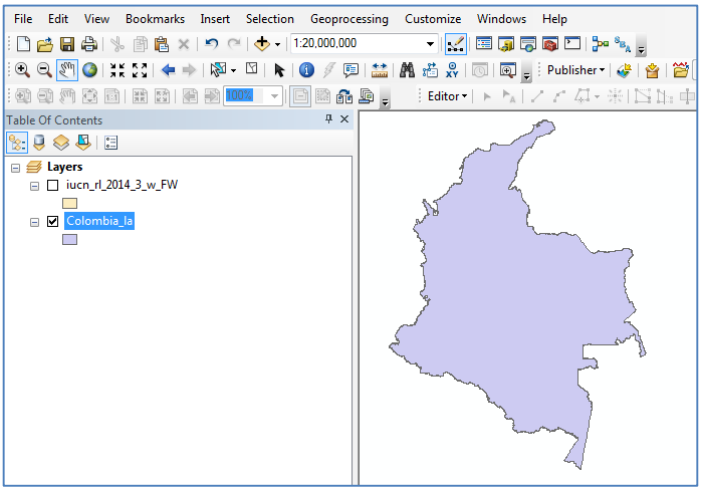
This section prepares the spatial data ready for analysis. The IUCN spatial dataset is a complex dataset as it contains many overlapping polygons for each species for the entire world. Even sub setting the dataset for your area of interest can be problematic so these set of instructions are important steps to make sure the analysis runs as smoothly as possible and to reduce the risk of errors in processing.



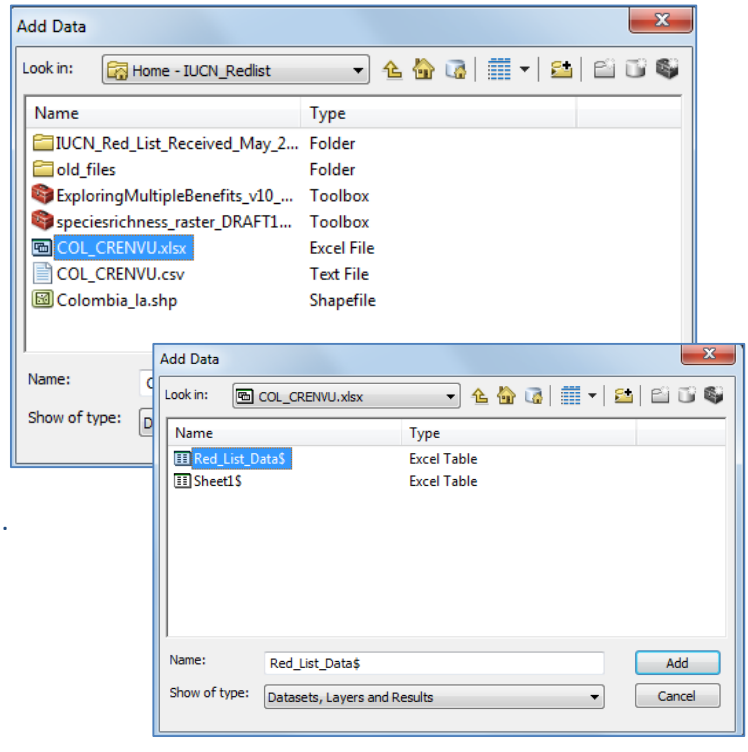

a. Open **ArcGIS**
b. Add in the **IUCN Species spatial dataset(s)** (the data are in geographic coordinate system (i.e. WGS84)
c. **Untick** the dataset in the table of contents to stop it drawing

d. **Add** in a polygon dataset of the area of interest (e.g. country boundary). e.g. in this example **Colombia_la.shp.**

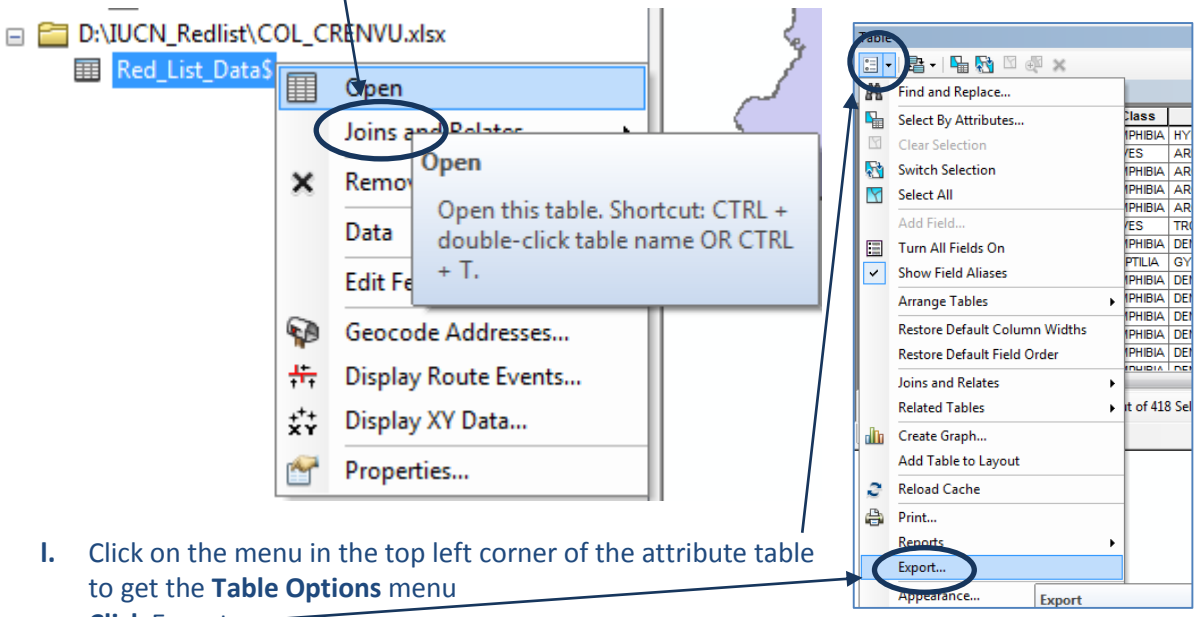
*Make sure the area of interest dataset is in the coordinate system you want to run the analysis in (i.e. in this example Lambert Azimuthal Equal Area)*




e. **Click** on the IUCN spatial dataset in the table of contents to make it the active layer e.g. **iucn_rl_2014_3_w_FW**
f. Add your **geodatabase file (or shapefiles) of the species EOO** polygons to ArcMAp
g. Next add the **,xls file** containing the species of interest (In this example **COL_CRENVU.xlsx)**
h. Click **Add** and the individual sheets within the excel file are listed
i. Select the sheet containing the Red List data (in this example we sheet **Red_List_Data**).
j. Click **Add** that sheet to ArcMap.

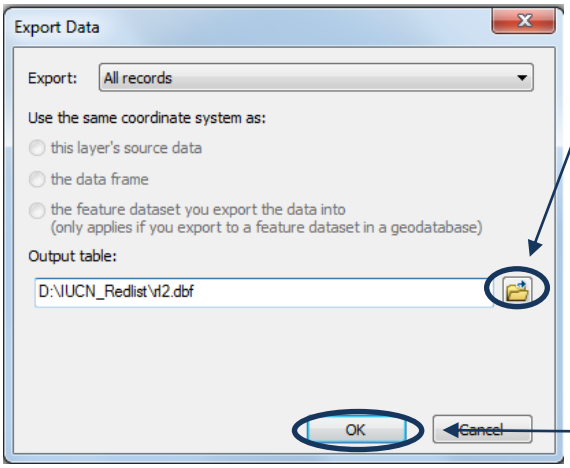


**k.** Right-click on the sheet just added to ArcMap and click **Open**

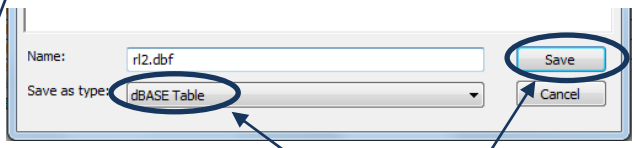



**l.** Click on the menu in the top left corner of the attribute table to get the **Table Options** menu

**m.** **Click** Export




**n.** Click on the **Browse** button to navigate to an output folder



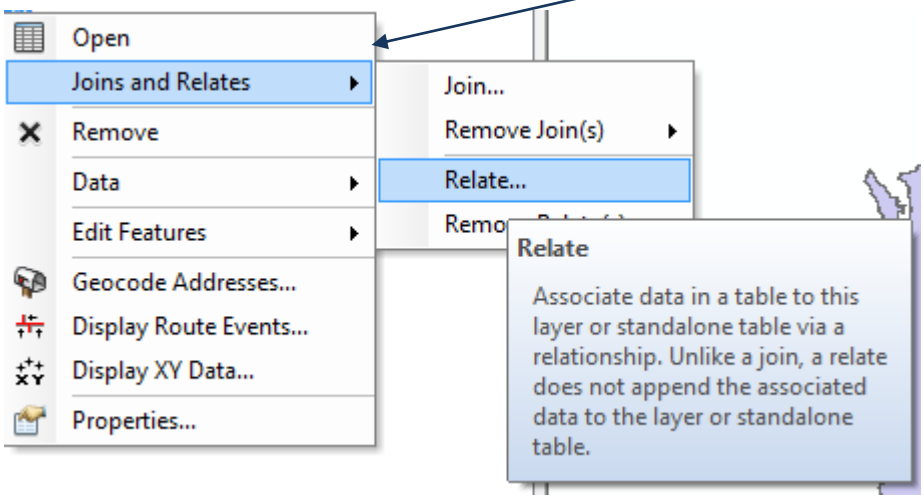

**o.** Change **Save as type** to **dBASE table**

**p.** Give the dbf a name (in this example **rl2.dbf**)

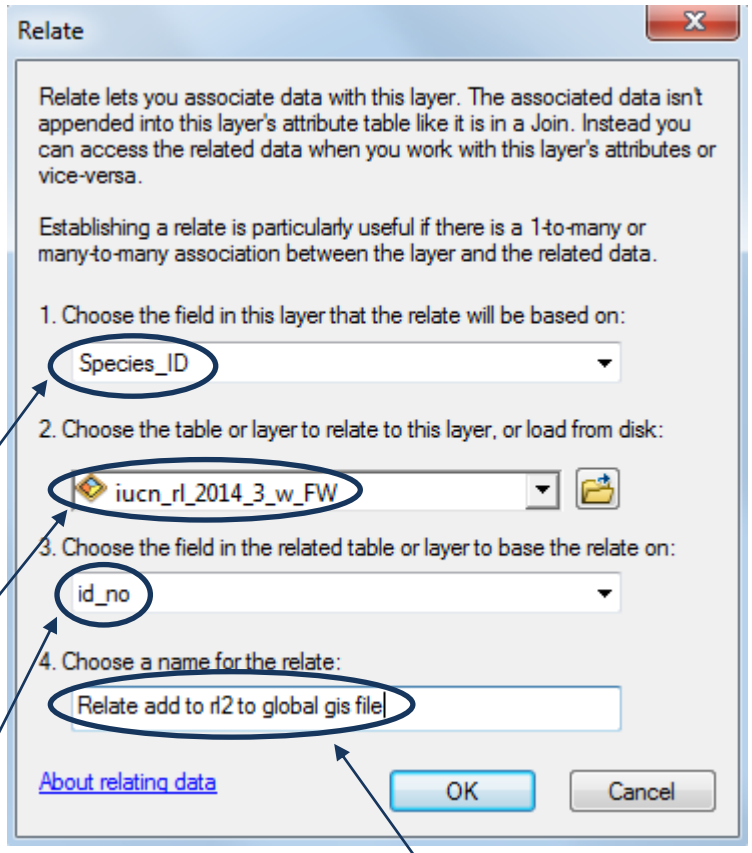
**q.** Click **Save**, then click **OK**

**r.** Click **Yes** to add the file to the ArcMap Session

**r.** Right click on your .dbf file i.e. in the example **rl2.dbf** and click **Joins and Relates>>Relate**.



In the relate window it is important to choose fields which relate the Red List species polygons and the .dbf file containing the species of interest list together, i.e. a common field to link both together. They do not necessarily have to have the same name but the information inside the field has to be common.




s. **The Field in this layer that the relate will be based on** is the field in the dbf file to use to join the table to the spatial data so in this example we will use **Species_ID.**

t. The table or layer to relate this layer is the IUCN Red List spatial data polygon file (e.g. in this example **iucn_rl_2014_3_w_FW)**

u. **The field in the related table or layer to base the relate on** is the field in the spatial dataset which relates to the field in the .dbf table (in example **id_no**)

v. Give the relate an appropriate name so it is clear what is the relate is representing

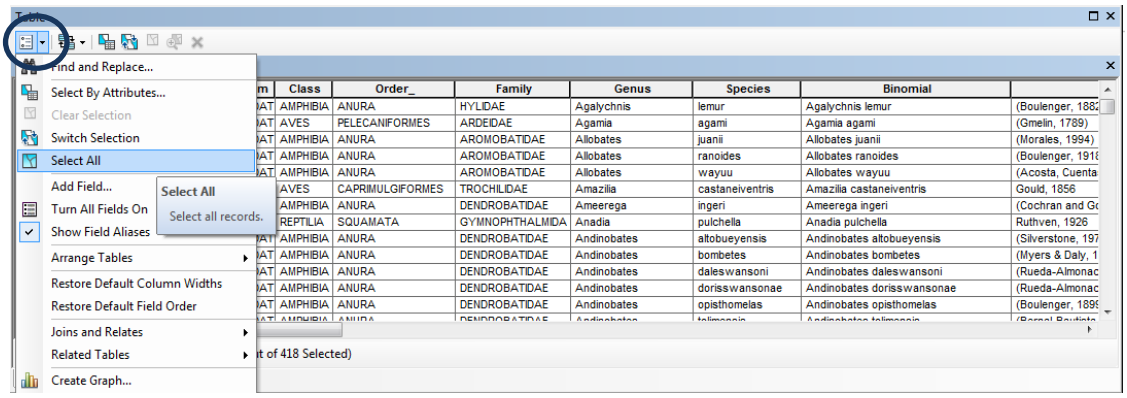
w. Click **OK**

*NOTE: Joining using Species_ID and id_no is more reliable than using the text field 'binomial'. Binomial can be used but is slower and due to there being some minor spelling inconsistencies between tables, and is therefore less likely to be able to join as many features correctly.*

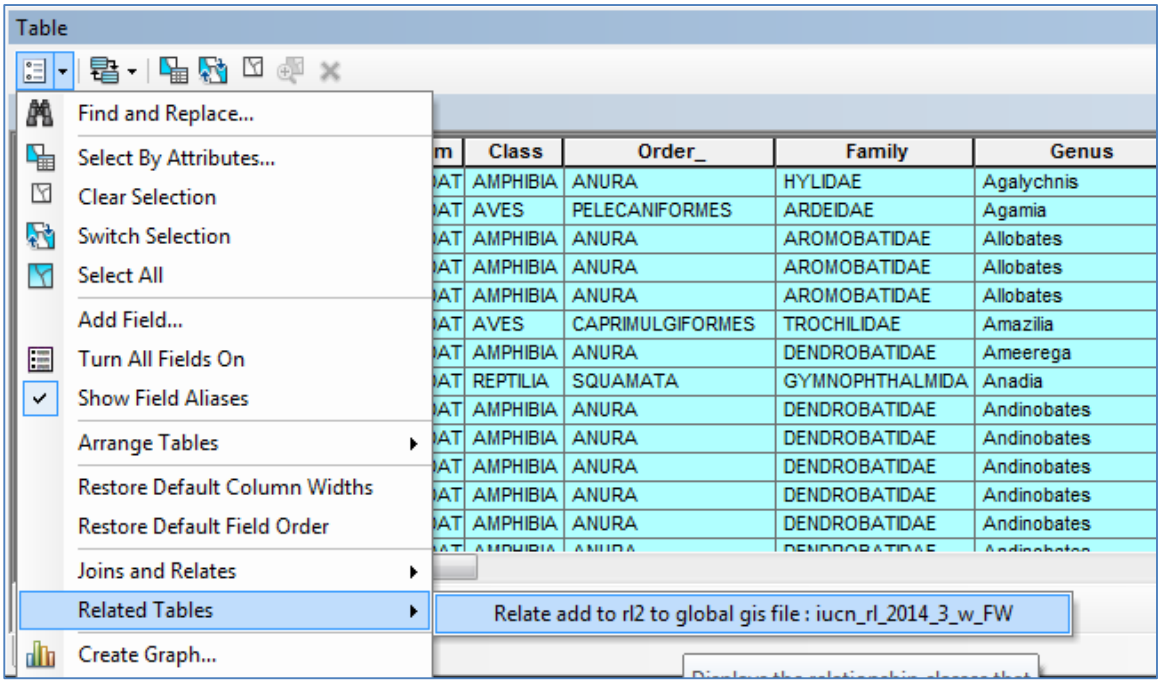
## 2.1. Using the relate to select the species polygons for species present in the table

a. Right click on your dbf file and click **Open** (e.g. in this example on rl2.dbf)

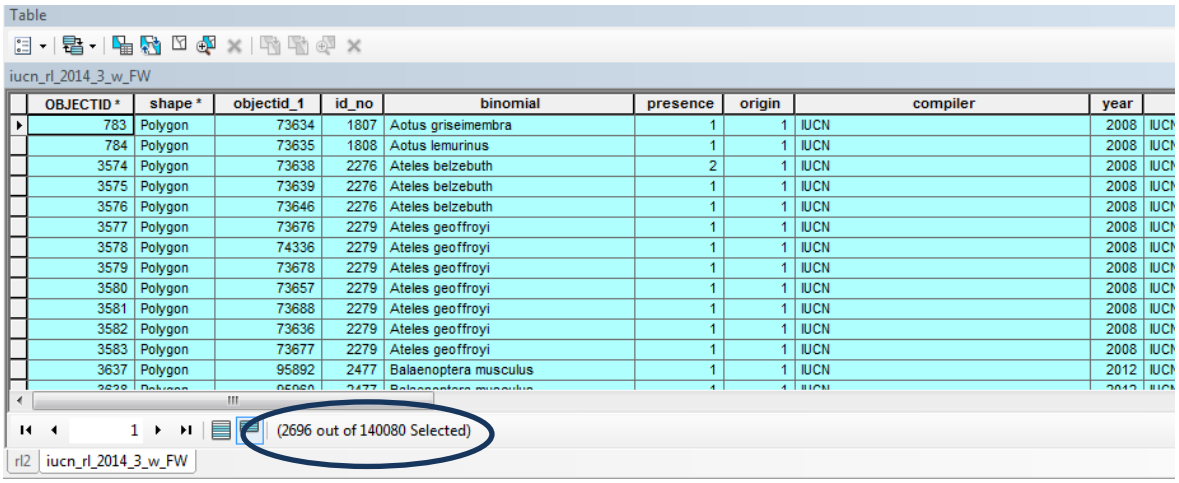
b. From the table options menu **Select all** records



**c.** From the table menu click **related tables** and click on your relate, In this example **Relate add to rl2 to global gis file: iucn_rl_2014_3_w_FW**

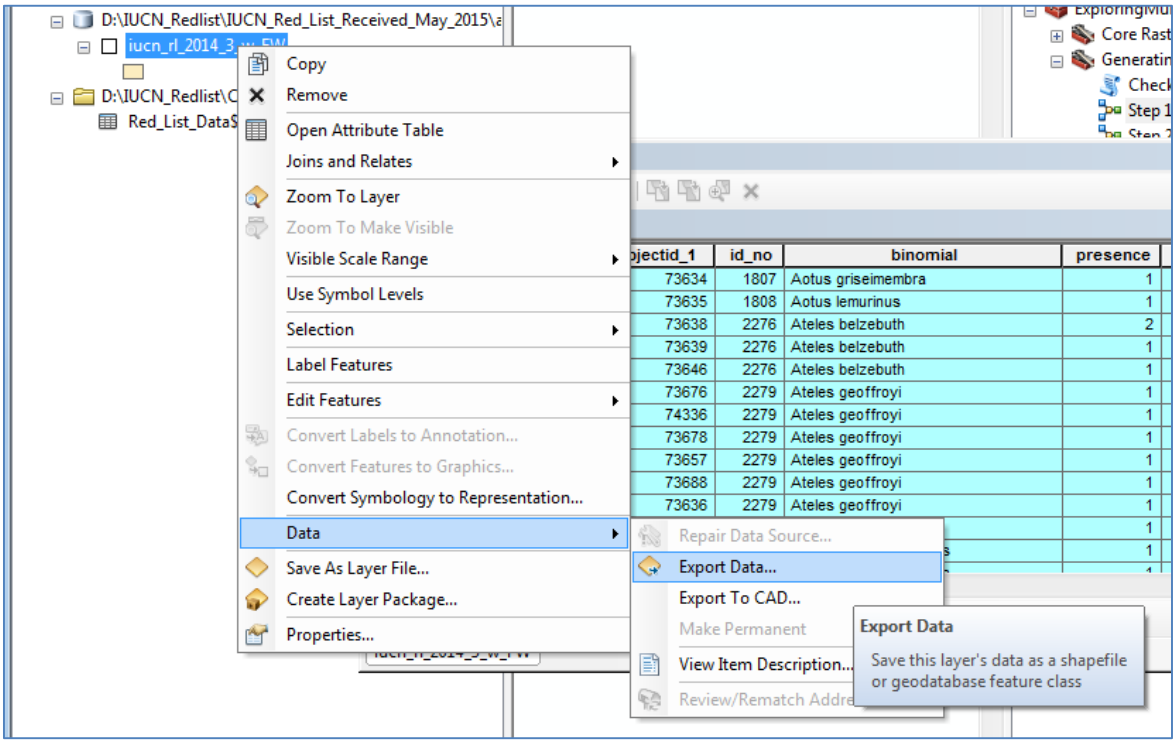



The species that were selected in your dbf file will be selected in the spatial dataset (i.e. in this case, the species polygons in **iucn_rl_2014_3_w_FW**). This selection may take several minutes, depending both on 1) how many species are being selected, and 2) whether you are working on the hard drive of your local computer or working on a network drive. The selection when finished, will show how many polygons have matched the species table (in this instance 2,696 polygons).

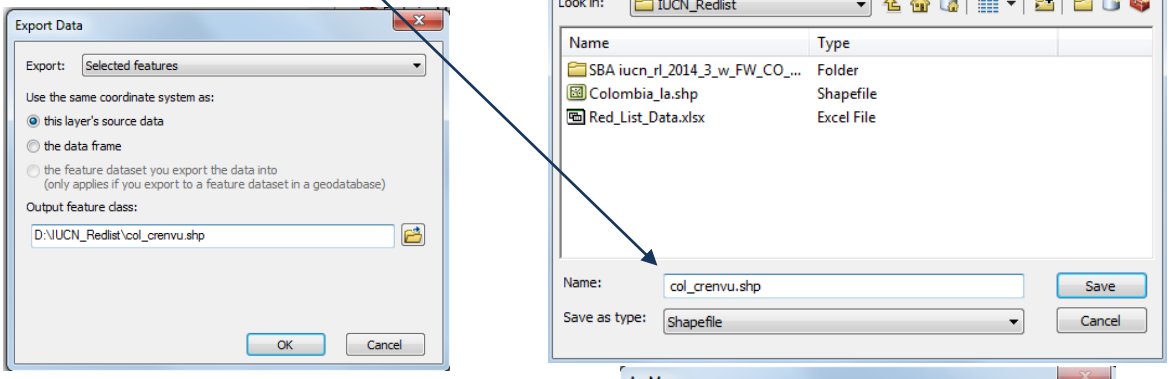



*NOTE: - If you are using a combined dataset of all species (mammal, birds, amphibians and reptiles all in a single shapefile or geodatabase), such a global dataset is very large. If processing data for a large number of species and at a global extent you may want to do some additional pre-processing steps to simplify the data first. UNEP-WCMC has developed a method to generate a simplified version of the global dataset - please contact UNEP-WCMC (ccb@unep-wcmc.org) for further information.*

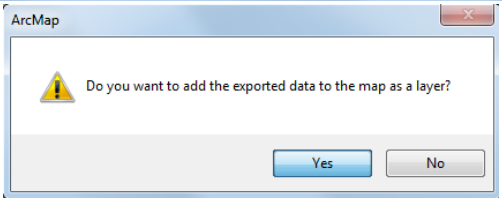
**d.** Return to the table of contents and right click on the species polygons dataset (i.e. in this example iucn_rl_2014_3_w_FW), then click **Data>>Export Data** to export the selected species polygon records to a new shapefile or geodatabase



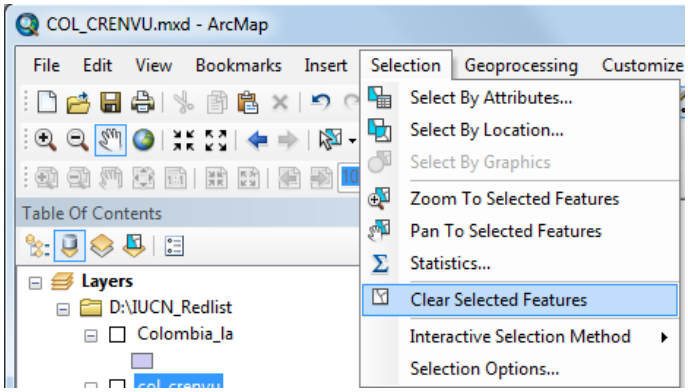

**e.** Save to a new shapefile e.g. in this example **col_crenvu.shp**.




**f.** Click **Save**, then **OK** and click **Yes** to add the exported data to the ArcMap session.



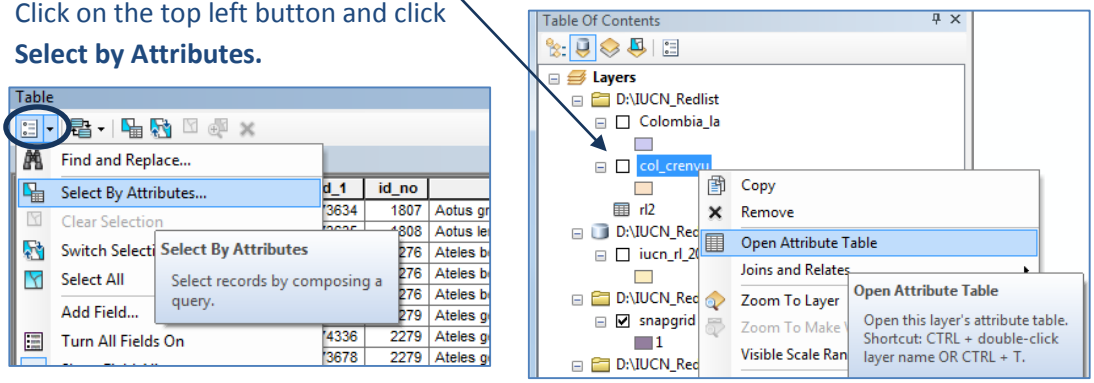

**g.** Then go to the top of the screen and from the **Selection** menu, click **Clear selected features**, so that you are no longer selecting the records in the global dataset.



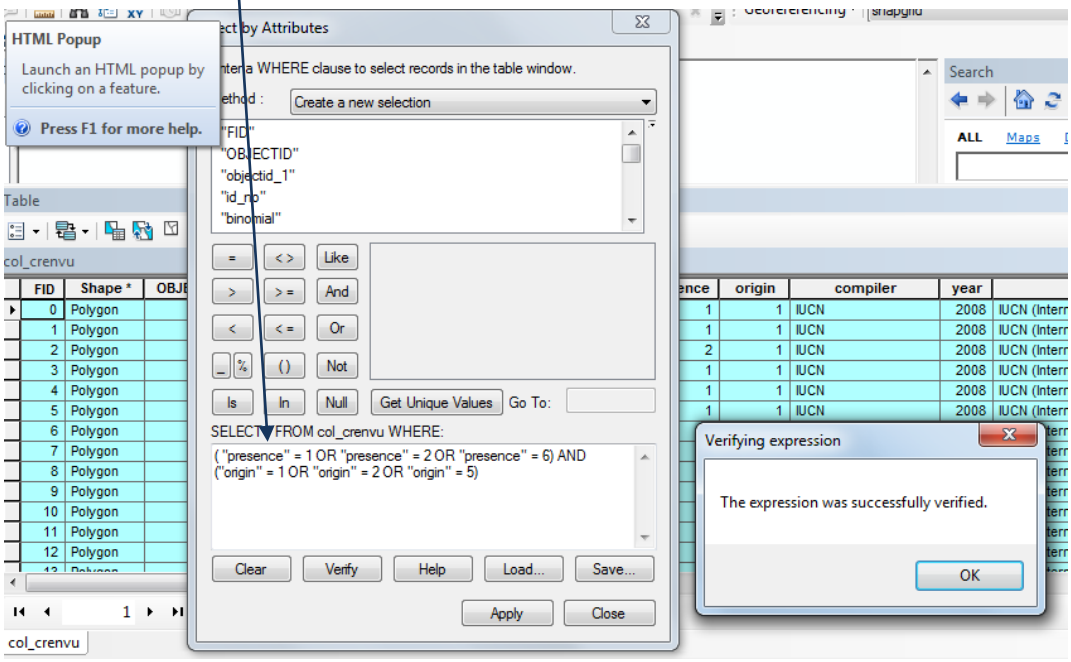
### 2.1.1. From the previous selection select out the current native species range

**a.** Right click on the newly added subset species layer **e.g. col_crenvu.shp** in this example and and click **Open attribute table.**

**b.** Click on the top left button and click **Select by Attributes.**




**c.** To only include categories as advised by IUCN Presence - 1 (extant); 2 (probably extant); 6 (presence uncertain) Origin – 1 (native); 2 (reintroduced); 5 (origin uncertain)
Put the following expression into the Select by Attributes window:-
**( "presence" = 1 OR "presence" = 2 OR "presence" = 6) AND ("origin" = 1 OR "origin" = 2 OR "origin" = 5)**




**d.** Click **Verify** to Check the expression, then click **OK** and **Apply**

**e.** Click **Close** to close the Select by Attributes window.

**f.** The attribute table will show the filtered records highlighted in blue, and the number of records that have been selected. **Close** the attribute table. **Right click** on the IUCN spatial dataset (e.g. **col_crenvu.shp)** and Click **Data>>Export Data.**

**g.** Ensure that you are exporting the **selected features,** then **save** the file with a new name, **e.g. col_crenvu_POselection.shp** (as file type shapefile) and click **Save.** It will ask you if you would like to add the new file to dataframe. Click **Yes.**

### 2.1.2. From the previous selection select out only terrestrial species ranges

**a.** Right click on the **newly added subset species layer** (e.g. **col_crenvu_POselection.shp** in this example) and and click **Open attribute table.**

**b.** Click on the top left button and click **Select by Attributes.**

**c.** To only include species which are terrestrial put the following expression into the Select by Attributes window:
**"biome_terr" = 't'**

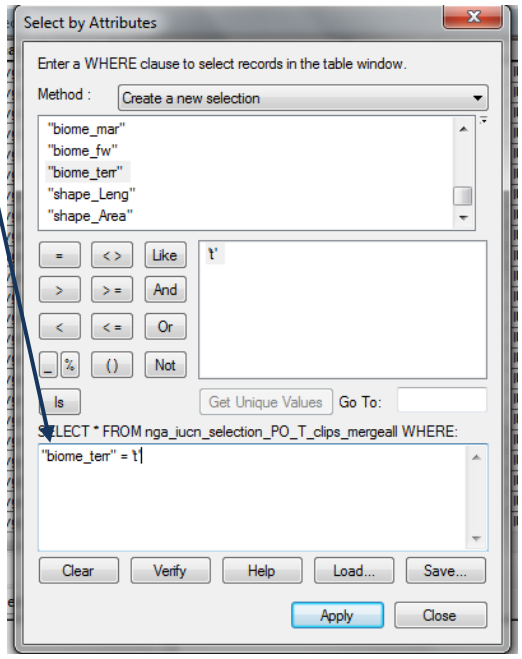
**d.** Click **Apply**

**e.** Click **Close** to close the Select by Attributes window.

**f.** The attribute table will show the filtered records highlighted in blue, and the number of records that have been selected.

**g.** Close the attribute table. **Right click** on the IUCN spatial dataset e.g. **col_crenvu_POselection.shp** in this example and **Click Data>>Export Data.**

**h.** Ensure that you are exporting the **selected features,** then **save** the file with a new name, **e.g. col_crenvu_POselection_T.shp** in this example and **Click Save.** It will ask you if you would like to add the new file to dataframe. **Click Yes.**




## 2.2. Instructions for adding the ExploringMultipleBenefits ArcGIS toolbox to ArcMap

The ExploringMultipleBenefits toolbox is designed to make spatial analysis steps quicker and easier to perform. In the standard ArcGIS toolbox there are multiple ways in which users can overlay datasets. Without the ExploringMultipleBenefits toolbox, users would need to find relevant tools, and understand how and when to use them. With Raster analyses in particular, it is important to use and apply appropriate environment settings to the data which are often hidden and forgotten. The ExploringMultipleBenefits toolbox not only standardizes the way that analysis is undertaken in a series of simple steps, but reduces the risk of errors.

The tools are designed to allow users to create their own workflows using combinations of tools in different orders. Each tool clearly outlines what user inputs are required for each of the defined 'parameters'. This information is also stored in the help pages, clearly visible from within the ExploringMultipleBenefits toolbox. There are also a series of modules which are designed to run a specific analysis step by step.

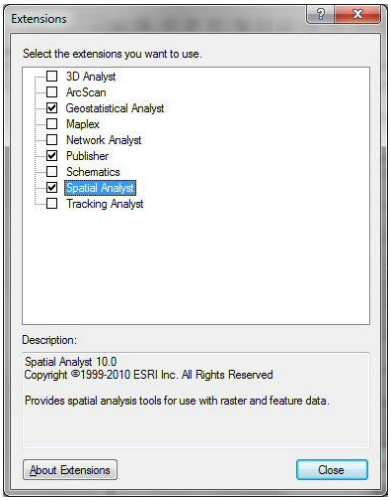
The following steps need to be taken in order to use the ExploringMultipleBenefits toolbox, available at http://bit.ly/GIStools-redd.

**a.** Unzip the **ExploringMultipleBenefits toolbox** and **save the file to chosen location**.

Note: the default area to which ArcGIS saves toolboxes is **c:\Documents and Settings\<username>\Application Data\ESRI\ArcToolbox\My Toolboxes.**

**b.** Make sure you keep the toolbox in a **sub-folder called ExploringMultipleBenefitsTools** otherwise the tools may show broken links.

*It may be preferable to save the toolbox within a current project folder.*

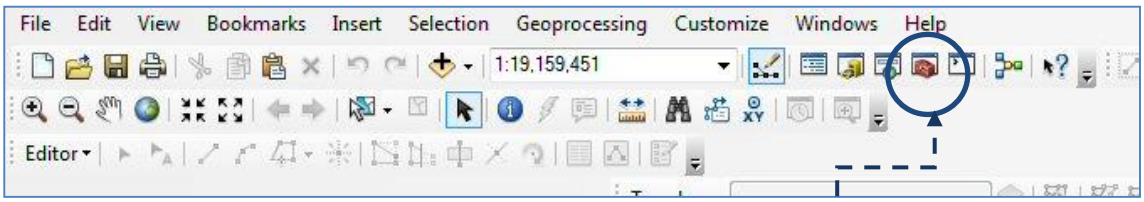



**c.** **Open the ArcMap** software and **activate** the spatial analysis extension by clicking on **Customize>>Extensions** and ensure that the **Spatial Analysis** extension is **ticked**.

**d.**

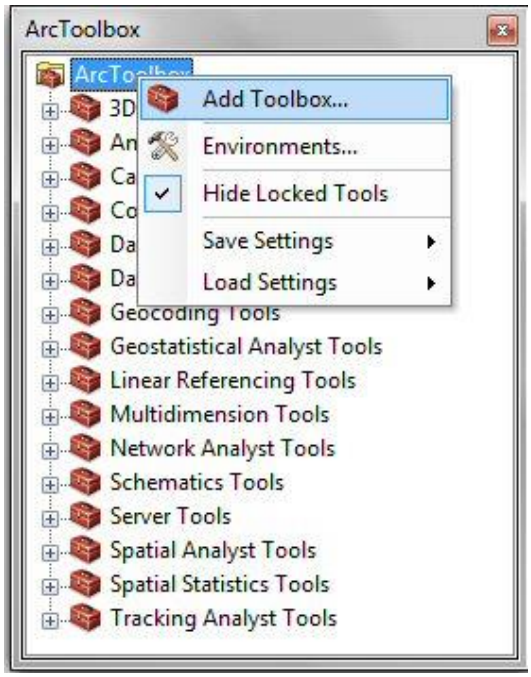
*Note: This extension is required to run the ExploringMultipleBenefits tools, therefore if this extension is not available the software vendor will need to be contacted to obtain a licence.*

**e.** Next you need to **Add** the **ExploringMultipleBenefits toolbox** to **ArcToolbox**.



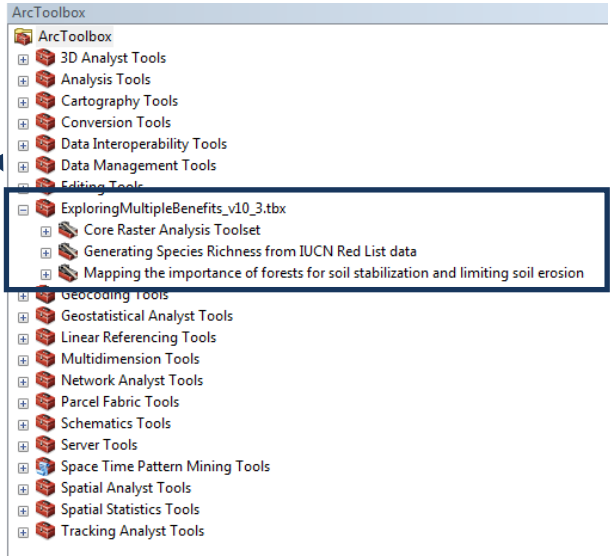

In ArcMap if the ArcToolbox is not already open, **click on the red toolbox button located in the main** horizontal menu bar or from the main menu, click on **Geoprocessing>>ArcToolbox**. The ArcToolbox window will open.

**f.** Right click on **ArcToolbox** and click **Add Toolbox**




**g.** Navigate to the folder in containing the toolbox (location determined in step a.) and click open

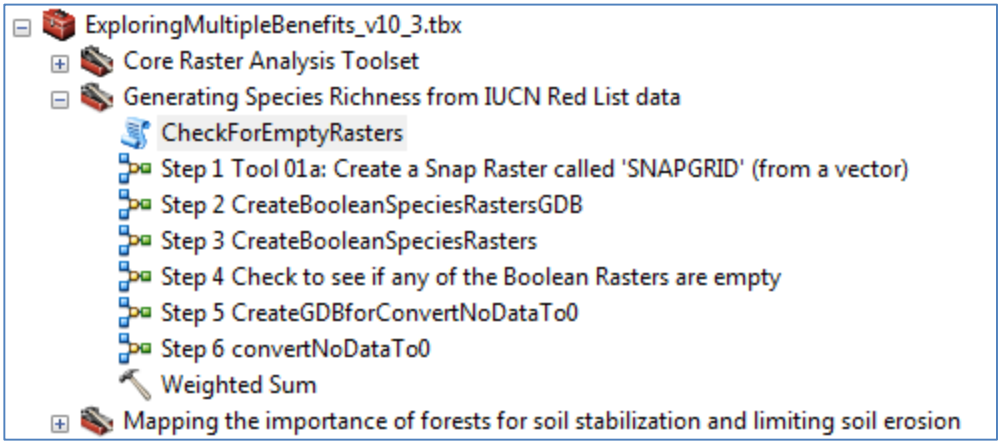
The toolbox will appear in the ArcToolbox




**h.** **Click** the + button to expand the toolbox to see the tools.

## 2.3. Running the species richness models in the Exploring multiple benefits toolbox

**a.** Expand the module **Generating Species Richness from IUCN Red List Data**.

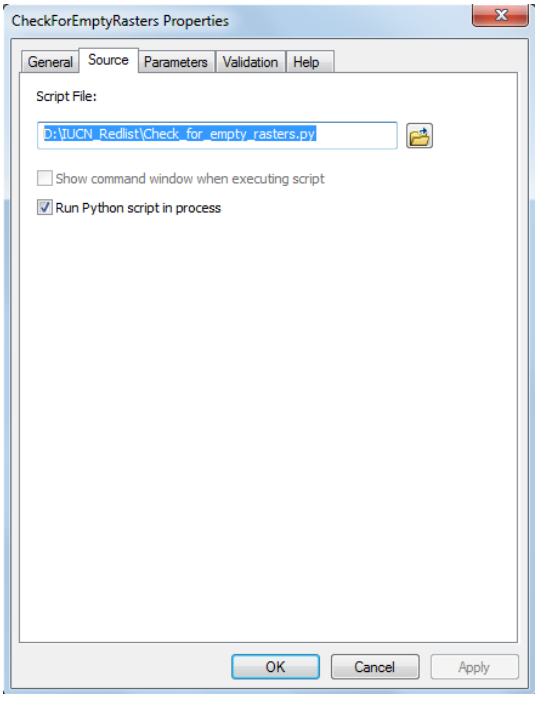



**b.** The script **CheckForEmptyRasters** is used the Step 4 model. Right click on the script and click **properties**.

**c.** Click on the **Source** tab

**d.** Check that the Script File is pointing to the location of the **Check_for_empty_rasters.py**.

**e.** Click **OK**



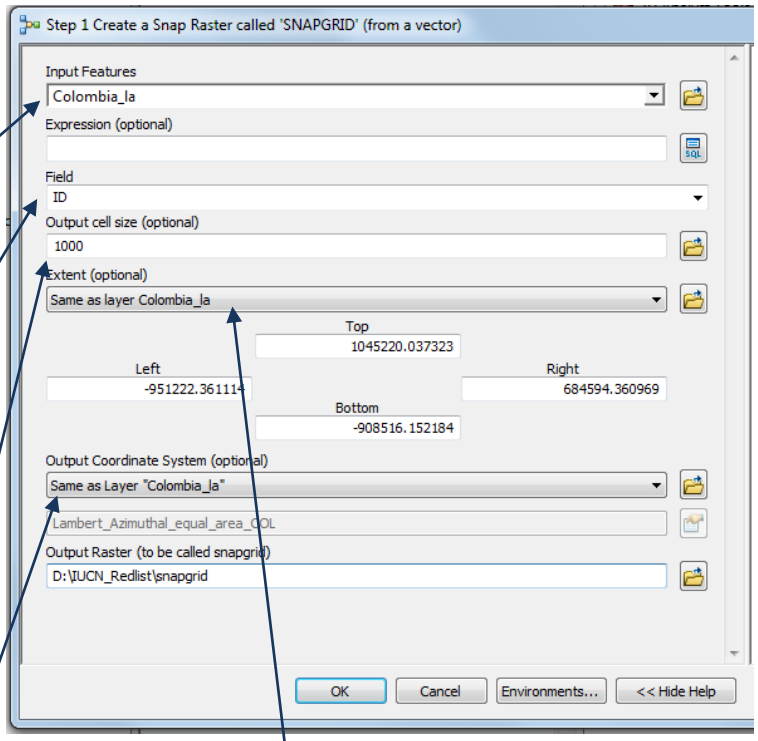

Now you are ready to run the models starting at Step 1.

### 2.3.1. Creating a snapraster

We want to create a snap raster in the projection used by the Colombia data – (i.e. Lambert Azimuthal Equal area, central meridian -73 degrees, Latitude of Origin 4 degrees.)

*NOTE: If you already have a raster which you want to use as your 'area of interest', rather than creating a new raster from a shapefile as is done in this step, and provided that it is the right cell size, you may want to skip Step 1. Alternatively if you want the cells of your final species richness raster to align to an existing raster, use **Tool 01b: Create a Snap Raster called 'SNAPGRID (from a raster**) from the **ExploringMultipleBenefits_v10_3.tbx** toolbox near the top of the **Core Raster Analysis Toolset**.*

**a.** Double click on **Step 1 Create a Snap Raster called 'SNAPGRID' (from a vector)** to open the tool dialogue




**b.** The input features is the area of interest file e.g. in this example from **Colombia_la.shp**.

**c.** Chose a numeric field for the **ID**. As the snap raster is only being used for setting the extent and snapping environment it does not matter what this field contains.

**d.** Chose a **cell size** for the analysis. The units are in the projection of your area of interest file.

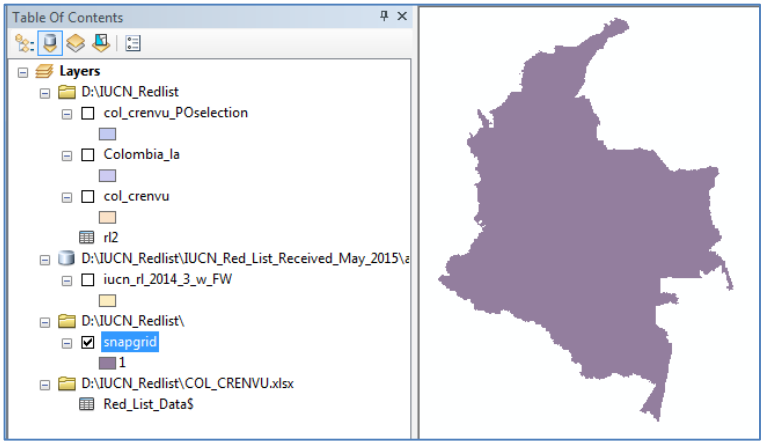
**e.** Set the extent to be the same as your area of interest file.

**f.** Set the output Coordinate system to be the same as your area of interest file.

**g.** Navigate to an output folder and call the output raster snapgrid.

**h.** Click **OK** to run Step 1.

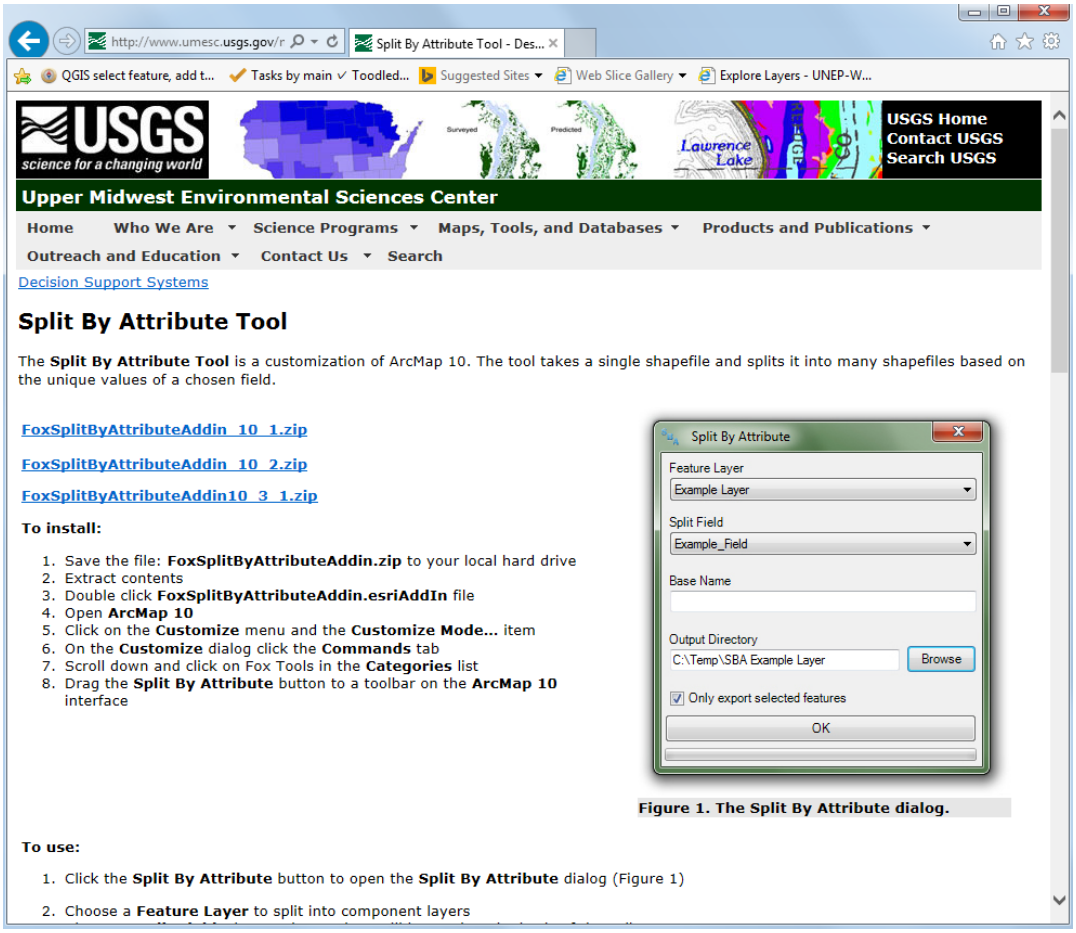
The resulting **snapgrid** is added automatically to the .mxd file in Arcgis 10.3, but in earlier versions you may have to find snapgrid and add it to the .mxd manually. If this has to be done, do not generate pyramids, if asked if you would like to do so.



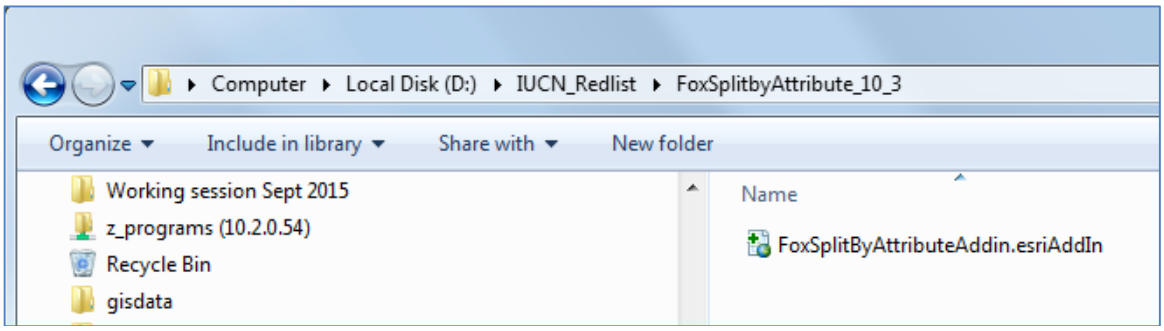
### 2.3.2. Split the species data into individual species files

The rest of the steps need the species dataset to be split into individual species (i.e. a single dataset per species. This will allow us to subsequently generate a 'heat' map showing how many species overlap in a particular area.

**a.** First, we need to download and use the following tool
http://www.umesc.usgs.gov/management/dss/split_by_attribute_tool.html

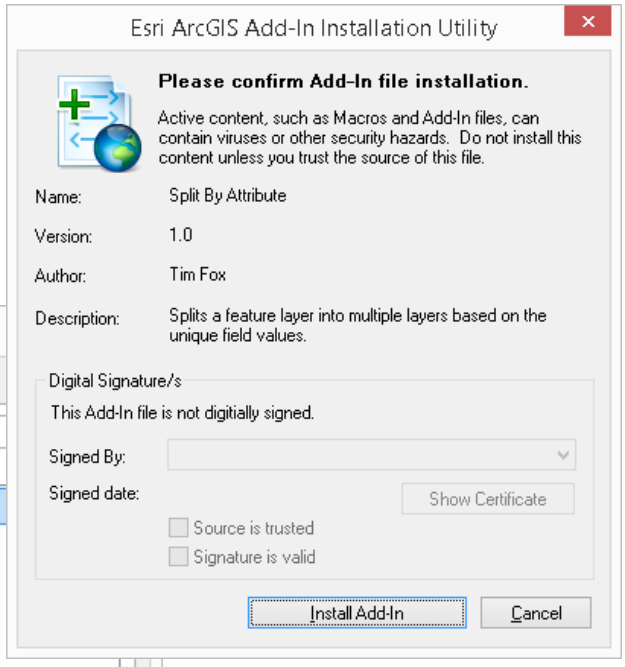


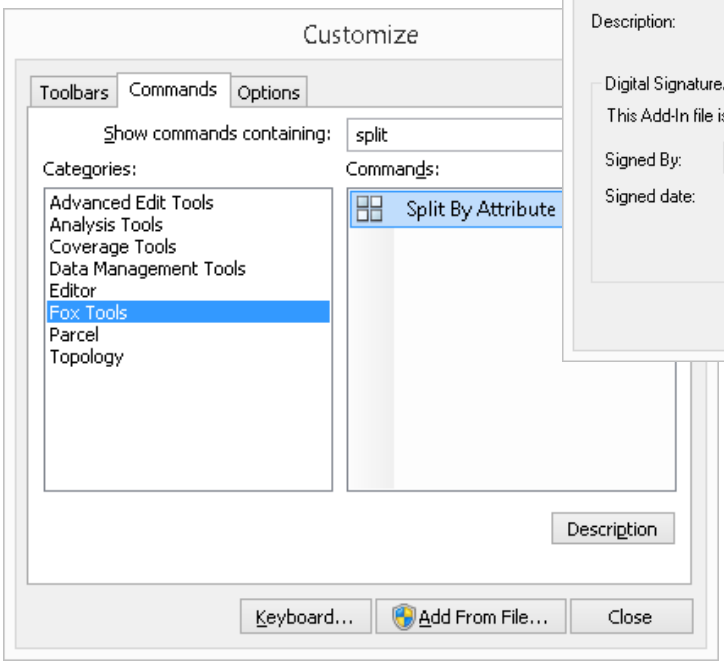

**b.** Select the version that matches your ArcGIS software. In this example we are using ArcGIS 10.3 so we download **FoxSplitByAttributeAddin10_3_1.zip** and save it into a chosen folder. In this example we have placed it into D:\IUCN_RedList. It puts it into a subfolder called **FoxSplitbyAttribute_10_3**




**c.** Double click on the split by attribute tool to install it

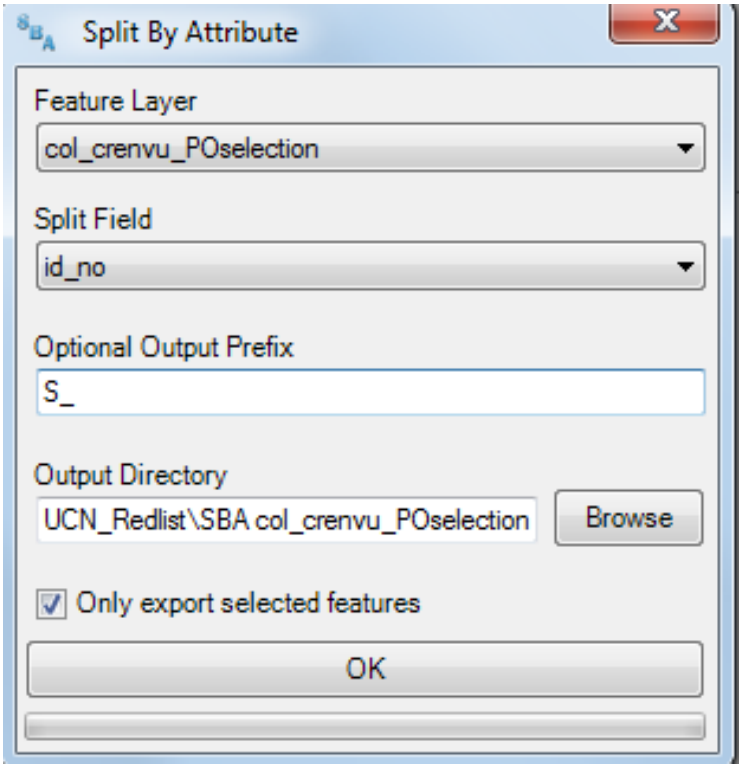
d. Click **install Addin**
e. In ArcMap click on **customize >> customise mode**
f. Click on the **commands tab** and type **split** in the box to filter. You should see Foxtools. Click on it.

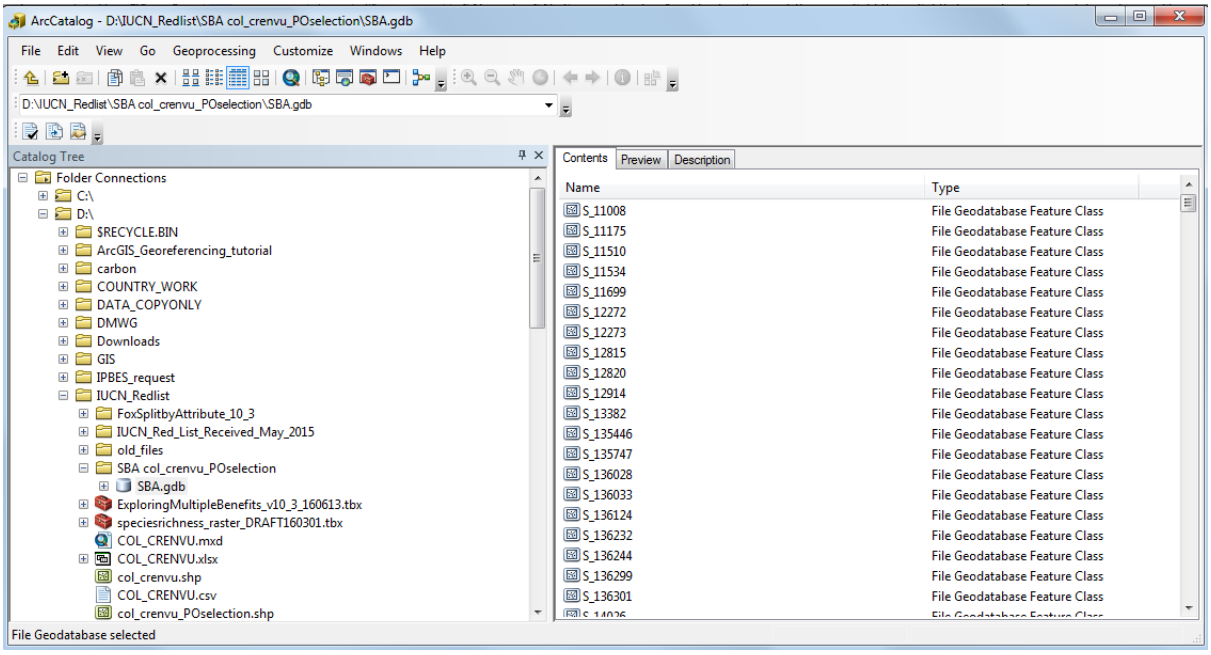


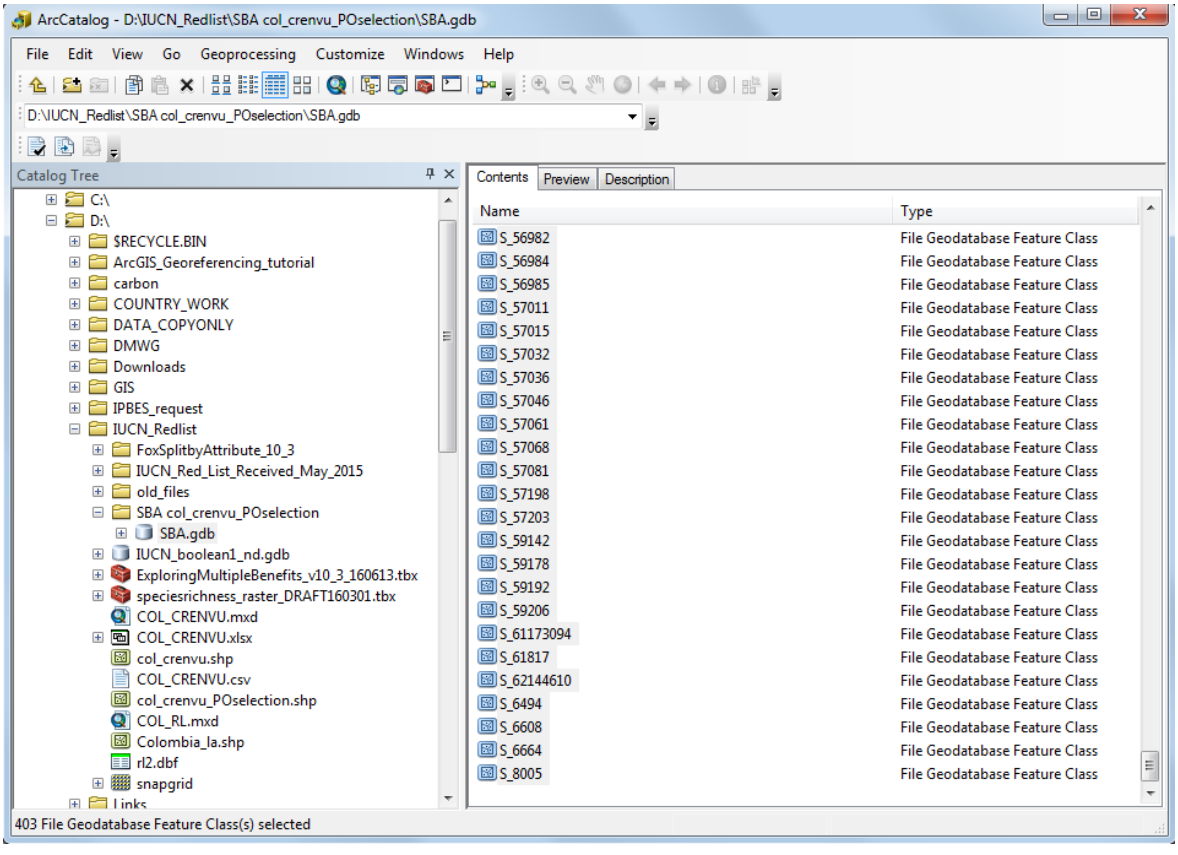

g. **Drag the icon and drop** into one of your menu bars
h. Click **Close**
i. Double click on the icon to run the tool

j. The feature layer is the one containing your species EOO polygons
k. The split field is the species id (id_no)
l. You can put a **prefix** e.g. **S_** (otherwise the names will just be the species id number and raster's starting with a number may cause trouble
m. Navigate to the folder you want to place it in. The tool will **automatically create a folder** called **SBA_name of your input file**
n. Click **OK** to finish. Within the File Geodatabase, the different species have now each got individual layers (see below):



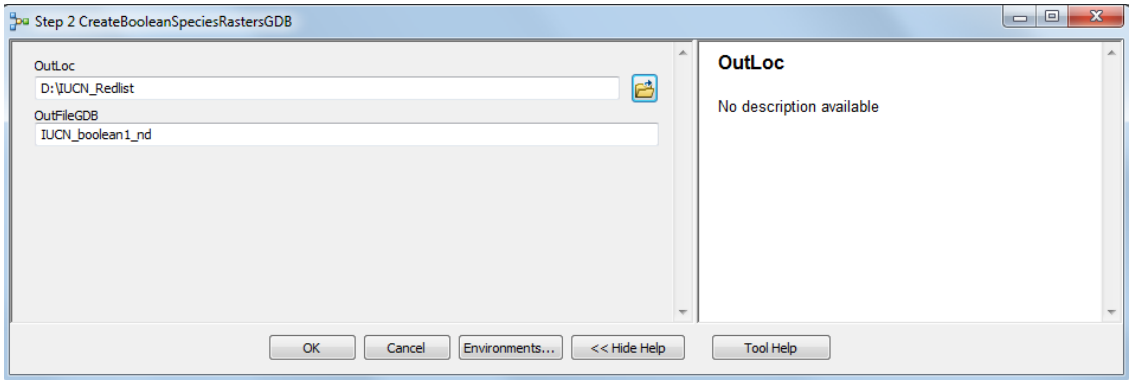



Check the number of Species layers in SBA.gdb. To do this, open ArcCatalog, **navigate to the SBA geodatabase e.g. in this example located in D:\IUCN_Redlist\SBA col_crenvu_POselection\SBA.gdb**, click on the **first file under Contents** (in this instance S_11008), then **scroll down to the bottom file** (in this instance S_8005), **hold the up arrow on your keyboard**, and click on the last file e.g. S_8005. The total number of layers is listed at the bottom of the ArcCatalog window. In this instance **403 layers were generated. Compare this to the original list e.g. rl2.dbf.** In this example there were originally 418. The 15 missing files will mean that either there was no polygon or that the polygon fell outside of the area of interest.



### 2.3.3. Create Boolean species rasters

**a.** Double click on **Step2 CreateBooleanSpeciesRasterGDB**




**b.** Specify and output location in the **OutLoc** tab.

**c.** Leave the filename as the default I**UCN_boolean1_nd**.

**d.** Click **OK** to run.

*This step only takes a few seconds to run as it simply creates an empty file Geodatabase ready for the next step.*

**e.** Now double click on **Step 3 CreateBooleanSpeciesRasters**. This model converts polygons to rasters for all the species in your SBA.gdb

**f.** Select the SBA geodatabase

**g.** Set the **Output Coordinate system, cell size, Extent, Mask and Snap Raster** to be **Same as Layer snapgrid.**

**h.** Then click Close when finished.

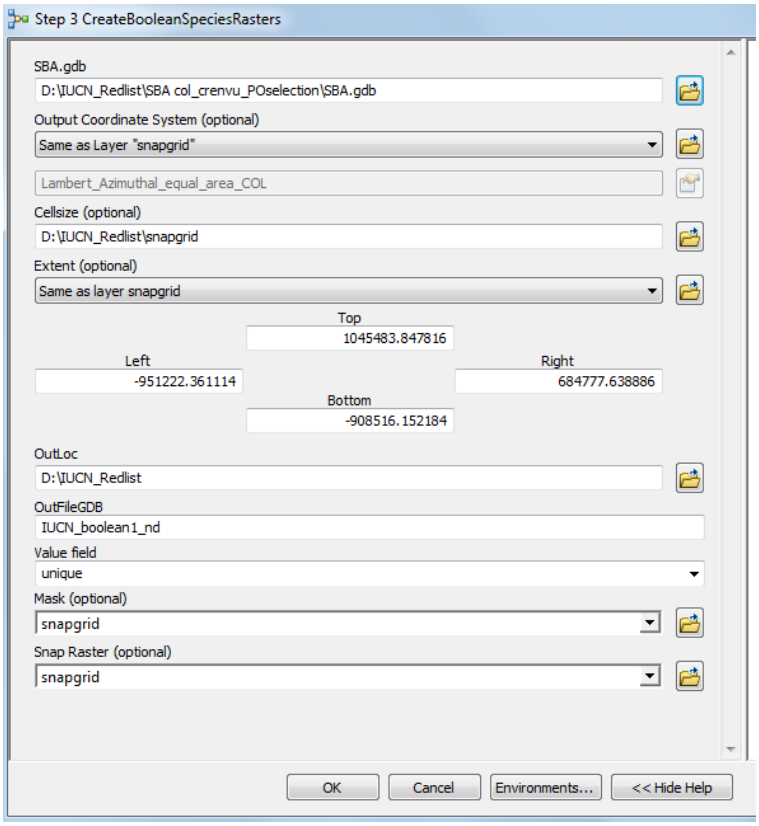
**i.** Check the number of rasters produced and compare with the original number of layers.

**j.** **Outloc** is the location you specified in step b)

**k.** The **OutfileGDB** is **IUCN_boolean1_nd**

**l.** **The value field leave as unique**

**m.** Click **OK** to **run the step**




**n.** Again, check the number of rasters using ArcCatalog in the same way. There should be the same number of rasters (in this example 403).

*This process took about half an hour to run in this example*

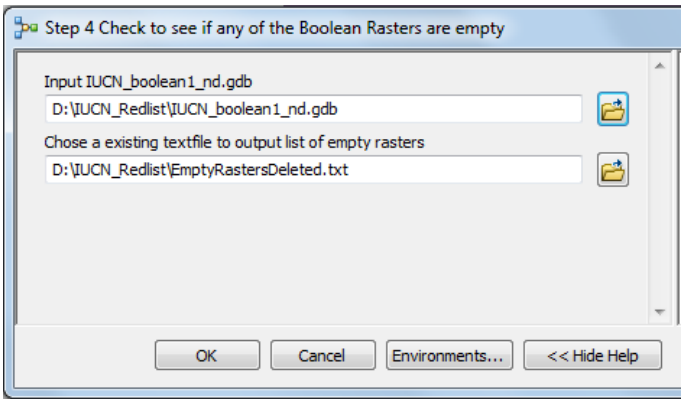
### 2.3.4. Check to see if any of the Boolean Rasters are empty

The next step is to check to see if any of the outputs from the previous step are blank as this would cause trouble in step 2.3.5. Blank outputs mean that the species polygon did not cross into the area of interest. This step deletes any of these empty rasters, and lists these in a file called **EmptyRastersDeleted.txt**.

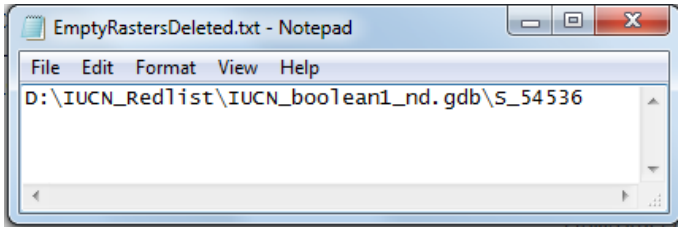
**a.** Double click on **Step 4 Check to see if any of the Boolean Rasters are empty** and navigate to the File geodatabase containing the rasters created in step 3 (**IUCN_boolean1_nd** ) and click **OK**.

**b.** Navigate to the **IUCN_boolean1_nd.gdb**

**c.** Outside of ArcMap, create a text file called **EmptyRastersDeleted .txt** and in ArcMap point step 4 to this file



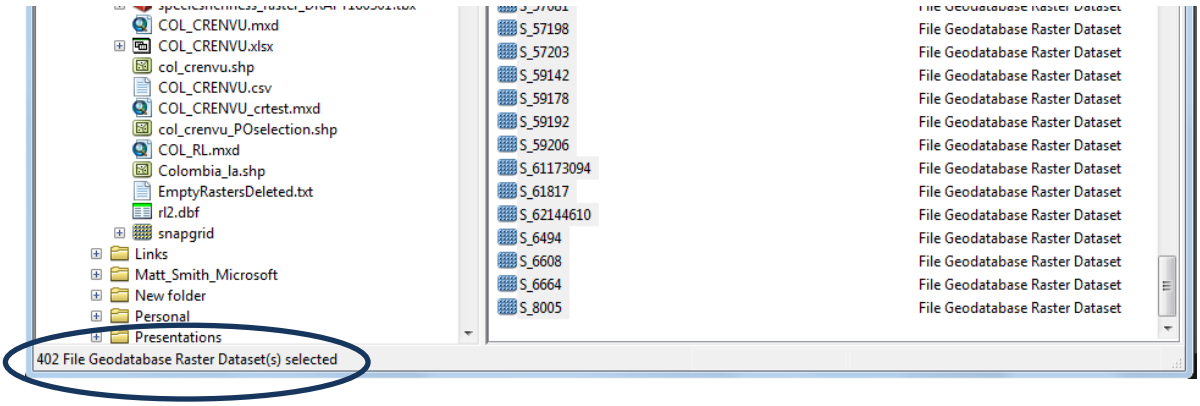

The model will delete any empty rasters and will list them in a text file




*This process takes around twice the length of time as the conversion to rasters. For this example, it took just under an hour.*

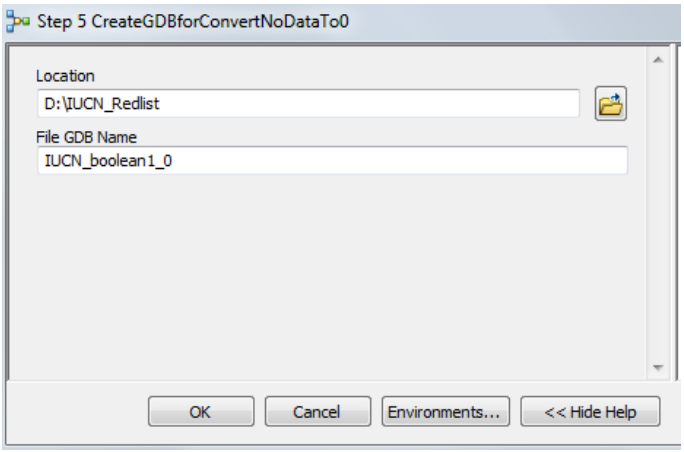
**d.** Click **Close** and then again check the number of rasters in the output geodatabase (**IUCN_boolean1_nd.gdb)** in ArcCatalog.

*In this example there are **402** rather than 403 rasters, indicating that one of the rasters were empty. This is confirmed by the one reference in the **EmptyRastersDeleted** text file which indicated which species was deleted.*



### 2.3.5. Convert no data to 0 in Boolean Rasters

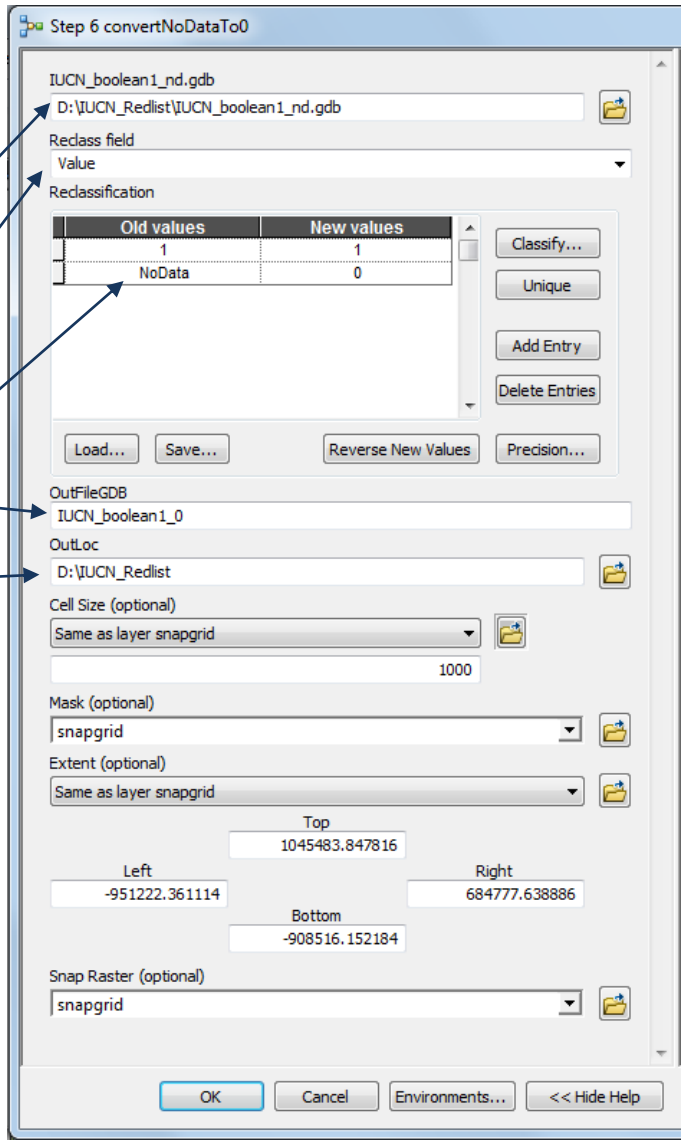
This next step will create a new file GDB contains the same rasters as the previous step but they will all have had their no Data values converted to 0 (zero). This is necessary to enable the raster to be successfully summed in the final step.




a. Double click on **Step5 CreateGDBforConvertNoDataTo0**
b. Specify and output location in the **OutLoc** tab.
c. Leave the filename as the default **IUCN_boolean1_0**.
d. Click **OK** to run.

*This step only takes a few seconds to run as it simply creates an empty file Geodatabase ready for the next step.*

o. Now double click on **Step 6 ConvertNoDataTo0**. This model converts no data values to 0 in all the species rasters in the **IUCN_boolean1_nd.gdb**
p. Select the **IUCN_boolean1_nd** geodatabase
q. Set the **reclass field** to **Value**
r. Set the reclassification, 1 to remain as 1 and **no data to become 0**.
s. The **OutfileGDB** is **IUCN_boolean1_0**
t. **Outloc** is the location you specified in step b)
u. Set the **cell size, Extent, Mask and Snap Raster** to be **Same as Layer snapgrid.**
v. Then click Close when finished.
w. Check the number of rasters produced and compare with the original number of layers.
x. Click **OK** to **run the step**
y. Again, check the number of rasters using ArcCatalog in the same way. There should be the same number of rasters (in this example 402).

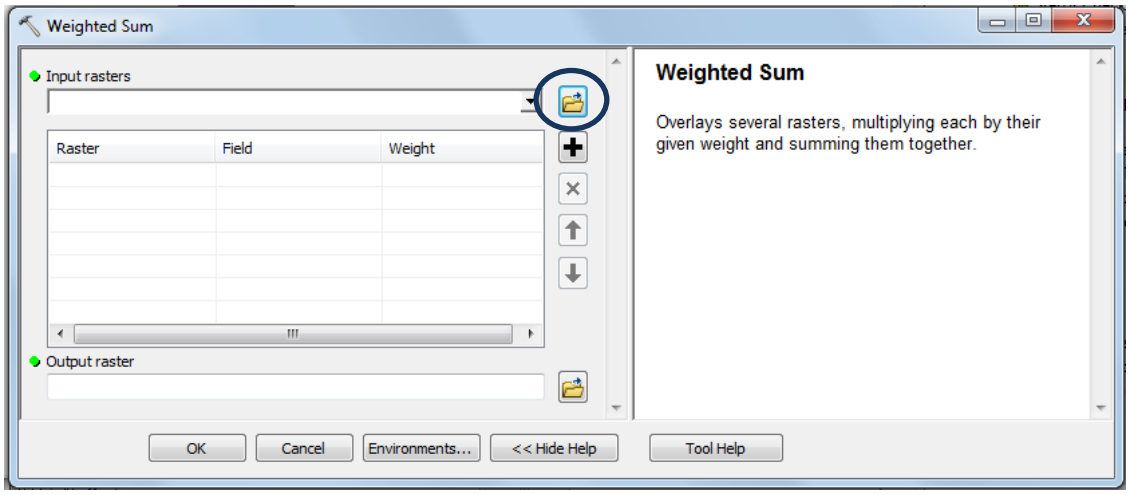


### 2.3.6. Sum the raster to create a species richness dataset

The last step is to run the weighted sum. All the datasets will be given the same weight so the tool will just sum each raster together.

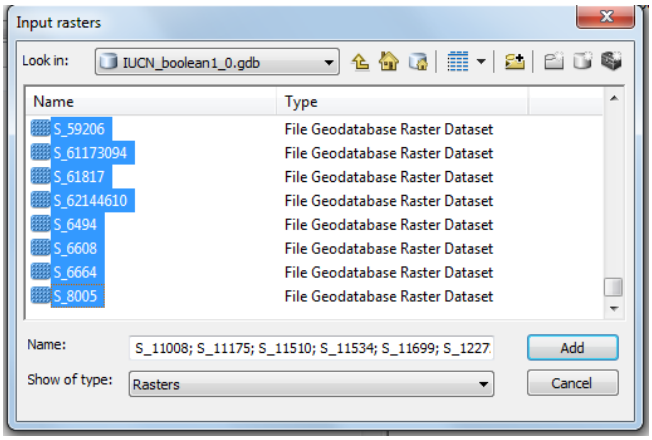
**a.** Double click on the Weighted Sum tool

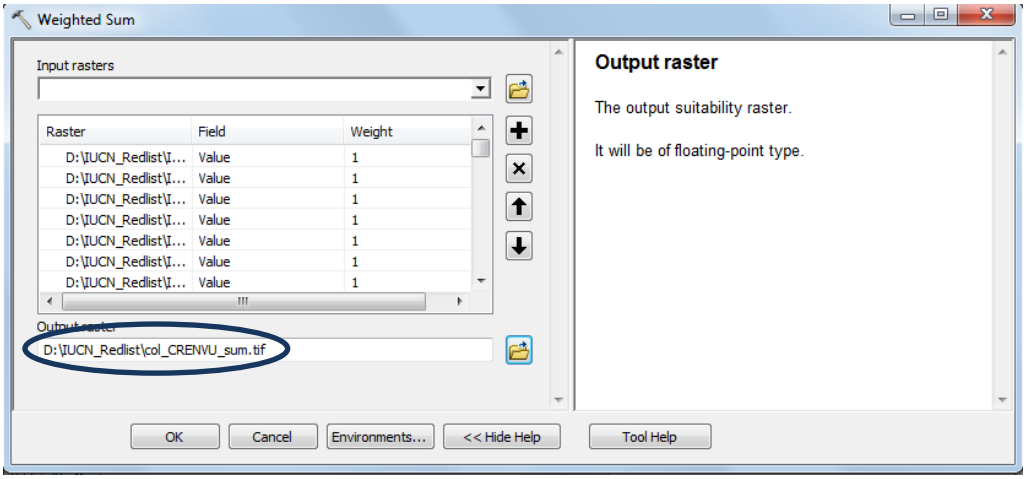
**b.** Click the folder button to navigate to the **IUCN_boolean1_0** geodatabase to pick up all the raster files.




**c.** Hold down **shift** and select all the files.

**d.** Click **Add**




**e.** Navigate to an **output folder** and give the species richness output raster a name.

**f.** Click **OK** to run this final step

*The final dataset can then be symbolized and placed in a map layout as in the example below. In this example the values refer to the total number of Critically Endangered, Endangered and Vulnerable species whose ranges include each grid cell. Remember that this does not guarantee species presence.*

### Example Species Richness Map