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 VECTOR METHOD IN A COMBINATION OF QGIS 1.8 AND 2.8

UN-REDD PROGRAMME

Food and Agriculture Organization of the United Nations

UNDP Empowered lives. Resilient nations.

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, Lucy Goodman, Blaise Bodin, Lisen Runsten and Matea Osti

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.

Citation: Ravilious, C., Goodman, L., Bodin, B., Runsten, L. and Osti, M. (2015) 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 vector method in a combination of QGIS 1.8 and 2.8. Prepared on behalf of the UN-REDD Programme. UNEP World Conservation Monitoring Centre, Cambridge, UK.

Acknowledgements: With thanks to support provided by IUCN, the Global Forest Resource Assessment of the FAO, the FAO-Finland Technical Collaboration Programme, Tanzanian Forest Service, FAO Tanzania, Sokoine University, André Mazinga (OSFAC) and Eric Lutete (OSFAC).

These training materials have been produced from materials generated for working sessions held in Tanzania with the National Forestry Resources Monitoring and Assessment of Tanzania, FAO Tanzania and Sokoine University, and the Democratic Republic of the Congo with OSFAC, to aid the production of multiple benefits maps to inform REDD+ planning and safeguards policies using open source GIS software.

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. Please note that the last part of the tutorial can currently only run in QGIS version 1.8 as it is reliant on the QMarxan plugin that is not yet available in more recent versions.

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

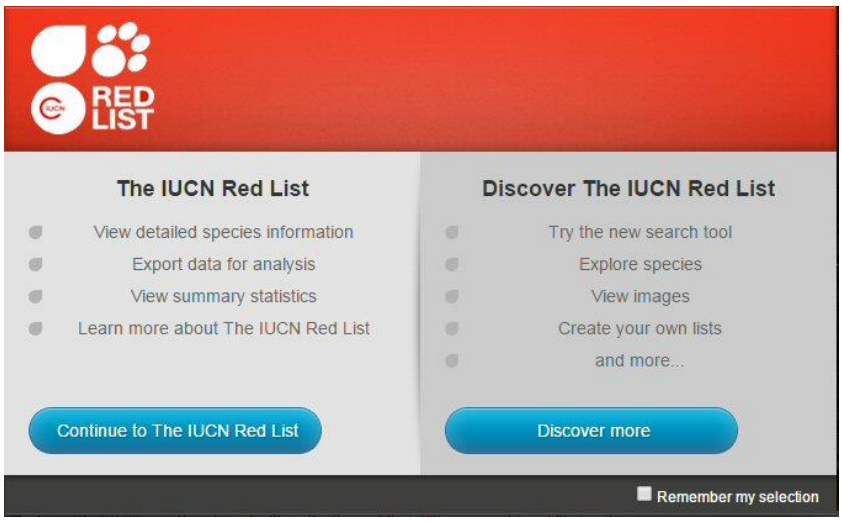
2.1. Selecting and downloading species data from the IUCN Red List website

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.

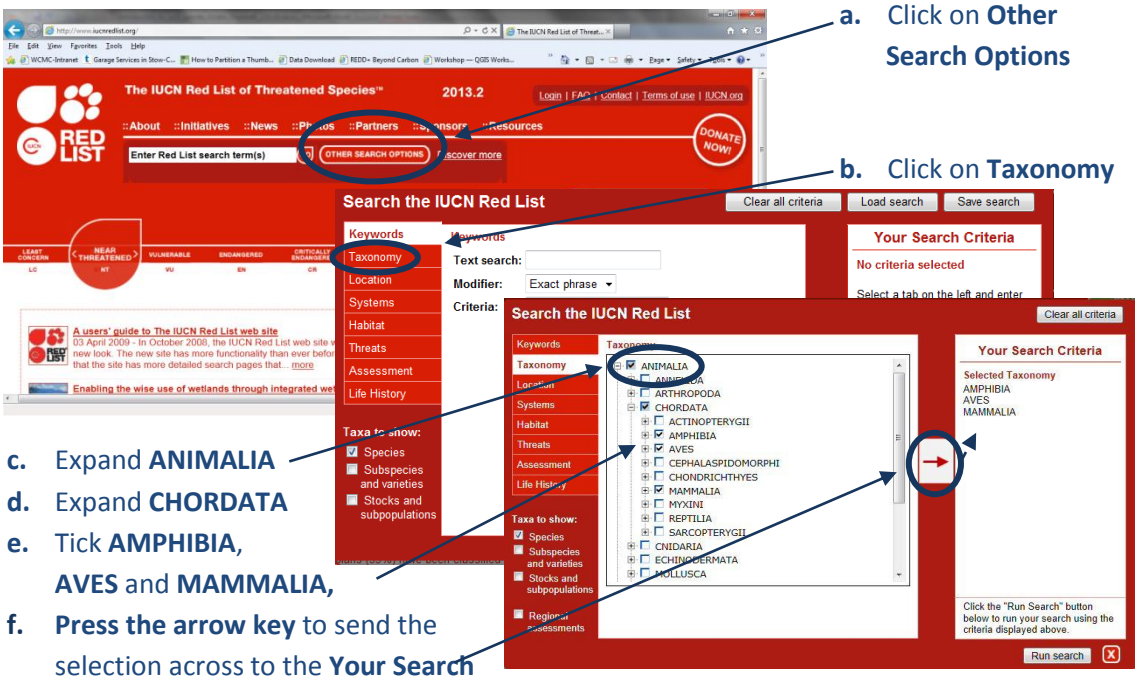
2.1.1. Searching for non-spatial data

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

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



This search below is an EXAMPLE search for mammals, birds and amphibians with threat status of Critically Endangered (CR), Endangered (EN), Vulnerable (VU), Lower Risk: Conservation Dependent (LR), Near Threatened (NT), Data Deficient (DD) or Least Concern (LC).



a. Click on **Other Search Options**

b. Click on **Taxonomy**

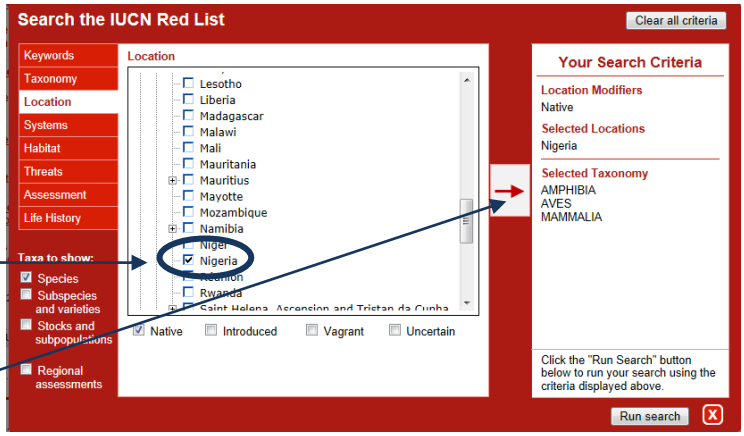
c. Expand **ANIMALIA**

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.

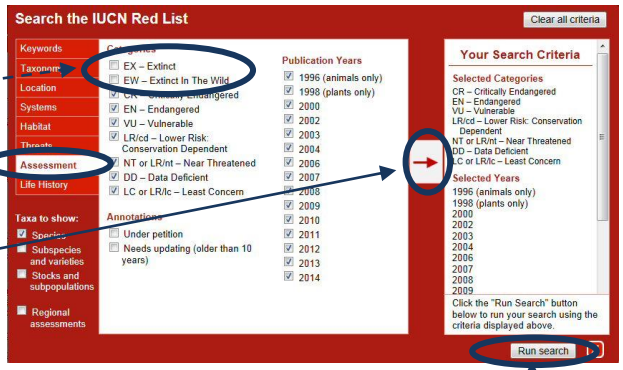


g. Click on **Location,** expand **land regions,** expand and tick the **country of interest**

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

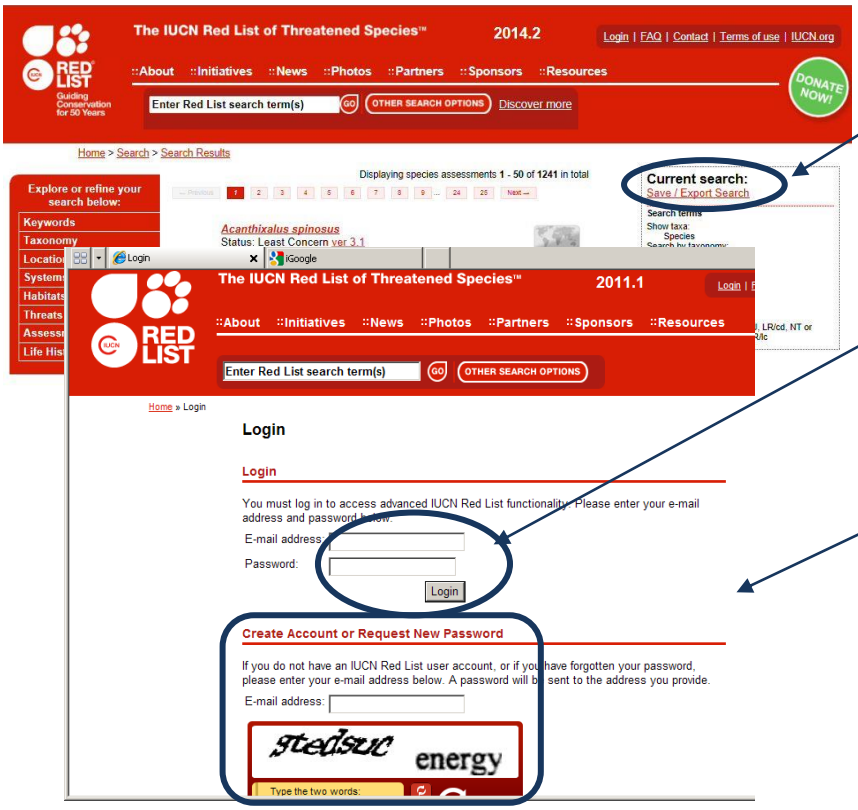
l. Click **Run search**

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 a list of species with 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, the 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



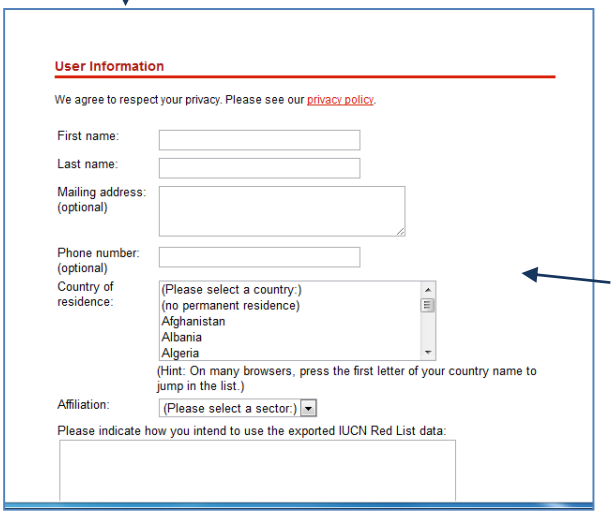
a. Click **Save/Export Search**

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

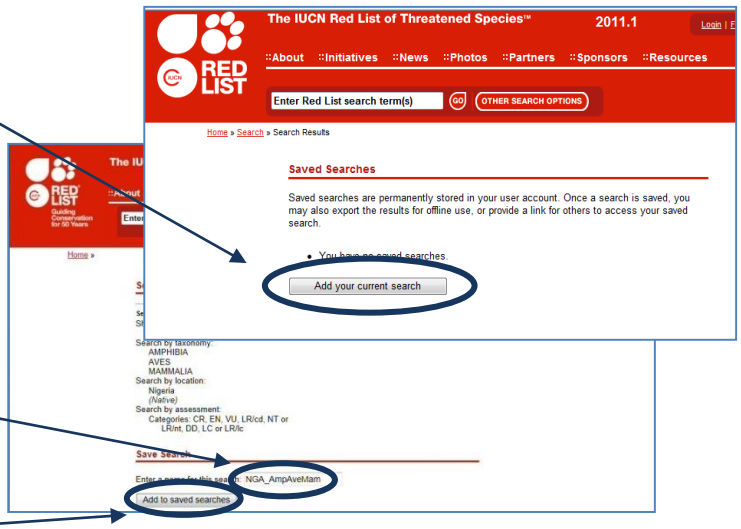


The first time new users export a search, they are required to fill out some information about themselves and the intended use of the data

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

Click on **Submit**

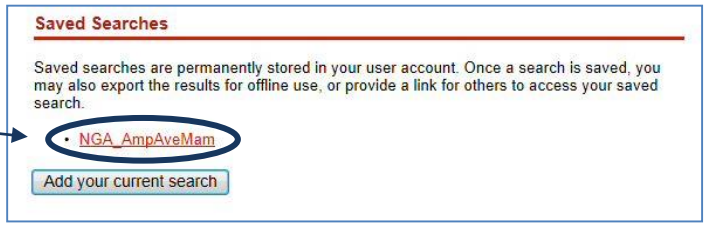
e. Once registered and/or logged in, Click on **Add your currentSearch**



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

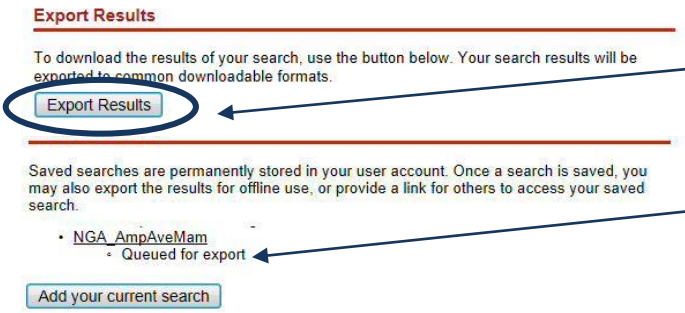
g. Click **add to saved searches**

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



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

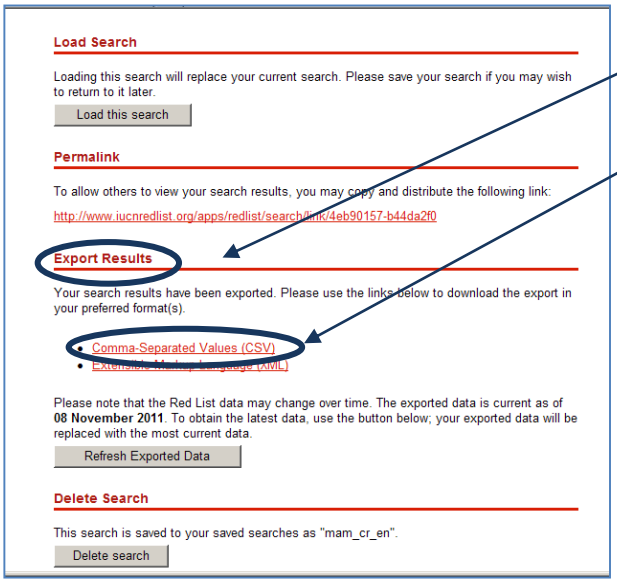
The dataset will then give a status of Queued for export.



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



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

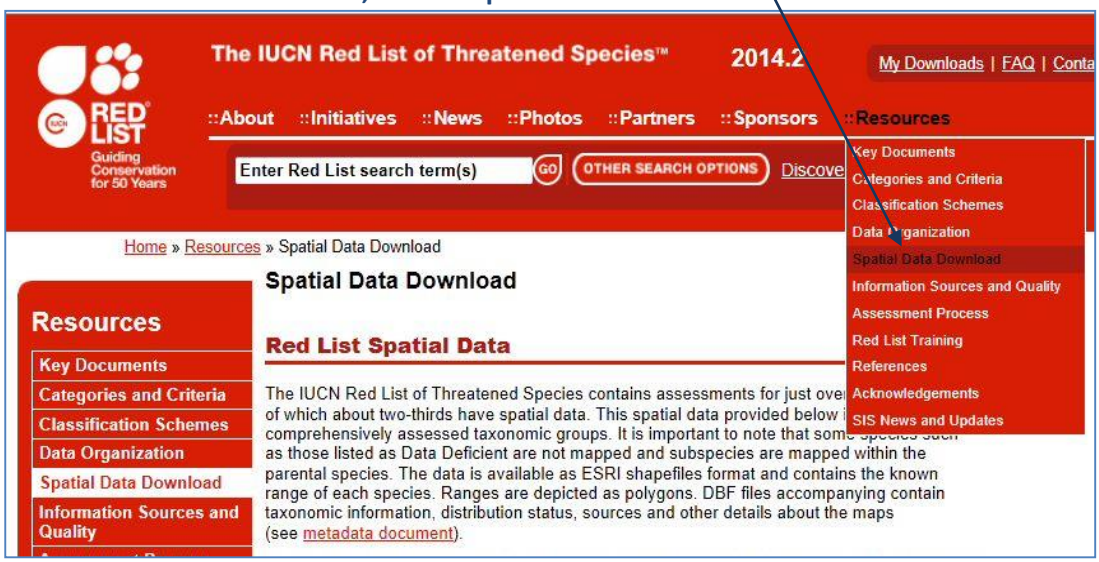
q. **Rename** the csv file e.g. **NGA_AmpAveMam.csv** in this example

2.1.3. Download the IUCN Red List spatial data layers

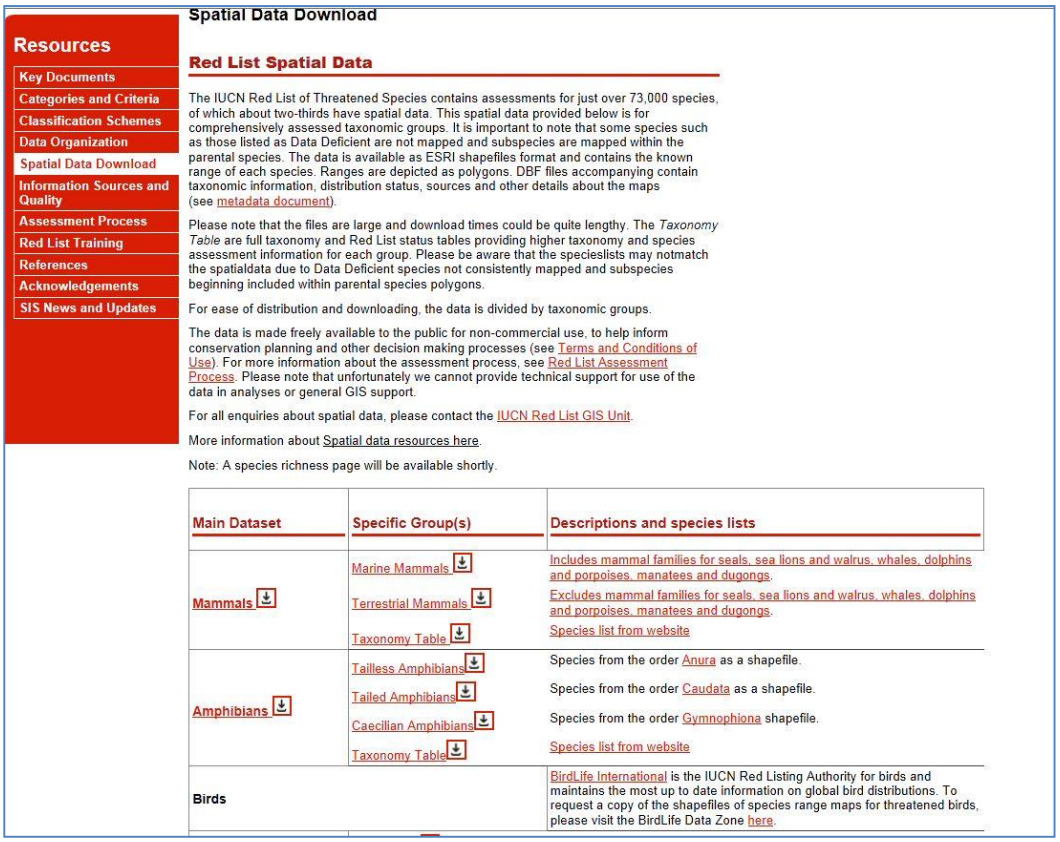
The next steps are for downloading spatial data. It is only possible to download the whole global dataset. It is not possible to filter by county prior to download. It is important to note that some of the spatial datasets are very large. If you have received the spatial data directly from IUCN you can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



Resources

- Key Documents
- Categories and Criteria
- Classification Schemes
- Data Organization
- Spatial Data Download
- Information Sources and Quality
- Assessment Process
- Red List Training
- References
- Acknowledgements
- SIS News and Updates

Spatial Data Download

Red List Spatial Data

The IUCN Red List of Threatened Species contains assessments for just over 73,000 species, of which about two-thirds have spatial data. This spatial data provided below is for comprehensively assessed taxonomic groups. It is important to note that some species such as those listed as Data Deficient are not mapped and subspecies are mapped within the parental species. The data is available as ESRI shapefiles format and contains the known range of each species. Ranges are depicted as polygons. DBF files accompanying contain taxonomic information, distribution status, sources and other details about the maps (see metadata document).

Please note that the files are large and download times could be quite lengthy. The *Taxonomy Table* are full taxonomy and Red List status tables providing higher taxonomy and species assessment information for each group. Please be aware that the speciesslists may notmatch the spatialdata due to Data Deficient species not consistently mapped and subspecies beginning included within parental species polygons.

For ease of distribution and downloading, the data is divided by taxonomic groups.

The data is made freely available to the public for non-commercial use, to help inform conservation planning and other decision making processes (see Terms and Conditions of Use). For more information about the assessment process, see Red List Assessment Process. Please note that unfortunately we cannot provide technical support for use of the data in analyses or general GIS support.

For all enquiries about spatial data, please contact the IUCN Red List GIS Unit.

More information about Spatial data resources here.

Note: A species richness page will be available shortly.

Main Dataset	Specific Group(s)	Descriptions and species lists
Mammals	Marine Mammals	Includes mammal families for seals, sea lions and walrus, whales, dolphins and porpoises, manatees and dugongs.
	Terrestrial Mammals	Excludes mammal families for seals, sea lions and walrus, whales, dolphins and porpoises, manatees and dugongs.
	Taxonomy Table	Species list from website
Amphibians	Tailless Amphibians	Species from the order Anura as a shapefile.
	Tailed Amphibians	Species from the order Caudata as a shapefile.
	Caecilian Amphibians	Species from the order Gymnophiona shapefile.
	Taxonomy Table	Species list from website
Birds		BirdLife International is the IUCN Red Listing Authority for birds and maintains the most up to date information on global bird distributions. To request a copy of the shapefiles of species range maps for threatened birds, please visit the BirdLife Data Zone here.

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)

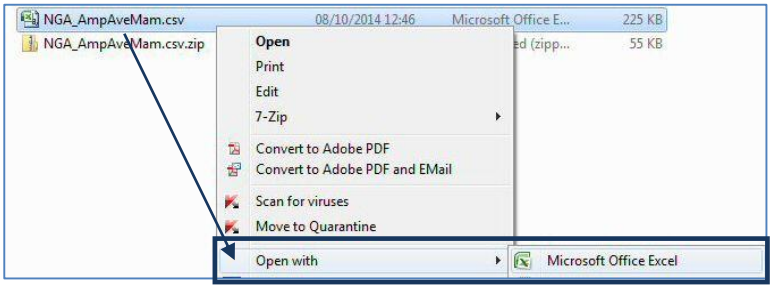
These files are all stored in geographic coordinate system (EPSG: 4326). Be aware the files are very large and will take some time to download.

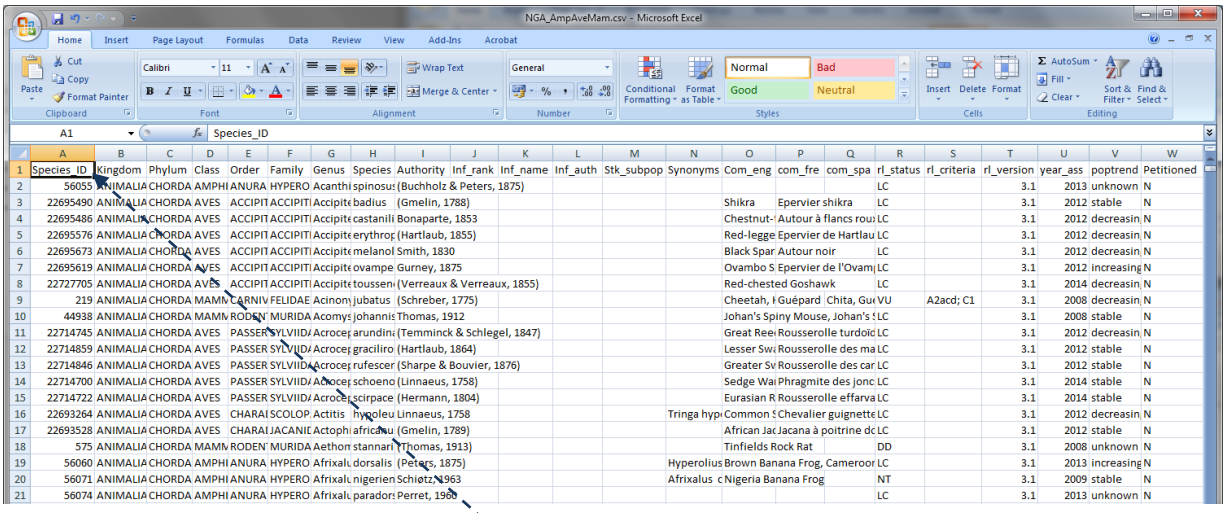
Note: If you have received the spatial data directly from IUCN they may have delivered as a single geodatabase containing all taxa in a single feature class rather than as separate files.

2.2. Vector Spatial Data Selection and Preparation

2.2.1. 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**

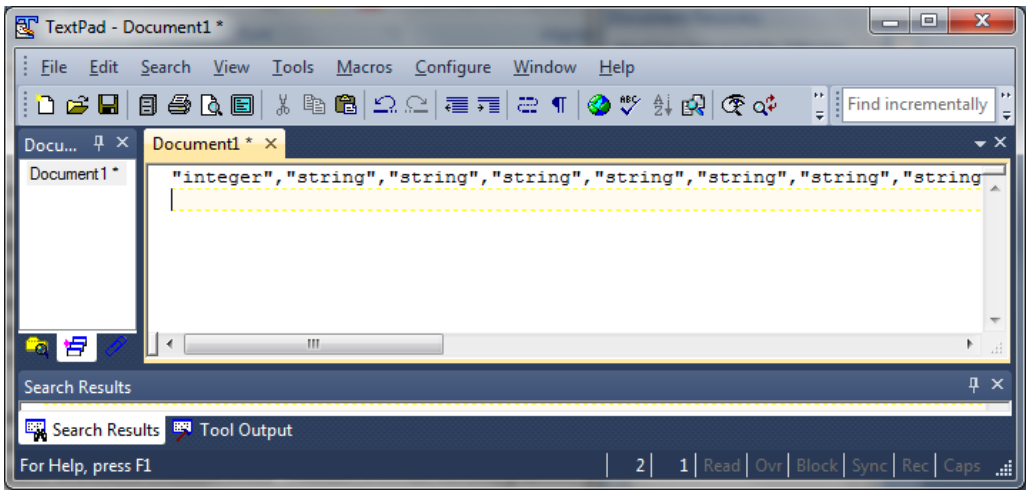
OLD Field Name		New Field Name
Species ID	=	Species_ID
Kingdom	=	Kingdom
Phylum	=	Phylum
Class	=	Class
Order	=	Order
Family	=	Family
Genus	=	Genus
Species	=	Species
Binomial	=	Binomial
Authority	=	Authority
Infraspecific rank	=	Inf_rank
Infraspecific name	=	Inf_name
Infraspecific authority	=	inf_auth
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 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).

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.

f. 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

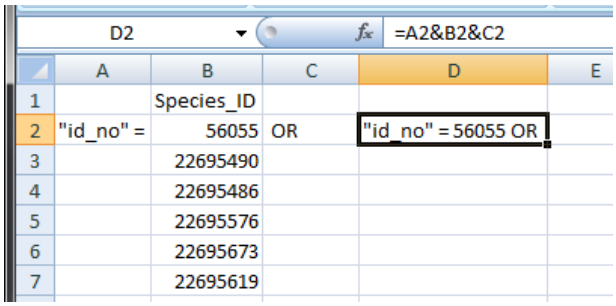
	A	B	C	D	E	F	G	H	I	J
1		Species_ID								
2		56055								
3		22695490								

g. 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

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

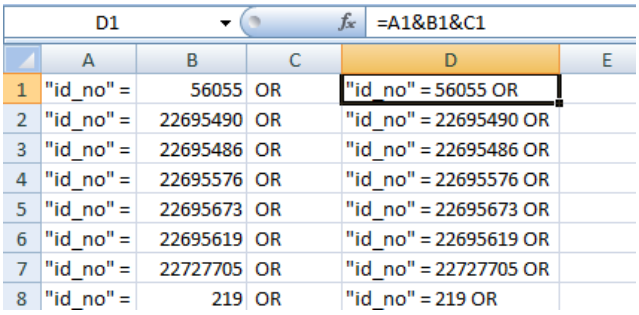
i. **In row 2** of **column D** type **=A2&B2&C2**

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



	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			

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



	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	

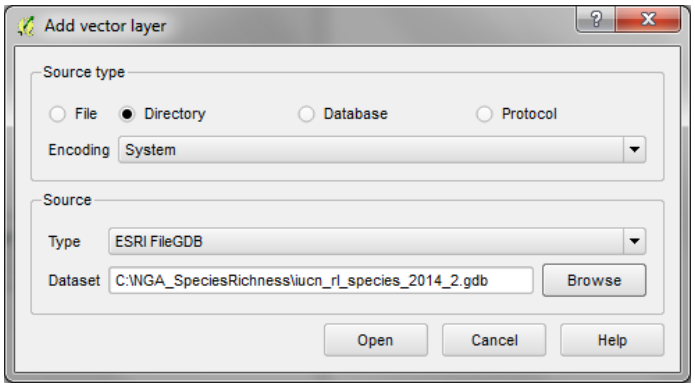
l. **Save** the worksheet for later to a **new file** e.g. in this example called **formatted_for_SQL_query.xlsx** and **close**

2.2.2. 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**

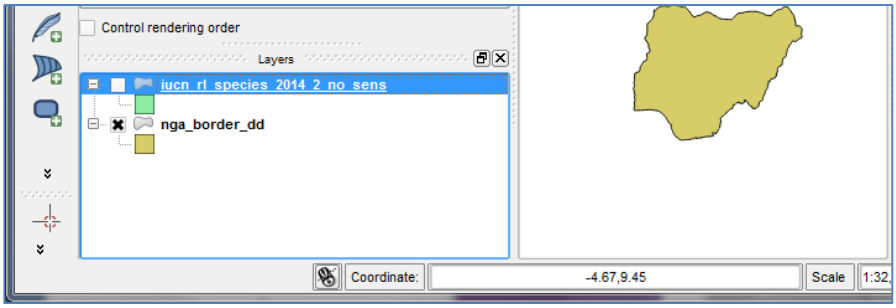
b. Add in the **IUCN Species spatial dataset(s)** (the data are in geographic coordinate system (i.e. EPSG:4326)



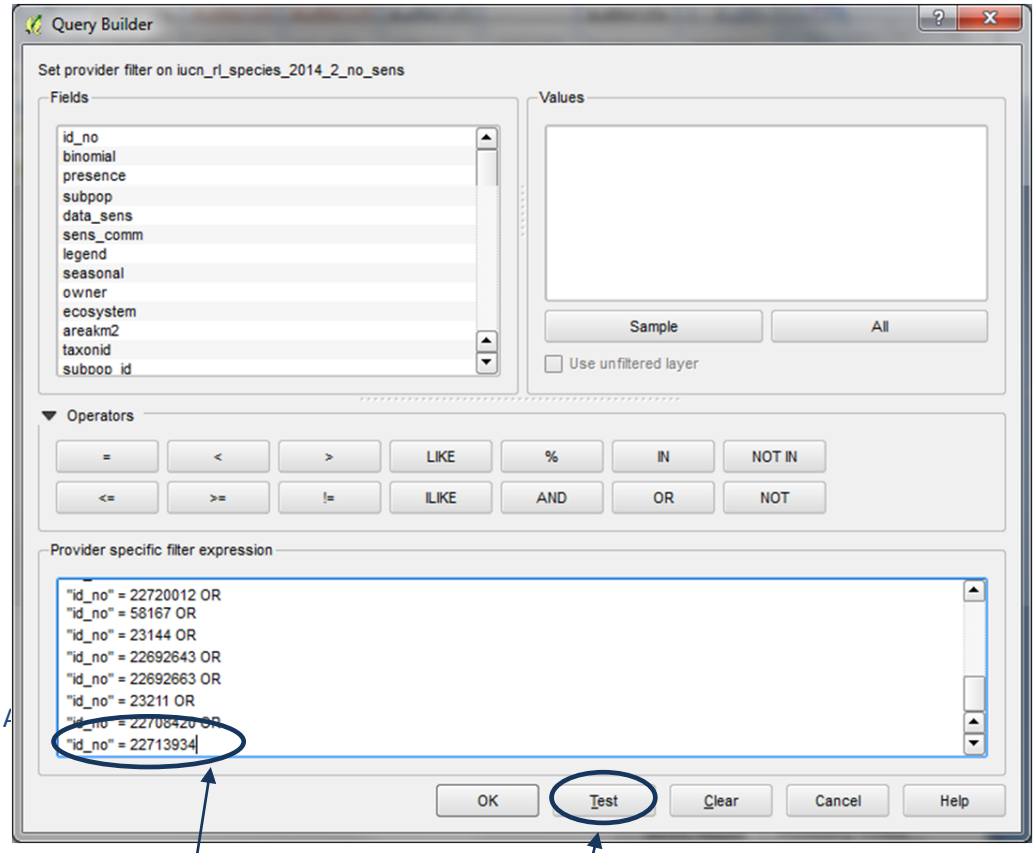
c. **Untick** the dataset in the table of contents to stop it drawing

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**

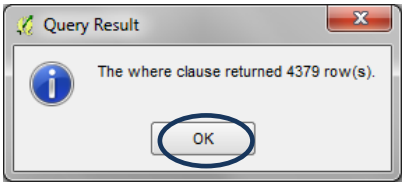


f. Right click on the IUCN spatial dataset and Click **Filter**



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

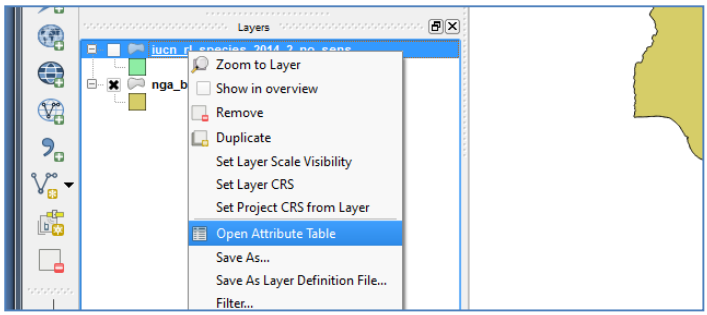


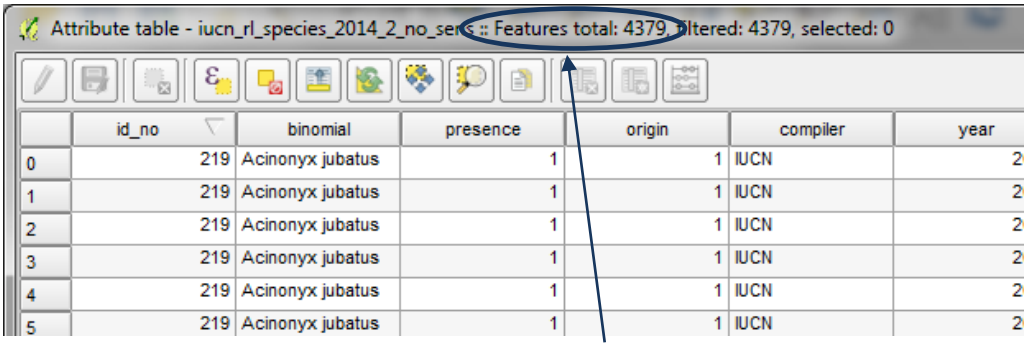
Note: This number does not equate to the number of species but to the number of polygons so you cannot use this to check that the number of species it has selected is correct.

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**

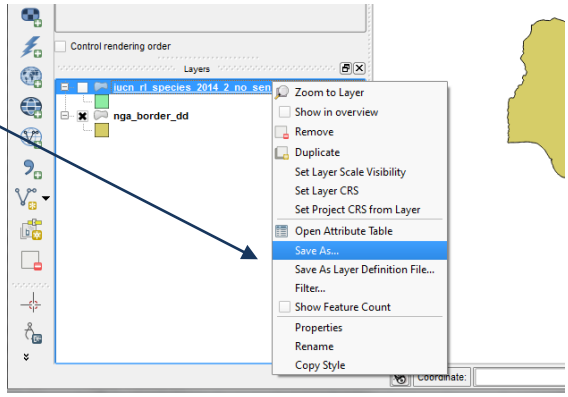


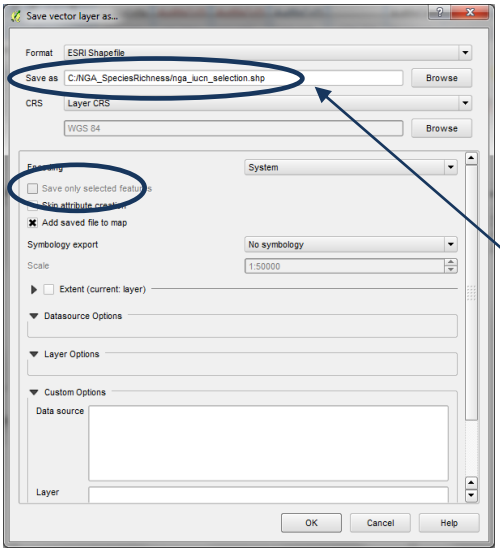


Note the attribute table shows only the records filtered by the SQL query.

l. **Close** the attribute table

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

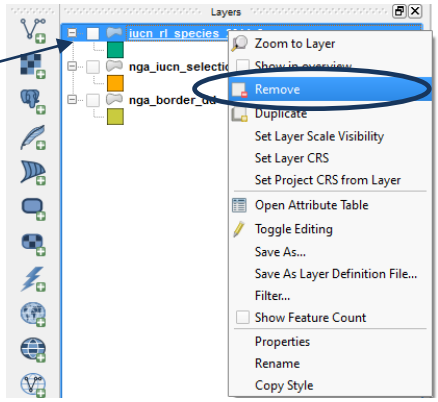




n. **Save** the file with a new name. **e.g. nga_iucn_selection.shp** in this example and **Click OK**

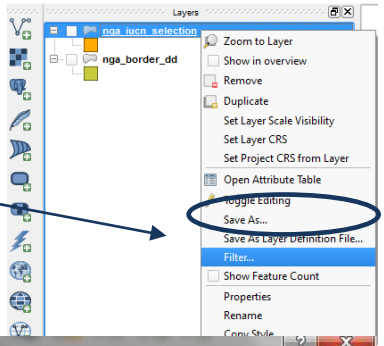
Note: Saving may take a long time (likely 40 minutes for a selection with about 1500 species from the global layer) so be patient.

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**



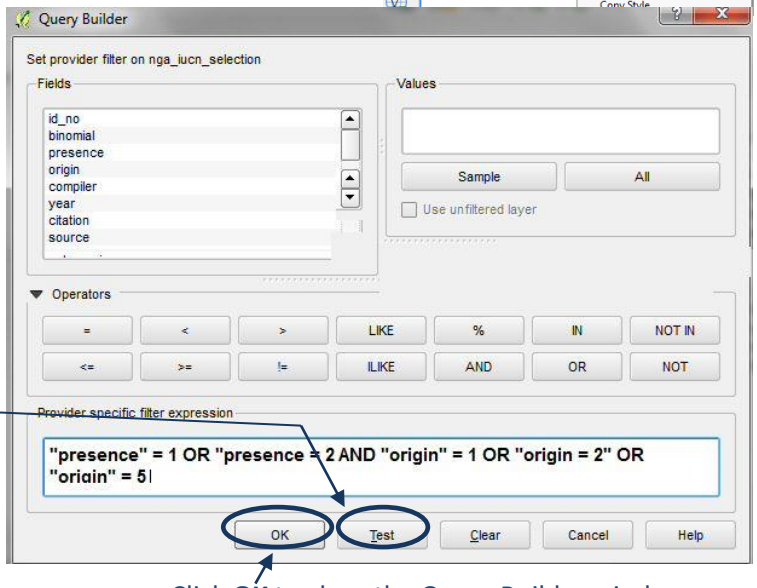
2.2.3. From the previous selection select out the current native species range

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



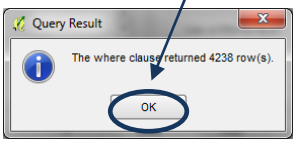
b. To only include categories as advised by IUCN Presence - 1 (extant); 2 (probably extant); 6 (presence uncertain) Origin – 1 (native); 2 (reintroduced); 5 (origin uncertain)

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

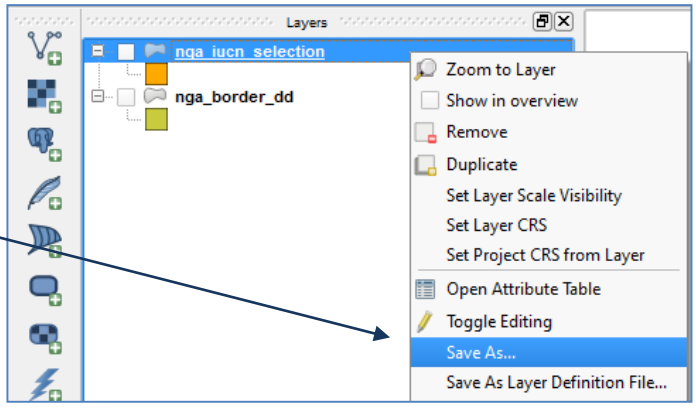


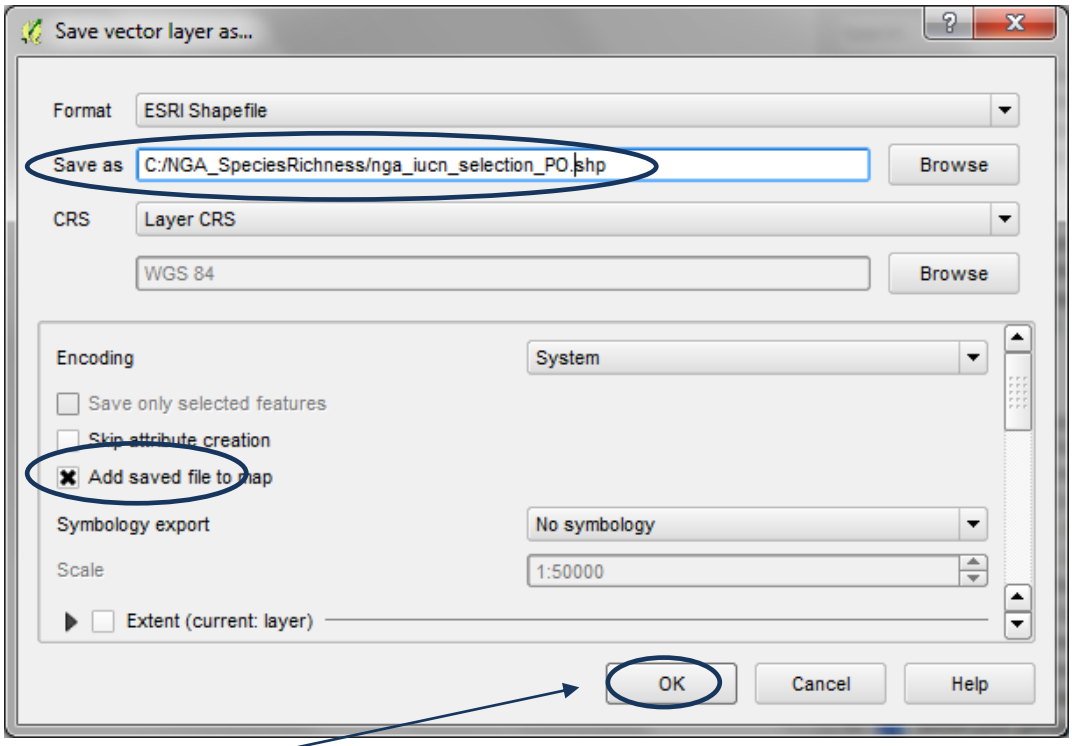
e. Click **OK** to close the Query Builder window

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

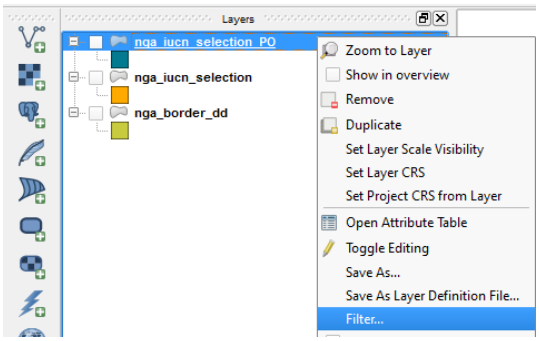




i. Click **OK**

2.2.4. From the previous selection select out terrestrial species ranges

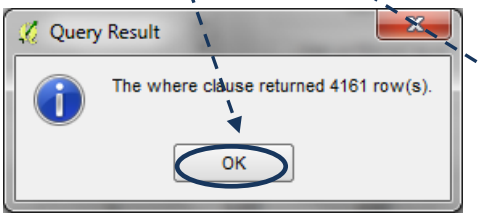
a. Right click on the **newly added subset species layer e.g. nga_iucn_selection_PO.shp** in this example and and **Click Filter**



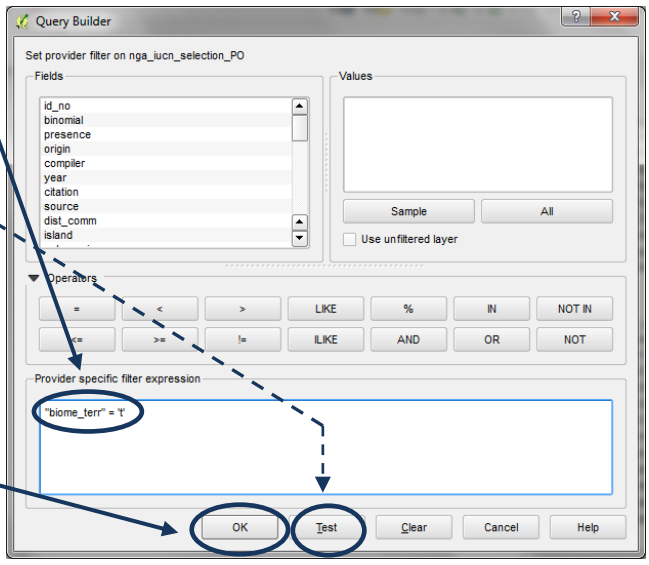
b. To only include species which are terrestrial put the following expression into the Query Builder window: **"biome_terr" = 't'**

c. Click **Test**

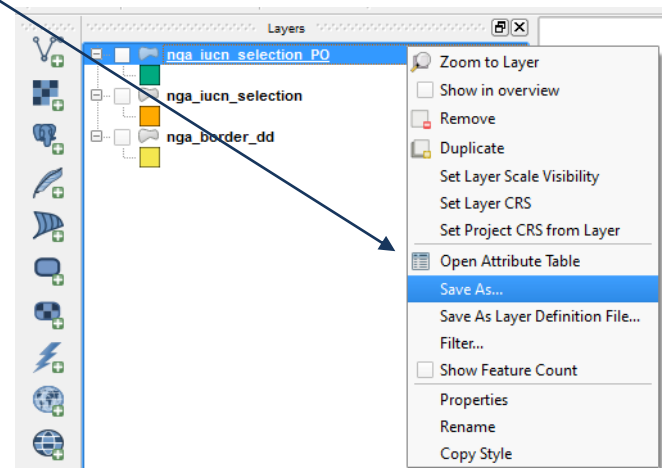
d. Click **OK** to close the Query Result window



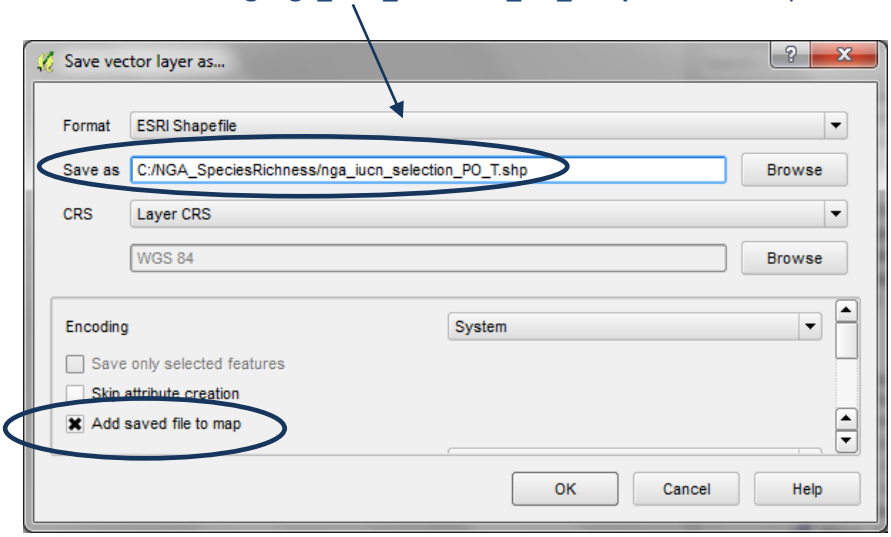
e. Click **OK** to close the Query Builder window



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

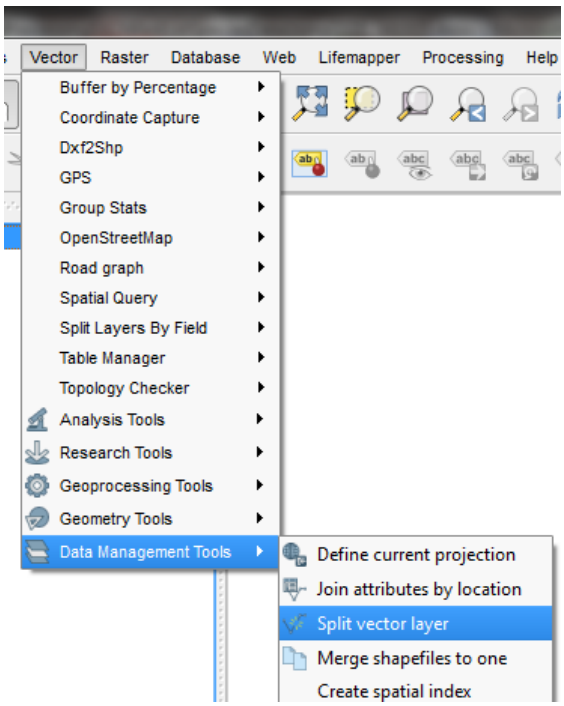


g. **Save** the file with a new name. **e.g. nga_iucn_selection_PO_T.shp** in this example

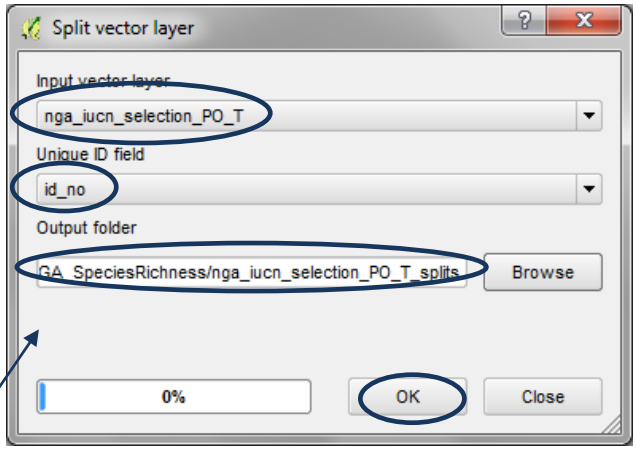


2.2.5. Split the final subset IUCN dataset into separate files by species

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**



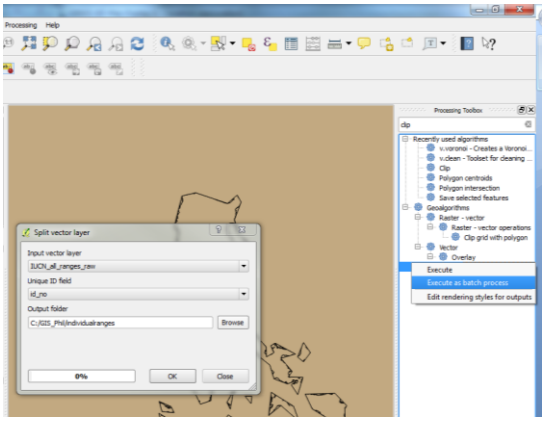
c. Under **unique ID field** choose the **field to base the split on**. Select **id_no**, this contains a unique ID for each species.

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**

2.2.6. Batch clip the separate species datasets to area of interest

a. In QGIS 1.8 go to **Analysis>>SEXTANTE toolbox** (or in QGIS 2.8. **Processing menu >> Toolbox**.

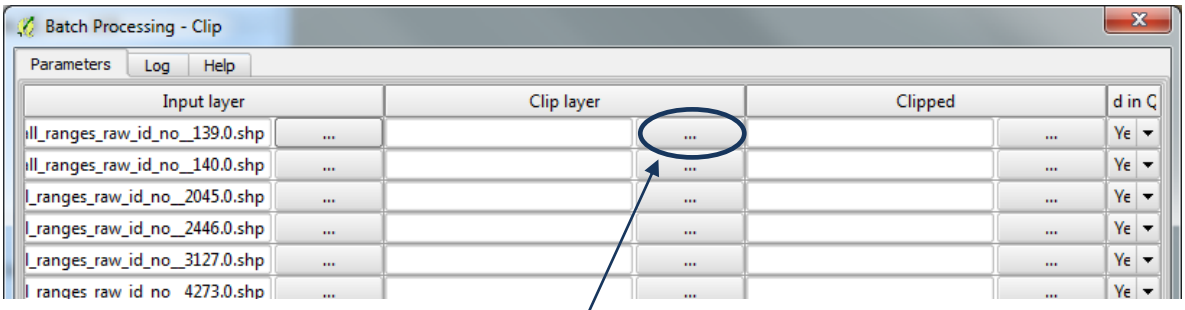


Note: - there has been significant improvement in QGIS 2.8 in the batch environment and therefore if possible use this rather than QGIS 1.8 which requires some manual filling of the inputs

b. In the **search box** at the top of the toolbox, **write clip**.

c. **Right click** on **clip** and choose **Execute as batch process.**

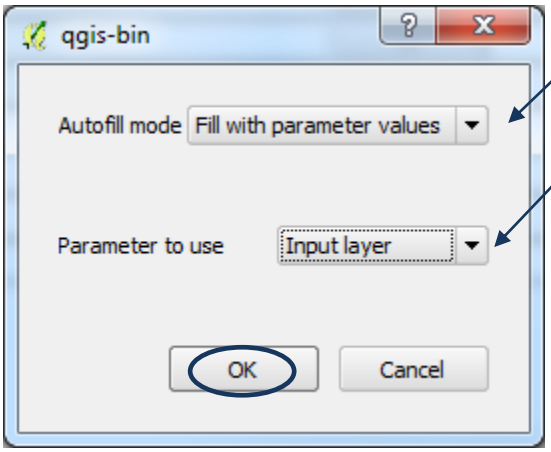
d. In the **input layer column**, click on the **'...'** box and select all of the species range files that you want to clip (**use the shift key** to select multiple files).



e. In the **clip layer** column, click on the **'...'** box and select the **vector boundary file** covering your area of interest.

f. **Double click** on the **top of the clip layer column**, to fill every cell. *(This is the bit that does not work in QGIS 1.8 and you have to copy and paste the contents into every row)*

g. In the **clipped column**, click on the **'...'** box and **select the location** to store your clipped files and **type a new name** e.g. clip.shp *(this will be the name preceding the filename of the clipped files)*

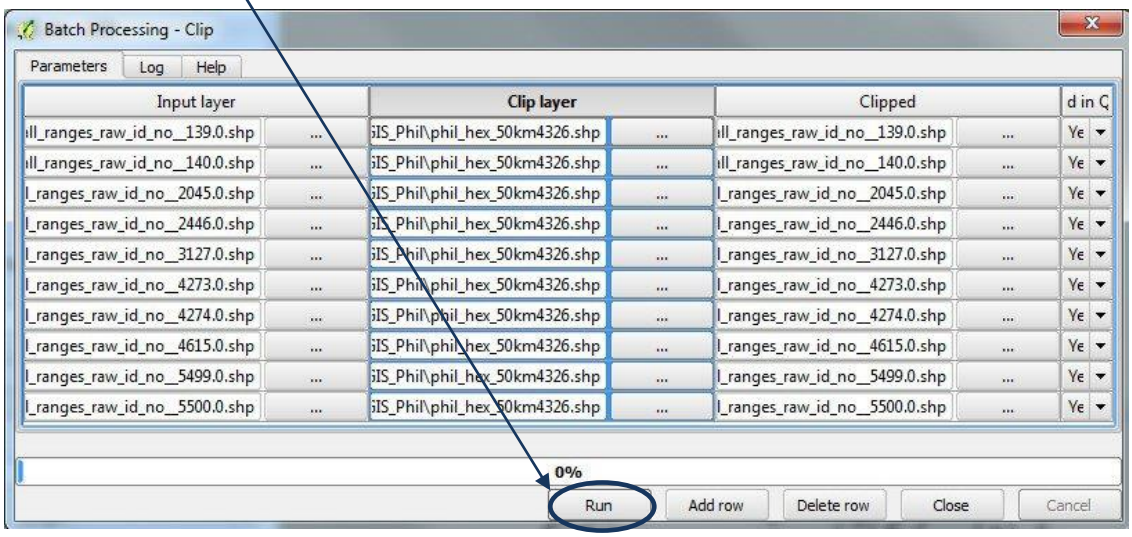


h. In the pop-up box, under **Autofill Mode** select **Fill with parameter values.**

i. These parameter values should be set from the **input layer**.

j. Click **OK**.

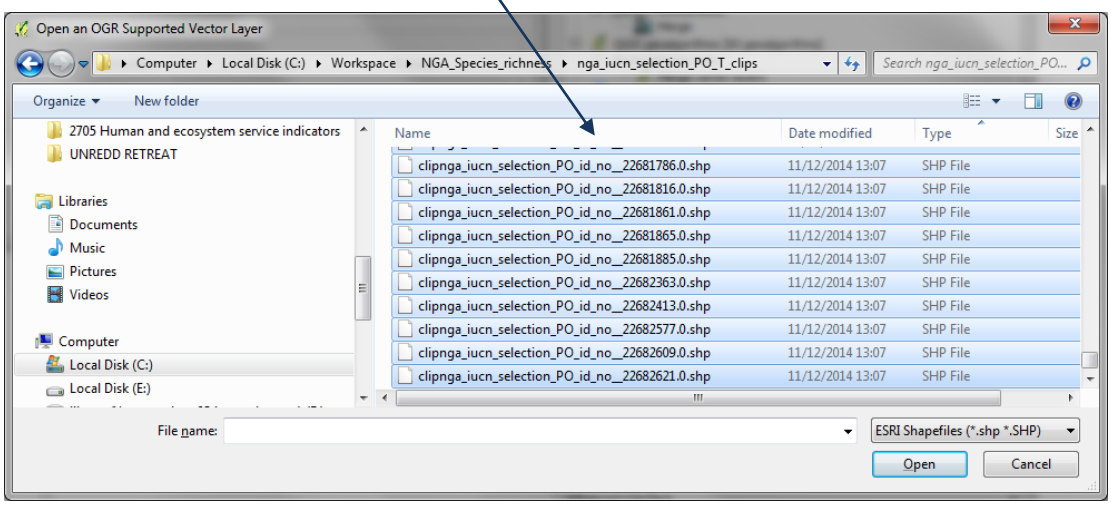
k. Click **Run**



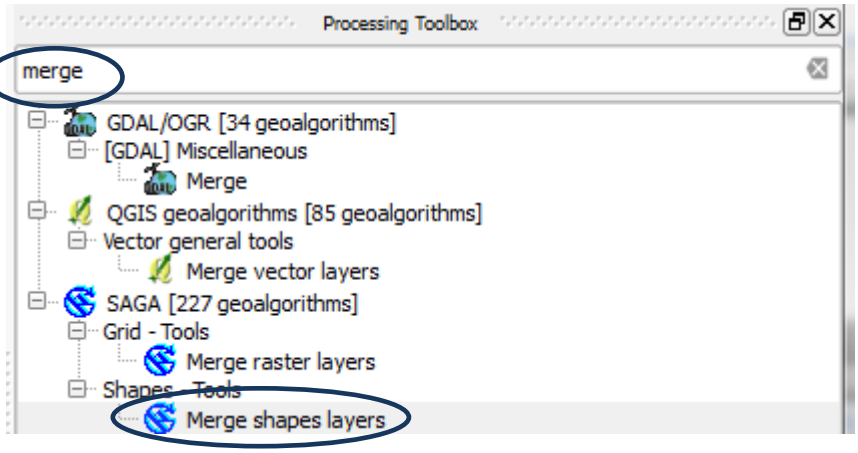
2.2.7. Merge individual files back into a single dataset

a. Remove all layers from your QGIS project

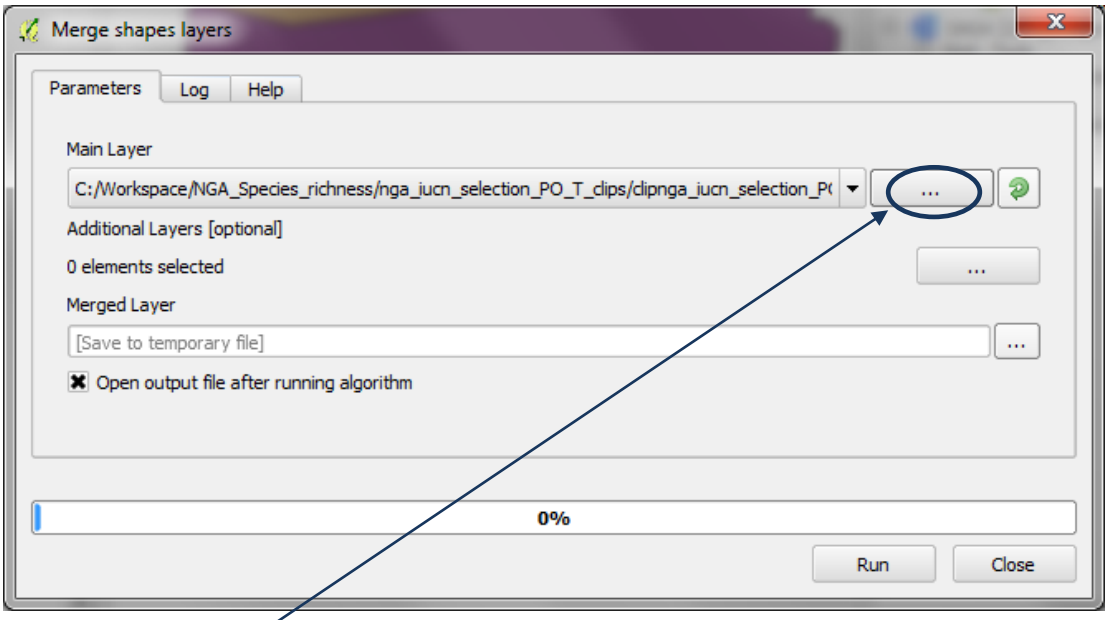
b. Add in all the clipped species shapefiles



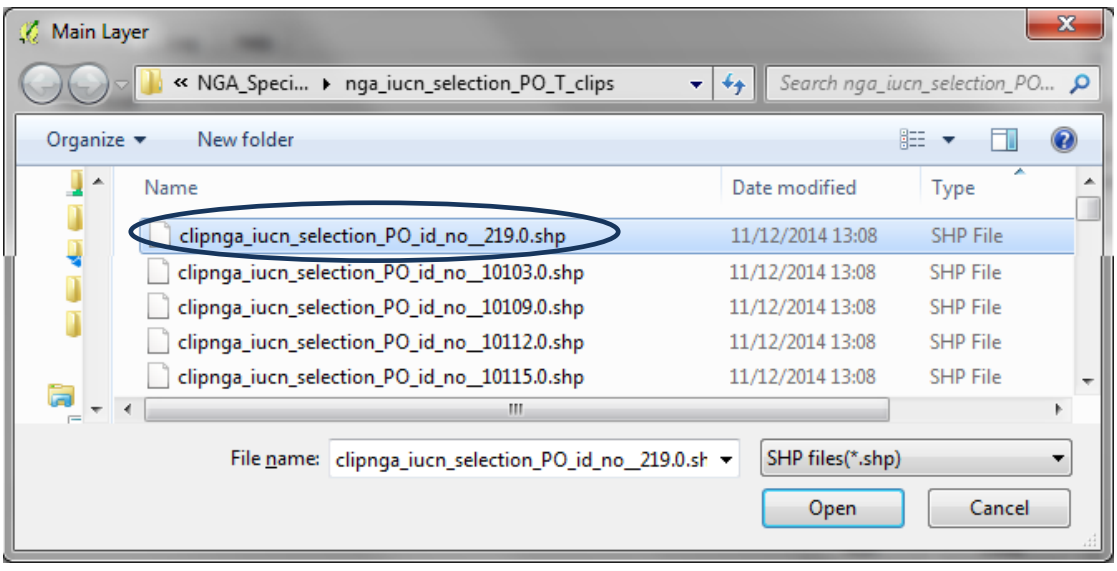
c. Search for **merge** in the **Processing toolbox**



d. Double click on the SAGA **Merge shapes layers** tool. This is the only tool currently available that lets you merge more than two shapefiles at once.



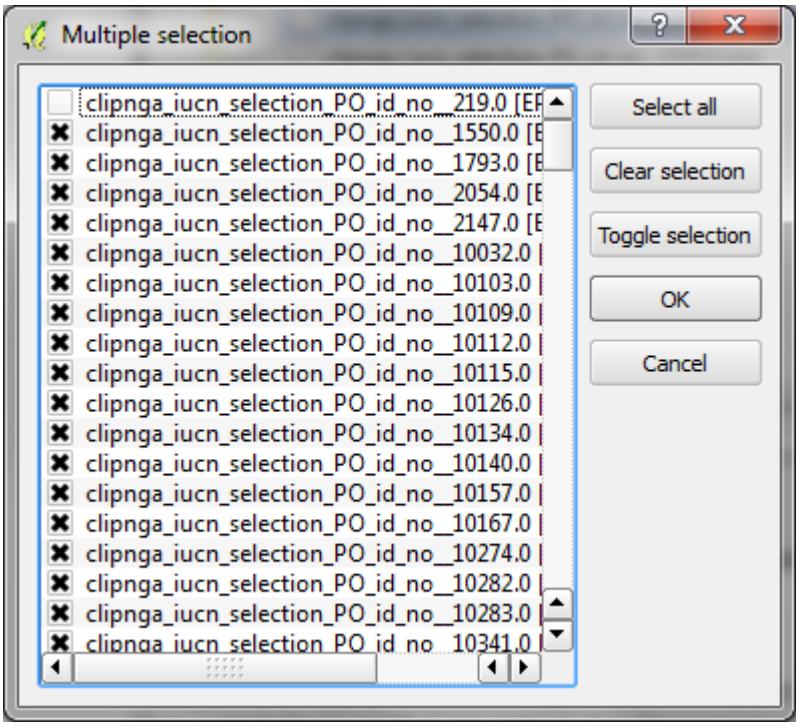
e. Click on the **…** next to the **Main Layer** and navigate to the folder containing the clipped shapefiles. Pick the **first shapefile** in the **list** e.g. in this example clipnga_iucn_selection_PO_id_no__219.0.shp



f. Click on the **…** next to **Additional Layers** and click Select All

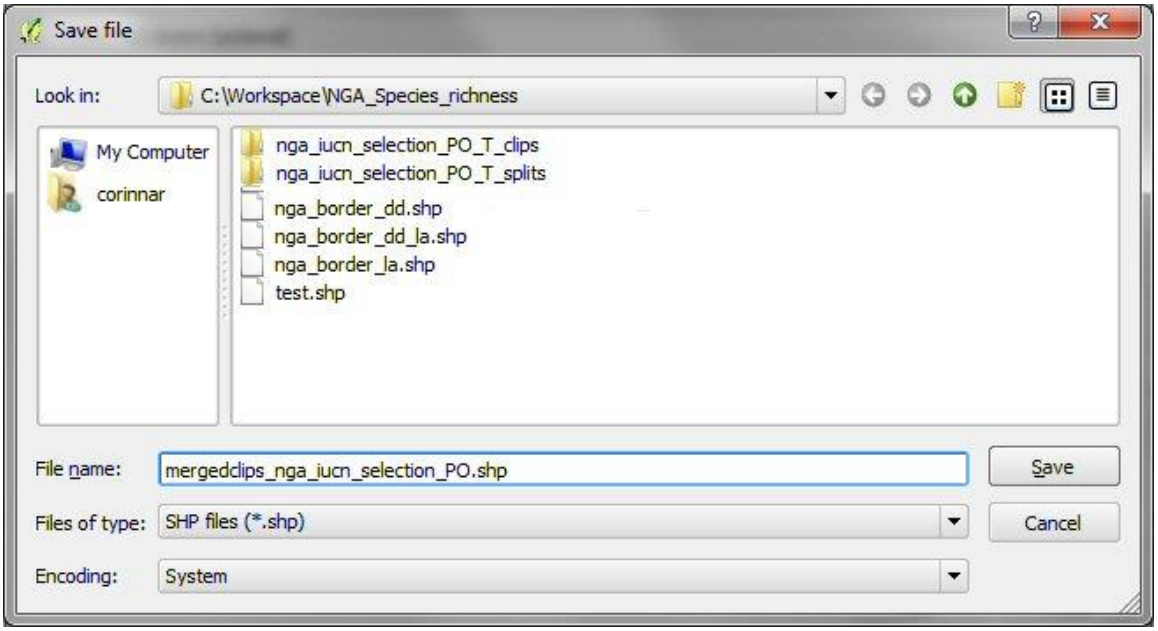
g. Then **untick the layer that you selected as the main layer.** E.g. in this example **clipnga_iucn_selection_PO_id_no__219.0.shp**

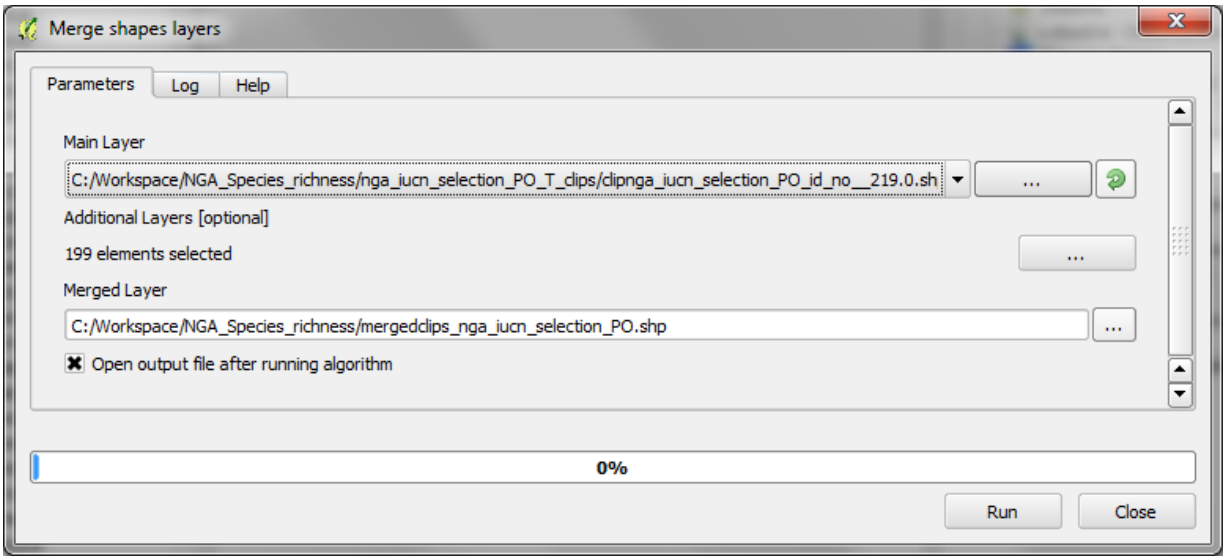
As we removed all other layers from the table of contents we can click 'select all'. This adds the rest of the species layers which will be merged with the layer chosen as the main layer.



h. Click OK

i. Click on the **…** next to **Merged Layer** and navigate to an output folder and save the Merged Layer with a new name e.g. in this example **mergedclips_nga_iucn_selection_PO.shp**





j. Click Run

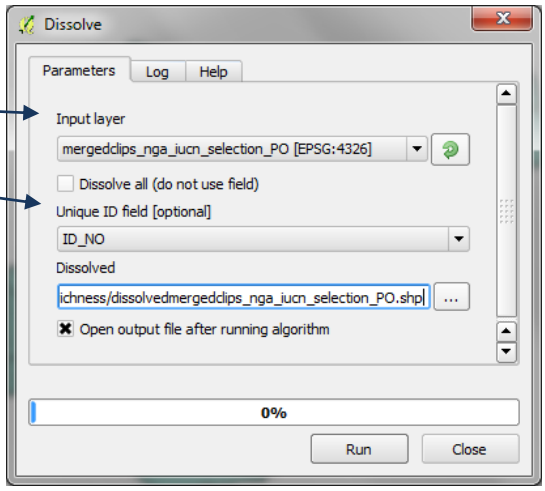
2.2.8. Dissolve and convert to single part features

a. From the main menu click on the **Vector>> Geoprocessing Tools>>Dissolve** tool

b. Select the **merged IUCN species range dataset for the input layer**

c. Select the species **id_no** as the **Unique ID** field (i.e. the field to dissolve on)

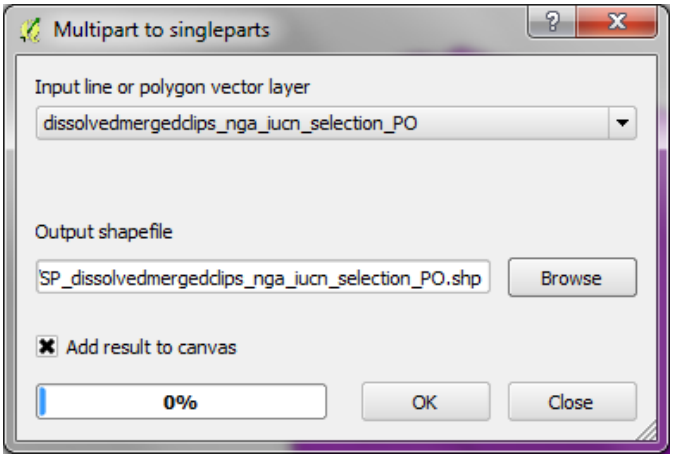
d. Navigate to the **output folder** to save the dissolved dataset with a new name e.g. in this example **C:\Workspace\NGA_Species_richness\ dissolvedmergedclips_nga_iucn_selection_PO .shp**



e. Next convert the dissolved dataset to single part features (i.e. so that there is one row in the attribute table for every polygon rather than one row for every group of polygons with the same attribute). From the main menu click on the **Vector>> Geometry Tools>>Multiparts to singlepart** tool

f. Select the **dissolved dataset** as the Input Layer e.g. in this example **C:\Workspace\NGA_Species_richness\ dissolvedmergedclips_nga_iucn _selection_PO .shp**

g. Navigate to the **output folder** to save the dissolved dataset with a new name e.g. in this example **C:\Workspace\NGA_Species_richness\ SP_dissolvedmergedclips _nga_iucn_selection_PO .shp**



h. Click **OK**

i. Remove all layers from your QGIS project except the singlepart species dataset generated in the previous step
e.g. in this example **C:\Workspace\NGA_Species_richness\SP_dissolvedmergedclips _nga_iucn_selection_PO .shp**

2.2.9. Save dataset to an equal area projection

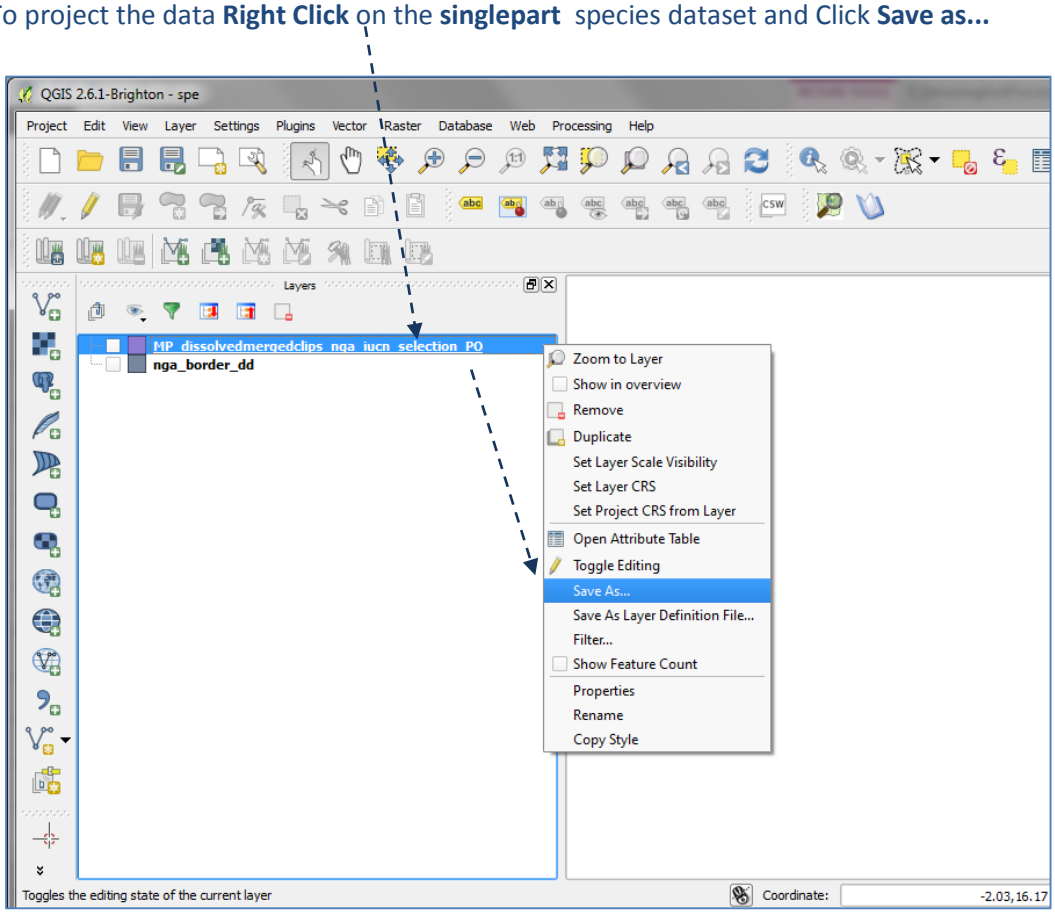
In subsequent steps a layer called a **planning unit layer** will be generated in order to **summarise the species range data to create a species richness map**. The planning unit layer may simply be a regular grid of squares or hexagons across the area of interest or an irregular summary unit for example territories within a country. The species range and the planning units layers must be projected to an equal area projection (e.g. Lambert Azimuthal Equal Area). Using an equal area projection allows the true area of the species ranges in each planning unit to be calculated. Whichever projection is chosen, both the species ranges and the planning units **must** be in exactly the same projection.

In this example, the data are in CRS EPSG:4326 (a geographic coordinate system with units in decimal degrees). In order to generate a planning units dataset of hexagons with a specific area, the data need to be projected into an equal area CRS with units of meters. In the following example Lambert-azimuthal-equal-area projection is used.

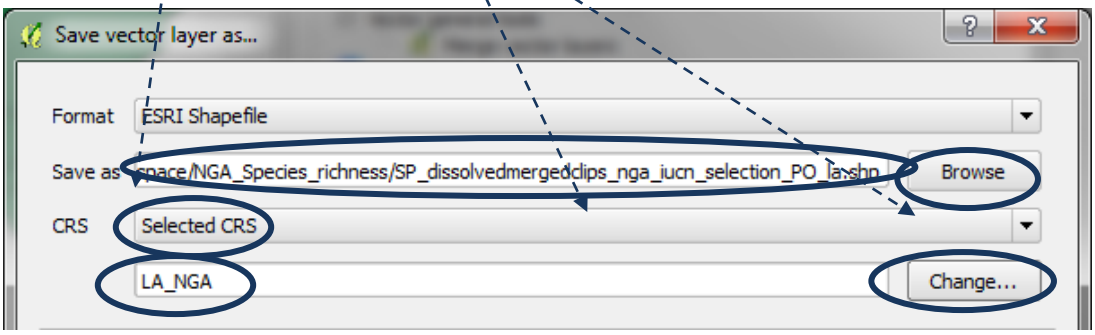
*Note: - The there is currently a bug in the project tool in QGIS 2.8 and therefore below we are using the **right-click>> save-as** option **to change the projection***

*There may be an appropriate equal area projection that is already defined within QGIS suitable for your area of interest, or you may have already defined a custom projection. To create a new a custom projection follow the instructions in **Box D.***

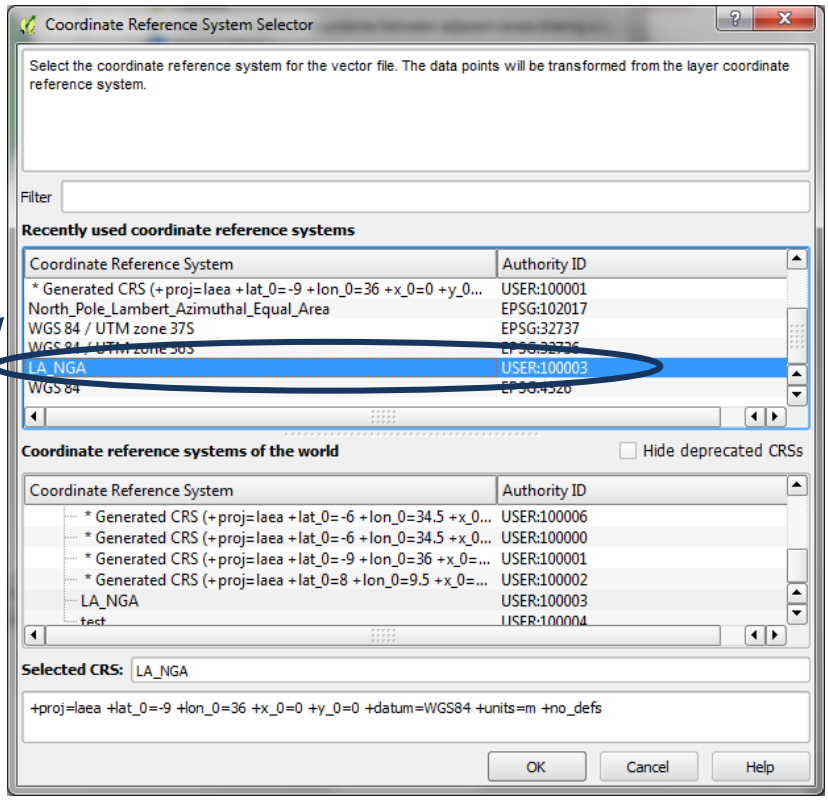
a. To project the data **Right Click** on the **singlepart** species dataset and Click **Save as...**



b. Choose **Selected CRS** and click **Browse** next to the **Save as** box to create a new output dataset e.g. **SP_dissolvedmergedclips_nga_iucn_selection_PO_la.shp** in this example



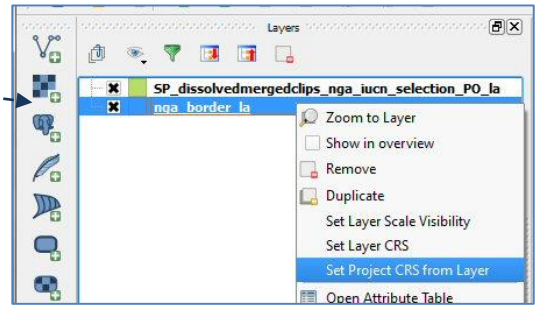
c. Click on **Change** to change the output ptojection. **In this example we are using a custom Lambert -azimuthal-equal-area projection.**



d. Add the **country boundaries** shapefile back into QGIS e.g. in this example **nga_border_dd.shp** and **repeat the save as step** to save it in same equal area projection as your species layer.

b. Remove the Geographic version of the datasets from the QGIS project to reduce confusion.

c. Finally**, Right click** on one of the layers and **Set Project CRS from Layer** so that the project projection is now the same as the layers



There should now just 2 files in the project :-

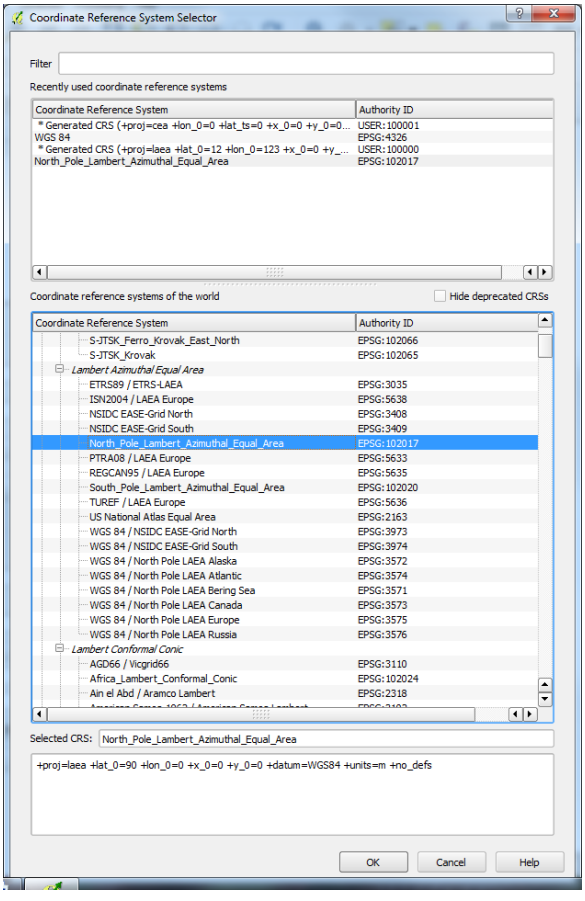
- *The projected species single part dataset: e.g.* ***SP_dissolvedmergedclips_nga_iucn_selection_PO_la.shp***
- *The projected country boundary dataset: e.g.* ***nga_border_la.shp***

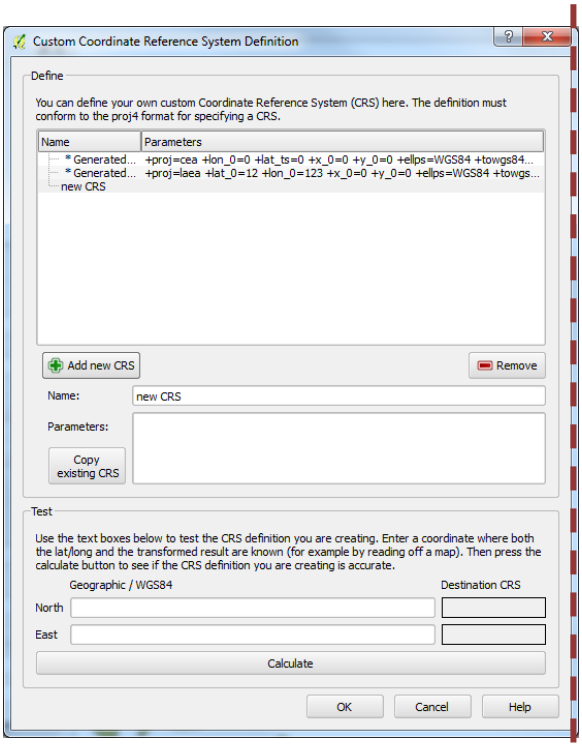
Box D

It may be useful (although not always necessary) to create a **custom projection**, for example a Lambert Azimuthal Equal Area projection centred on a particular country or world region. In this example, the projection is centred on the Philippines, with a Central Meridian (longitude of origin) of 123 and a Latitude of Origin of 12. To centre the projection on a different country or region, a different Central Meridian and Latitude of Origin are required.

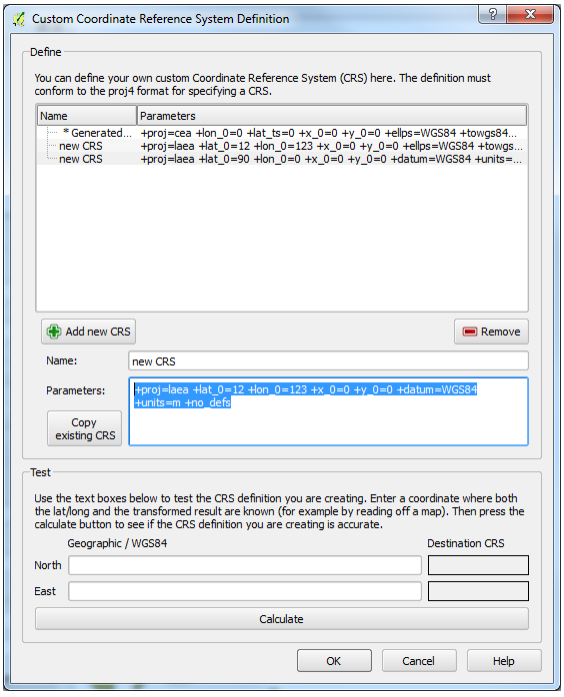
To create a custom projection, go to the settings menu in QGIS and choose **Custom CRS**. Click **Add new CRS**, and give your projection a name.

Choose the parameters. For a Lambert Azimuthal Equal Area projection, click on **Copy existing CRS**, and select **North_Pole_Lambert_Azimuthal_Equal_Area**. Click **OK**.





Then edit the information in the parameters box to change the central meridian and latitude of origin to centre the projection on a particular country or region. For the Philippines this means setting lat_0=12 and lon_0=123. Click **OK**.

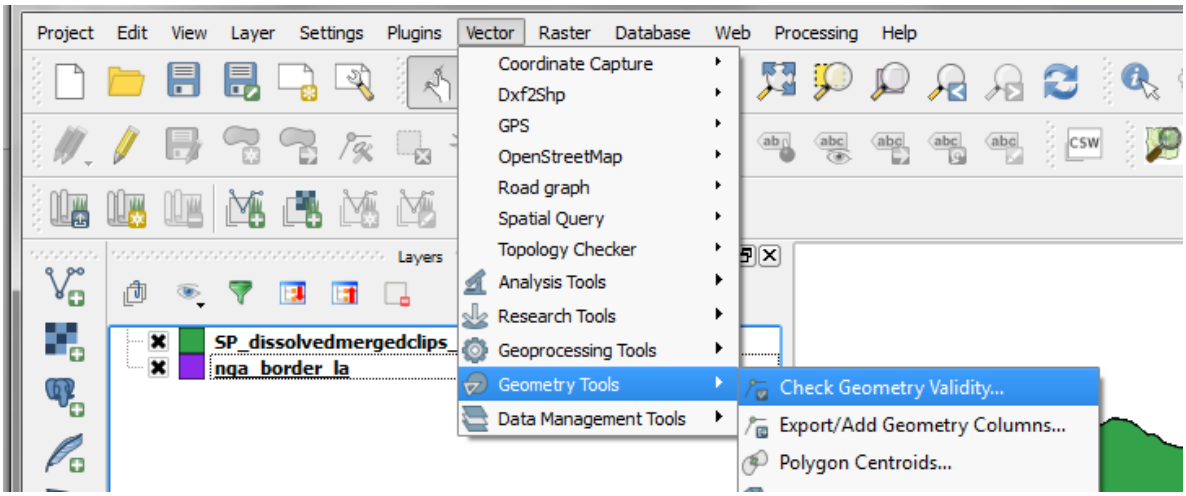


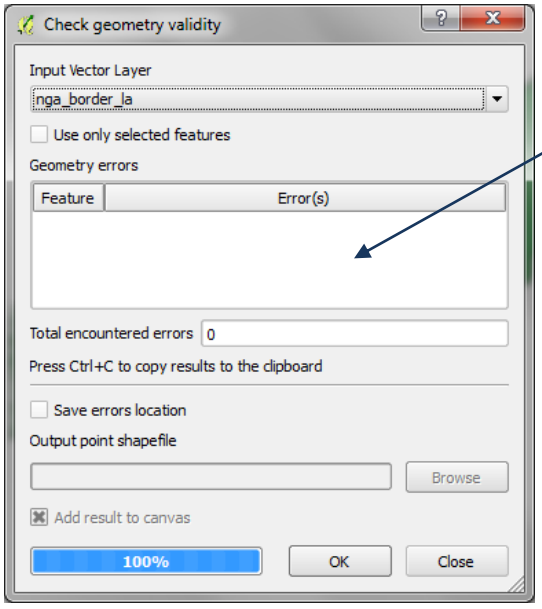
2.2.10. Check data for topological errors

Check for topological errors in the data as these could prevent the Qmarxan plugin working correctly.

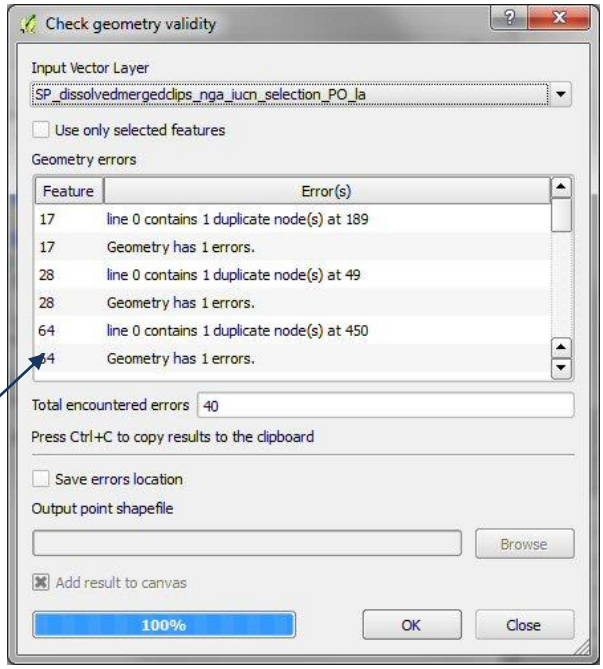
Check for geometry errors in the projected IUCN and the country boundaries shapefiles

j. From the vector menu click **Geometry Tools>>Check geometry validity**. Run for **both** dataset. (Remember to click **OK** to run the tool)





k. In this example the country boundaries file reported **0 errors**



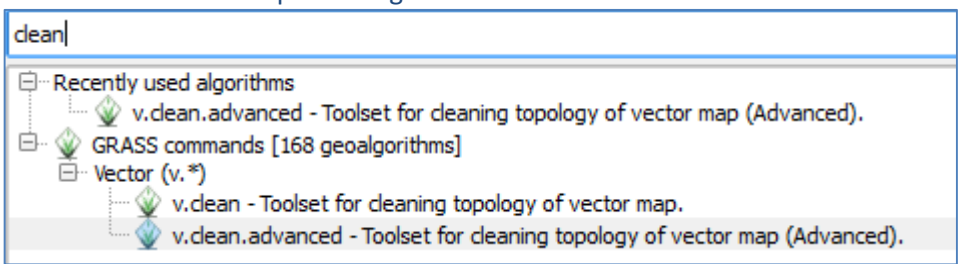
l. BUT In the IUCN data there are some **errors to fix.**

*Note the **Feature Ids** that contain errors. These refer to the record id's of the polygons in the spatial dataset*

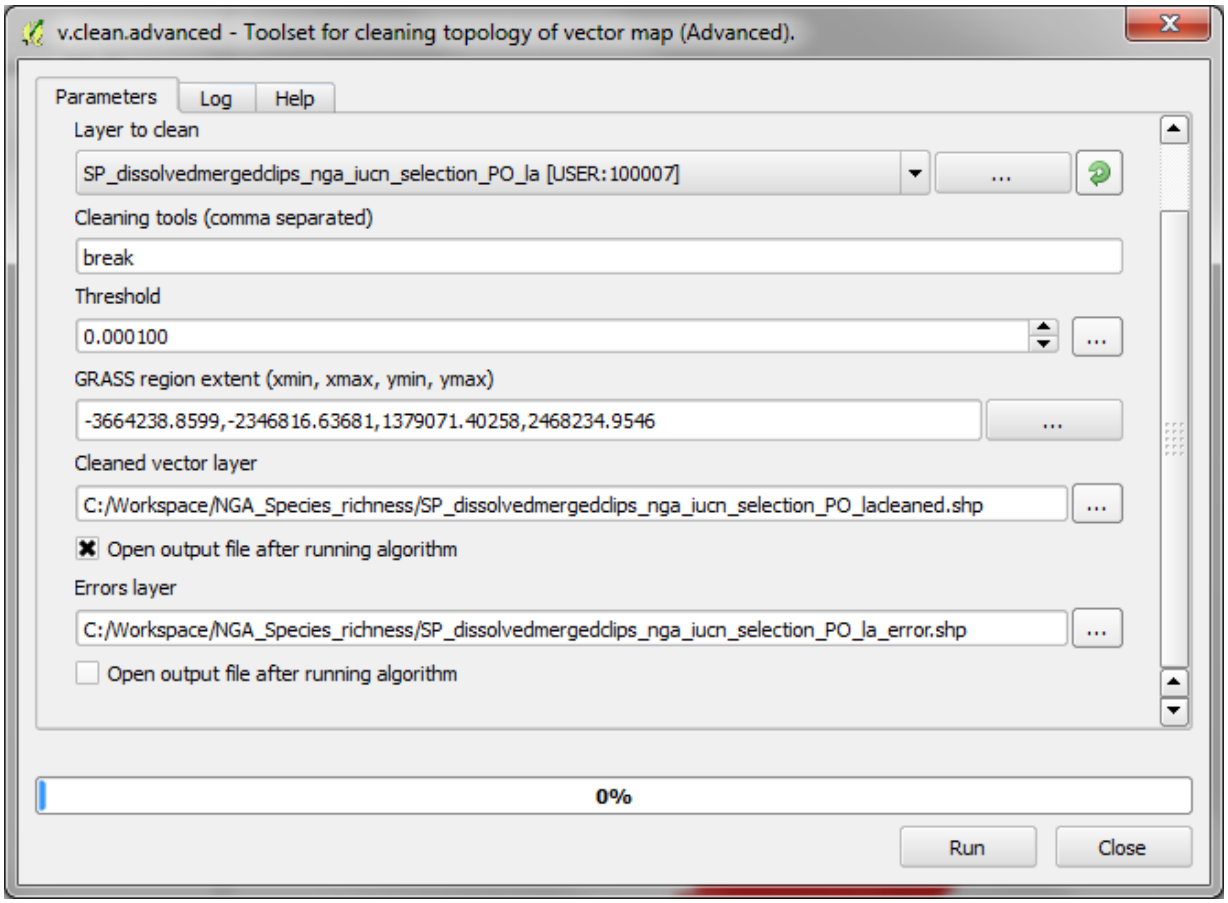
If errors are reported continue to step 2.2.11, otherwise go straight to section 2.3

2.2.11. Clean the dataset to remove the errors

Search for **clean** in the processing toolbox



Double click on the **v.clean.advanced** tool

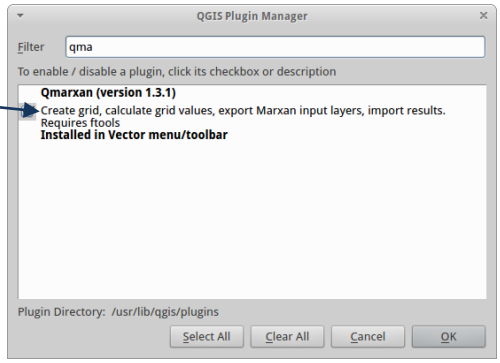


Note: If the dataset is very large and QGIS is failing to clean the dataset the clean tool can be run in the native GRASS interface. Some guidance notes are provided in the Annex for cleaning a dataset natively in GRASS.

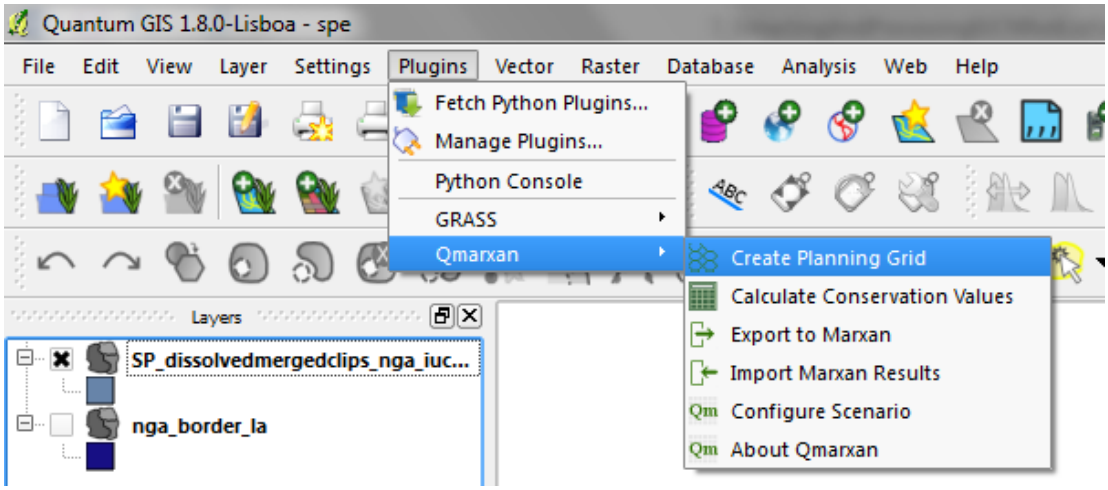
2.3. Vector analysis to create species richness (in QGIS 1.8 only as requires QMarxan plugin)

2.3.1. Generate a dataset of hexagons or squares using the Qmarxan plugin

a. **Fetch** the **latest QMarxan plugin** from the QGIS tool repository and activate it from the **Plugins>>Manage Plugins** menu



b. From the Plugins menu click **Qmarxan>>Create Planning Grid**



c. Select the **projected Area of interest file** e.g. nga_border_la.shp and click **Update extents from layer**

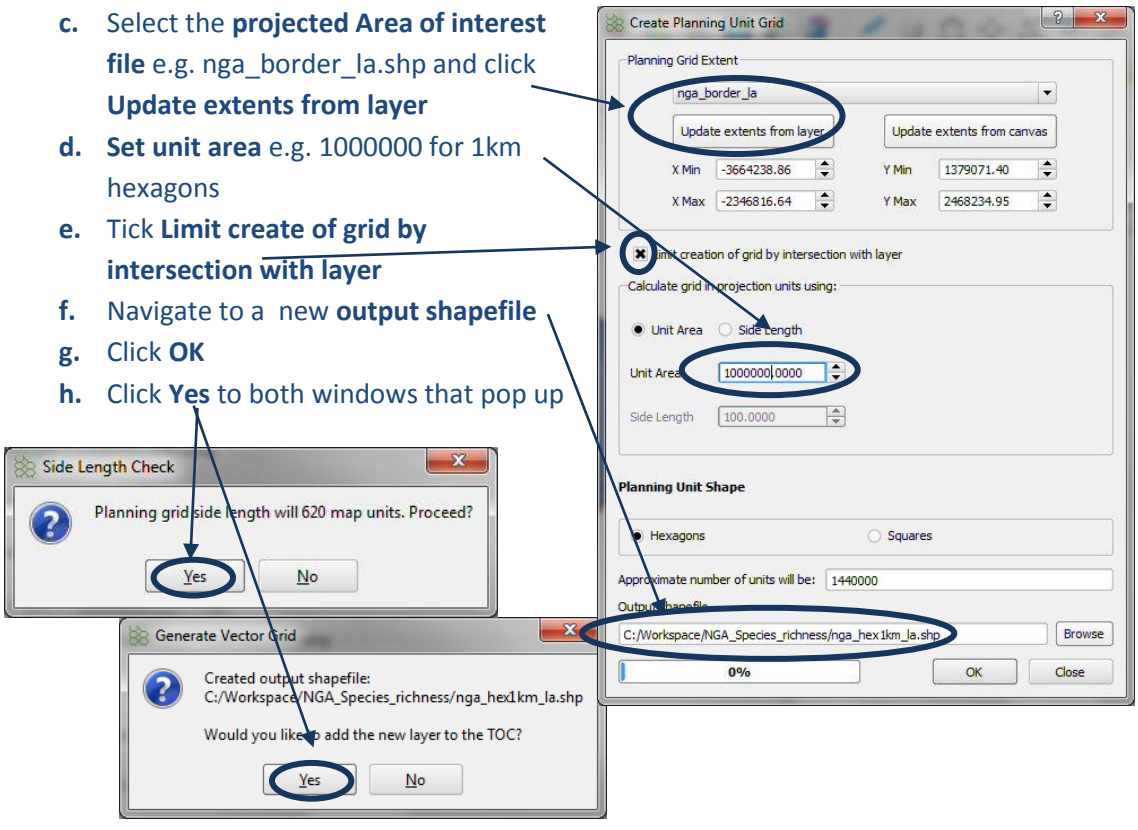
d. **Set unit area** e.g. 1000000 for 1km hexagons

e. Tick **Limit create of grid by intersection with layer**

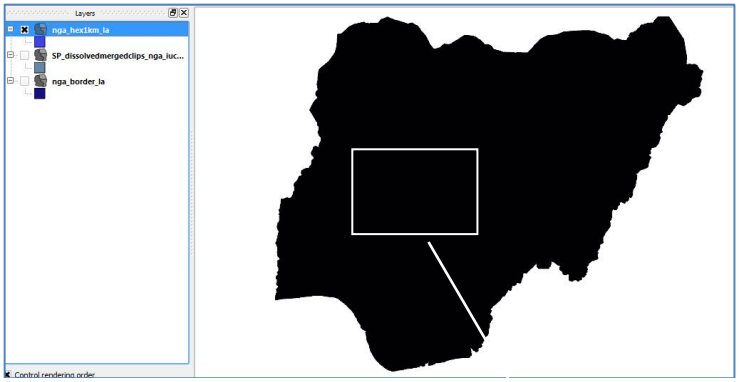
f. Navigate to a new **output shapefile**

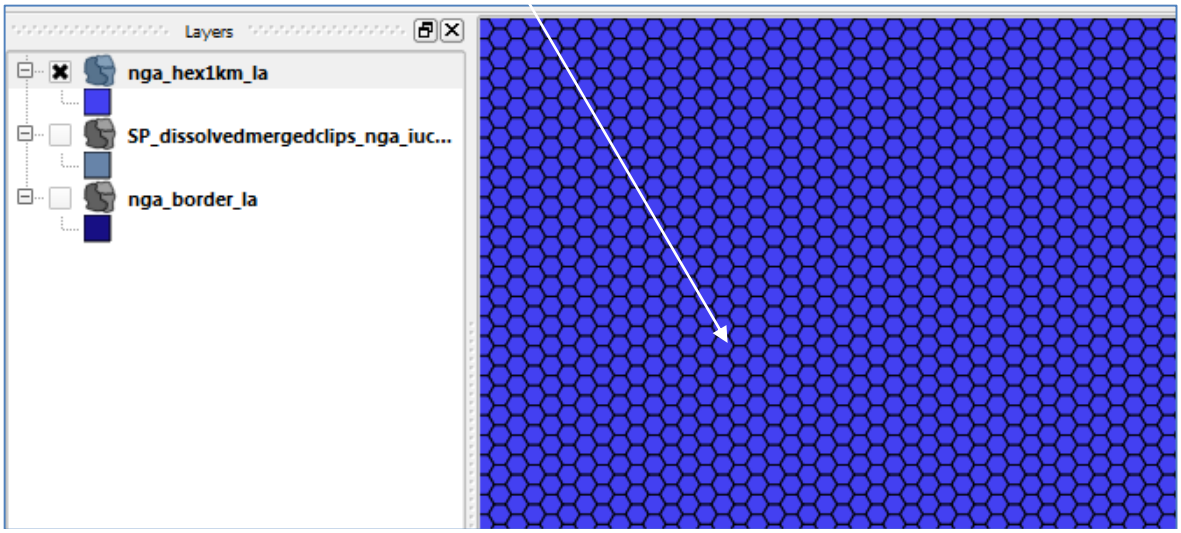
g. Click **OK**

h. Click **Yes** to both windows that pop up



i. Zoom in to check that the hexagons have been created correctly

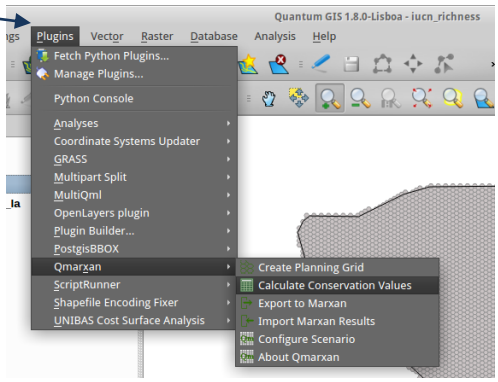


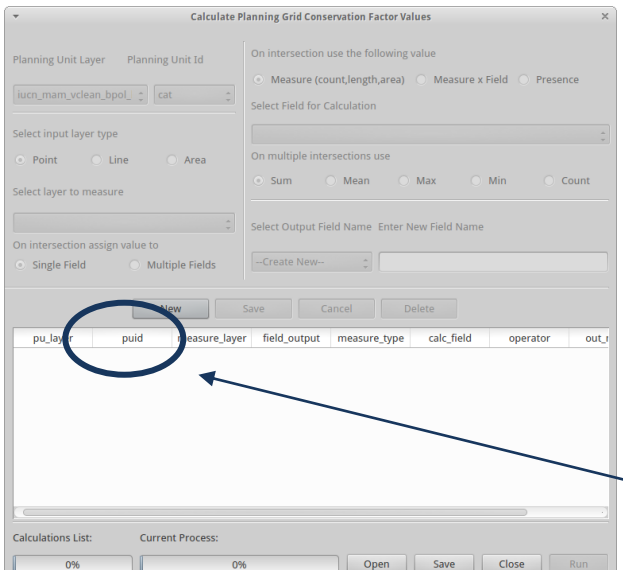


2.3.2. Generate species richness using the Qmarxan plugin

a. The next step is to use the planning units file to generate a count of number of threatened species in each planning unit hexagon

b. From the **Plugins** menu click **Qmarxan>>Calculate Conservation Values**

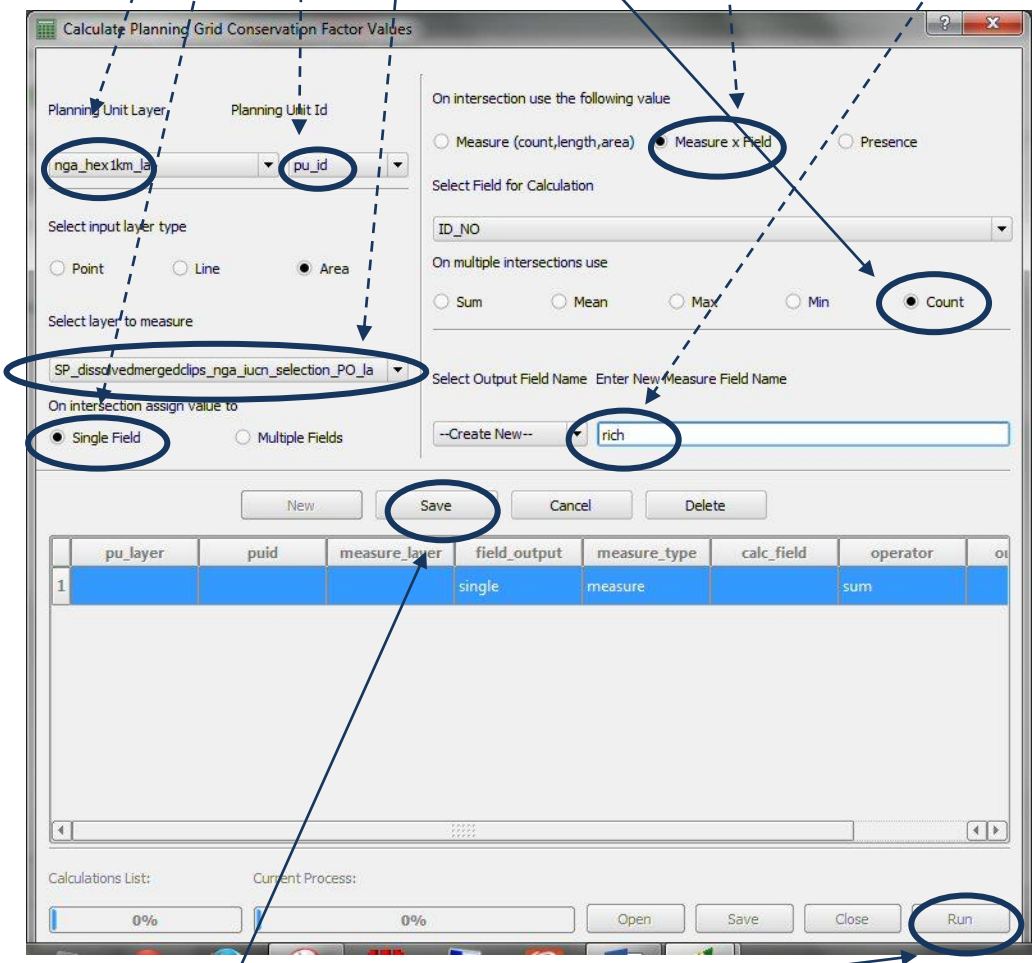




c. The **Calculate Planning Grid Conservation Factor Values** window opens

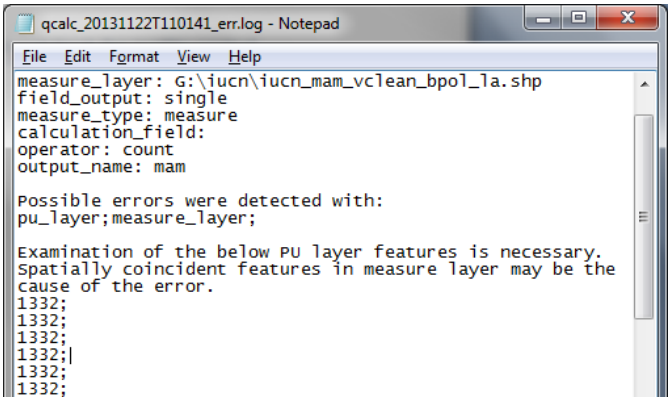
d. Click **New**

e. Select the **Planning Unit Layer** generated in the previous step
f. Select the **Planning Unit Id** (this is unique ID for each hexagon in the planning units dataset upon which the summaries will be made)
g. Set **On intersection assign value** to **Single field**
h. Set the **On intersection use the following value** to **Measure X Field**
i. Set the **Select Field for Calculation** to either the **species ID** or **binomial**
j. Set the **On multiple operations use** to **Count**
k. Set the **new Output Field Name** to be added to the planning units e.g. mam



l. Click **Save**
m. Click **Run**

2.3.3. Check any errors located in the error log and spot-check for quality control



a) In the Planning Units folder **open the error log** generated by the previous step

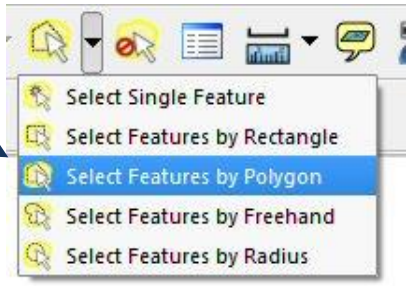
For each of the planning units listed manually check the results of the features listed

b) **Right Click** on the **Planning Unit Layer** and **open the attribute table**

c) **Select** the **PU** and **zoom to it in the map canvas**

d) Click on the IUCN species layer in the table of contents

e) Then Click on the **Select Features by Polygon tool** and **draw a polygon** around the hexagon (PU) to select features within the IUCN dataset corresponding to that hexagon

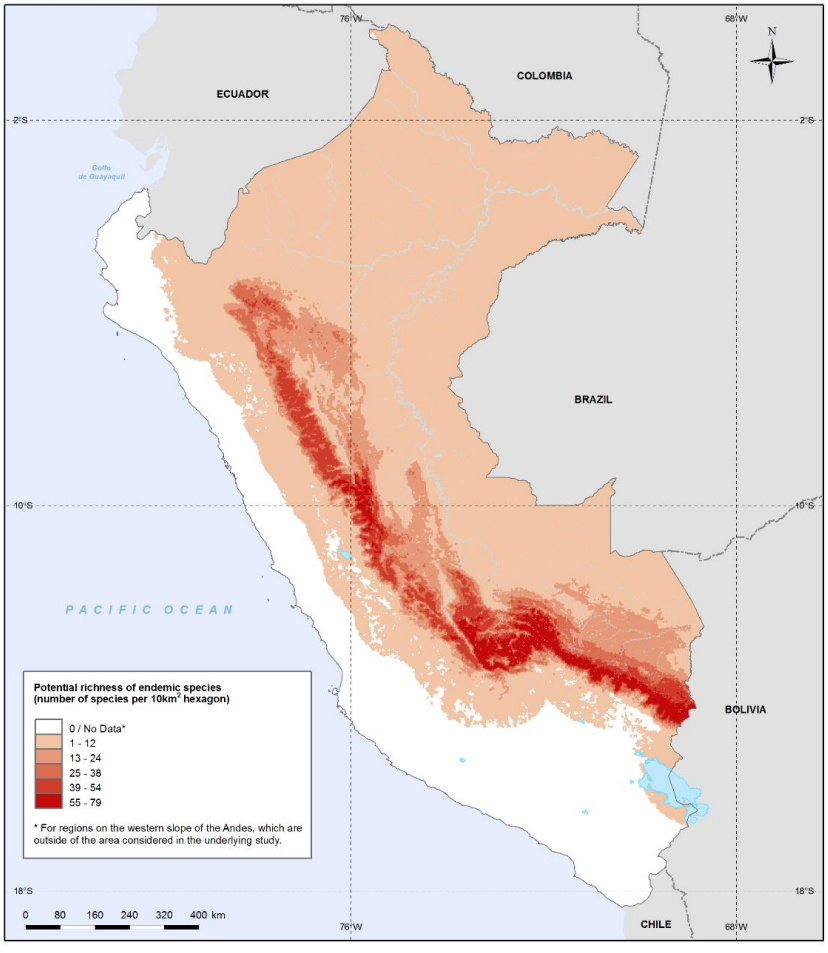


f) The number selected should match with the count in the 'mam' field in the Planning Unit Layer. Check again by drawing the polygon around the hexagon and if necessary alter the value in the 'mam' field to match the number selected

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

Annex1 : Cleaning the topology using GRASS GIS

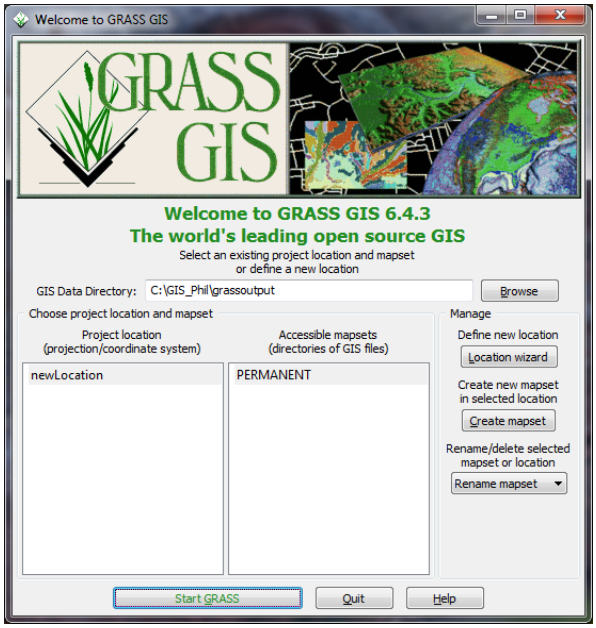
GRASS GIS works best as a standalone programme, although it does have a QGIS plug-in, so many of the GRASS tools are also available in QGIS. *You may have used the GRASS v.clean tool from within in QGIS).* This example runs through cleaning of the IUCN data which can be a very large dataset depedning on your area of interest and how many species you are working with. The standalone version of GRASS is automatically installed when you install QGIS.

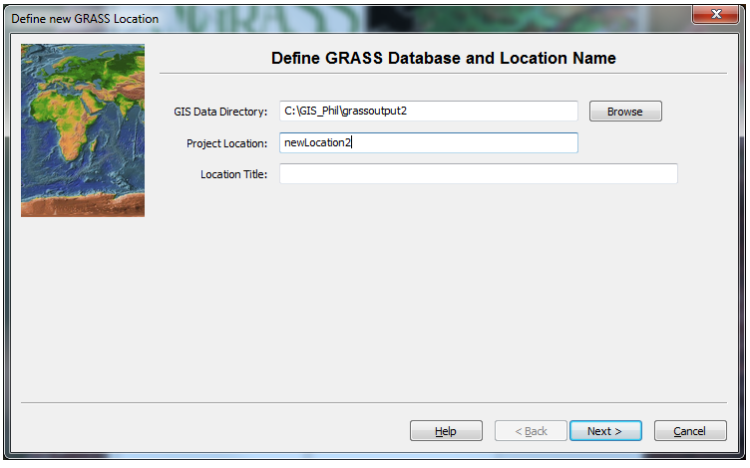
a. Click on **Education>>GRASS GIS** to open GRASS

To use GRASS as a standalone programme, it is necessary to set the **project location** and **mapset**.

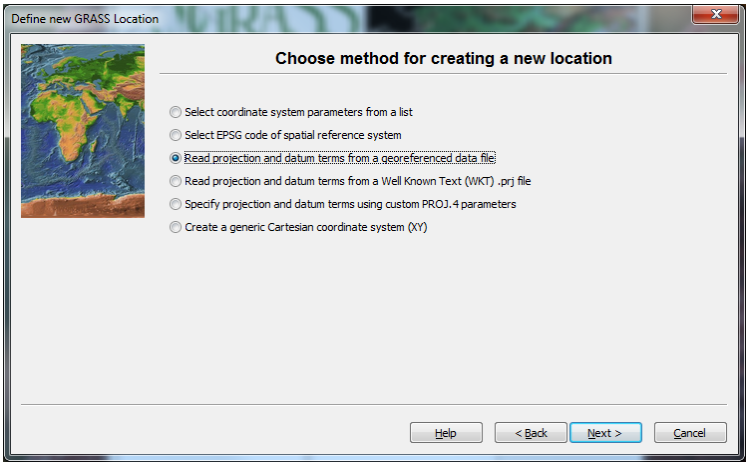
b. Click on the **Location Wizard** and choose the location of the GIS data directory, plus a folder name for the project location.
For faster computation, choose a location on your local drive and avoid spaces in folder names.

c. Click on **Start Grass**



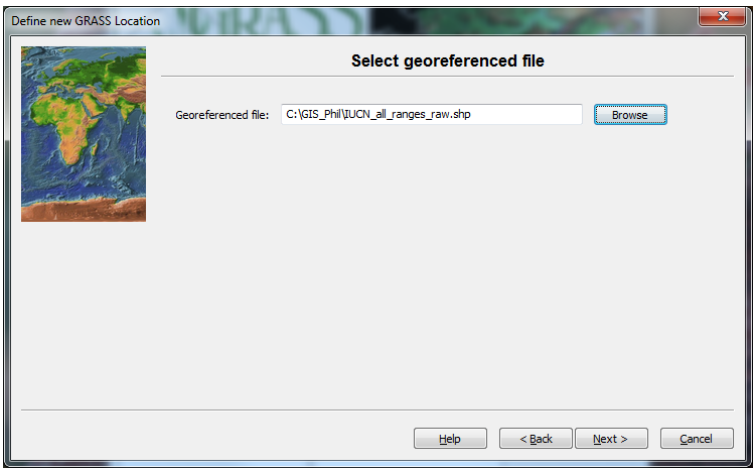


d. Click **Next**



e. Choose the option **Read projection and datum terms from a georeferenced data file**

f. Click **Next**



g. **Select** the shapefile containing the clipped and projected species range data with the topological errors.

h. Click **Next**

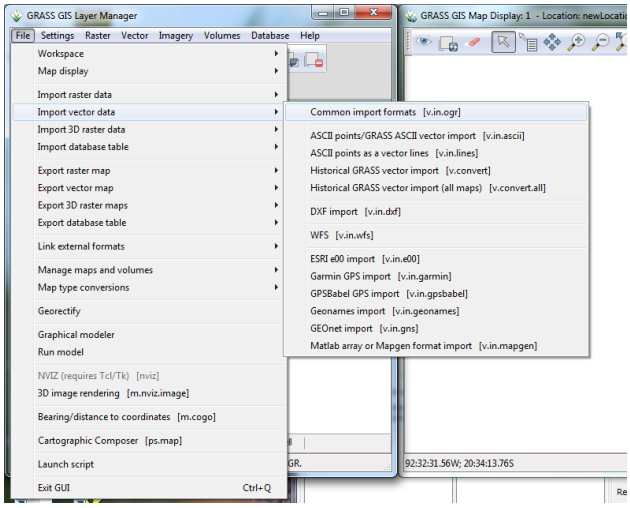
i. Click **Finish**

j. Click **OK**

Wait for GRASS to create the new project location.

Now import the species range data.

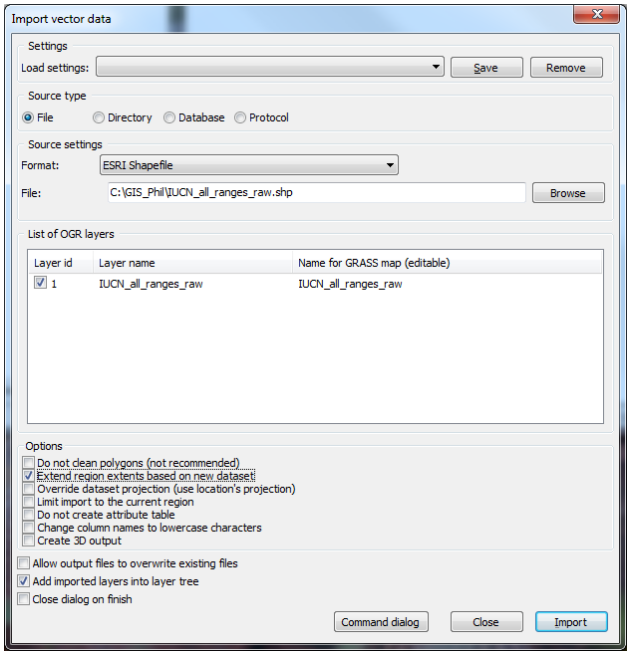
k. In the **GRASS GIS Layer Manager**, go to the **File menu >> Import vector data >> Common import formats [v.in.ogr]**



l. Click **Browse** to choose the shapefile containing the clipped and projected species ranges. Under **options** select the option **extend region extents based on new dataset**.

m. Click **Import**.

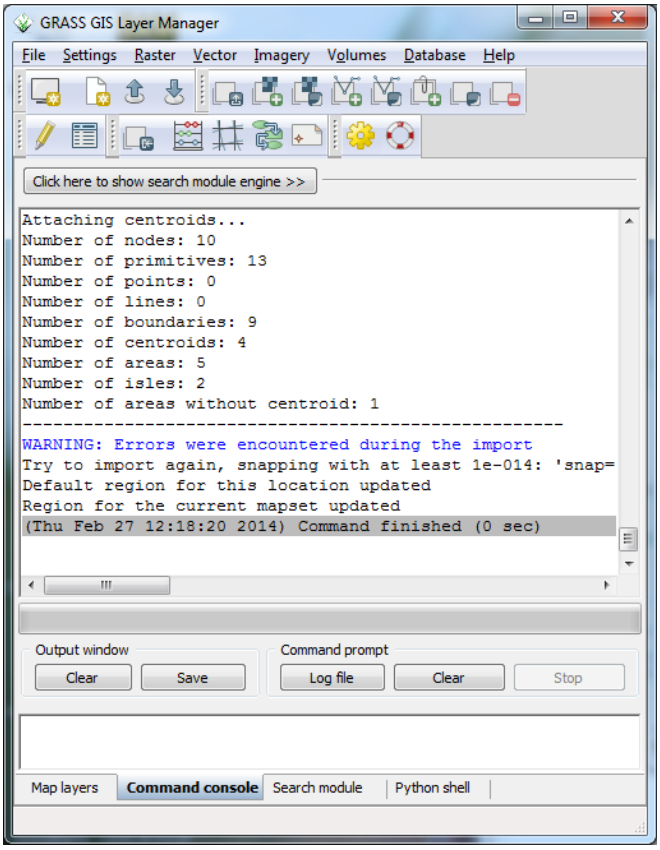
A range of cleaning processes will be automatically undertaken during the import process. ***This could take several hours depending on the size of the file being imported.***



n. When the import is complete, check the command console in the GRASS GIS Layer Manager.

o. If there is no warning message you can go straight to **step p** and **simply export the file from GRASS**.

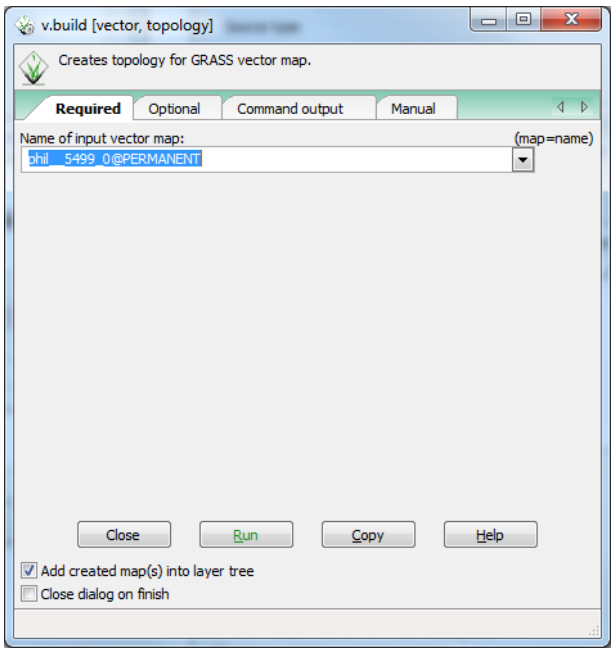
*If there is a **warning message** (see screenshot), the next step is to use the **v.build** procedure to **rebuild the topology** (see Box A: Rebuild topology below)*



Box A: Rebuild topology

a. In GRASS GIS go to the **Vector menu >> Topology maintenance >> Create or rebuild topology [v.build]**.

*Make sure name of **input vector map shows your file** (it will have **@PERMANENT** at the end of the file name)*



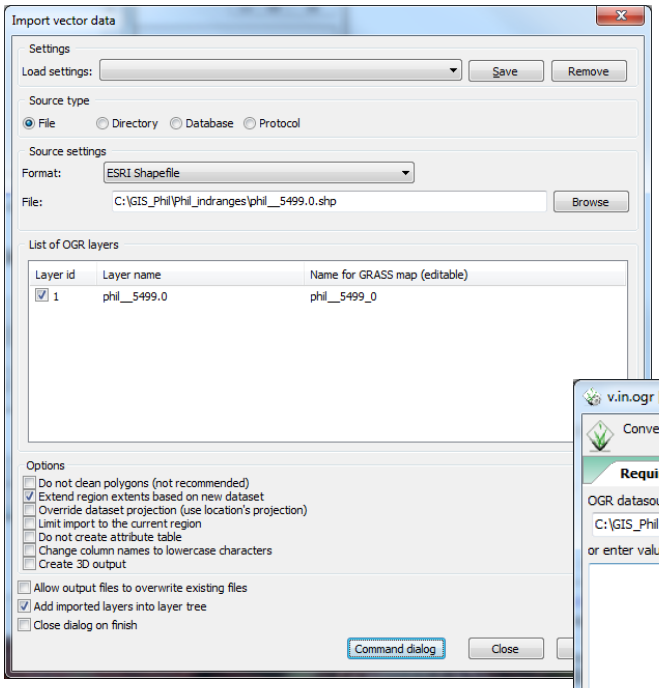
b. Click **Run**.

c. Check the **command console** to find the results of the v.build. **If there is no warning message** you can now export the file from GRASS (**goto step p**)

***If there is an error message**, you now have **two choices** (see Box B or Box C)*

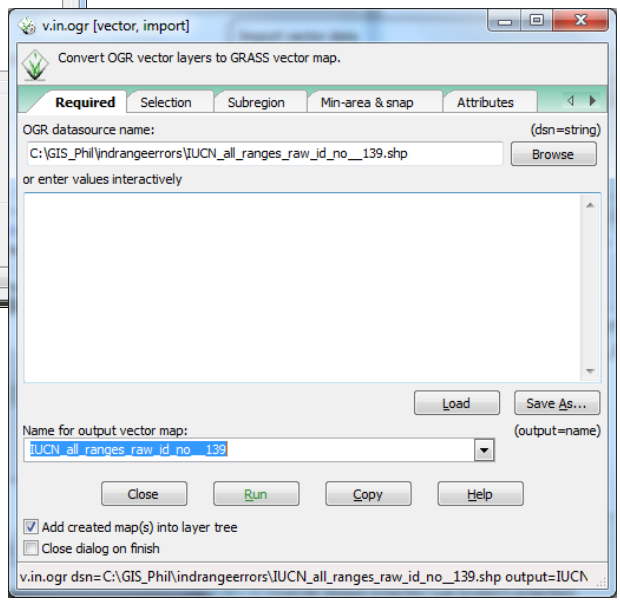
Box B: Rebuild topology (option 1)

If the import didn't take too long, you might prefer to re-import the file into GRASS, but this time setting **a snapping threshold**.

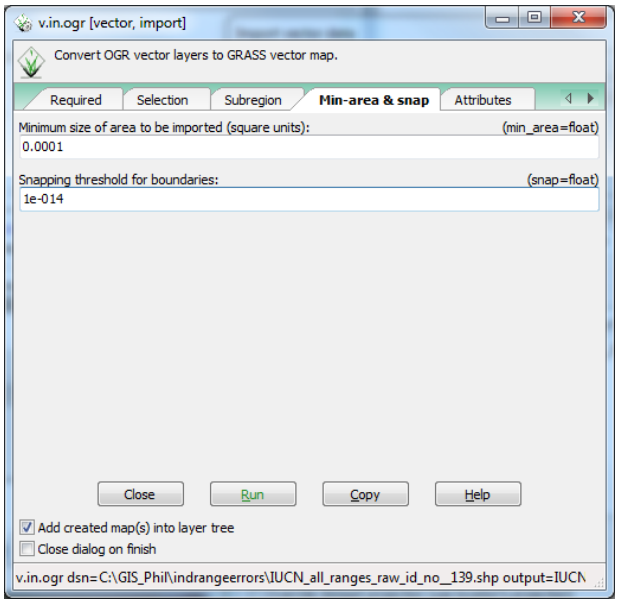


a. To re-import the file and set a snapping threshold, **go back to [v.in.ogr], as in step k,** but this time inlude an additional step and click **Command dialog**

b. In the new window, **browse** to find your species range file, and select a **name for output vector map** (the name of the new file within GRASS)



c. Go to the Min-area & snap tab. Write **'1e-014'** as the snapping threshold. It is important to set a low threshold, otherwise snapping can introduce errors. If the distance between two points is lower than the snapping threshold, these points will be assumed to be in the same place. This can correct many topological errors, but it can also cause errors if the snapping threshold is set too high. Even with a very low threshold it is still possible to introduce errors, and you will later need to check that the cleaned species ranges match the original ranges.



d. Click **run** and wait for the import to complete. Again, this may take some time.

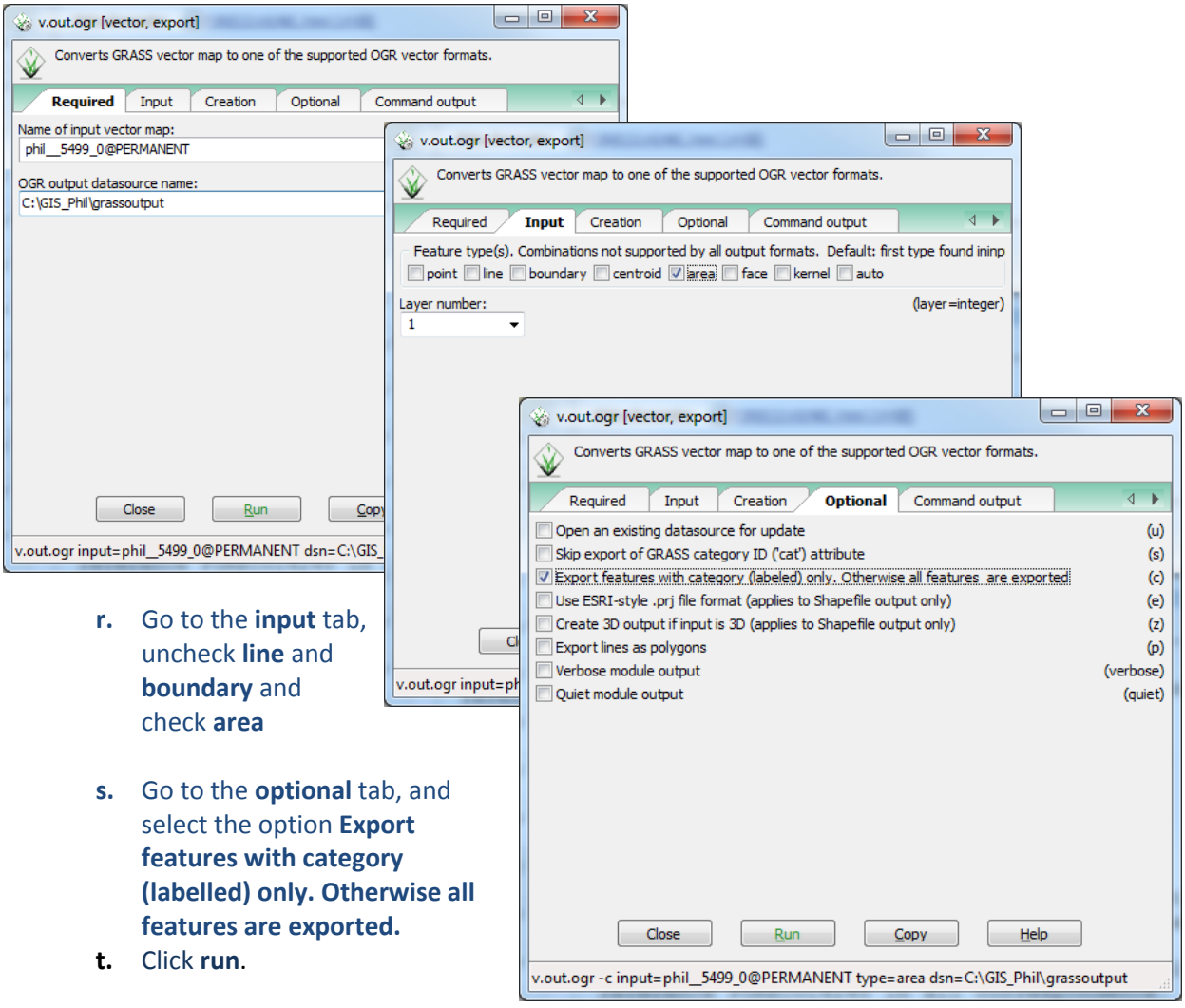
e. Then go **step (p)** to export the cleaned data from GRASS GIS.

Box C: Rebuild topology (option 2)

If the import was very slow, the other option is to continue using the uncleaned species range file (the one that existed prior to the import into GRASS). Follow sections 2.9 and 2.10 to reproject the file and to split it, creating separate files for each species. Then check for topology errors in these separate species files (section 2.7) and where necessary clean these in GRASS, by repeating the process described in section 2.8. If the files have been reprojected, they will require a new 'project location' in GRASS (simply repeat the process described in 2.8 a).

p. To export the file from GRASS, go to the **File menu >> Export vector map > >Common export formats [v.out.ogr]**

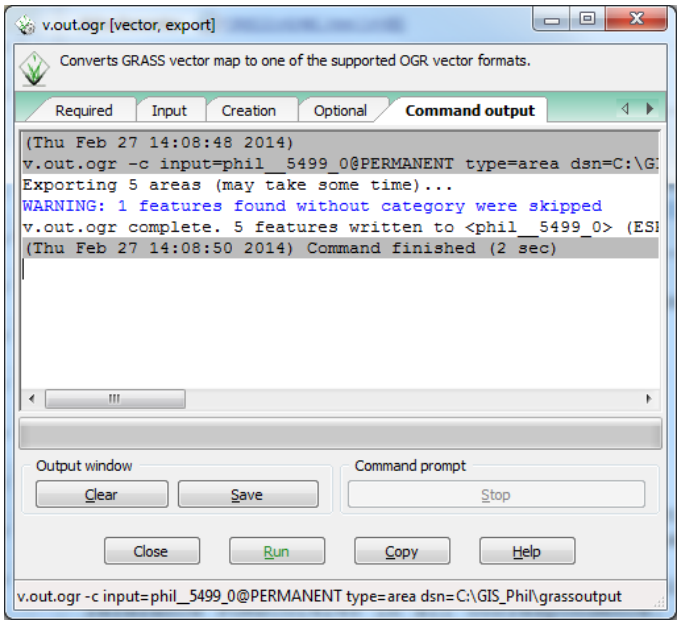
q. Select the name of the file you want to export (it will have **@PERMANENT** at the end of the file name) and under **OGR output datasource name** write the file path of the chosen export location.



r. Go to the **input** tab, uncheck **line** and **boundary** and check **area**

s. Go to the **optional** tab, and select the option **Export features with category (labelled) only. Otherwise all features are exported.**

t. Click **run**.



In the command output, ignore any warnings that features found without category were skipped.

u. Close GRASS.

v. **Open QGIS** and **add** the cleaned file that you exported from GRASS.

w. Use the '**Add Vector layer** button.

x. Check whether any **topological errors** remain (**see section 2.7**).

Make note of the species that are still affected by these errors, you may need to check these manually and select them out and clean them on their own.