Eco-evolutionary hypothesis testing with Machine Learning (ML)

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```
library(ecoevor)
library(here)
library(Boruta)
library(randomForest)
library(caTools)
```

1 Overview

The goal of this vignette is to illustrate how to use machine learning (more specifically a random forest algorithm; Breiman 2001; Liaw & Wiener 2002) to classify an observed feature set (in this instance summary statistics from a simulated 'observed data set'), i.e. assign posterior probabilities to an observed dataset for each of a set of alternative hypothesized models.

For an example observed dataset, use the same simulation of population and trait dynamics in a 3-species model of growth and competition (a Leslie-Gower model, which is a discrete-time Lotka-Volterra model, with potentially evolving population growth rate) that is the focus of the ecoevo-ABC vignette (Pantel & Becks 202x, Box 2).

There are 2 key differences from the ABC version presented in Pantel & Becks (2022x) Box 2 / the vignette ecoevo-ABC - first, we use as an observed dataset a coarse time series population size every 14 days and the beginning and end trait values (x_1,x_{300}) (note that the x_1 values aren't included as features, but they are nevertheless known because they were supplied to the simulatin command LV_evol - see full ecoevo-ML.rmd code to confirm this). Second, the random forest does not perform as well as ABC for this model + dataset. We leave it in as an example of how ML can be used for eco-evolutionary hypothesis testing in R.

2 Prepare ML

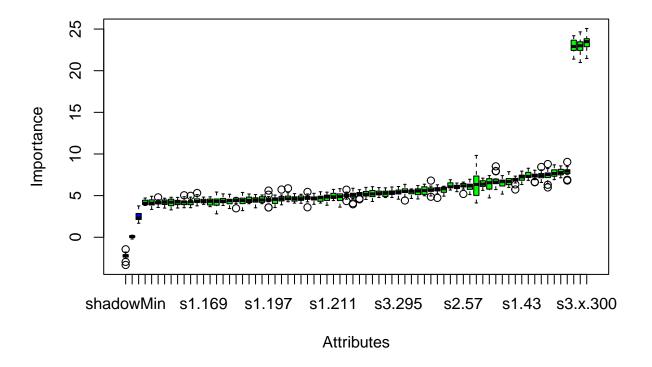
To determine how the summary statistics contribute to identifying the model that generated a dataset, we first use feature selection via a boruta algorithm (Kursa & Rudnicki 2010). We focus on the simulated dataset produced in the vignette ecoevo-ABC, a dataset with population size every 14 days and the end trait values (x_{300}) . We use the same vector of model parameter values and associated summary statistics saved in the accompanying dataset $abc_lv.rda$.

```
datapath <- here::here("data")
load(file.path(datapath, "abc_lv.rda"))
list2env(abc_lv,globalenv())</pre>
```

3 Fitting observed data to model via ABC

Step 1. Perform initial feature selection procedure

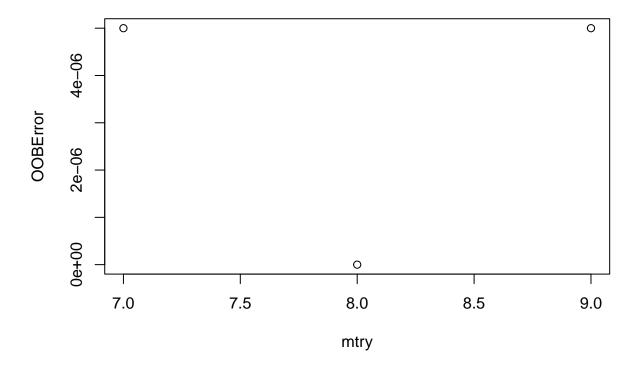
This step is quite lengthy, so we show the code here, but call the saved object rf_lv.rda for subsequent use.



Interestingly, we see that the trait features are most important.

Step 2. Tune hyperparameters for model

Use tuneRF to search for an optimal value of mtry given the data. mtry is a parameter in the random forest algorithm that determines the number of variables randomly sampled as candidates at each split, and the optimal values reduces the 'out-of-bag' score (where random sub-samples of the original training data are taken, random forest models are generated using these subsets, and the prediction error for the remaining "out-of-bag" samples are calculated; Pichler & Hartig 2022). Again, this step can be lengthy, so we load this from the $rf_lv.rda$ environment.



In this instance changing the mtry (Number of variables randomly sampled as candidates at each split) doesn't impact the "Out-of-Bag" error estimate. Bagging uses subsampling with replacement to create training samples for the model to learn from. OOB error is the mean prediction error on each training sample x_i , using only the trees that did not have x_i in their bootstrap sample.

Step 3. Train ML classifier on the simulations using the summary statistics as features and the model (No-Evol, Evol) as the target variable

```
fac_sim_mod <- factor(abc_sim_mods)

sample <- caTools::sample.split(fac_sim_mod, SplitRatio = 0.75)
train_y <- subset(fac_sim_mod, sample == TRUE)
train_x <- subset(abc_sim_summ, sample == TRUE)</pre>
```

```
test_y <- subset(fac_sim_mod, sample == FALSE)</pre>
test_x <- subset(abc_sim_summ, sample == FALSE)</pre>
tune <- as.data.frame(tune)</pre>
m <- tune$mtry[tune$00BError == min(tune$00BError, na.rm = TRUE)]</pre>
rf <- randomForest(train_x, train_y, mtry = m)</pre>
rf_lv <- list(bor = bor, tune = tune, rf = rf)</pre>
save(rf_lv, file = "data/rf_lv.rda")
rf
#>
#> Call:
\# randomForest(x = train_x, y = train_y, mtry = m)
                   Type of random forest: classification
#>
                         Number of trees: 500
#> No. of variables tried at each split: 8
#>
#>
           OOB estimate of error rate: 0%
#> Confusion matrix:
           evol no_evol class.error
#> evol
           75000
                        0
                                     0
#> no_evol 0 75000
                                     0
```

The confusion matrix indicates a 100% classification accuracy. We now try a test dataset, and again it accurately classifies 100%:

```
pred <- predict(rf, newdata = test_x)
cm <- table(test_y, pred)
cm
#> pred
#> test_y evol no_evol
#> evol 25000 0
#> no_evol 0 25000
```

Step 4. Posterior model probabilities for 2 'observed' datasets

The model prediction is incorrect for the Evolution dataset, even though we have known trait values at t_1 and t_{300} , the beginning and end of the simulated experiment.

References

Breiman, L. (2001). Random forests. Machine Learning 45(1), 5-32.

Kursa, M.B. and Rudnicki, W.R. (2010) Feature Selection with the Boruta Package. J. Stat. Softw. 36, 1-13

Liaw and M. Wiener (2002). Classification and Regression by randomForest. R News 2(3),18-22.

Pichler, M. and Hartig, F. (2022) Machine Learning and Deep Learning – A review for Ecologists https: //doi.org/10.48550/arXiv.2204.05023