REDD-PAC modelling work

Land use change modelling was carried out by IIASA/INPE using the GLOBIOM model – see full technical reports for detailed description of the model (\\wcmc-data-03\programs\PROJECTS\6100s\06175.00.E REDD - PAC Scenarios\Final outputs).

Biodiversity analysis methods are also described in the full reports.

The biodiversity analysis was undertaken using the statistical programme R. The graphs were produced using excel. In general, in order to update (produce) the graphs the final outputs from the R scripted were copied and pasted into the excel file of graphs.

The R scripts are stored in the file: \\wcmc-data-03\programs\PROJECTS\6100s\06175.00.E REDD - PAC Scenarios\Work in progress\Modelling\R. There are separate folders for each of the iterations of the model runs and each region. Each folder has a genera structure of:

* Main folder containing:
  + R files with the analysis code in them, these are numbered and should generally be ran in sequence
  + Excel file called Graphs which contain the graphs developed from the R code outputs.
* Subfolders:
  + Inputs
    - Containing the input data including raw GLOBIOM outputs
  + Outputs
    - Containing the outputs files created by the R code
  + Maps
    - Containing the maps that are linked directly to the outputs folder. So if the codes are re-run and new outputs produced the maps should update automatically.

The R scripts are annotated, and start with an explanation for what the code does. So it should be possible to read through them to see exactly what analysis was carried out. The most up to date script for Brazil is in the folder - Brazil1611\_AnalysisForPaper, and for the Congo Basin is in folder Congo1603\_AnalsysisForReports.

**NOTEs:**

1. I ran the scripts from my c drive so that they would run faster. Therefore, the pathnames will not be correct for them to run directly off the p drive (e.g. they point to the c drive not the p drive). This would have to be updated before they can be ran.
2. Re-running the script will overwrite the files that are currently in the outputs folder. So that it is possible to go back to past outputs and explore differences it is advisable to create a new folder **AND update the outputpath in the script to point at this,** when analysis is being re-ran on new data.
3. Some of the inputs were created through spatial analysis – including the proportion of the gridecells that are covered by particular species or biodiversity priority areas. Ideally, this would be re-ran with updated data for new analysis in Brazil or Indonisa (e.g. updated IUCN data, or even better – national data). Andy Arnell carried out the overlap analysis for me for the REDD-PAC work – since the ICUN data is so large this is a process intensive step.
4. For the Congo Basin analysis – there is code to select whether the analysis should be for the whole region or a specific country.
5. In the ‘Brazil1510\_AnalysisForReports’ folder there are two word documents that I created as full guides to the analysis for the workshop with ICMBio. These should also be helpful for understanding the code and analysis. However, the code in these word documents does NOT run perfectly (it has a few bugs in it) AND it is not the latest code – so it needs to be carefully compared to the final code in the code files.
6. The column headings for the GLOBIOM outputs were sometimes missing or different (e.g. caps/not caps) in the files I got from IIASA – this needs to be checked before trying to run the code. To check compare the file to the files in the inputs in earlier analysis.
7. If new GLOBIOM outputs are being sent and used in an analysis do some simple sense checks before using the data, lots of bugs in the IIASA GLOBIOM script were picked up this way during the REDD-PAC project. Simple checks include:
   1. Does the total amount of land in a simulation unit add up to the total area of the simulation unit
   2. Is the total land area in a simulation unit (summed across different land use categories) constant over time
8. To do the analysis with new scenarios each code file has to be updated with the new scenario names. Using Ctrl find is the quickest way of doing this. If the number of scenarios changes then the code for a scenario can be copied and pasted to increase the number of scenarios analysed. NOTE that if the number of scenario’s change it can cause problems in the code for the summary tables – make sure all scenarios are being picked up in the summary tables and that it is not trying to include scenarios that are no longer relevant. Also changes in the number of scenarios may require modifications to the graphs excel file.
9. In the species analysis the final output from the R files are the data for a histograms (e.g. number of species in different categories of habitat loss). To add this into the excel to create the graph – copy and paste the final outputs and then convert from text to columns in excel.

During the work in the REDD-PAC project one of our key roles was to ask questions of the GLOBIOM model. Notes and working papers from these discussions are stored in: \\wcmc-data-03\programs\PROJECTS\6100s\06175.00.E REDD - PAC Scenarios\Work in progress\Modelling\Discussion with IIASA. Issues that arose and may arise again are:

* How to deal with PAs in the model (in the end they are dealt with in a on/off way but it would be good if this could be more sophisticated). We put a lot of thought into this and the main isssues were outlined in a word doc: Protected areas issues for REDD-PAC.
* What the different land use/land cover categories within GLOBIOM represent – especially what type of land cover/use is included within the ‘other natural land’ category of GLOBIOM. Due to the way the input land use maps to GLOBIOM are created (see full project reports for details), this category will include both natural shrubland and previously abandond farmland.
* Regeneration times (including of carbon).