Biomapper – file preparation and preliminary analysis 6 steps to create 1-0 (Boolean) files for species data in Arc Map

Before starting...

- Make sure that the study area raster (or shapefile) and the species presence data files are in the same datum and projections!
- You may need to convert the study area feature file into a raster (use feature to raster). It may make sense to set the environments to those of some other file that you will use in the analysis from the EGV layers (eg the DEM).
- Make sure you name each new file created using some sensible nomenclature scheme saving each set of files in clearly labeled folders helps. Make sure you have all master files backed up in a directory separate from your working directory!
- Verify that the point coordinate data for species presence is correctly entered.
- 1) Add new field to shapefiles of species and code uniformly to some number eg (2) (Create a new field in the attribute table eg "new_values".. Make sure that this is a different value from the background value of the study area shapefile with which the species file has to be merged. Use the "same as …" option.
- 2) Convert feature (shapefile) to raster (Conversion Tools). Make sure you select the newly added field with a constant value for all animal locations (eg '2') in the field ID. In the Environment section, go to "general" and set the extent the same as the study area raster. Under raster analysis settings, set the cell size to that of the study area raster.
- 3) "Mosaic to new raster" (toolbox data management, alternatively, the raster calculator in spatial analyst can also be used after standardizing the extent and cell size). Put in the study area raster and the species raster → mosaic. Once again, you need to set the extent and cell size to that of the study area raster (in environments). In the list of added raster files (that are to be merged), keep your species raster below the study area raster!
- 4) Reclassify (Spatial Analyst) ensure the background (beyond the study area has boundary) is assigned 'no data'. The background within the study area should be assigned "0". The species locations should be assigned "1". This is a Boolean map.
- 5) Using spatial analyst mask to insure that extent and boundaries match up with other layers (including EVG's). Spatial analyst → options → set the mask to a layer whose boundaries you want your species maps to conform to. Make sure you also set the cell size and extent to this same layer. Raster calculator. Select the species + study area merged grid file of interest (one at a time) from the list, and click evaluate. These files will appear in arc map with the title 'calculation'. Right click → data → export → save as a GRID with a new filename and specify the folder in which you want your files saved.
- 6) Convert to Idrisi format. The plug in is often quirky. Usually works best of the 1-0 species GRID file is rendered in the 'stretched' mode (properties- symbology), before the GRID \rightarrow IDRISI conversion is carried IDRISI out. The GRID \rightarrow from convertor can be downloaded off ESRI or http://www.terracs.de/ArcGIS 9 x/Grid2ldrisi/grid2idrisi1.html and has plug ins for both Arc Map and Arc View. Make sure all files are saved in a hard drive (internal or external) – but not on the desktop/ my documents for this convertor to work. If at first the conversion does not work, retry several times, it usually eventually works! Hint: Sometimes it will appear as though the output .rst (idrisi) file is not Boolean. Go into properties \rightarrow symbology in arc and select "classified". Click ok. Go back into properties and select 'stretched'. Your .rst file may appear as a binary or Boolean file now!

STEP 1: Adding a new field and entering a new value. (make sure files are projected into the projection system that will be used here on – same as EVG rasters, eg. UTM WGS 84, Zone 37N).





STEP 2 Converting species shapefile to raster. Add the study area raster into your display window on Arc Map.



STEP 3: Mosaic raster – merging the species and study area rasters.

(Click on the Arc Toolbox. Click on Index and type "Mosaic". Select "Mosaic to New Raster".)

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STEP 4: Reclassify merged raster to Boolean.

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Reclassify merged raster so that background (study area is "0", all species points are "1" and the rest is "NoData".

STEP 5: Creating consistent 'boundaries' using Spatial Analyst

(This step may or may not need to be carried out – it is important to follow of the boundaries of your nmerged, binary species raster do not conform exactly to boundaries of EVG's at this stage).





STEP 6: Conversting GRID raster files to .rst (IDRISI) raster files.

Note: At this point all file converted into .rst will <u>lose all spatial information</u>! This is alright so long as all the files that go through this conversion have EXACTLY the same projection, cell size and extent prior to conversion. Files in Biomapper need to have a projection and they will 'sit' on one another without problem if consistence is maintained throughout the entire process.



Sometimes the converted (.rst) file does not render correctly. This may not be a problem. To ascertain whether the conversion has been sussessful, selected 'strectched' in Symbology. The File should render correctly as a binary raster now. $\label{eq:linear} \label{eq:linear} where the the two states are the$