### Offshore distribution of yelkouan shearwaters in the north-western Adriatic Sea: insight from machine learning
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Prep

python imports

```
import numpy as np
import pandas as pd
import random
from sklearn.model_selection import train_test_split
from sklearn.metrics import roc_curve, roc_auc_score
import matplotlib.pyplot as plt
pip install interpret
from interpret.glassbox import ExplainableBoostingClassifier
from interpret import show
```

Import data

```
df_sw = pd.read_csv("myNewDataForInterpret.csv")
X_sw = df_sw.drop(columns = ['presence'])
y_sw = df_sw['presence']
```

Models

Model on full data

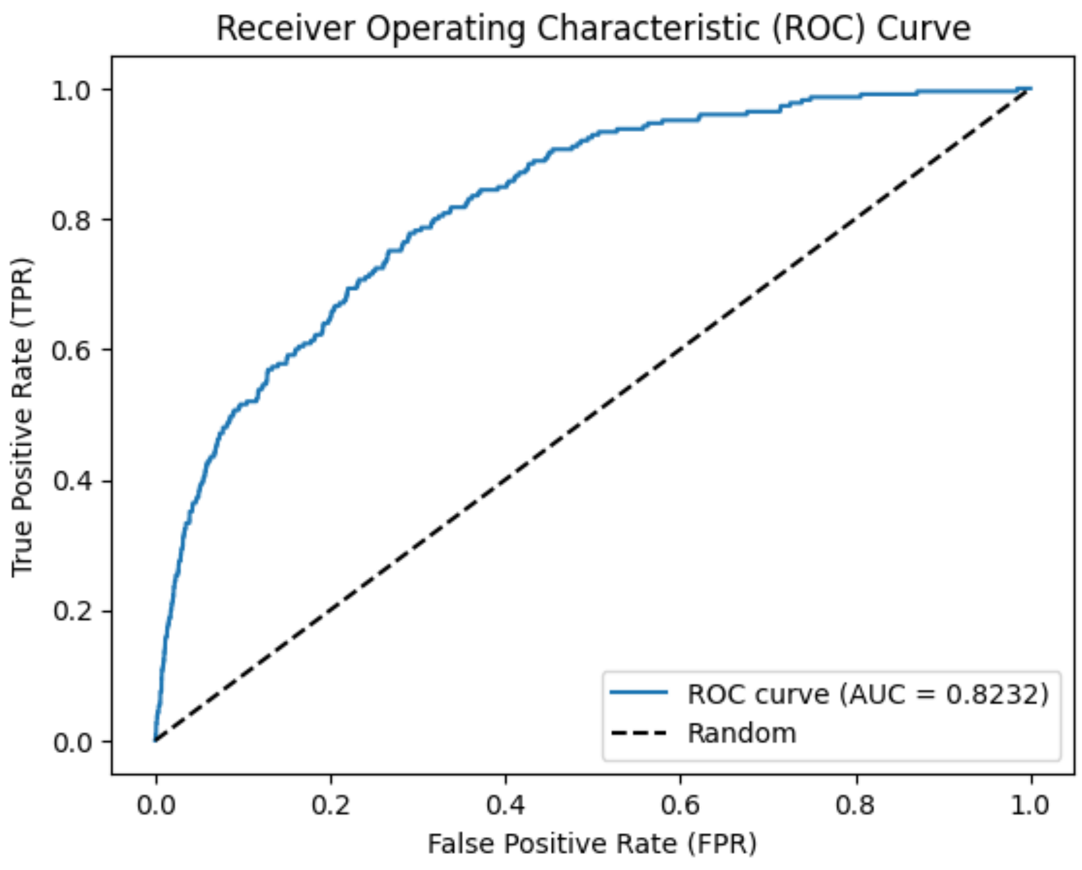
```
ebm_sw = ExplainableBoostingClassifier(outer_bags = 25, inner_bags = 25)
ebm_sw.fit(X_sw, y_sw)
ExplainableBoostingClassifier(inner_bags=25, outer_bags=25)
show(ebm_sw.explain_global())
auc = roc_auc_score(y_sw, ebm_sw.predict_proba(X_sw)[:, 1])
print("AUC: {:.3f}".format(auc))
AUC: 0.908
```

AUC is 0.908

Models using five-fold cross-validation

```
seed = 20240103

k_fold_predictions = np.arange(0, 33227, 1.0) # just to create a vector of the correct length
pyando = np.arange(33227) % 5 # 0 to 653 mod 5; i.e., 0's through 4's
pyando = pyando.tolist()
random.shuffle(pyando) # shuffles pyando
for i in np.arange(5):
  train_set = [True if x != i else False for x in pyando]
  test_set = [True if x == i else False for x in pyando]
  X_sw_i = X_sw[train_set]
  y_sw_i = y_sw[train_set]
  X_sw_test_i = X_sw[test_set]
  y_sw_test_i = y_sw[test_set]
  ebm_sw_i = ExplainableBoostingClassifier(outer_bags = 25, inner_bags = 25)
  ebm_sw_i.fit(X_sw_i, y_sw_i)
  k_fold_predictions[test_set] = ebm_sw_i.predict_proba(X_sw_test_i)[:, 1]
```

```
y_true_k = y_sw
y_scores_k = k_fold_predictions
fpr_k, tpr_k, thresholds_k = roc_curve(y_true_k, y_scores_k)

# Calculate the area under the ROC curve (AUC)
auc_k = roc_auc_score(y_true_k, y_scores_k)

# Plot the ROC curve
plt.plot(fpr_k, tpr_k, label='ROC curve (AUC = {:.4f})'.format(auc_k))
plt.plot([0, 1], [0, 1], 'k--', label='Random')
plt.xlabel('False Positive Rate (FPR)')
plt.ylabel('True Positive Rate (TPR)')
plt.title('Receiver Operating Characteristic (ROC) Curve')
plt.legend(loc='lower right')

# Display the plot
plt.show()
```



Runs 1-10, AUCs are 0.8158, 0.8227, 0.8182, 0.8266, 0.8172, 0.8167, 0.8226, 0.8101, 0.8141, 0.8232
mean is 0.819, sd is 0.005

```
# Export predicted values for further analysis
df = pd.DataFrame([y_sw, k_fold_predictions])
df = df.T
df.to_csv('modelOutput.csv')
```

What happens if random variables are included?

Data for these tests was generated externally using R.

One uniform random variable

```
df_honk = pd.read_csv("dataPlusRandom/greatHonkU1_5.csv")
X_honk = df_honk.drop(columns = ['presence'])
y_honk = df_honk['presence']
ebm_honk = ExplainableBoostingClassifier(outer_bags = 25, inner_bags = 25)
ebm_honk.fit(X_honk, y_honk)
show(ebm_honk.explain_global())
```

test 1: unif comes after all other variables in importance

tests 2-5: same, or even after the first interaction term

One normal random variable

```
df_honk = pd.read_csv("dataPlusRandom/greatHonkN1_5.csv")
X_honk = df_honk.drop(columns = ['presence'])
y_honk = df_honk['presence']
ebm_honk = ExplainableBoostingClassifier(outer_bags = 25, inner_bags = 25)
ebm_honk.fit(X_honk, y_honk)
show(ebm_honk.explain_global())
```

test 1: norm comes after all other variables in importance

tests 2-5: same, or even after the first interaction term

Five uniform random variables

```
df_honk = pd.read_csv("dataPlusRandom/greatHonkU5_5.csv")
X_honk = df_honk.drop(columns = ['presence'])
y_honk = df_honk['presence']
ebm_honk = ExplainableBoostingClassifier(outer_bags = 25, inner_bags = 25)
ebm_honk.fit(X_honk, y_honk)
show(ebm_honk.explain_global())
```

test 1: all uniform variables fall below all other main variables, some below interactions

tests 2-5: same

Five normal random variables

```
df_honk = pd.read_csv("dataPlusRandom/greatHonkN5_5.csv")
X_honk = df_honk.drop(columns = ['presence'])
y_honk = df_honk['presence']
ebm_honk = ExplainableBoostingClassifier(outer_bags = 25, inner_bags = 25)
ebm_honk.fit(X_honk, y_honk)
show(ebm_honk.explain_global())
```

test 1: all normal variables fall below all other main variables, some below interactions

tests 2-5: same
NB, dist X sst interaction is the only one that commonly (but not universally) falls above random

Export plots for each predictor for improvement (?) in R

In retrospect, I'm not sure this is any better than just using the plots from the entire dataset, but here's the strategy: partition the dataset into five pieces, and generate and export the plots of each variable for each piece. Then average the plots together in R and add a smoother.

```
pyando = np.arange(33227) % 5 # 0 to 653 mod 5; i.e., 0's through 4's
pyando = pyando.tolist()
random.shuffle(pyando) # shuffles pyando
```

```
# Run the following for each i from 0 to 4:
i = 0
train_set = [True if x != i else False for x in pyando]
test_set = [True if x == i else False for x in pyando]
X_sw_i = X_sw[train_set]
y_sw_i = y_sw[train_set]
X_sw_test_i = X_sw[test_set]
y_sw_test_i = y_sw[test_set]
ebm_sw_i = ExplainableBoostingClassifier(outer_bags = 25, inner_bags = 25)
ebm_sw_i.fit(X_sw_i, y_sw_i)
ebm_sw_i_expl = ebm_sw_i.explain_global()
show(ebm_sw_i_expl)
```

In the following, use 0 for dist_coast, 1 for depth, 2 for chla_month, 3 for sst_day, 4 for salinity_month, 5 for cell_effort_value, 6 for day_of_year, and 9 for dist X sst. Then export the resulting JSON data to R for further use.

```
ebm_sw_i_expl.data(0)
{'type': 'univariate',
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```
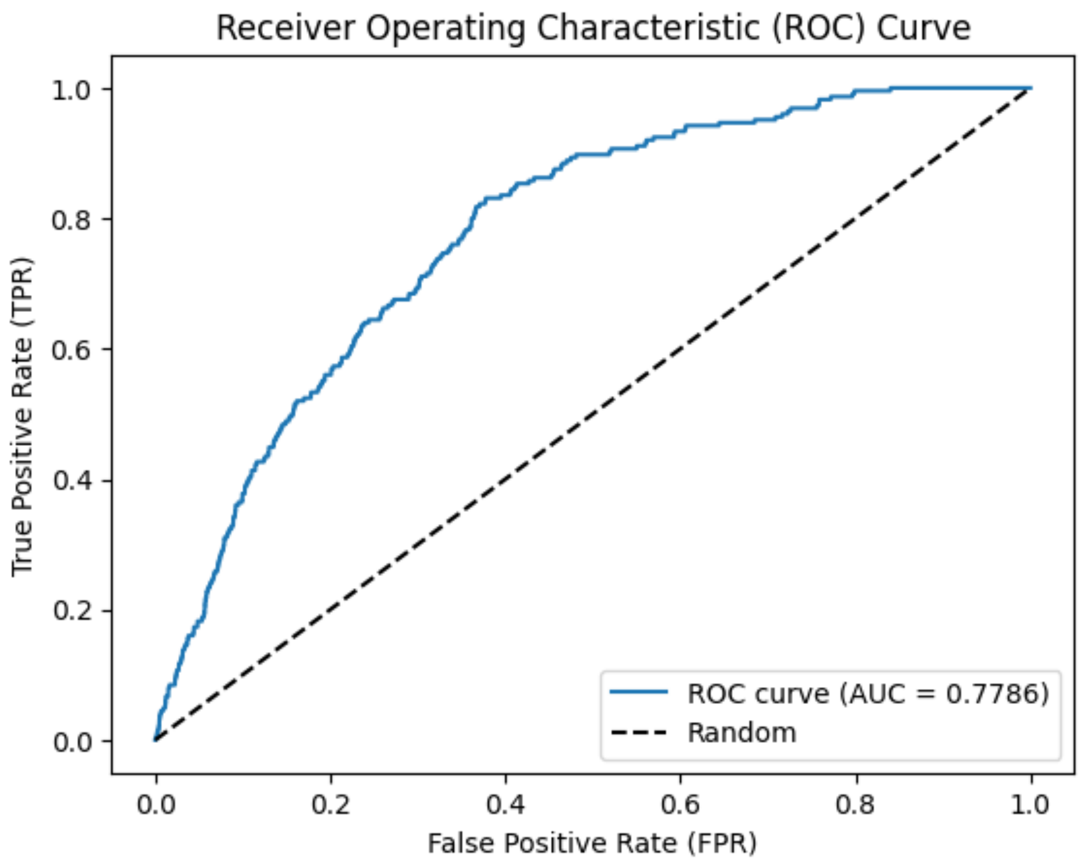

Does using ROSE improve anything on cross-validation?

Whether or not ROSE is implemented in python, it is easier to use it in R and import. The same 5-fold cross-validation procedure is followed as above, except each training set is augmented using the ROSE technique.

```
ROSE_train_0 = pd.read_csv("../TryROSE/ROSEtrain0.csv")
ROSE_X_train_0 = ROSE_train_0.drop(columns = ['presence'])
ROSE_y_train_0 = ROSE_train_0['presence']
ROSE_test_0 = pd.read_csv("../TryROSE/ROSEtest0.csv")
ROSE_X_test_0 = ROSE_test_0.drop(columns = ['presence'])
ROSE_y_test_0 = ROSE_test_0['presence']
```

```
ebm_sw_ROSE_0 = ExplainableBoostingClassifier(outer_bags = 25, inner_bags = 25)
ebm_sw_ROSE_0.fit(ROSE_X_train_0, ROSE_y_train_0)
ROSE_pred = ebm_sw_ROSE_0.predict_proba(ROSE_X_test_0)[:, 1]
ROSE_truth = ROSE_y_test_0.to_numpy()
ROSE_train_1 = pd.read_csv("../TryROSE/ROSEtrain1.csv")
ROSE_X_train_1 = ROSE_train_1.drop(columns = ['presence'])
ROSE_y_train_1 = ROSE_train_1['presence']
ROSE_test_1 = pd.read_csv("../TryROSE/ROSEtest1.csv")
ROSE_X_test_1 = ROSE_test_1.drop(columns = ['presence'])
ROSE_y_test_1 = ROSE_test_1['presence']

ebm_sw_ROSE_1 = ExplainableBoostingClassifier(outer_bags = 25, inner_bags = 25)
ebm_sw_ROSE_1.fit(ROSE_X_train_1, ROSE_y_train_1)
ExplainableBoostingClassifier(inner_bags=25, outer_bags=25)
ROSE_pred = np.concatenate((ROSE_pred, ebm_sw_ROSE_1.predict_proba(ROSE_X_test_1)[:, 1]),
axis = 0)
ROSE_truth = np.concatenate((ROSE_truth, ROSE_y_test_1.to_numpy()), axis = 0)
ROSE_train_2 = pd.read_csv("../TryROSE/ROSEtrain2.csv")
ROSE_X_train_2 = ROSE_train_2.drop(columns = ['presence'])
ROSE_y_train_2 = ROSE_train_2['presence']
ROSE_test_2 = pd.read_csv("../TryROSE/ROSEtest2.csv")
ROSE_X_test_2 = ROSE_test_2.drop(columns = ['presence'])
ROSE_y_test_2 = ROSE_test_2['presence']

ebm_sw_ROSE_2 = ExplainableBoostingClassifier(outer_bags = 25, inner_bags = 25)
ebm_sw_ROSE_2.fit(ROSE_X_train_2, ROSE_y_train_2)

ROSE_pred = np.concatenate((ROSE_pred, ebm_sw_ROSE_2.predict_proba(ROSE_X_test_2)[:, 1]),
axis = 0)
ROSE_truth = np.concatenate((ROSE_truth, ROSE_y_test_2.to_numpy()), axis = 0)
ROSE_train_3 = pd.read_csv("../TryROSE/ROSEtrain3.csv")
ROSE_X_train_3 = ROSE_train_3.drop(columns = ['presence'])
ROSE_y_train_3 = ROSE_train_3['presence']
ROSE_test_3 = pd.read_csv("../TryROSE/ROSEtest3.csv")
ROSE_X_test_3 = ROSE_test_3.drop(columns = ['presence'])
ROSE_y_test_3 = ROSE_test_3['presence']

ebm_sw_ROSE_3 = ExplainableBoostingClassifier(outer_bags = 25, inner_bags = 25)
ebm_sw_ROSE_3.fit(ROSE_X_train_3, ROSE_y_train_3)

ROSE_pred = np.concatenate((ROSE_pred, ebm_sw_ROSE_3.predict_proba(ROSE_X_test_3)[:, 1]),
axis = 0)
ROSE_truth = np.concatenate((ROSE_truth, ROSE_y_test_3.to_numpy()), axis = 0)
ROSE_train_4 = pd.read_csv("../TryROSE/ROSEtrain4.csv")
ROSE_X_train_4 = ROSE_train_4.drop(columns = ['presence'])
ROSE_y_train_4 = ROSE_train_4['presence']
ROSE_test_4 = pd.read_csv("../TryROSE/ROSEtest4.csv")
ROSE_X_test_4 = ROSE_test_4.drop(columns = ['presence'])
ROSE_y_test_4 = ROSE_test_4['presence']

ebm_sw_ROSE_4 = ExplainableBoostingClassifier(outer_bags = 25, inner_bags = 25)
ebm_sw_ROSE_4.fit(ROSE_X_train_4, ROSE_y_train_4)
```

```
ROSE_pred = np.concatenate((ROSE_pred, ebm_sw_ROSE_3.predict_proba(ROSE_X_test_4)[:, 1]),
axis = 0)
ROSE_truth = np.concatenate((ROSE_truth, ROSE_y_test_4.to_numpy()), axis = 0)
ROSE_fpr_k, ROSE_tpr_k, ROSE_thresholds_k = roc_curve(ROSE_truth, ROSE_pred)

# Calculate the area under the ROC curve (AUC)
ROSE_auc_k = roc_auc_score(ROSE_truth, ROSE_pred)

# Plot the ROC curve
plt.plot(ROSE_fpr_k, ROSE_tpr_k, label='ROC curve (AUC = {:.4f})'.format(ROSE_auc_k))
plt.plot([0, 1], [0, 1], 'k--', label='Random')
plt.xlabel('False Positive Rate (FPR)')
plt.ylabel('True Positive Rate (TPR)')
plt.title('Receiver Operating Characteristic (ROC) Curve')
plt.legend(loc='lower right')

# Display the plot
plt.show()
```



Worse