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

STEP-BY-STEP TUTORIAL: EXTRACTING AND PROCESSING IUCN RED LIST SPECIES DATA USING A RASTER METHOD IN QGIS 2.8

UN-REDD PROGRAMME

FAO UNDP UNEP

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 the United Nations Environment Programme (UNEP).

The United Nations Environment Programme World Conservation Monitoring Centre (UNEP-WCMC) is the specialist biodiversity assessment centre of the United Nations Environment Programme (UNEP), the world's foremost intergovernmental environmental organisation. The Centre has been in operation for over 30 years, combining scientific research with practical policy advice.

Prepared by Corinna Ravilious

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

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Contents

1. Introduction

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. 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.

Open Source GIS software can be used to undertake spatial analysis of datasets of relevance to multiple benefits and environmental safeguards for REDD+. Open-source software is released under a license that allow software to be freely used, modified, and shared (http://opensource.org/licenses). Open Source GIS software can be used to undertake spatial analysis of datasets of relevance to multiple benefits and environmental safeguards for REDD+. Open-source software is released under a license that allow software to be freely used, modified, and shared (http://opensource.org/licenses). Therefore, using open source software has great potential in building sustainable capacity and critical mass of experts with limited financial resources.

This tutorial demonstrates how a species richness grid could be created using species range data from the IUCN Red List (IUCN, 2013). It provides full instructions of how to select and 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 QGIS, an open-source desktop GIS software.

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

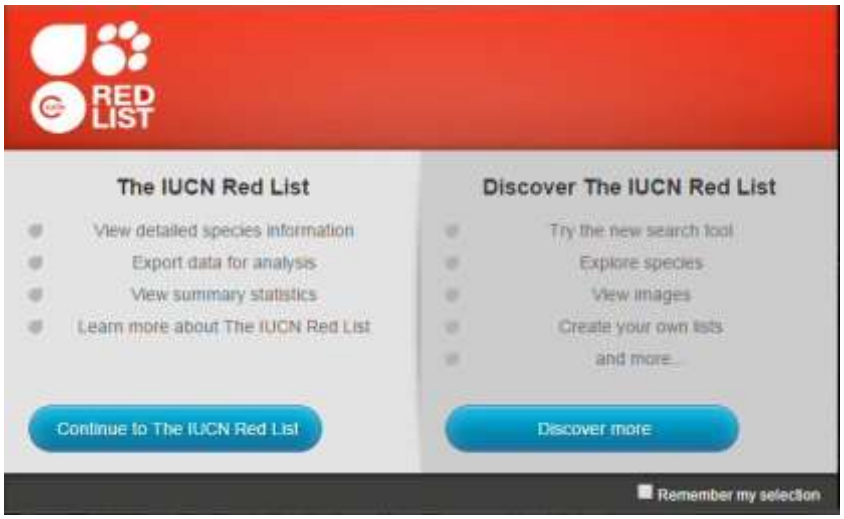
2.1. Selecting and downloading species data from the IUCN Red List website

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.

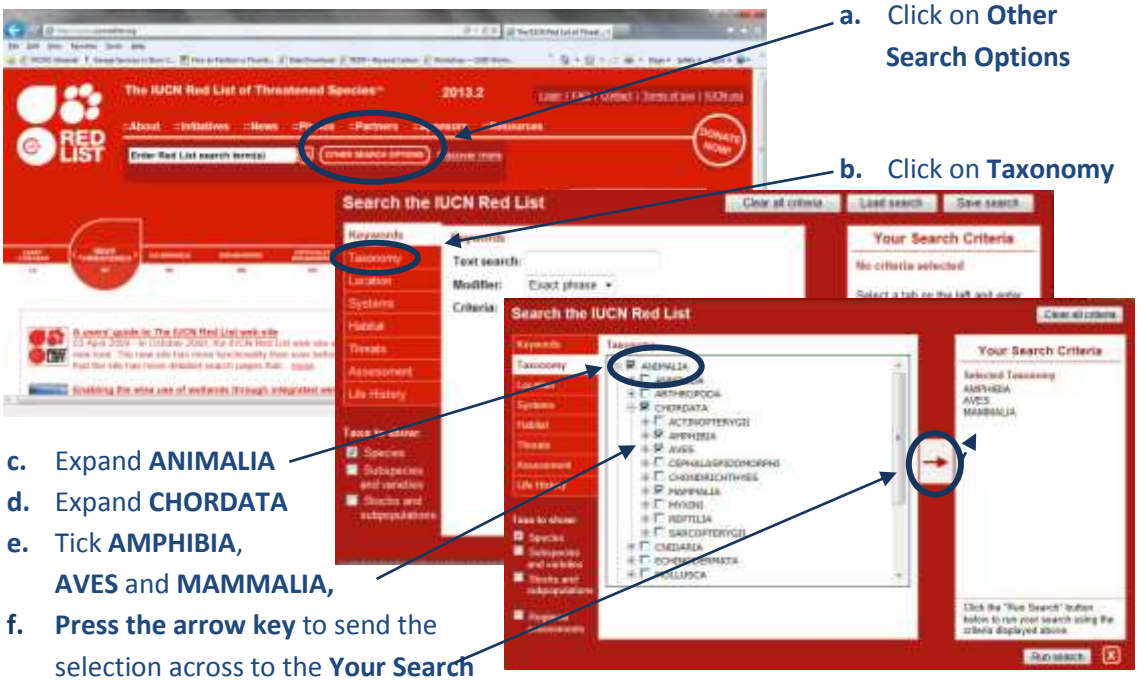
2.2. Searching for non-spatial data

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

Click on **continue to the IUCN Red List**



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



a. Click on **Other Search Options**

b. Click on **Taxonomy**

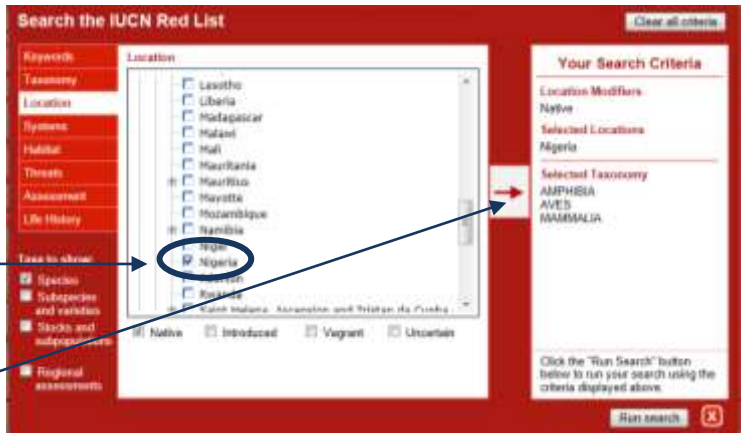
c. Expand **ANIMALIA**

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

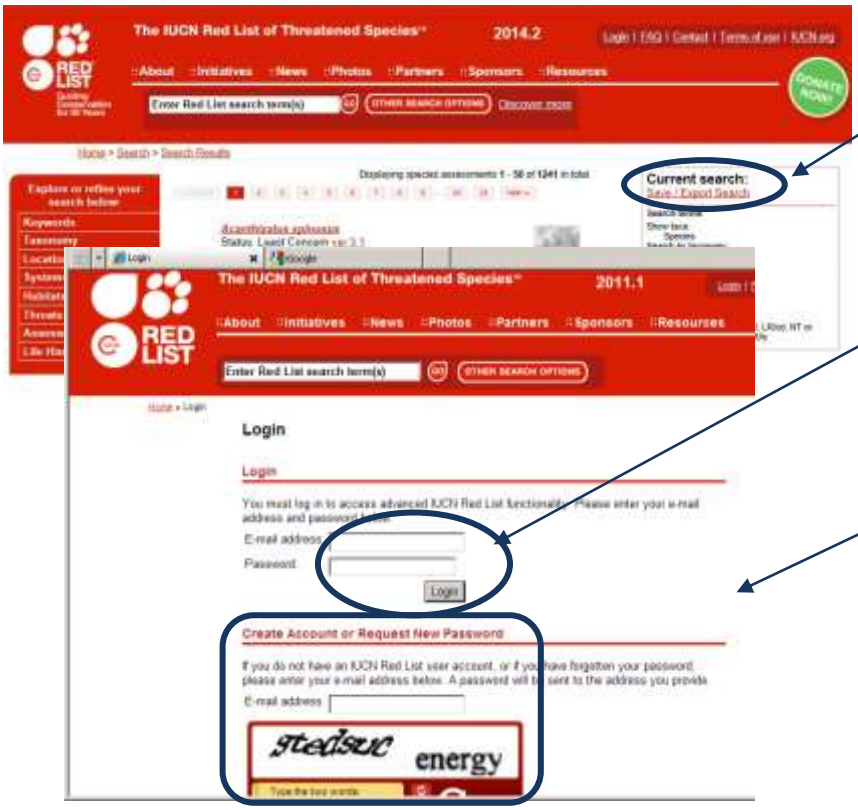
l. Click **Run search**

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.

2.3. 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

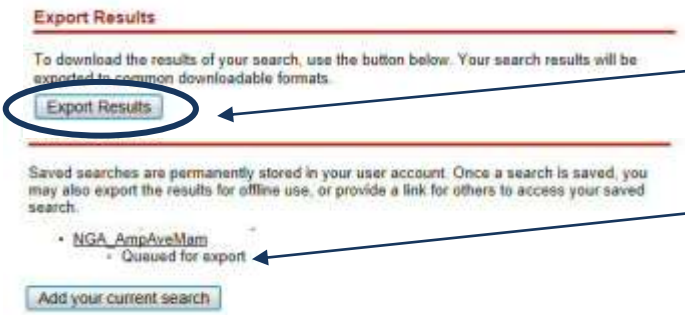
Click on **Submit**

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



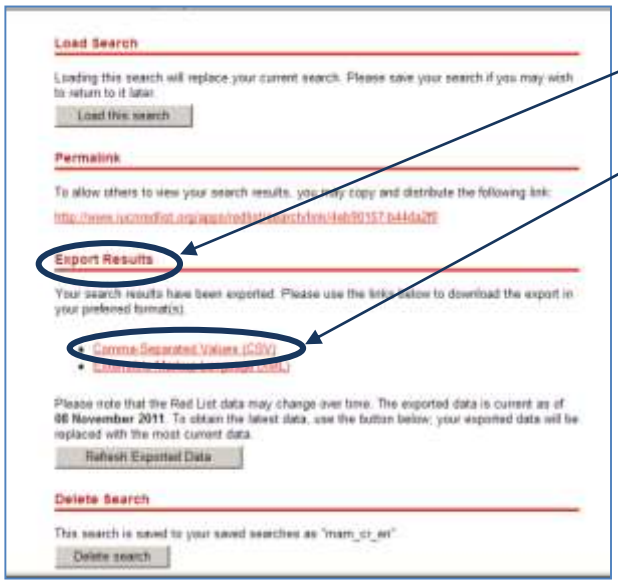
i. **Scroll down to Export results** and click on **Export results**

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



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

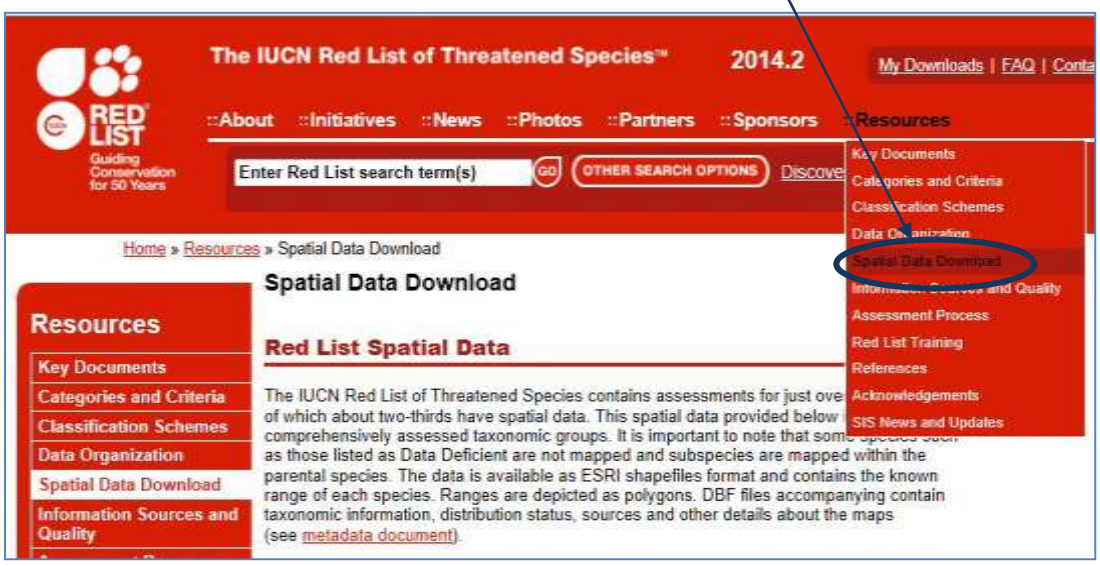
q. **Rename** the csv file e.g. **NGA_AmpAveMam.csv** in this example

2.4. Download the IUCN Red List spatial data layers

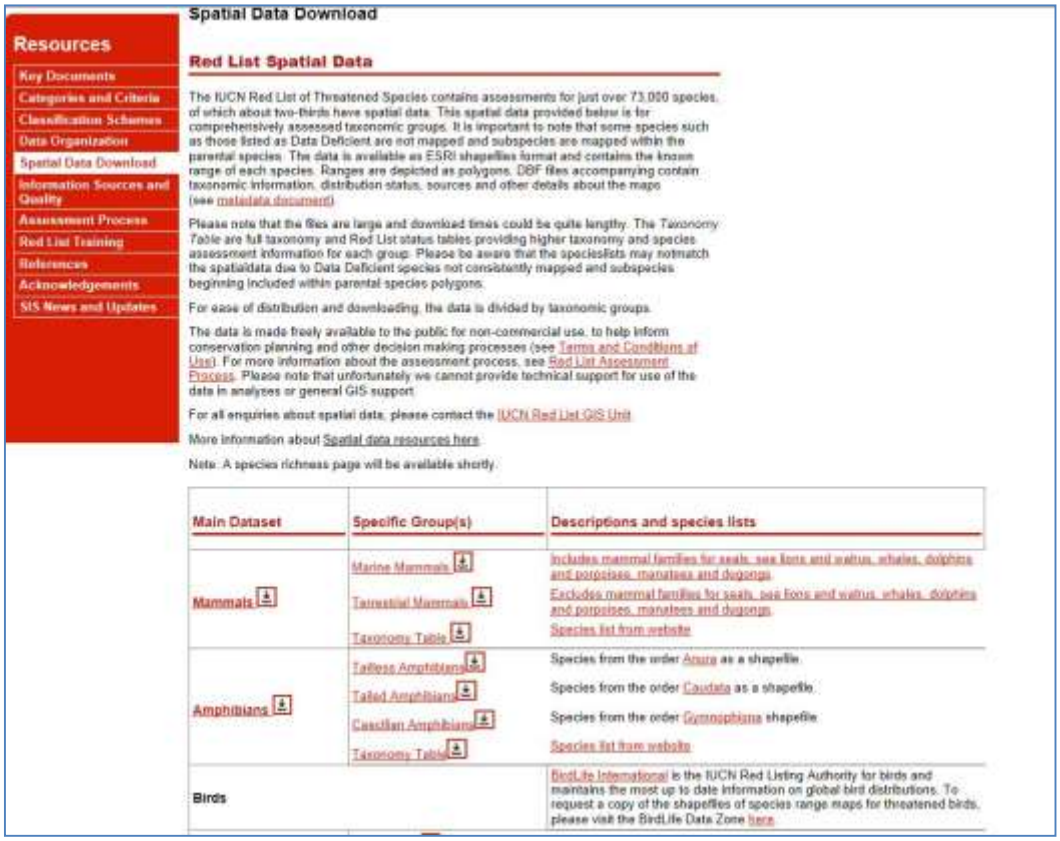
The next steps are for downloading spatial data. It is only possible to download the whole global dataset. It is not possible to filter by county prior to download. It is important to note that some of the spatial datasets are very large. If you have received the spatial data directly from IUCN you can 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)

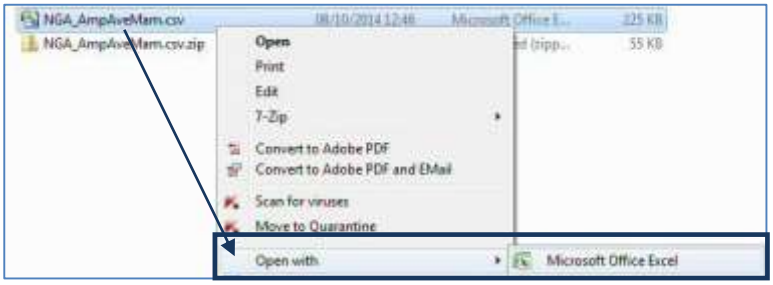
(Leave Reptiles for now as assessment is not yet complete for all species)

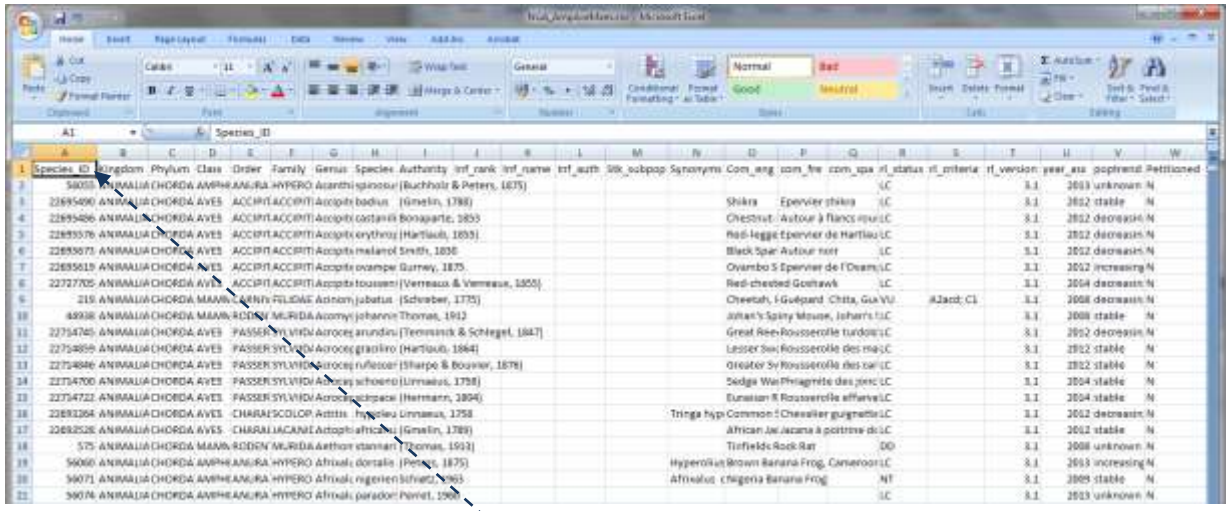
These files are all stored in geographic coordinate system (EPSG: 4326). Be aware the files are very large and will take some time to download.

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

2.5. Format species CSV file in preparation for joining to the spatial data

a. Open the 'exported search' results csv file (that was downloaded in section 2.3 step m) e.g. **NGA_AmpAveMam.CSV in this example. Open the file Excel** (or if using completely open source software in **Gnumeric or Libre Office Calc)** (The Screengrab examples below use Excel.





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

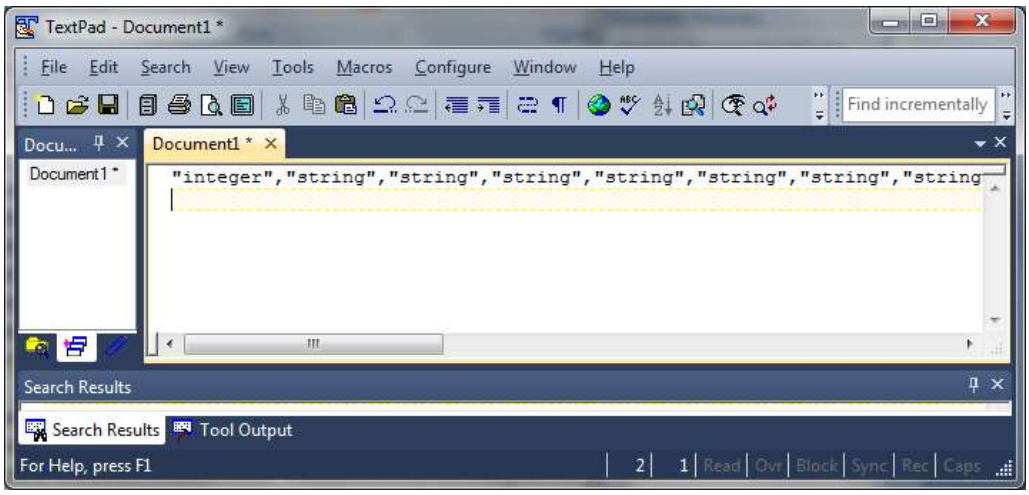
OLD Field Name		New Field Name
Species ID	=	Species_ID
Kingdom	=	Kingdom
Phylum	=	Phylum
Class	=	Class
Order	=	Order
Family	=	Family
Genus	=	Genus
Species	=	Species
Binomial	=	Binomial
Authority	=	Authority
Infraspecific rank	=	Inf_rank
Infraspecific name	=	Inf_name
Infraspecific authority	=	inf_auth
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 (keeping the file format as csv). If it asks if you want to keep the file in this format **click yes**

Keep the CSV file open as it will be used in section 2.6 where we will use the 'species_id' column to prepare an SQL query to be used in QGIS.

d. Open a **text editor** and **create a new file empty csv file** and **add** the following text to correspond to the data types of each of the columns in the .csv file**. e.g. the Species_ID column should contain integer values**

"integer","string","string","string","string","string","string","string","string","integer","string","string","string","string","string","string","string","string","string","string","string","string","string"



These are the data types for each of the fields in the species csv file.

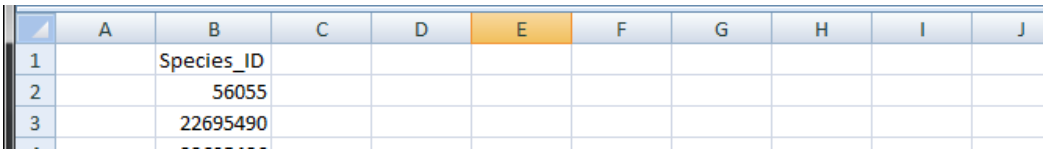
e. **Save the file** with **the same name and in the same folder** as the species csv file but with the a **.csvt** ending **e.g. NGA_AmpAveMam.csvt** in this example

This will ensure that when the file is opened later in QGIS that the numeric (Integer) fields are read with the correct data type, otherwise QGIS will default to making all the fields text (string).

2.6. Prepare SQL query for selecting species of interest

The next steps will prepare an SQL query which will be used QGIS to select out the polygons from the large spatial dataset which are in the species list. This method is being used rather than using a 'join' to join the species list to the spatial data because the join function often fails or causes errors on this very large spatial dataset.

a. Go back to the 'species list csv file. e.g. **NGA_AmpAveMam.CSV**
Then **copy and paste** the Species_ID column into **column B** a **new** excel worksheet



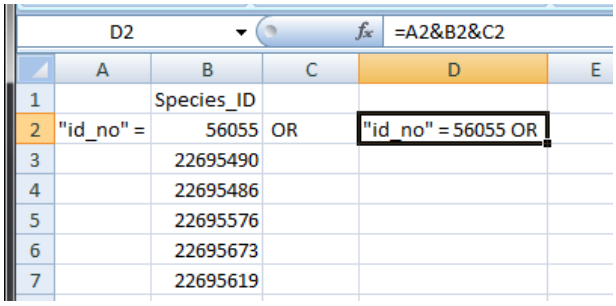
	A	B	C	D	E	F	G	H	I	J
1		Species_ID								
2		56055								
3		22695490								

b. In **row 2** of **column A** type **"id_no" =**a (make sure you put a space after the equals sign as this is important for the SQL syntax we are creating

c. **In row2** of **column C** type a **OR** (this time make sure you put a space **before** the OR as this is important for the SQL syntax we are creating)

d. **In row 2** of **column D** type **=A2&B2&C2**

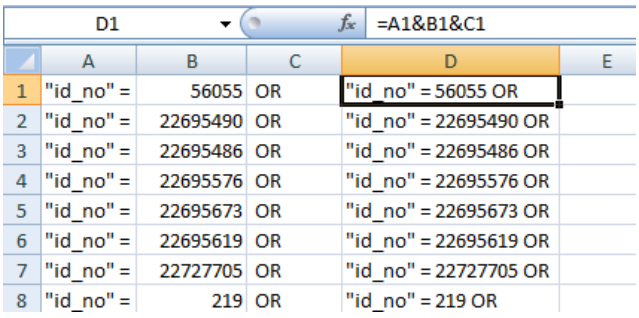
e. Next **fill Columns A, B, C and D** by double clicking on the bottom right hand corner of **each cell in row 2**



D2 =A2&B2&C2

	A	B	C	D	E
1		Species_ID			
2	"id_no" =	56055	OR	"id_no" = 56055 OR	
3		22695490			
4		22695486			
5		22695576			
6		22695673			
7		22695619			

f. Delete the entire first row so that the file now looks similar to the illustration below



D1 =A1&B1&C1

	A	B	C	D	E
1	"id_no" =	56055	OR	"id_no" = 56055 OR	
2	"id_no" =	22695490	OR	"id_no" = 22695490 OR	
3	"id_no" =	22695486	OR	"id_no" = 22695486 OR	
4	"id_no" =	22695576	OR	"id_no" = 22695576 OR	
5	"id_no" =	22695673	OR	"id_no" = 22695673 OR	
6	"id_no" =	22695619	OR	"id_no" = 22695619 OR	
7	"id_no" =	22727705	OR	"id_no" = 22727705 OR	
8	"id_no" =	219	OR	"id_no" = 219 OR	

g. **Save** the worksheet for later to a **new file** e.g. in this example called **formatted_for_SQL_query.xlsx** and **close**

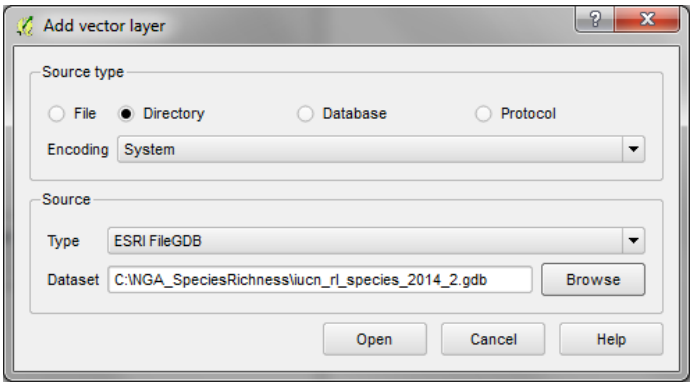
2.7. Use SQL query to select species of interest from spatial dataset

The next 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 subsetting 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 **QGIS**

b. Add in the **IUCN Species spatial dataset(s)** (the data are in geographic coordinate system (i.e. EPSG:4326)

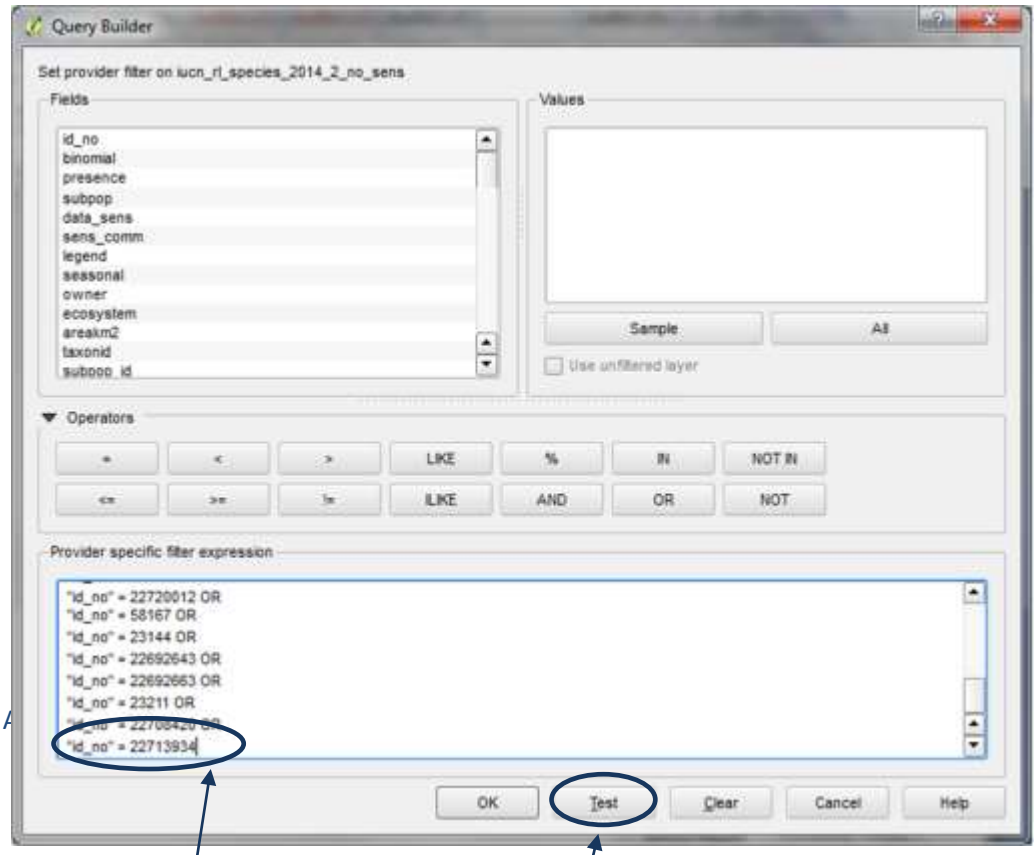
c. **Untick** the dataset in the table of contents to stop it drawing



d. **Add** in a polygon dataset of the area of interest (e.g. country boundary). e.g. in this example **nga_border_dd.shp.** Make sure the dataset is in geographic coordinate system (i.e. EPSG:4326) to match the coordinate system of the IUCN spatial data

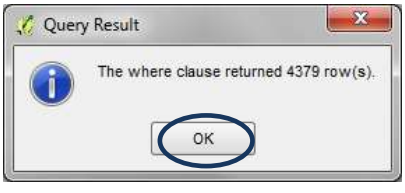
e. **Click** on the IUCN spatial dataset in the table of contents to make it the active layer e.g. in this example **iucn_rl_species_2014_2_no_sens**

f. Right click on the IUCN spatial dataset and Click **Filter**



g. A Query window appears**. Copy and paste** into the Query window **the SQL query** that you created earlier. This will select out only those species present in the exported species list

h. **Remove** the **OR** from the last row and click **Test** to check you got the syntax correct. This may take 5 - 10 minutes or longer depending on how many records are being selected. If correct it should return the number of rows selected

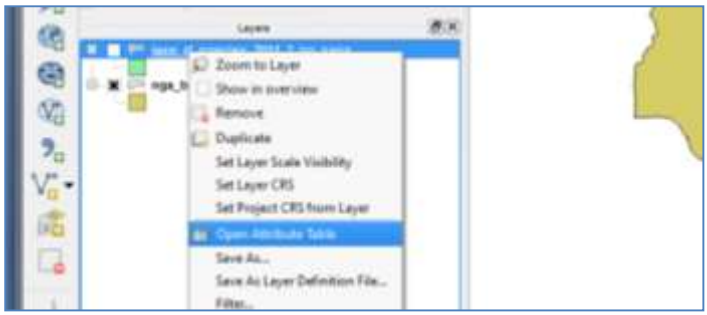


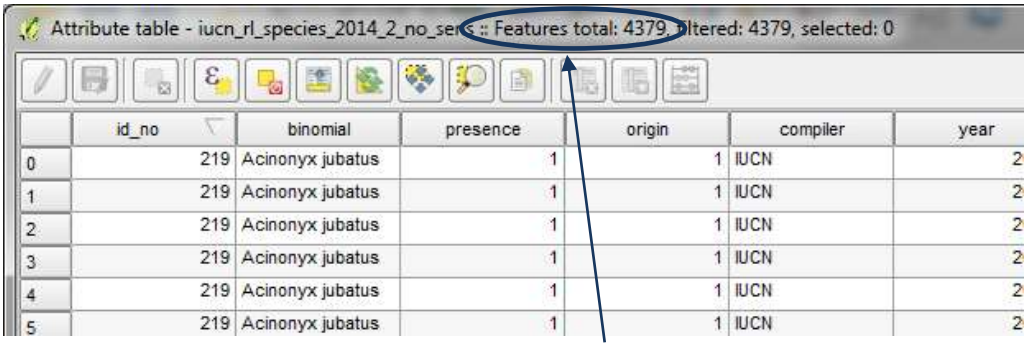
Note: This number does not equate to the number of species but to the number of polygons so you cannot use this to check that the number of species it has selected is correct.

i. **Click OK** to close the Query Result window

j. **Click OK** to apply the filter to the IUCN spatial dataset and close the Query Builder window.

k. To see that the dataset now only shows the filtered records **right click** on the IUCN spatial dataset and click on **Open Attribute table**



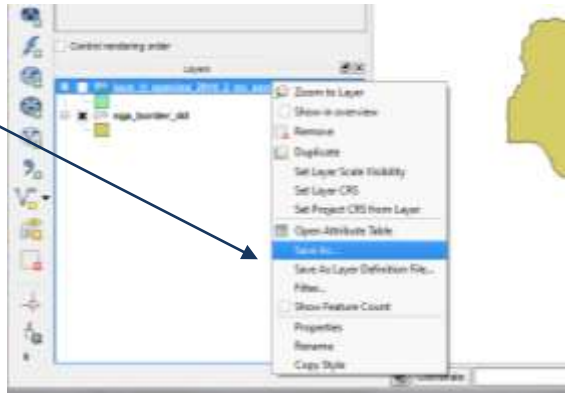


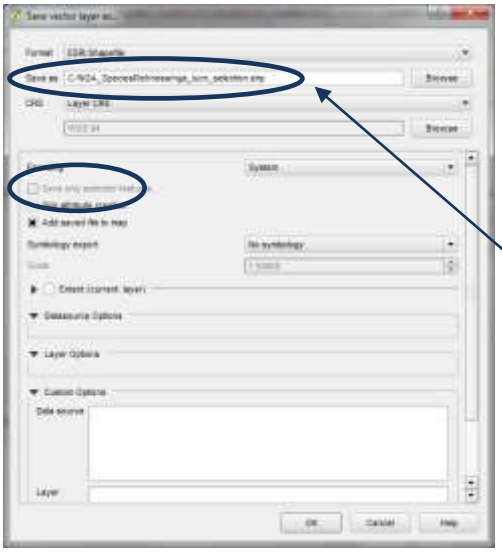
	id_no	binomial	presence	origin	compiler	year
0	219	Acinonyx jubatus	1	1	IUCN	2
1	219	Acinonyx jubatus	1	1	IUCN	2
2	219	Acinonyx jubatus	1	1	IUCN	2
3	219	Acinonyx jubatus	1	1	IUCN	2
4	219	Acinonyx jubatus	1	1	IUCN	2
5	219	Acinonyx jubatus	1	1	IUCN	2

Note the attribute table shows only the records filtered by the SQL query.

l. **Close** the attribute table

m. **Right click** on the IUCN spatial dataset and **Click Save as**





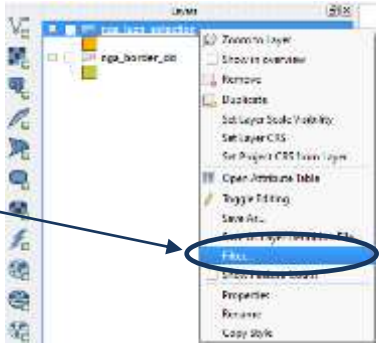
n. **Save** the file with a new name. **e.g. nga_iucn_selection.shp** in this example and **Click OK**

Note: Saving may take a long time (likely 40 minutes for a selection with about 1500 species from the global layer) so be patient.

o. **Right click and Remove** the IUCN spatial dataset in the table of contents e.g. in this example remove **iucn_rl_species_2014_2_no_sens**

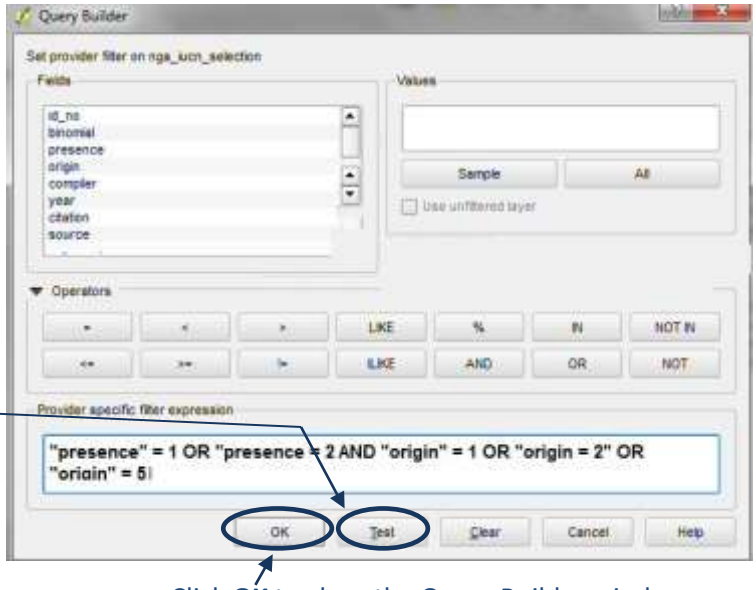
2.8. From the previous selection select out the current native species range

a. Right click on the newly added subset species layer **e.g. nga_iucn_selection.shp** in this example and and **Click Filter**



b. 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 Query Builder window:- **"presence" = 1 OR "presence" = 2 AND "origin" = 1 OR "origin" = 2 OR "origin" = 5**



c. Click **Test**

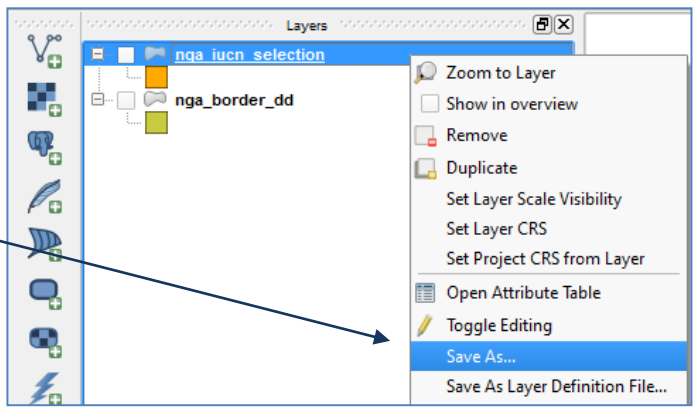
d. Click **OK** to close the Query Result window

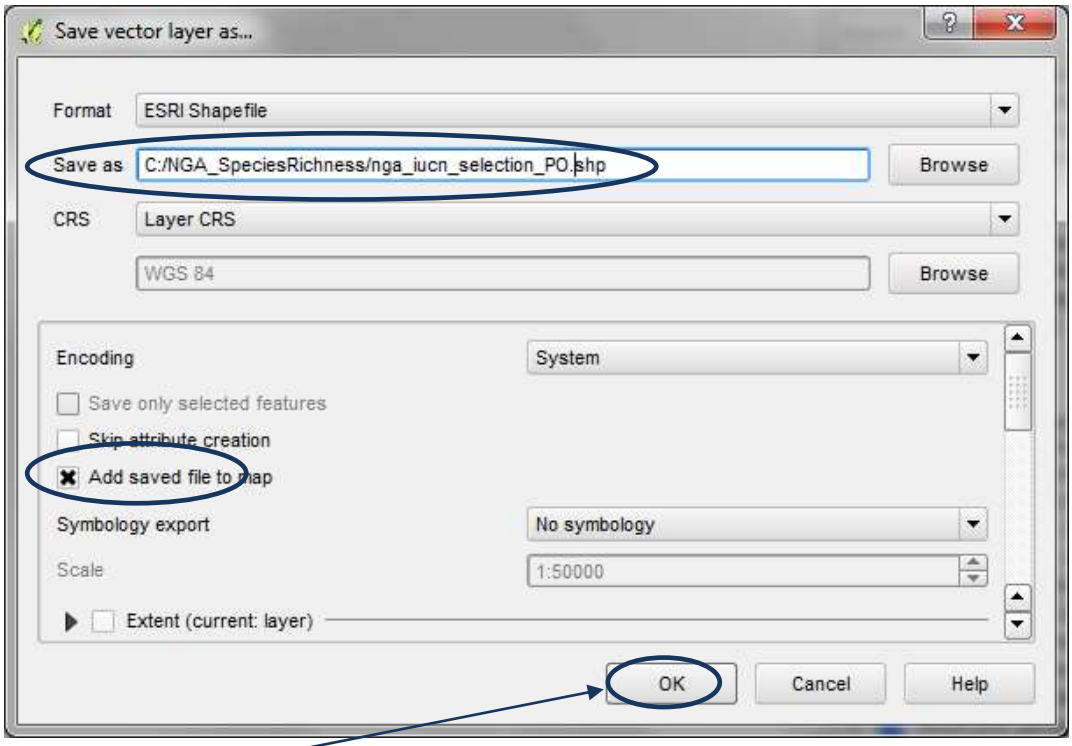
e. Click **OK** to close the Query Builder window

f.

g. Right click on the subset IUCN spatial dataset e.g **nga_iucn_selection.shp** in this example and Click **Save as**

h. **Save** the file with a new name. **e.g. nga_iucn_selection_PO.shp** in this example

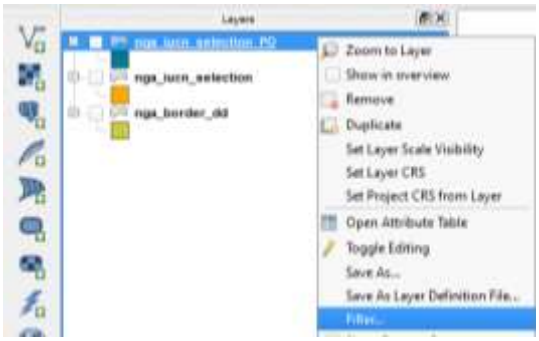




i. Click **OK**

2.9. From the previous selection select out terrestrial species ranges

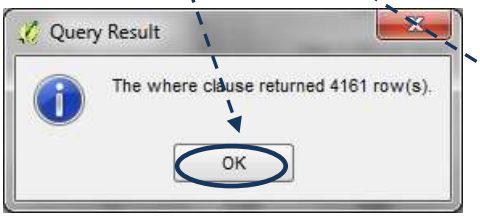
a. Right click on the **newly added subset species layer e.g. nga_iucn_selection_PO.shp** in this example and and **Click Filter**



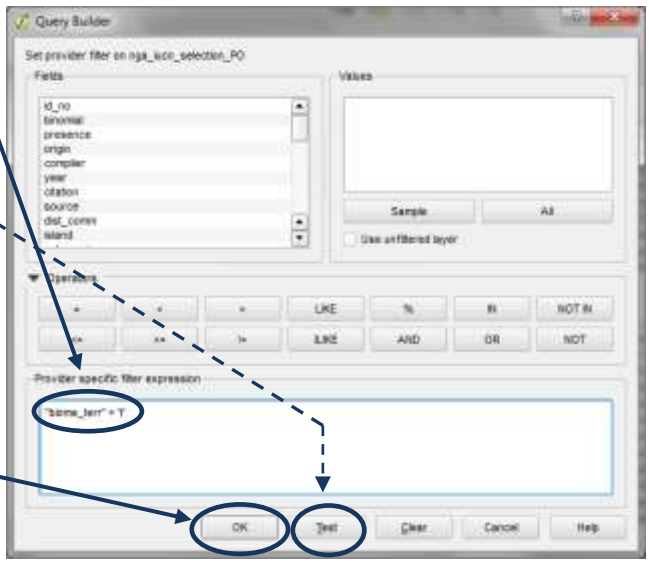
b. To only include species which are terrestrial put the following expression into the Query Builder window: **"biome_terr" = 't'**

c. Click **Test**

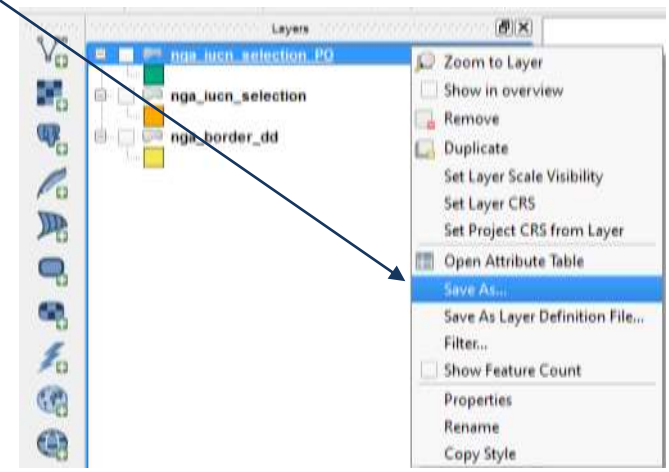
d. Click **OK** to close the Query Result window



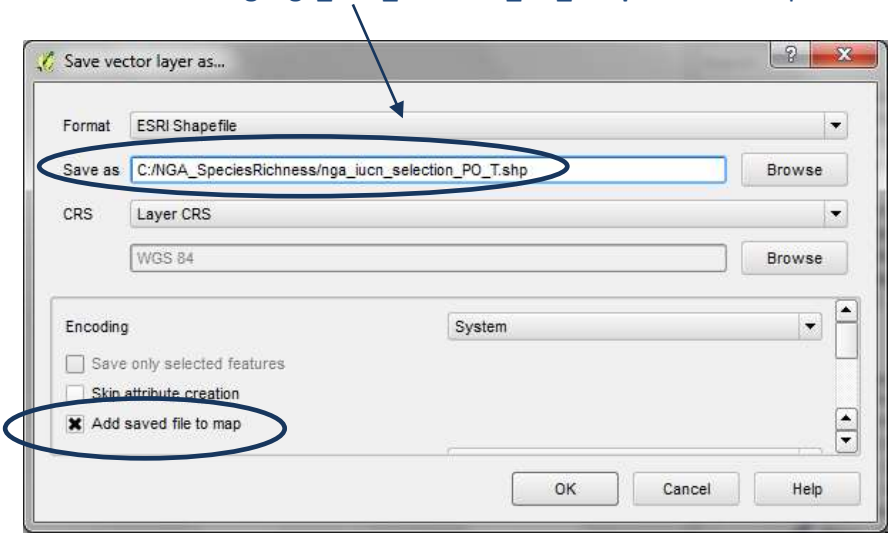
e. Click **OK** to close the Query Builder window



f. Right click on the subset IUCN spatial dataset e.g **nga_iucn_selection_PO.shp** in this example and Click **Save as**

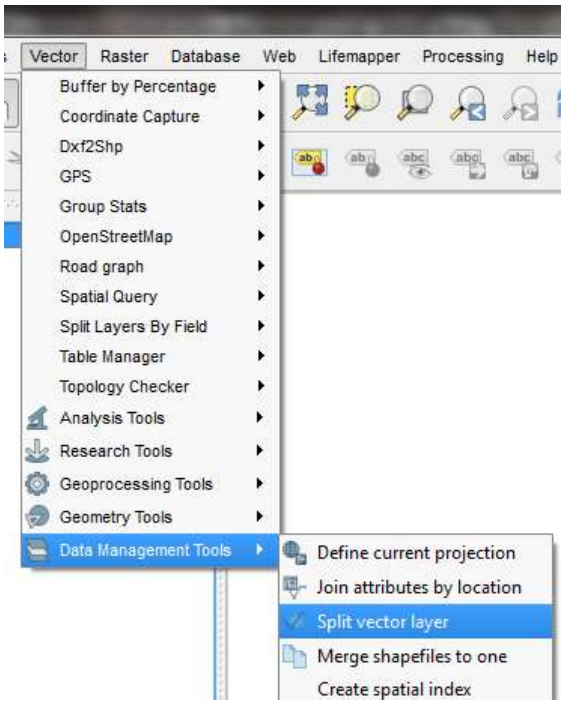


g. **Save** the file with a new name. **e.g. nga_iucn_selection_PO_T.shp** in this example

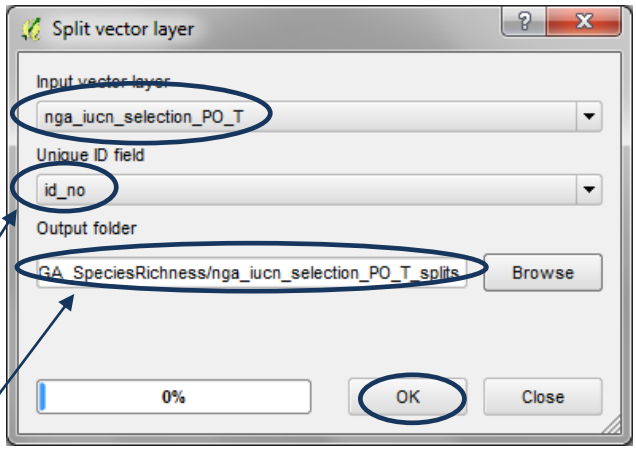


2.10. Split the the final subset IUCN dataset into separate files by species

a. From the **Vector menu >> Data management tools >> Split vector layer**



b. Under **input vector layer** choose the name of the **species range file you want to split**. e.g. in this example **nga_iucn_selection_PO_T.shp**



c. Under **unique ID field** choose the **field to base the split on**. Select **id_no**, this contains a unique ID for each species.

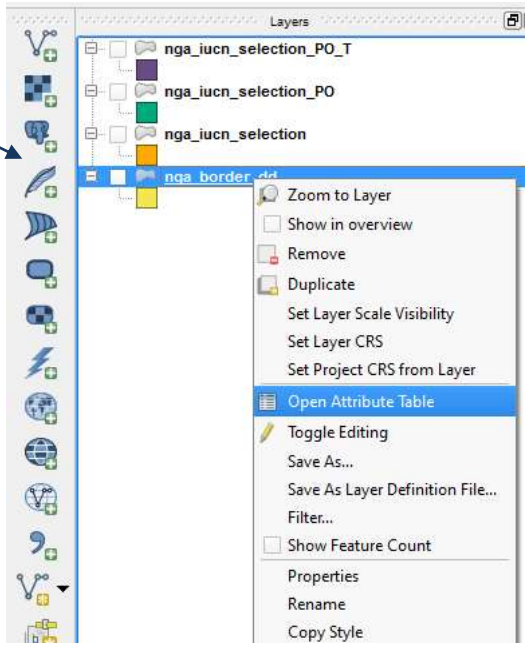
d. Select an **output folder** for the split species range files. e.g. in this example **C:\NGA_SpeciesRichness\nga_iucn_selection_PO_T_splits**

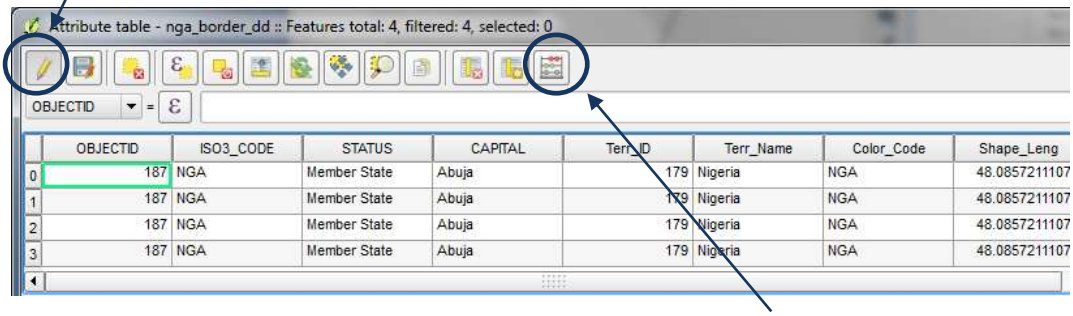
e. Click **OK**

2.11. Create Raster for Area of interest with all pixels having value of 1

a. Right click the Vector layer of the area of interest **e.g. nga_border_dd.shp** in this example and open Attribute table

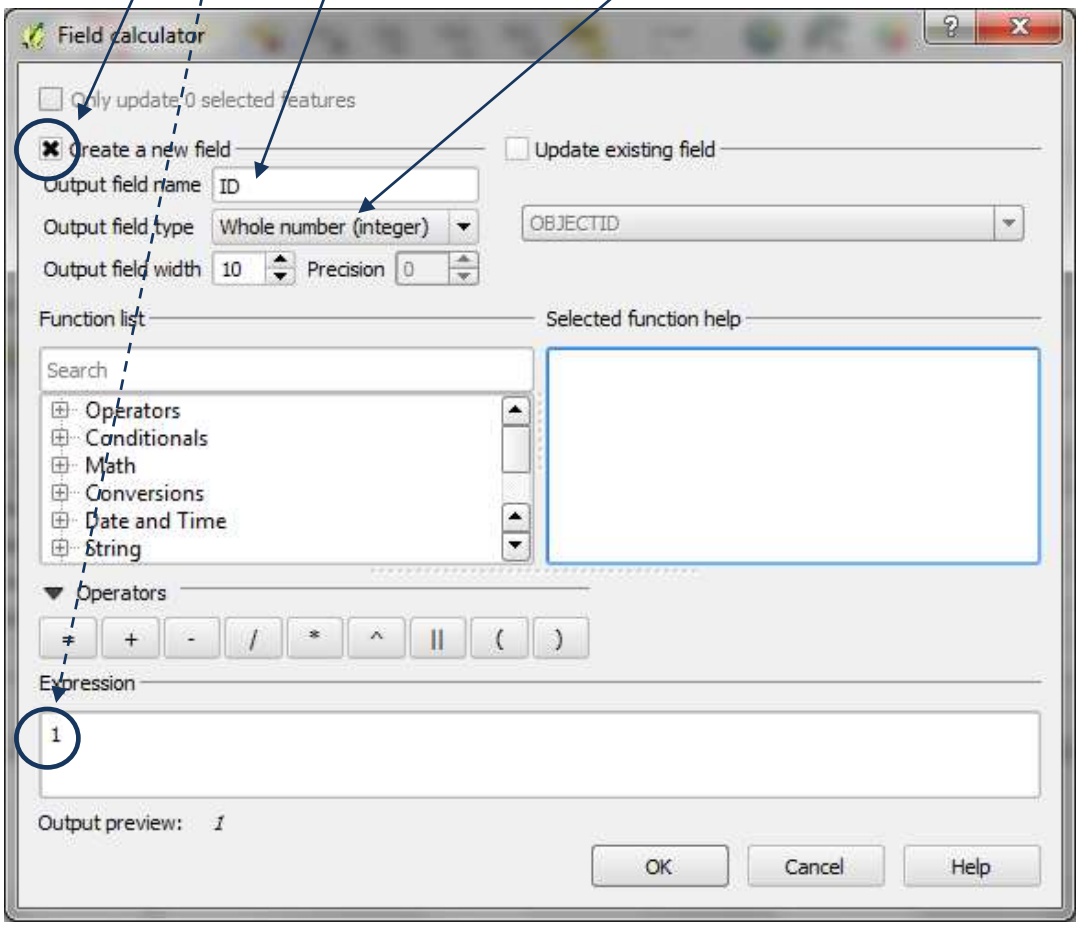
b. Click on the toggle editing button in the attribute table window



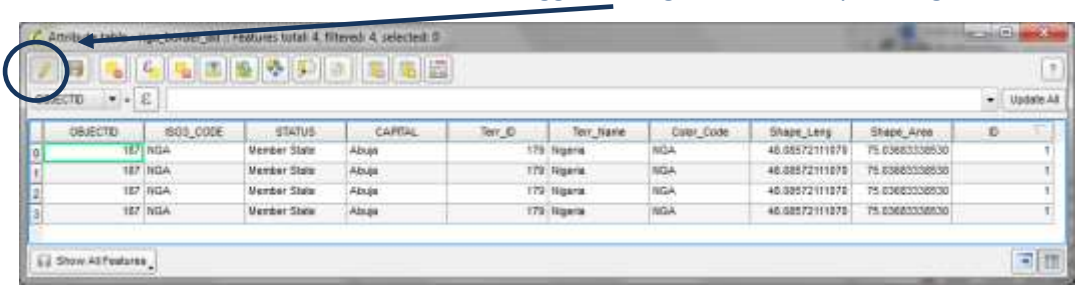


c. The calculator button becomes active. **Click** on the **Calculator button**

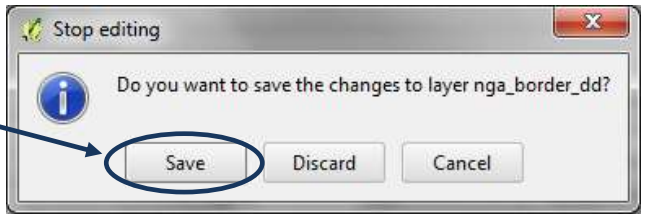
d. **Create a new field** called **ID** (in this example) of type **integer** and calculate all the values in that field as **1**



e. An ID field is added to the table. Click the toggle editing button to stop editing

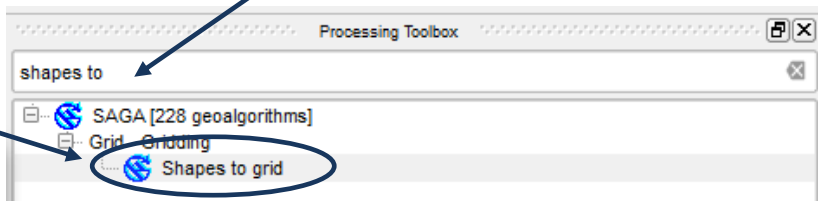


f. Click **Save** to save the edits

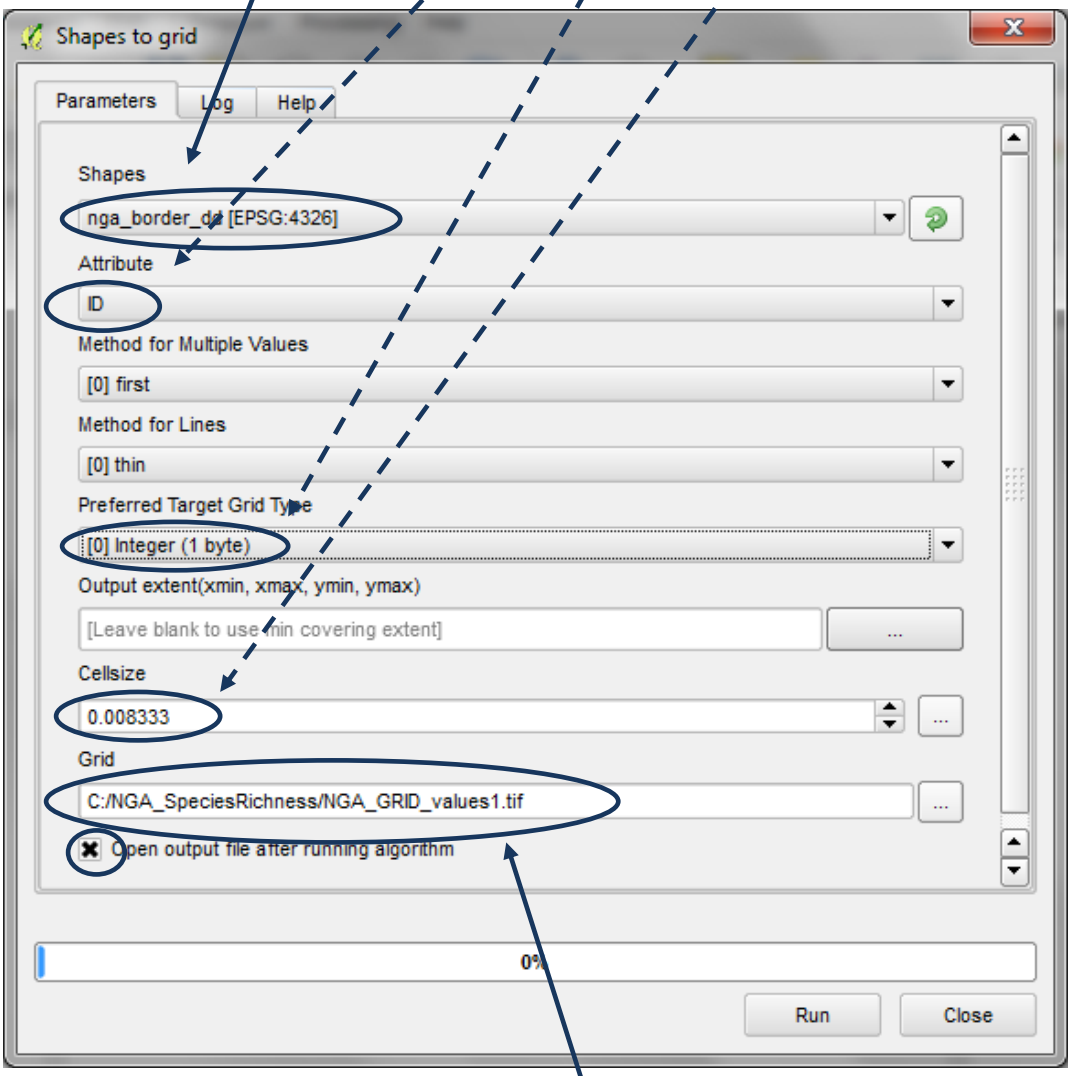


g. In the Processing Toolbox, search for the **SAGA - shapes to Grid tool**

h. Double click on the **Shaped to grid** tool



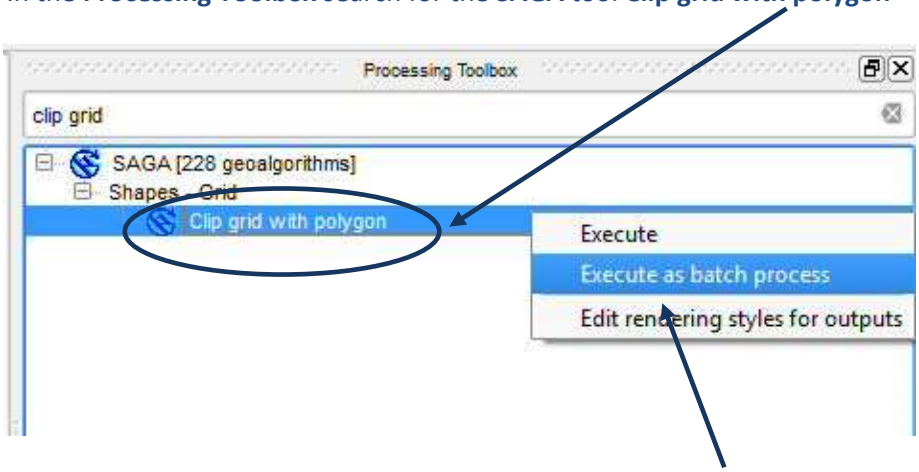
i. Set the Shapes to the **Area of Interest shapefile**
j. Set the attribute to use for the grid values as **ID** (i.e. all the grid values will be 1)
k. Set the Preferred Target Grid Type to **Integer (1 byte)**
l. Set the cellsize in **decimal degrees** e.g. in this example 0.008333 (equivalent to 1km)



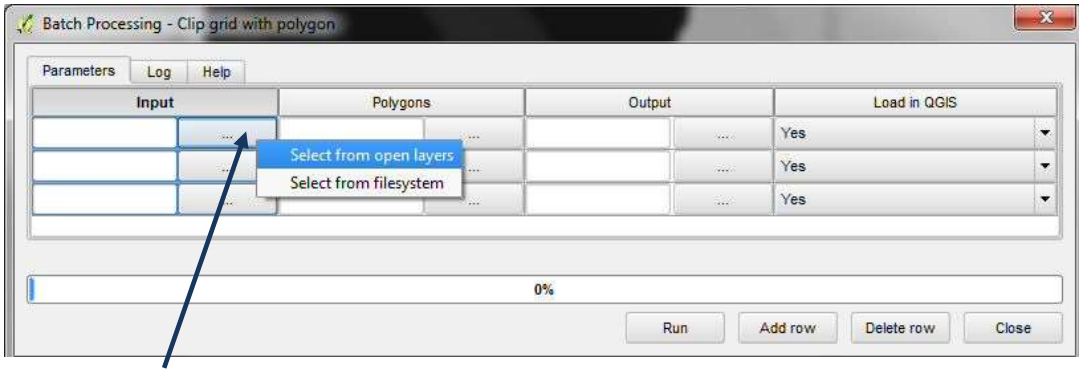
m. Give the output Grid a **new name and save in .tif format** e.g. in this example **C:\NGA_SpeciesRichness\NGA_GRID_values1.tif**
n. Once run click **Close** to close the dialogue box. It appears as Grid in the table of contents. All values are **1** and no data is value **129**
o. Right click on Grid and **rename** it **AOI** (for area of interest)

2.12. Batch clip Area of Interest Raster with Each Species Range

a. In the **Processing Toolbox** search for the **SAGA** tool **Clip grid with polygon**



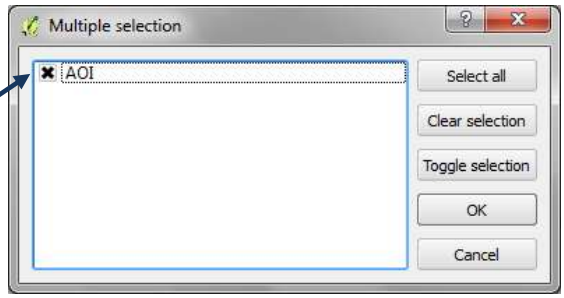
b. **Right click** on the **Clip grid with polygon** tool and **Execute as batch process**



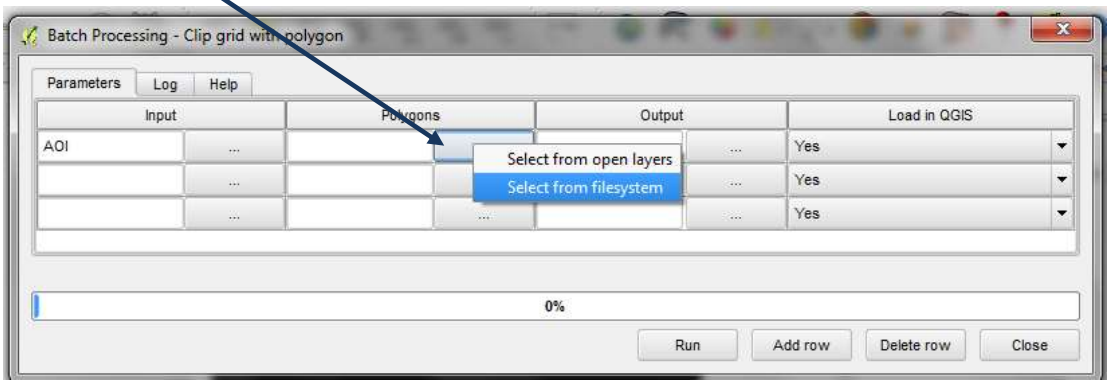
c. Click on the ... in the first row of the input column and **select from open layers**

d. Select **AOI** (i.e.the grid of the area of interest where all cells contain the value of 1)

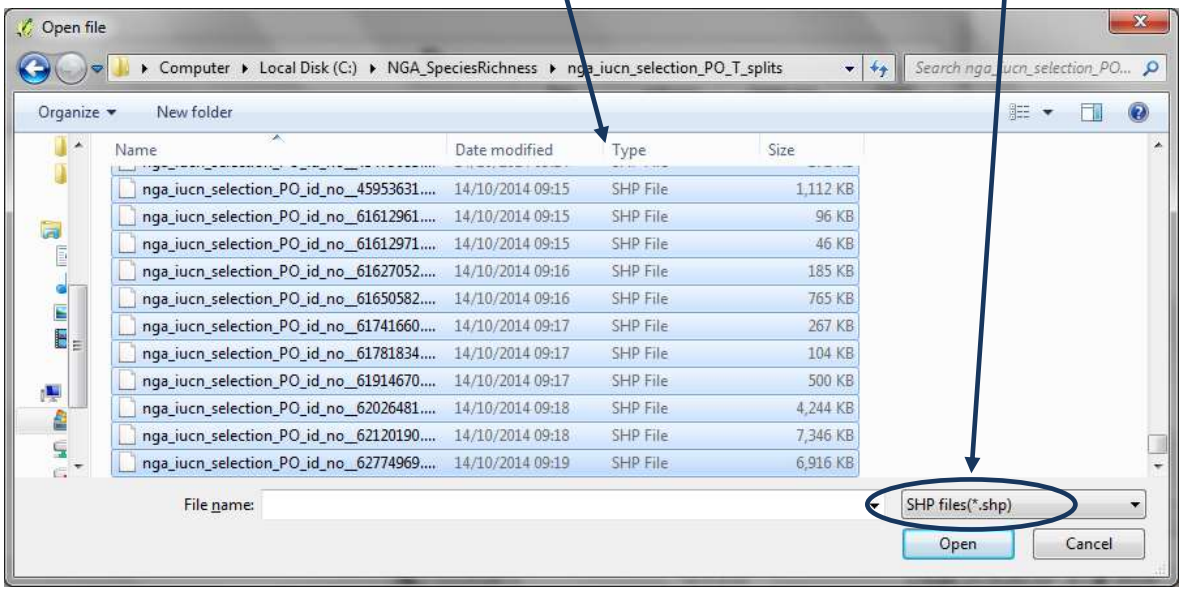
e. Click **OK**



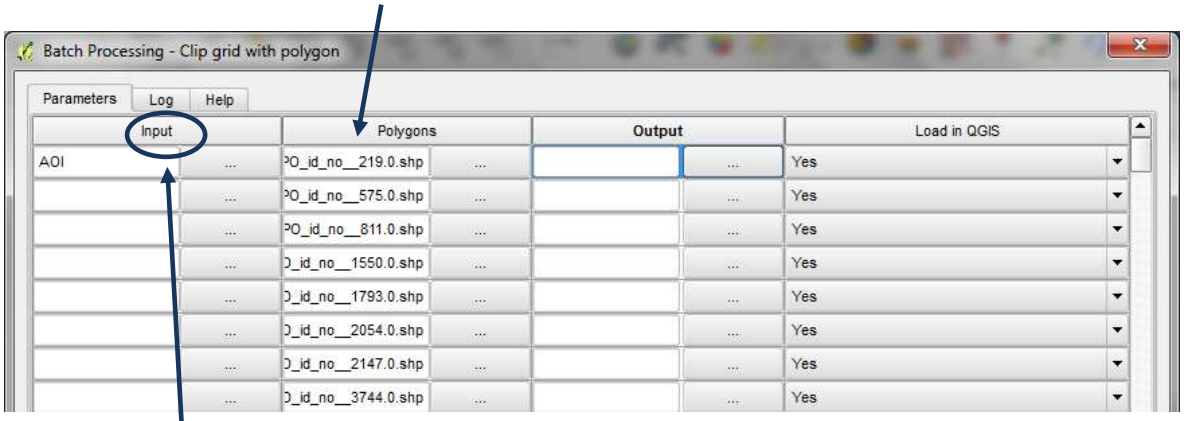
f. Click on the **...** in the first row of the **Polygons** column and **select from file system**



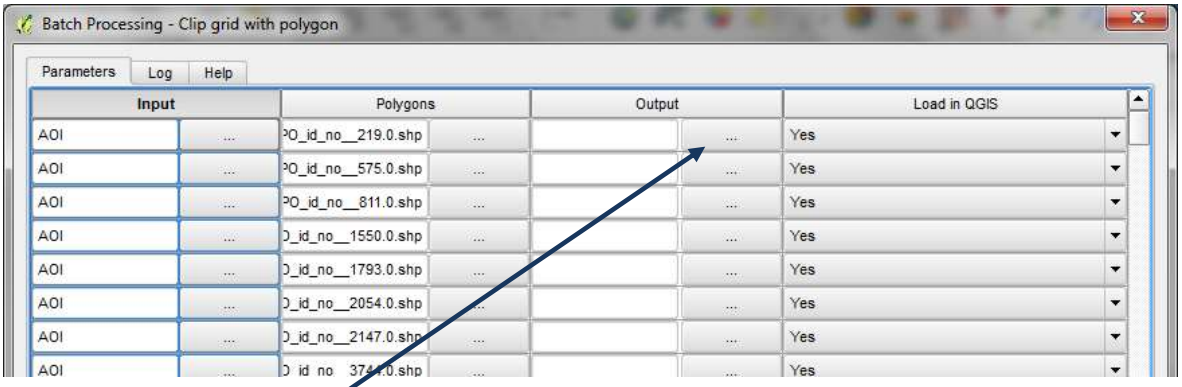
g. Navigate to the folder containing the split up shapefiles, change the type shp and hold down the **shift key** and **select all the species** files. e.g. in the folder C:\NGA_SpeciesRichness\nga_iucn_selection_PO_T_splits in this example



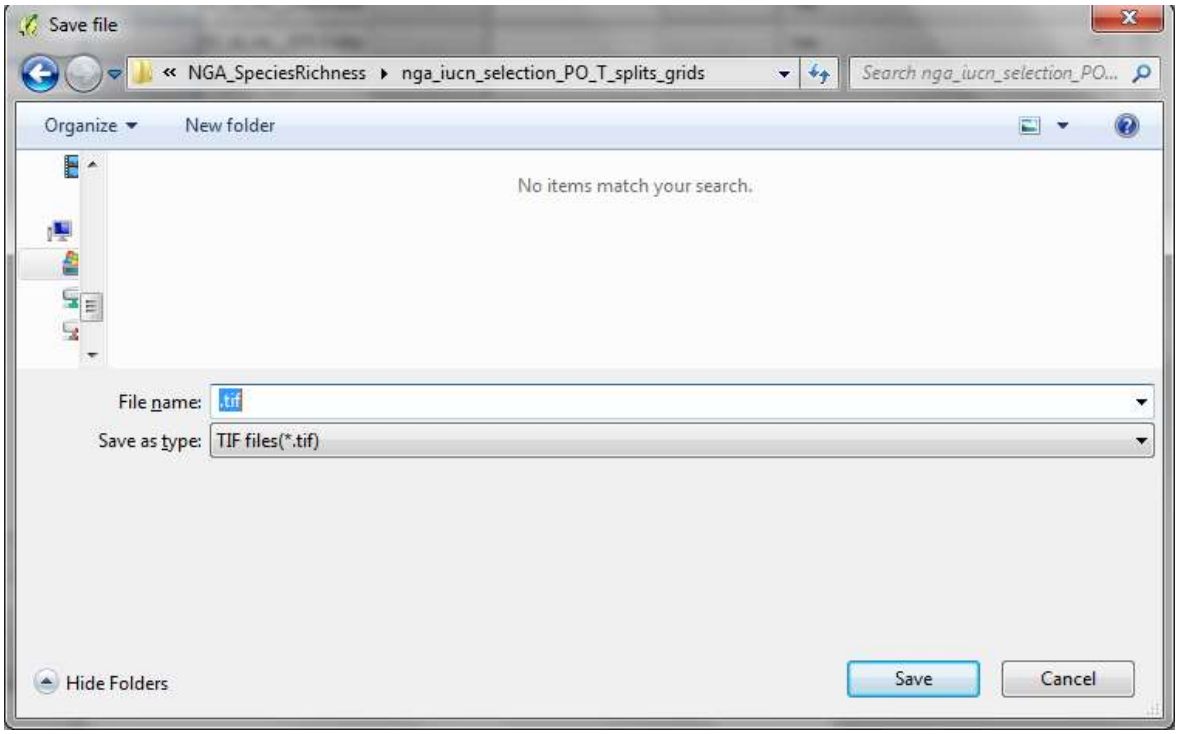
A single row per species file is added for the batch process



h. **Double click** on the **Input** heading to auto populate the AOI down the input column



i. Click on the **...** in the first row of the **Output** column and **select from file system**



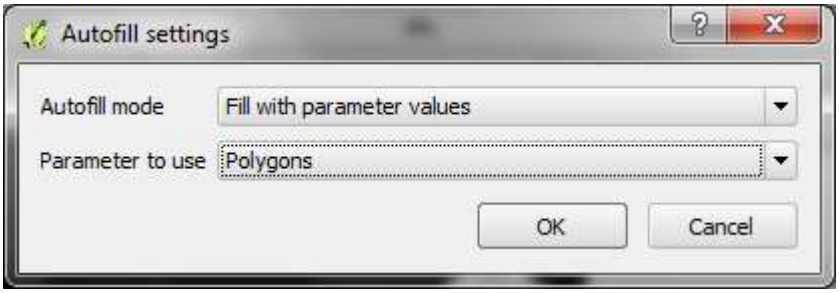
j. Create a **new folder** to put the output species rasters e.g. in this example **C:\NGA_SpeciesRichness\nga_iucn_selection_PO_T_splits_grids**

k. In the file name box put **.tif**

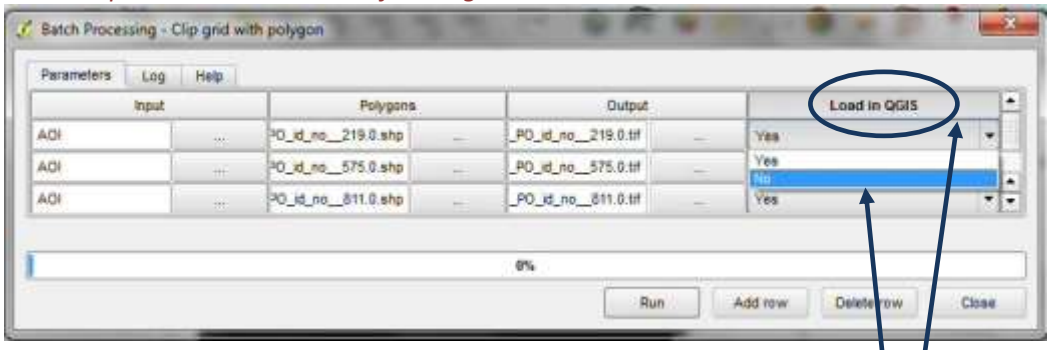
l. In the Save as type box pick Tif files(.tif)

m. Click **Save**

n. In the Autofill mode box that appears pick **Fill with parameter values** and for the Parameter to use pick **polygons**

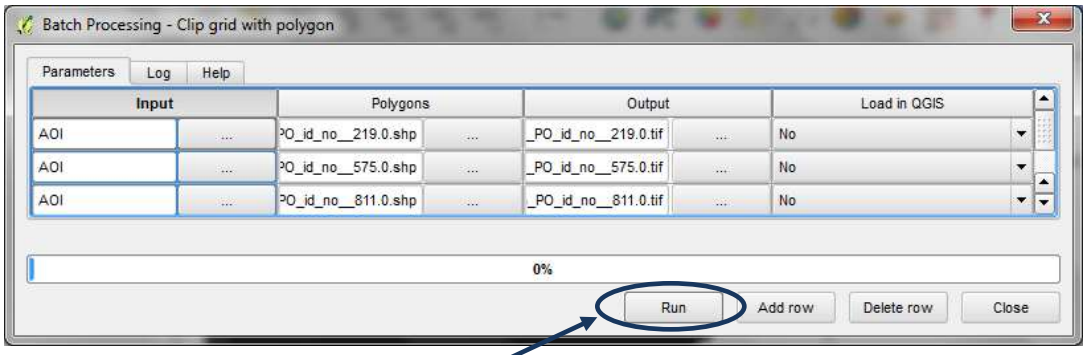


A single row per species file is added for the batch process with an output name the same as the input name but with a .tif ending.



o. Click on the **...** in the first row of the **Load in QGIS** column and change to **No**

p. Double click on the **Load in QGIS** column title to auto-change every row to **No**



q. Click **Run** to run the batch process

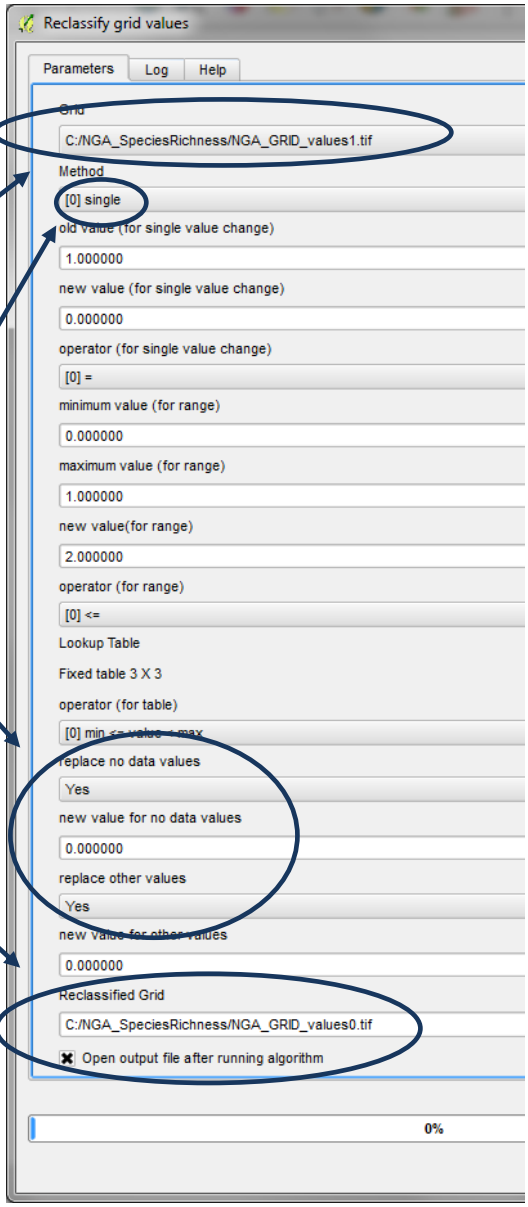
r. In a windows explorer window navigate to the output folder to see the new species raster's being created

Once the process is complete there should be a .tif file for each species which contains values of 1 where present and nodata (129). The extent of the file does not cover the whole of the area of interest (AOI) file only the extent of the individual species.

2.13. Extend extent in species raster to Area of Interest Raster

In order to sum the individual species raster's it is important that they all cover the same extent (i.e. that of the AOI).

First, reclassify the Mask raster so that all the values are reclassified to 0



a. Set the input **AOI** raster. e.g. **NGA_GRID_values1.shp** in this example

b. Set the Method to **Single**

c. Set the **old Value** to **1** and the **new value** to **0**

d. Set **replace no data value** to **Yes**

e. Set **new value for no data values** to **0**

f. Set **replace other values** to **Yes**

g. Set **new value for other values** to **0**

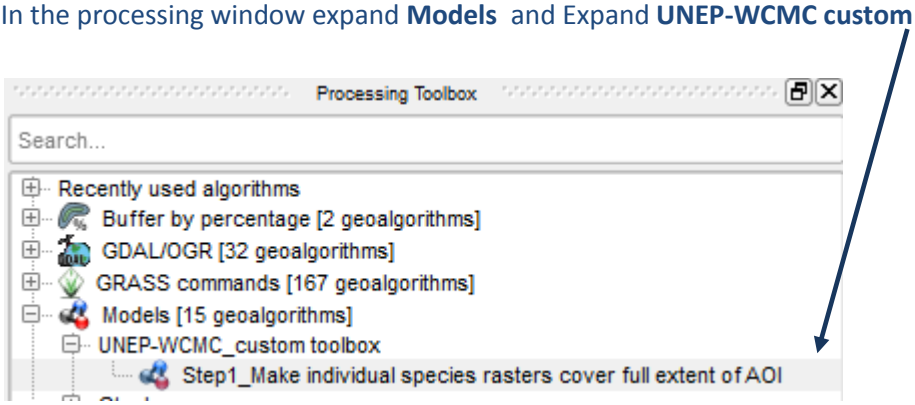
h. Give the new reclassified Grid a new name e.g. **NGA_GRID_values0.shp** in this example

The reclassified Grid should contain 0 values only for the full extent of the area of interest

Next, use the reclassified the Mask raster containing the 0 values to combine with the individual species raster to

ensure they all have the full extent of the area of interest.

i. In the processing window expand **Models** and Expand **UNEP-WCMC custom toolbox**



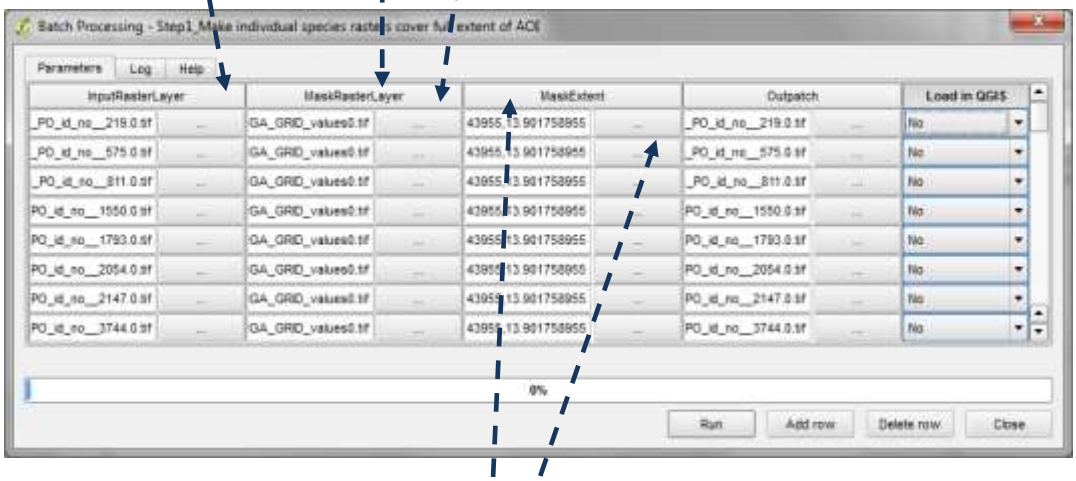
j. Right click on **Step1_Make individual species rasters cover full extent of AOI** and **execute as batch**

k. Click on the **...** in the first row of the **InputRasterLayer** column and **select from file system.** Hold down **shift** and select all **the species tifs** generated in the previous section.

l. Click on the **...** in the first row of the **MaskRasterLayer column** and **select from open layers.**

m. Tick the **AOI** raster containing the 0 values**. e.g. NGA_GRID_values0.tif** in this example.

n. Double click on the column heading **MaskRasterLayer** to populate AOI down the column

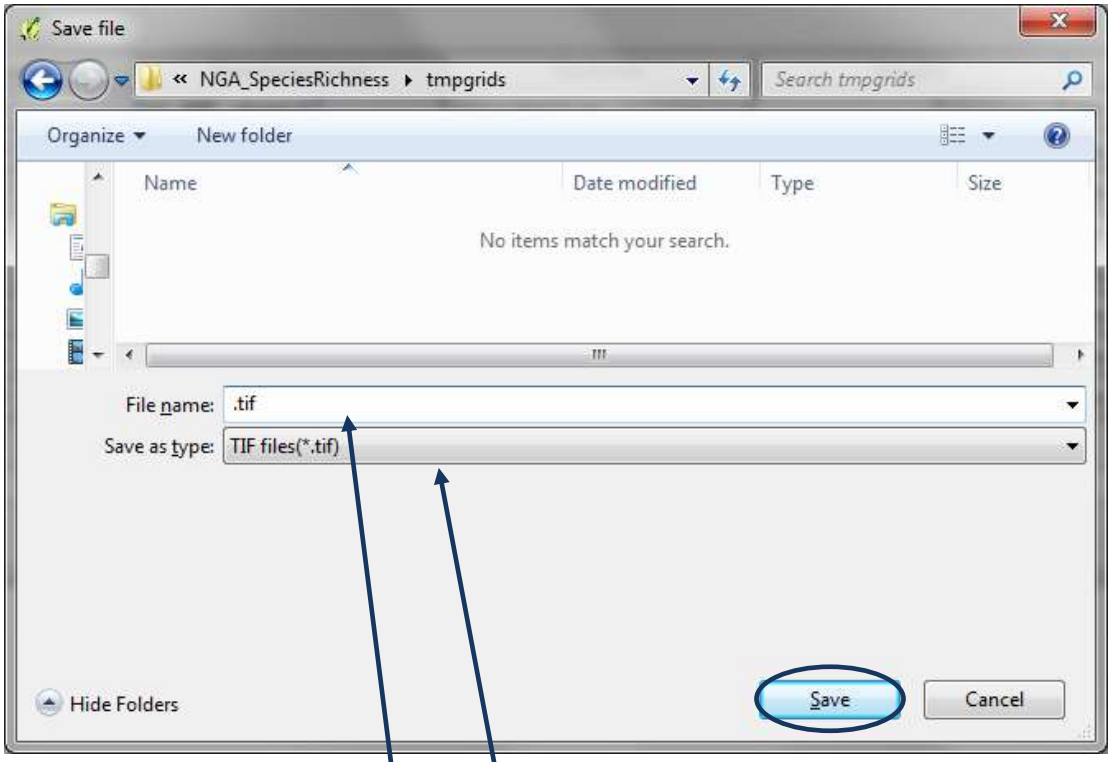


o. Click on the **...** in the first row of the **MaskExtent** column and **use layer/canvas extent** and change to **AOI e.g. NGA_GRID_values0.tif** in this example and Click **OK.**

p. Double click on the column heading **MaskExtent** to populate the AOI extent down the column

q. Click on the **...** in the first row of the **Outpatch** column

r. Create a **new folder** to put some **temporary** output species raster's e.g. in this example C:**\NGA_SpeciesRichness\tmpgrids**

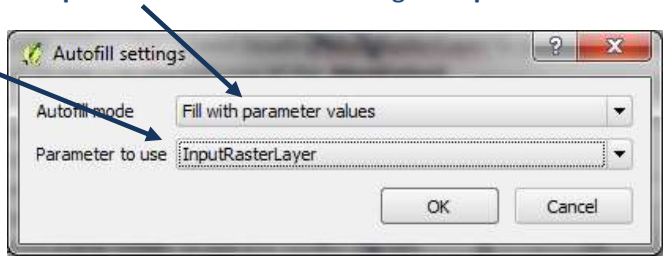


s. In the **file name** box put **.tif**

t. In the **Save as type** box pick **Tif files(.tif)**

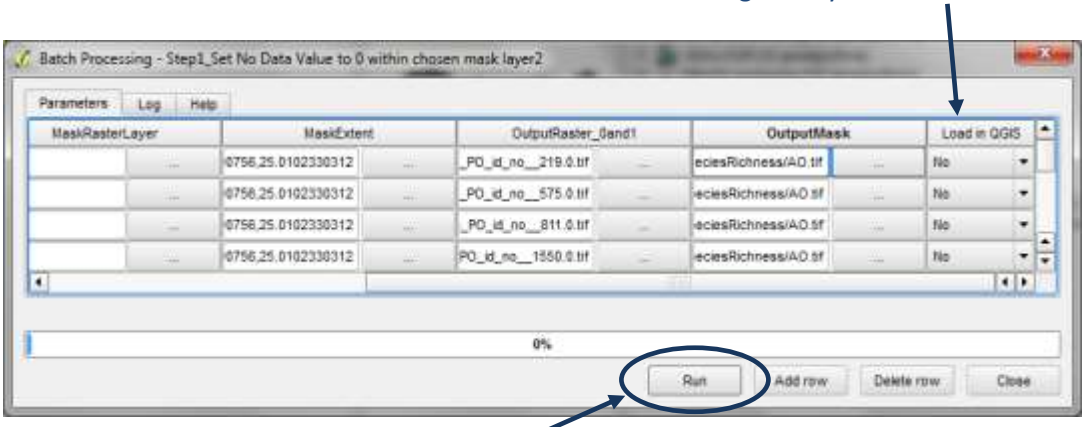
u. Click **Save**

v. **Change** the **Autofill** mode to **Fill with parameter values** and change the **parameter to use** to **InputRasterLayer**



w. Click on the **...** in the first row of the **Load in QGIS** column and change to **No**

x. Double click on the **Load in QGIS** column title to auto-change every row to No.



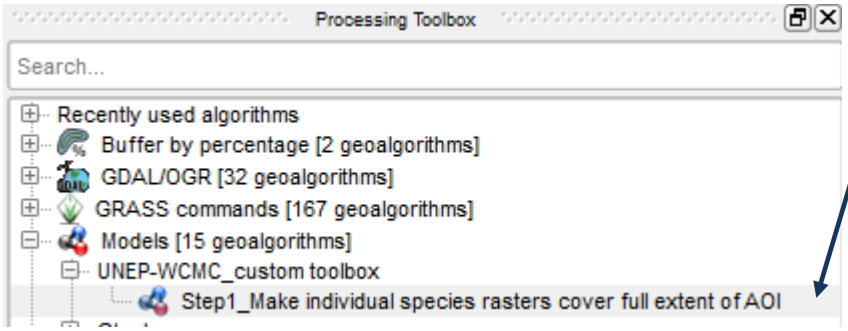
y. Click **Run** to run the batch process

z. In a windows explorer window navigate to the **temporary output folder** to see the new species raster's being created e.g. **C:\NGA_SpeciesRichness\tmpgrids** in this example.

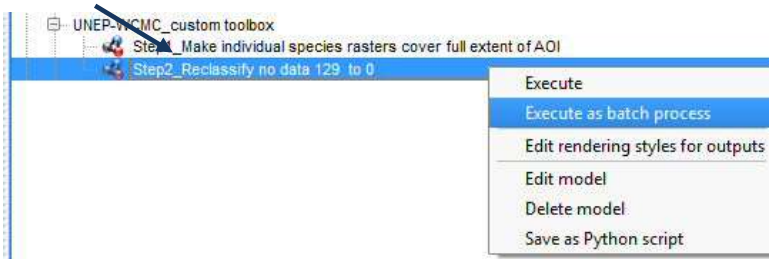
If the process is successful this box will appear once the batch process is complete. Note: If the tool fails after the first few files. Try clicking run again. It may take a few attempts (not sure why!). If that fails the try closing QGIS and reopening it.

2.14. Batch Reclassify nodata values of 129 to 0

a. In the processing window expand **Models** and Expand **UNEP-WCMC custom toolbox**

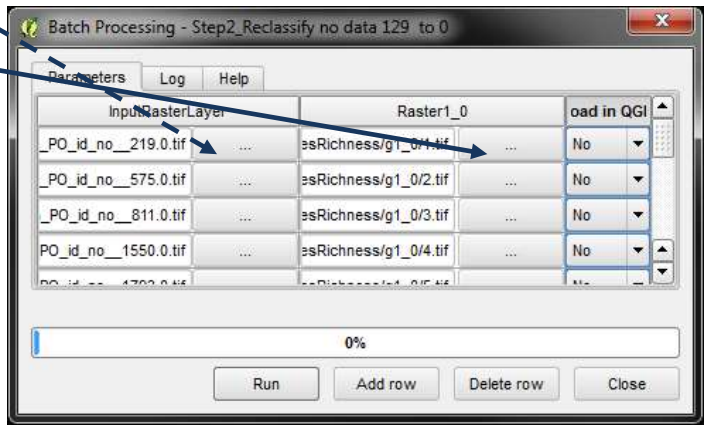


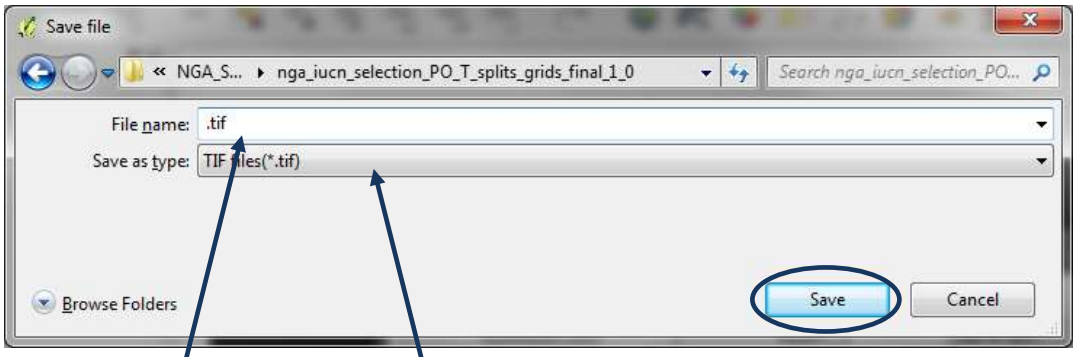
b. Right click on **Step2_Reclassify no data 129 to 0** and **execute as batch**



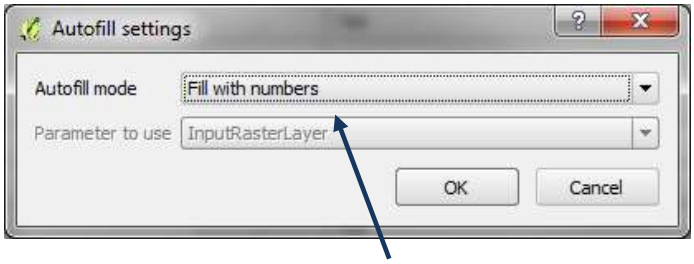
c. Click on the **...** in the first row of the **InputRasterLayer** column and **select from file system.** Hold down **shift** and select all **the species tifs** generated in the previous section e.g. **C:\NGA_SpeciesRichness\tmpgrids** in this example

d. Click on the **...** in the first row of the **Raster1_0.** Create a **new folder** to put some the **final** output species raster's in e.g. in this example **C:\NGA_SpeciesRichness\nga_iucn_selection_PO_T_splits_grids_final_1_0**





e. In the **file name** box put **.tif**
f. In the **Save as type** box pick **Tif files(.tif)**
g. Click **Save**



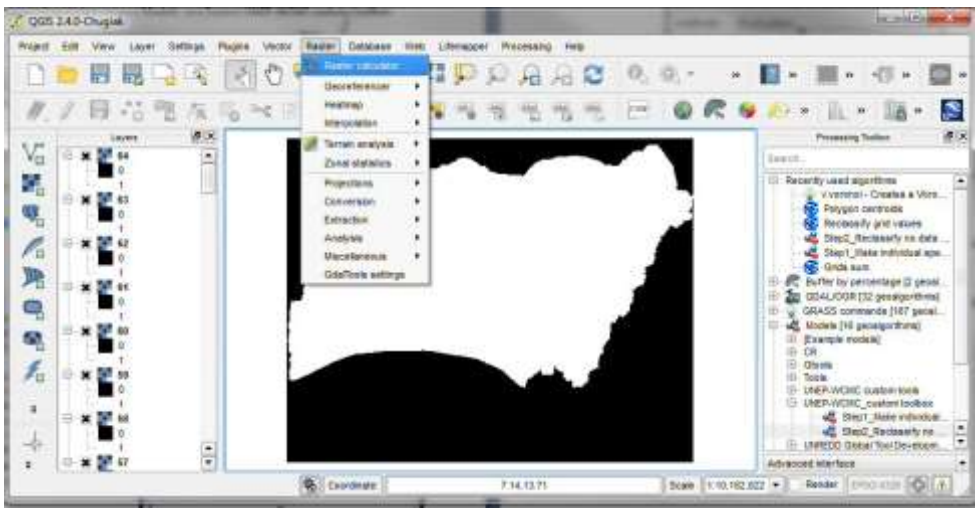
h. **Change** the **Autofill** mode to **Fill with number values**
i. **Change** the **Load in QGIS** to **No** (as this can use too much memory and cause the function to fail half way through when processing many files)

This will label the files from 1 to x. We are using number rather than the names from the input as the next step requires the file names to be very short.

2.15. Create Species Richness Raster

Now that all the individual species raster files have a value of 1 for present and 0 for absent, the final step is to sum them together to make a richness grid.

a. **Load** all the rasters from the previous step into QGIS **e.g. C:\NGA_SpeciesRichness\ nga_iucn_selection_PO_T_splits_grids_final_1_0** in this example.
b. **Press Ctrl+Shft+H** to turn the layers i.e.e to stop them drawing
c. From the main menu pick **Raster>>Raster Calculator**



d. Open **Excel**

e. In **row 1 of column A** type **1**

f. **In row 1 of column B** type **"**

g. **In row 1 of column C** type **=B1&A1&"@1"&B1&" + "**

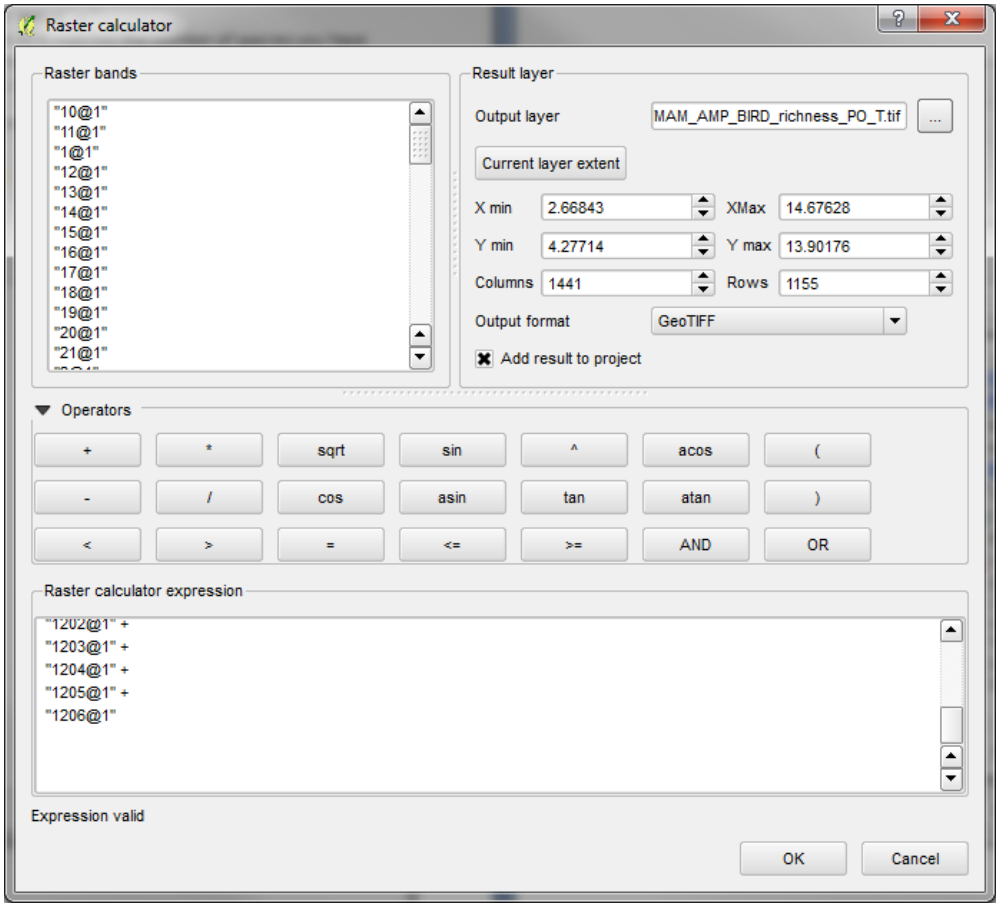
h. **Auto increment the number in Column A** so it matches the number of species you have in the final species rasters folder**. e.g.** 1206 in this example

i. Fill the rest of the columns so it looks similar to the image right

C1 =B1&A1&"@1"&B1&" + "

	A	B	C	D	E	F	G	H
1	1	"	"1@1" +					
2	2	"	"2@1" +					
3	3	"	"3@1" +					
4	4	"	"4@1" +					
5	5	"	"5@1" +					
6	6	"	"6@1" +					
7	7	"	"7@1" +					
8	8	"	"8@1" +					
9	9	"	"9@1" +					
10	10	"	"10@1" +					
11	11	"	"11@1" +					
12	12	"	"12@1" +					

j. Copy and paste the contents of column C into the raster calculator window in QGIS

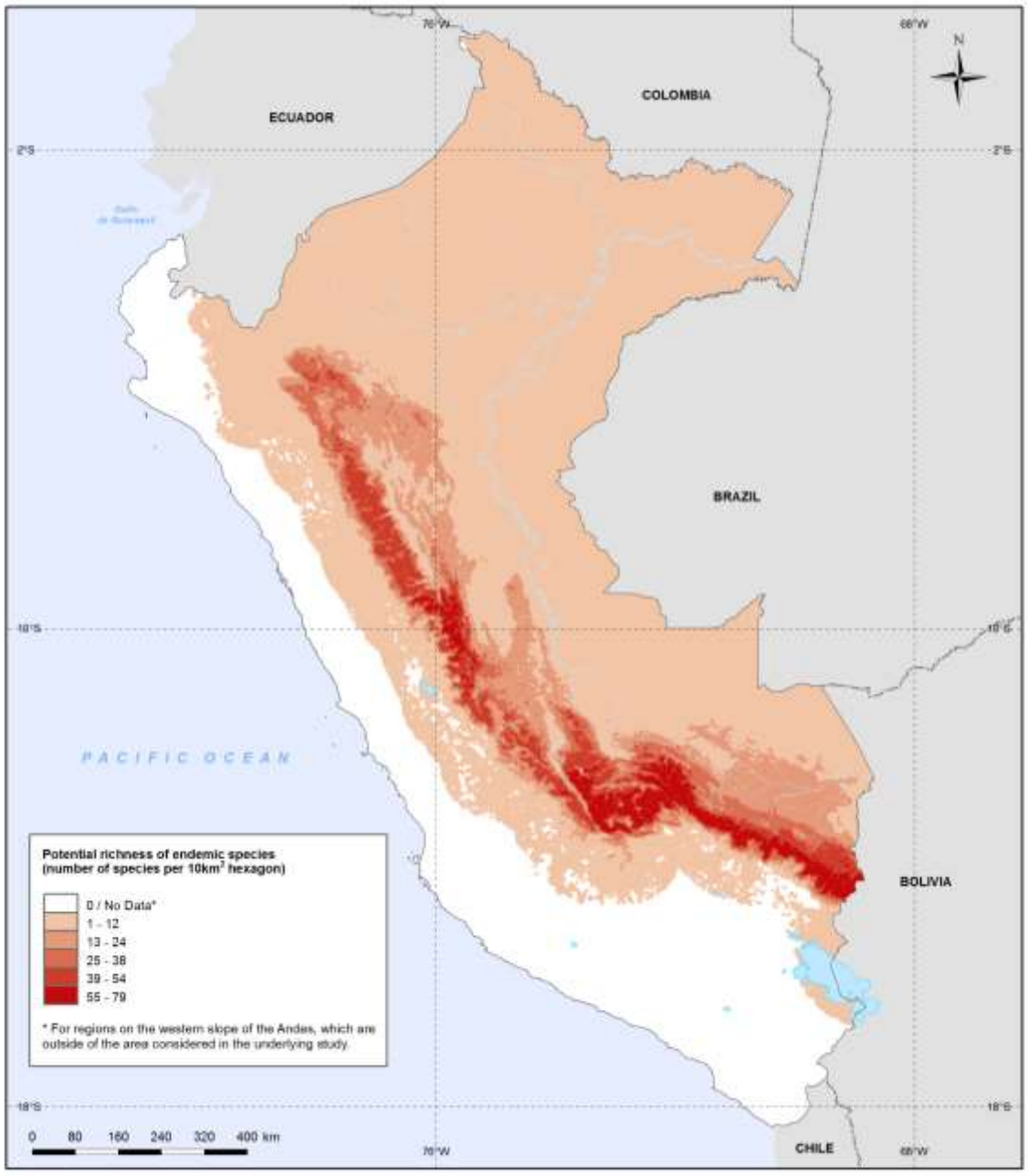


k. Click on the ... , navigate to the folder to place the output and give it a new name. e.g. **C:/NGA_SpeciesRichness/MAM_AMP_BIRD_richness_PO_T.tif** in this example.

This is the final species richness dataset

The dataset can then be symbolized and placed in a map layout as in the example below
Below is an Example map output

Example Map



Methods and data sources:
Endemic species distribution (amphibians, mammals and birds): Young, BE, Beck S, Córdova J, Embert D, Franke I, Hernandez P, Herzog S, Pacheco V, Timaná M, Tovar C, and Vargas J. 2007. Digital distribution maps of species endemic to the east slope of the Andes in Peru and Bolivia. NatureServe, Arlington, Virginia, USA.
Data provided by NatureServe in collaboration with the Centro de Datos para la Conservación (CDC) of the Universidad Nacional Agraria La Molina, the Museo de Historia Natural de la Universidad Mayor de San Marcos, and many participating natural history museums and herbaria. See: http://www.natureserve.org/conservation-tools/data-maps-tools/modeled-distribution-maps-species-endemic-east-slope-andes-peru