**Test Summary**

This test is to check that the output of the brt model 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 brt model and evaluation” as the name for this experiment.
5. Enter “Phascolarctos cinereus brt model, default parameters, current projection, and model evaluation” as the description of experiment
6. Click Next
7. Select Boosted Regression Trees under Species Distribution Model Production Algorithms
8. Expand configuration parameters
9. Check the default parameter are as follows:
   1. tree.complexity = 1
   2. learning.rate = 0.01
   3. bag.fraction = 0.75
   4. var.monotone = rep(0, length(predictors))
   5. n.folds = 10
   6. prev.stratify = TRUE
   7. family = “bernoulli”
   8. n.trees = 50
   9. max.trees = 10000
   10. tolerance.method = “auto”
   11. tolerance = 0.001
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 generate by model algorithm
2. current.tif – brt model projected onto current climate layers
3. combined.modelEvaluation.csv – table of all accuracy measures provided by dismo and biomod2 packages
4. dismo.eval.object.RData – binary evaluation output provided by dismo’s evaluate() function
5. brt.Rout – R output file, text file containing record of commands sent to R, generated automatically when using R CMD BATCH
6. AUC.png – Area Under the Receiver Operating Characteristic (ROC) Curve; threshold-independent plot of model predictive performance with test statistic value as figure title
7. \*\_response.png – response plot for each current climate layer used during model creation
8. biomod2\_like\_VariableImportance.csv – table of variable importance using biomod2’s procedure
9. maxent\_like\_VariableImportance.csv – table of variable importance using maxent’s permutation importance procedure
10. results.html – html file displaying AUC.png and combined.modelEvaluation.csv

**Comments**

Test Step #11,12 Names likely to change when using Gerhard’s koala data

Test Step #12 should be the selection of individual climate layers, not ones already packaged