**Test Summary**

This test is to check that the output of the Generalized Linear Model (glm) SDM experiment is accurate. The modeling script uses the default parameter arguments and includes the production of evaluation measures.

**Preconditions & Test Data-sets Required**

occur.csv

bkgd.csv

current climate layers (current.76to05 | bioclim01-bioclim19.tif)

**Test Steps**

1. Log in to the BCCVL
2. Select Experiments tab
3. Click new SDM Experiment
4. Enter “Phascolarctos cinereus glm model and evaluation” as the name for this experiment.
5. Enter “Phascolarctos cinereus glm model, default parameters, current projection, and model evaluation” as the description of experiment
6. Click Next
7. Select Generalized Linear Model under Species Distribution Model Production Algorithms
8. Expand configuration for Generalized Linear Model
9. Check the default parameters are as follows:
   1. n-fold cross-validation = 10
   2. data split = 100
   3. weighted response weights = None
   4. resampling = 0
   5. do.full.models = TRUE
   6. type = “quadratic”
   7. interaction level = 0
   8. test = “AIC”
   9. family = “binomial”
   10. mustart = 0.5
   11. control: epsilon = 1e-08
   12. control: maxit = 50
   13. control: trace = FALSE
10. Click Next
11. Select Occurence Data for Phascolarctos cinereus
12. Click Next
13. Select Absence Data for Phascolarctos cinereus
14. Select Current climate layers for Australia, 2.5arcmin (~5km)
15. Click Next
16. Click start Experiment

**Expected output in files:**

1. model object.RData – binary model output file generated by model algorithm
2. current.tif – glm model projected onto current climate layers
3. current\_ClampingMask.tif – glm model projected onto current climate layers with a clamping mask applied. This mask identifies locations where predictions are uncertain because the values of the variables are outside the range used for calibrating the models.
4. combined.modelEvaluation.csv – table of all accuracy measures provided by dismo and biomod2 packages
5. biomod2.modelEvaluation.txt – evaluation output provided by biomod2’s getModelsEvaluations() function
6. glm.Rout – R output file, text file containing record of commands sent to R, generated automatically when using R CMD BATCH
7. AUC.png – Area Under the Receiver Operating Characteristic (ROC) Curve; threshold-independent plot of model predictive performance with test statistic value as figure title
8. mean\_response\_curves.png – response plots for each current climate layer used during model creation
9. results.html – html file displaying AUC.png and combined.modelEvaluation.csv

**Comments**

Test Step #14 should be the selection of individual climate layers, not ones already packaged

biomod2 automatically creates additional files in the working directory, I’m not sure if these are exposed to the user. The folder/files are:

* Phascolarctos.cinereus/.BIOMOD\_DATA/Phascolarctos\_cinereus/calib.lines
* Phascolarctos.cinereus/.BIOMOD\_DATA/Phascolarctos\_cinereus/formatted.input.data
* Phascolarctos.cinereus/.BIOMOD\_DATA/Phascolarctos\_cinereus/models.evaluation
* Phascolarctos.cinereus/.BIOMOD\_DATA/Phascolarctos\_cinereus/models.options
* Phascolarctos.cinereus/.BIOMOD\_DATA/Phascolarctos\_cinereus/models.prediction
* Phascolarctos.cinereus/.BIOMOD\_DATA/Phascolarctos\_cinereus/models.prediction.eval
* Phascolarctos.cinereus/models/Phascolarctos\_cinereus/Phascolarctos.cinereus\_AllData\_Full\_GLM
* Phascolarctos.cinereus/proj\_current/Phascolarctos.cinereus.current.projection.out
* Phascolarctos.cinereus/Phascolarctos.cinereus.Phascolarctos\_cinereus.models.out