Z Score Classifier

Preparing data and motivation

```
import pandas as pd
import os
import random
import numpy as np
import matplotlib.pyplot as plt
from great_tables import GT, md
from scipy.signal import detrend
test_file_names = os.listdir("test/")
test_file_names.sort()
test_files = []
#for file in test_file_names:
  test_files.append(pd.read_csv(f"test/{file}", sep=";"))
#NOTE: I'm changing the way the data is imported by preprocessing
# it while being imported. In the official colab, this should be done separately
for file in test_file_names:
    data = pd.read_csv(f"test/{file}", sep=";")
    data['Value1'] = detrend(data['Value1'])
    test_files.append(data)
train_file_names = os.listdir('train/')
train_files = []
for train in train_file_names:
  train_files.append(pd.read_csv(f'train/{file}',sep=';'))
```

The test data is **normally distributed** meaning normal outlier detection techniques like **z** scores and IQR is applicable.

The Model

```
from sklearn.base import BaseEstimator, ClassifierMixin
from sklearn.metrics import recall_score
from sklearn.metrics import mean_squared_error, mean_absolute_error
class StatsModel(BaseEstimator, ClassifierMixin):
  Ensemble stats outlier classifier using:
  - Normal z scores
  - Rolling z_scores
  - Mean Absolute Deviation
  def __init__(self, w_smooth=51, w = 61,
               iqr_threshold = 1.5,
               mad_threshold = 2.465,
               normal_z_threshold = 2,
               rolling_z_threshold = 2,
               metric_consensus =3):
    self.w = w
    self.w_smooth = w_smooth
    self.iqr_threshold = iqr_threshold
    self.mad_threshold = mad_threshold
    self.normal_z_threshold = normal_z_threshold
    self.rolling_z_threshold = rolling_z_threshold
    self.metric_consensus = metric_consensus
  def _determine_rolling_z_mask(self, X :np.array) -> np.array:
    k = np.ones(self.w_smooth) / self.w_smooth
    smooth = np.convolve(X, k, mode='same')
    # I'm quite sure this step makes it less applicable for machine learning so
    # its not used in fit
    resid = X- smooth
    kw = np.ones(self.w) / self.w
```

```
mu = np.convolve(resid, kw, mode='same')
 mu2 = np.convolve(resid * resid, kw, mode='same')
 var = np.maximum(mu2 - mu*mu, 1e-08)
 sigma= np.sqrt(var)
  z_rolling = np.abs((resid - mu) / (sigma + 1e-08))
 return np.abs(z_rolling > self.rolling_z_threshold)
def fit(self, X : np.array, y=None) -> None:
  self.iqr_ = np.quantile(X, 0.75) - np.quantile(X, 0.25)
  self.mean_ = np.mean(X)
 self.std_ = np.std(X)
  self.median_ = np.median(X)
  self.mad_ = np.sum(np.abs(X - self.mean_)) / len(X)
  self.iqr_ub_ = self.mean_ + self.iqr_threshold * self.iqr_
  self.iqr_lb_ = self.mean_ - self.iqr_threshold * self.iqr_
 return self
def predict(self, X = None) -> np.array:
  IQR_mask = (X > self.iqr_ub_) | (X < self.iqr_lb_)</pre>
  MAD_mask = np.abs(X - self.median_) > self.mad_ * self.mad_threshold
  Normal_Z_Mask = np.abs((X - self.mean_) / self.std_) > self.normal_z_threshold
  Rolling_Z_Mask = self._determine_rolling_z_mask(X)
  mask_df = pd.DataFrame({
    'IQR' : IQR_mask,
    "MAD" : MAD_mask,
    'Normal_z' : Normal_Z_Mask,
    'Rolling_Z' : Rolling_Z_Mask
  })
 mask_df['outlier'] = mask_df.sum(axis=1) >= self.metric_consensus
 return mask_df['outlier'].to_numpy()
def score(self, X , y_true) -> float:
  y_pred = self.predict(X)
 return recall_score(y_true, y_pred)
```

Helper Functions

```
from benchmarking import Benchmarking
import time
def run_benchmark(model,show_printout=True):
 benchmark_df = pd.DataFrame()
 file_no = 1
 for df in test_files:
   if show_printout:
     model = model
   X = df['Value1']
   y_true = df['Labels']
   model.fit(X)
   y_pred = model.predict(X)
   results = Benchmarking.evaluate_model(y_true, y_pred,show_printout=show_printout)
   results = results.rename(columns={'Score' : f'File {file_no}'})
   benchmark_df = pd.concat([benchmark_df, results],axis=1)
   file_no += 1
 return benchmark_df
def create_benchmark_table(benchmark_df: pd.DataFrame,
                         model_name :str = "Stats Model" ,
                          subtitle: str = "results **before hyperparameter turning**") -> No
 totals = benchmark_df.sum(axis=1) / 10
 totals = totals.apply(lambda x: round(x,\frac{2}{2}))
 totals = totals.to_frame().transpose()
 totals['group'] = 'AGGREGATE'
 benchmark_df = benchmark_df.transpose()
 benchmark_df['group'] = 'File'
 benchmark_df = pd.concat([benchmark_df, totals])
  benchmark_df = benchmark_df.reset_index().rename(columns={'index': 'File'})
 benchmark_df
   GT(benchmark_df)
    .tab_header(title=md(f'Benchmark Results: **{model_name}**'),
```

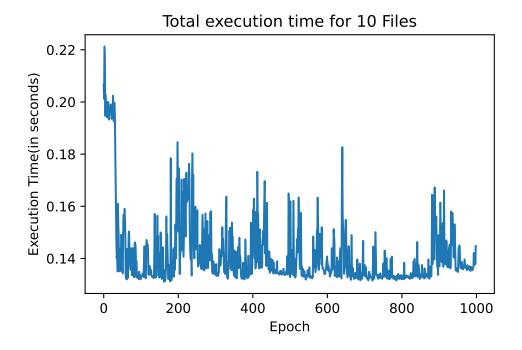
```
subtitle=md(subtitle))
.tab_source_note(md('See benchmarks for how penalised group accuracy is calculated'))
.tab_stub(rowname_col='File',groupname_col='group')
).show()
```

Benchmarking Time complexity

```
start = time.perf_counter()
ms = []
for epoch in range(1,1000):
    start = time.perf_counter()
    model = StatsModel()
    run_benchmark(model,show_printout=False)
    end = time.perf_counter()
    ms.append((end-start))
end = time.perf_counter()
print('Time for 1000 epochs', end-start)
```

Time for 1000 epochs 0.14482370900003616

```
plt.plot(ms)
plt.title('Total execution time for 10 Files')
plt.xlabel('Epoch')
plt.ylabel('Execution Time(in seconds)')
plt.show()
```



The execution time varies from 24 ms to 300 ms meaning we can tune this model for thousands of iterations to determine the optimal parameters

Base Benchmark

```
benchmark_df = run_benchmark(StatsModel())
create_benchmark_table(benchmark_df)
```

11 anomaly groups identified 10 anomaly groups identified Model predicts 1 more than 10 Model predicts 1 more than 10

11 anomaly groups identified 10 anomaly groups identified Model predicts 1 more than 10

Model predicts 1 more than 10	
=======File	3===========
12 anomaly groups identified 10 anomaly groups identified Model predicts 2 more than 10 Model predicts 2 more than 10	
======File	4==========
10 anomaly groups identified 10 anomaly groups identified Number of groups match! Number of groups match!	
======File	5======
10 anomaly groups identified 10 anomaly groups identified Number of groups match! Number of groups match!	
File	6
11 anomaly groups identified 10 anomaly groups identified Model predicts 1 more than 10 Model predicts 1 more than 10	
======File	7==========
11 anomaly groups identified 10 anomaly groups identified Model predicts 1 more than 10 Model predicts 1 more than 10	
======File	8=======
11 anomaly groups identified 10 anomaly groups identified Model predicts 1 more than 10 Model predicts 1 more than 10	

10 anomaly groups identified 10 anomaly groups identified Number of groups match!

Number of groups match!

11 anomaly groups identified 10 anomaly groups identified Model predicts 1 more than 10 Model predicts 1 more than 10

Benchm	Benchmark Results: Stats Model							
results l	before hyp	erparamet	er turn	ing				
	Accuracy	Precision	Recall	Balanced Accuracy	Group Accuracy	Penalised Group Accuracy		
File	00.69	00.07	04.75	00.07	00.0	01.00		

	·				•	
File						
File 1	98.63	99.87	84.75	92.37	90.0	81.82
File 2	96.66	99.86	68.79	84.39	80.0	72.73
File 3	96.64	99.78	57.27	78.63	70.0	58.33
File 4	97.84	99.83	73.26	86.62	90.0	90.0
File 5	98.99	99.76	80.31	90.15	90.0	90.0
File 6	97.04	99.86	70.62	85.3	90.0	81.82
File 7	98.18	99.68	77.81	88.89	100.0	90.91
File 8	96.0	99.81	57.37	78.68	70.0	63.64
File 9	96.81	99.76	56.62	78.3	80.0	80.0
File 10	97.57	99.87	75.99	87.99	90.0	81.82
AGGRE	EGATE					
0	97.44	99.81	70.28	85.13	85.0	79.11

See benchmarks for how penalised group accuracy is calculated

Base Benchmark with different grouping hyperparameters

The grouping function used for anomalous regions has two hyperparameters:

• merge_tolerance

acceptable gap between predicted anomalous regions for when a merge is appropriate

• noise_tolerance

 minimum length of an anomalous region(end - start) for it to be classified as an anomalous region

The group accuracy is penalised if precision or recall is very high. Given each set has a recall of 100%, we can hyperparameter tune the model to maximize recall to get these two metrics closer together.

Given precision is 100% (no false positives) this indicates all true anomalies are detected by the model. The problem is that there is false negatives in the model indicating multiple false indications of anomalous regions.

Hyperparameter Tuning for Penalised Group Accuracy

```
from sklearn.model selection import GridSearchCV, RandomizedSearchCV
from tqdm import tqdm
param_grid = {
    "w_smooth": [31, 51, 71, 91, 111, 131, 151, 171],
    "w": [41, 61, 81, 101, 121, 141, 161, 181],
    "iqr_threshold": [1.5, 1.75, 2],
    "mad_threshold": [ 2.2, 2.465, 2.7, 3],
    "normal_z_threshold": [2.25, 2.5, 3],
    "rolling_z_threshold": [2.0, 2.25, 2.5],
    "metric_consensus": [3, 4]
combined = pd.concat(test_files)
def calculate_estimated_tuning_time(params: dict, cv :int):
  total iterations = 1
  for key, value in params.items():
    total_iterations *= len(value)
  print(total_iterations)
  print('Estimated Tuning Time', (total_iterations / 16)*cv, 'seconds')
calculate_estimated_tuning_time(param_grid,5)
import itertools
import numpy as np
def grid_search(model, X, y, param_grid):
```

```
best_score = -np.inf
best_params = {}
for combination in tqdm(itertools.product(*param_grid.values()),desc='Iterations'):
    params = dict(zip(param_grid.keys(), combination))
    model.set_params(**params)
    model.fit(X, y)
    score = model.score(X, y)
    if score > best_score:
        best_score = score
        best_params = params
return best_params, best_score
```

13824 Estimated Tuning Time 4320.0 seconds

```
#grid.best_params_
```

```
'w': 41,
                    'w_smooth': 31}
best_recall_clf = StatsModel()
best_recall_clf.set_params(**best_recall_params)
benchmark_df = run_benchmark(best_recall_clf)
create_benchmark_table(benchmark_df,model_name='Z_Score Model',
                 subtitle="results **after hyperparameter tuning for recall**")
11 anomaly groups identified
10 anomaly groups identified
Model predicts 1 more than 10
Model predicts 1 more than 10
10 anomaly groups identified
10 anomaly groups identified
Number of groups match!
Number of groups match!
11 anomaly groups identified
10 anomaly groups identified
Model predicts 1 more than 10
Model predicts 1 more than 10
10 anomaly groups identified
10 anomaly groups identified
Number of groups match!
Number of groups match!
11 anomaly groups identified
```

10 anomaly groups identified	
Model predicts 1 more than 10	
Model predicts 1 more than 10	
=======File 6	6========
11 anomaly groups identified	
10 anomaly groups identified	
Model predicts 1 more than 10	
Model predicts 1 more than 10	
-	
======File 7	7========
11 anomaly groups identified	
10 anomaly groups identified	
Model predicts 1 more than 10	
Model predicts 1 more than 10	
Francisco Communication	
=======File 8	8=========
10 anomaly groups identified	
10 anomaly groups identified	
Number of groups match!	
Number of groups match!	
Number of groups materi.	
=======File 9	9===========
ille :	J
10 anomaly groups identified	
10 anomaly groups identified	
Number of groups match!	
Number of groups match!	
Number of groups match:	
=======File :	10=========
tite	
11 anomaly groups identified	
10 anomaly groups identified	
Model predicts 1 more than 10	
Model predicts 1 more than 10	
TOTAL PROGRESS I MOTO SHOW TO	

Benchmark Results: **Z_Score Model** results after hyperparameter tuning for recall

	Accuracy	Precision	_	Balanced Accuracy	Group Accuracy	Penalised Group Accuracy
File						
File 1	98.54	99.87	83.74	91.87	90.0	81.82
File 2	96.49	99.72	67.29	83.63	80.0	80.0
File 3	96.51	99.77	55.61	77.8	70.0	63.64
File 4	97.82	99.83	73.01	86.5	90.0	90.0
File 5	98.9	99.5	78.74	89.36	90.0	81.82
File 6	96.86	99.86	68.82	84.41	90.0	81.82
File 7	98.11	99.68	76.94	88.46	100.0	90.91
File 8	95.82	99.62	55.56	77.77	70.0	70.0
File 9	96.76	99.52	56.07	78.02	80.0	80.0
File 10	97.38	99.87	74.11	87.05	90.0	81.82
AGGRE	EGATE					
0	97.32	99.72	68.99	84.49	85.0	80.18

See benchmarks for how penalised group accuracy is calculated

11 anomaly groups identified 10 anomaly groups identified Model predicts 1 more than 10 Model predicts 1 more than 10

10 anomaly groups identified 10 anomaly groups identified Number of groups match! Number of groups match!

11 anomaly groups identified

10 anomaly groups identified	
${\tt Model\ predicts\ 1\ more\ than\ 10}$	
Model predicts 1 more than 10	
File	4
10 anomaly groups identified 10 anomaly groups identified Number of groups match! Number of groups match!	
======File	5=======
11 anomaly groups identified 10 anomaly groups identified Model predicts 1 more than 10 Model predicts 1 more than 10	
=======File	6===========
11 anomaly groups identified 10 anomaly groups identified Model predicts 1 more than 10 Model predicts 1 more than 10	
======File	7=======
11 anomaly groups identified 10 anomaly groups identified Model predicts 1 more than 10 Model predicts 1 more than 10	
======File	8======
10 anomaly groups identified 10 anomaly groups identified Number of groups match! Number of groups match!	
======File	9======
10 anomaly groups identified 10 anomaly groups identified	

```
Number of groups match!
Number of groups match!
```

=======File 10==============

11 anomaly groups identified 10 anomaly groups identified Model predicts 1 more than 10 Model predicts 1 more than 10

Benchmark Results: **Z Score Model** results after hyperparameter tuning for balanced accuracy

	Accuracy	Precision	Recall	Balanced Accuracy	Group Accuracy	Penalised Group Accuracy
File						
File 1	98.55	100.0	83.74	91.87	90.0	81.82
File 2	96.51	100.0	67.29	83.65	80.0	80.0
File 3	96.52	100.0	55.61	77.81	70.0	63.64
File 4	97.83	100.0	73.01	86.5	90.0	90.0
File 5	98.91	99.75	78.74	89.36	90.0	81.82
File 6	96.87	100.0	68.82	84.41	90.0	81.82
File 7	98.12	99.84	76.94	88.47	100.0	90.91
File 8	95.83	99.81	55.56	77.77	70.0	70.0
File 9	96.77	99.76	56.07	78.03	80.0	80.0
File 10	97.39	100.0	74.11	87.05	90.0	81.82
AGGRE	EGATE					
0	97.33	99.92	68.99	84.49	85.0	80.18

See benchmarks for how penalised group accuracy is calculated

```
true_groups = np.array(Benchmarking.create_anomaly_groups(y))
print('Pred Groups\n',pred_groups)
print('Actual Groups\n',true_groups)
5 anomaly groups identified
10 anomaly groups identified
Model predicts 5 less than 10
Model predicts 5 less than 10
8 anomaly groups identified
10 anomaly groups identified
Model predicts 2 less than 10
Model predicts 2 less than 10
11 anomaly groups identified
10 anomaly groups identified
Model predicts 1 more than 10
Model predicts 1 more than 10
9 anomaly groups identified
10 anomaly groups identified
Model predicts 1 less than 10
Model predicts 1 less than 10
10 anomaly groups identified
10 anomaly groups identified
Number of groups match!
Number of groups match!
```

10 anomaly groups identified 10 anomaly groups identified Number of groups match! Number of groups match!

11 anomaly groups identified 10 anomaly groups identified Model predicts 1 more than 10 Model predicts 1 more than 10

12 anomaly groups identified 10 anomaly groups identified Model predicts 2 more than 10 Model predicts 2 more than 10

12 anomaly groups identified 10 anomaly groups identified Model predicts 2 more than 10 Model predicts 2 more than 10

7 anomaly groups identified 10 anomaly groups identified Model predicts 3 less than 10 Model predicts 3 less than 10

Benchmark Results: **Stats Model** results **before hyperparameter turning**

Accuracy Precision Recall Balanced Accuracy Group Accuracy Penalised Group Accuracy File File 1 93.48 99.59 27.0263.530.0 15.0 File 2 93.86 99.78 42.5571.2760.0 48.0 File 3 50.3863.64 96.199.7575.19 70.0

Benchmark Results: Stats Model

results	before	\mathbf{hyp}	erparamet	er turni	\mathbf{ing}
	Λ		D:-:	D 11	D - 1

	Accuracy	Precision	Recall	Balanced Accuracy	Group Accuracy	Penalised Group Accuracy
File 4	95.96	99.75	49.88	74.93	70.0	63.0
File 5	98.8	99.74	76.57	88.28	90.0	90.0
File 6	93.91	99.75	39.44	69.72	70.0	70.0
File 7	95.87	99.5	49.32	74.65	80.0	72.73
File 8	95.17	99.78	48.5	74.25	60.0	50.0
File 9	96.47	99.74	51.98	75.98	80.0	66.67
File 10	94.71	99.79	47.62	73.8	50.0	35.0
AGGRE	EGATE					
0	95.43	99.72	48.33	74.16	66.0	57.4

See benchmarks for how penalised group accuracy is calculated

```
8 anomaly groups identified
10 anomaly groups identified
Pred Groups
 [[2928 2979]
 [3834 3927]
 [4758 4879]
 [6850 6953]
 [7919 7955]
 [8379 8429]
 [9112 9221]
 [9403 9472]]
Actual Groups
 [[2206 2326]
 [2864 2979]
 [3483 3566]
 [3834 3927]
 [4758 4879]
 [6850 6958]
 [7852 7955]
 [8319 8429]
 [9112 9226]
 [9372 9472]]
```

```
for file in test_files:
  model = StatsModel().set_params(**best_balanced_acc_params)
  X = file['Value1']
  y = file['Labels']
```

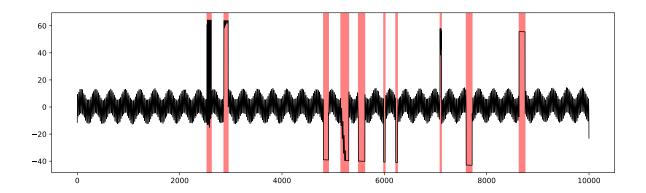
```
model.fit(X)
y_pred = model.predict(X)

pred_groups = Benchmarking.create_anomaly_groups(pd.Series(y))
true_groups = Benchmarking.create_anomaly_groups(y)

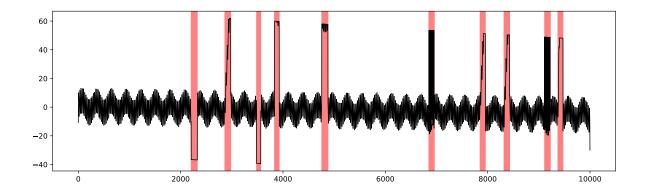
plt.figure(figsize=(14,4))
plt.plot(X, color='black',lw=1)
#for start,end in true_groups:
# plt.axvspan(start, end, color='green',alpha=0.3)

for start,end in pred_groups:
    plt.axvspan(start,end, color='red',alpha=0.5)
plt.show()
```

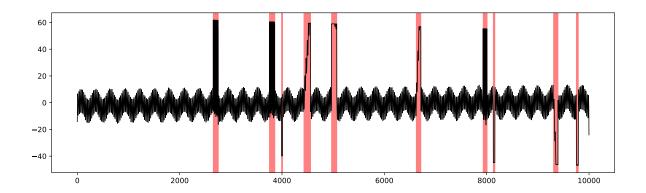
10 anomaly groups identified 10 anomaly groups identified



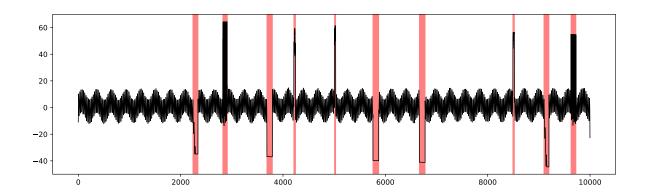
10 anomaly groups identified 10 anomaly groups identified



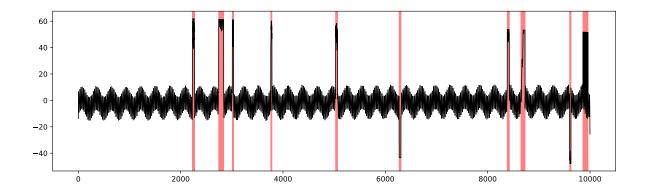
10 anomaly groups identified 10 anomaly groups identified



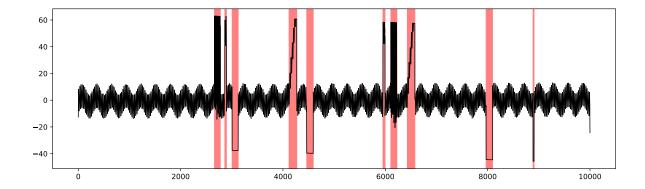
10 anomaly groups identified 10 anomaly groups identified



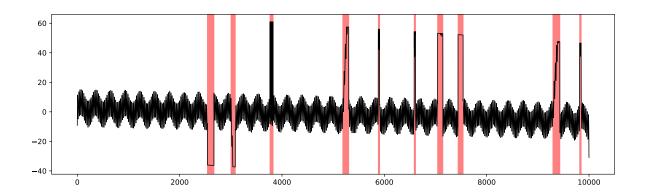
- 10 anomaly groups identified $% \frac{1}{2}\left(\frac{1}{2}\right) =\frac{1}{2}\left(\frac{1}{2}\right$
- 10 anomaly groups identified



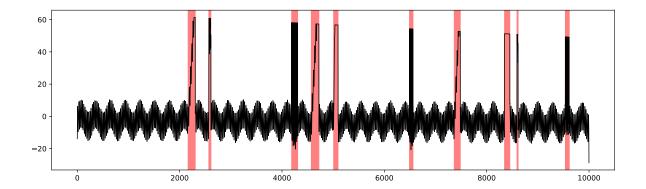
10 anomaly groups identified 10 anomaly groups identified



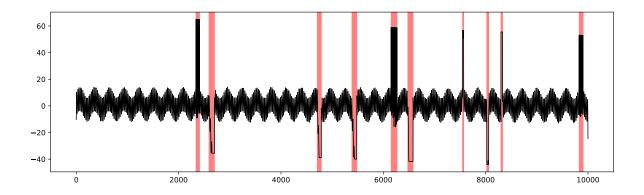
10 anomaly groups identified 10 anomaly groups identified



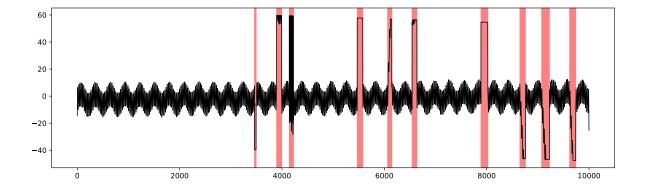
- 10 anomaly groups identified $\,$
- 10 anomaly groups identified



- 10 anomaly groups identified
- 10 anomaly groups identified

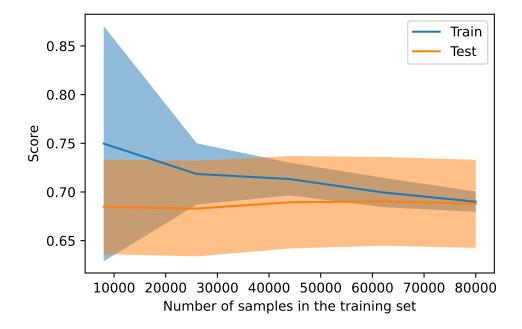


- 10 anomaly groups identified
- 10 anomaly groups identified

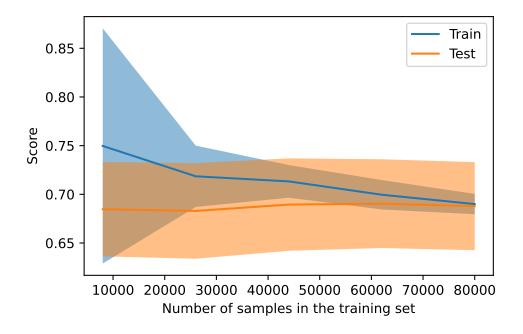


```
from sklearn.model_selection import LearningCurveDisplay

LearningCurveDisplay.from_estimator(
   StatsModel().set_params(**best_balanced_acc_params),
   combined['Value1'],
   combined['Labels']
)
plt.show()
```



```
LearningCurveDisplay.from_estimator(
   StatsModel().set_params(**best_recall_params),
   combined['Value1'],
   combined['Labels']
)
plt.show()
```

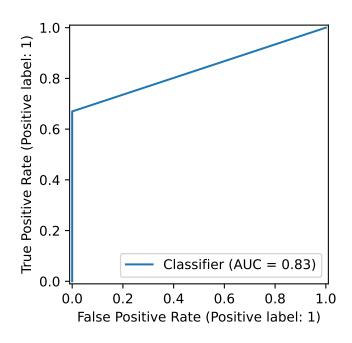


```
from sklearn.metrics import roc_curve
from sklearn.metrics import RocCurveDisplay

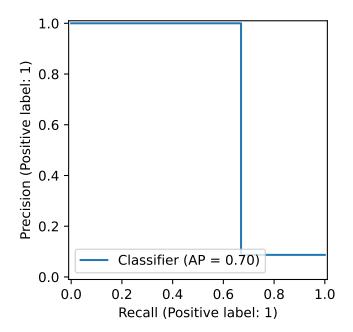
model = StatsModel().set_params(**best_balanced_acc_params)

Test = combined[-20000:]
model.fit(combined[:80000]['Value1'])
y_pred = model.predict(Test['Value1'])
y_true = Test["Labels"]
fpr, tpr, thresholds = roc_curve(y_true, y_pred)

RocCurveDisplay.from_predictions(y_true, y_pred)
plt.show()
```



from sklearn.metrics import PrecisionRecallDisplay
PrecisionRecallDisplay.from_predictions(y_true, y_pred)
plt.show()



```
model = StatsModel()
for idx, train in enumerate(train_files):
  model = StatsModel()
  model.fit(train['Value1'])
  y_pred = model.predict(test_files[idx]['Value1'])
  y_true= test_files[idx]['Labels']
  results = Benchmarking.evaluate_model(y_true, y_pred)
  print(results)
```

2 anomaly groups identified 10 anomaly groups identified Model predicts 8 less than 10 Model predicts 8 less than 10 Score 8.78 Accuracy Precision 8.79 Recall 98.43 49.22 Balanced Accuracy Group Accuracy 0.00 Penalised Group Accuracy 0.00 6 anomaly groups identified 10 anomaly groups identified Model predicts 4 less than 10 Model predicts 4 less than 10 Score 8.13 Accuracy Precision 8.34 Recall 76.19 Balanced Accuracy 38.10 Group Accuracy 0.00 Penalised Group Accuracy 0.00 4 anomaly groups identified 10 anomaly groups identified Model predicts 6 less than 10 ${\tt Model\ predicts\ 6\ less\ than\ 10}$ Score Accuracy Precision Recall Balanced Accuracy

6.98 7.04 89.03 44.52

Group Accuracy	0.00
Penalised Group Accuracy	0.00
4 anomaly groups identifie	d
10 anomaly groups identifi	ed
Model predicts 6 less than	. 10
Model predicts 6 less than	. 10
	Score
Accuracy	7.71
Precision	7.74
Recall	95.90
Balanced Accuracy	47.95
Group Accuracy	0.00
Penalised Group Accuracy	0.00
7 anomaly groups identifie	d
10 anomaly groups identifi	
Model predicts 3 less than	
Model predicts 3 less than	
_	Score
Accuracy	4.03
Precision	4.07
	79.33
	39.67
Group Accuracy	0.00
Penalised Group Accuracy	0.00
8 anomaly groups identifie	
10 anomaly groups identifi	
Model predicts 2 less than	
Model predicts 2 less than	
_	Score
Accuracy	8.34
Precision	8.48
	83.07
	41.53
Group Accuracy	0.00
Penalised Group Accuracy	
7 anomaly groups identifie	
10 anomaly groups identifi	
Model predicts 3 less than	
Model predicts 3 less than	
_	Score
Accuracy	6.09
Precision	6.22
	75.09
INCOULT	10.03

Using the provided Train Files

There is no anomalies in these files and is not normally distributed meaning it will most likely perform very poorly.

Important

The data must be normally distributed

```
def run_benchmark(model,show_printout=True):
 benchmark_df = pd.DataFrame()
 file_no = 1
 for idx,df in enumerate(test_files):
   if show_printout:
     X_train = train_files[idx]['Value1']
   y_train = train_files[idx]['Labels']
   X_test = df['Value1']
   y_true = df['Labels']
   model.fit(X_train)
   y_pred = model.predict(X_test)
   results = Benchmarking.evaluate_model(y_true, y_pred,show_printout=show_printout)
   results = results.rename(columns={'Score' : f'File {file_no}'})
   benchmark_df = pd.concat([benchmark_df, results],axis=1)
   file_no += 1
 return benchmark_df
model = StatsModel().set_params(**best_recall_params)
create_benchmark_table(run_benchmark(model))
-----File 1------
2 anomaly groups identified
10 anomaly groups identified
Model predicts 8 less than 10
Model predicts 8 less than 10
6 anomaly groups identified
10 anomaly groups identified
Model predicts 4 less than 10
Model predicts 4 less than 10
```

======File	3
4 anomaly groups identified	
10 anomaly groups identified	
Model predicts 6 less than 10	
Model predicts 6 less than 10	
======File	4=======
4 anomaly groups identified	
10 anomaly groups identified	
Model predicts 6 less than 10	
Model predicts 6 less than 10	
•	
=======File	5=======
7	
7 anomaly groups identified	
10 anomaly groups identified	
Model predicts 3 less than 10	
Model predicts 3 less than 10	
File	6=======
O crowely ground identified	
8 anomaly groups identified	
10 anomaly groups identified	
Model predicts 2 less than 10	
Model predicts 2 less than 10	
======File	7========
7 anomaly groups identified	
10 anomaly groups identified	
Model predicts 3 less than 10	
Model predicts 3 less than 10	
======File	8
9 anomaly groups identified	
10 anomaly groups identified	
Model predicts 1 less than 10	
Model predicts 1 less than 10	
prodroso r roop ondir ro	

1 anomaly groups identified 10 anomaly groups identified Model predicts 9 less than 10 Model predicts 9 less than 10

2 anomaly groups identified 10 anomaly groups identified Model predicts 8 less than 10 Model predicts 8 less than 10

Benchmark Results: Stats Model							
results before hyperparameter turning							

	Accuracy	Precision	Recall	Balanced Accuracy	Group Accuracy	Penalised Group Accuracy		
File								
File 1	8.77	8.78	98.32	49.16	0.0	0.0		
File 2	7.95	8.17	74.51	37.25	0.0	0.0		
File 3	6.98	7.04	89.03	44.52	0.0	0.0		
File 4	7.71	7.74	95.9	47.95	0.0	0.0		
File 5	4.03	4.07	79.33	39.67	0.0	0.0		
File 6	8.34	8.48	83.07	41.53	0.0	0.0		
File 7	6.09	6.22	75.09	37.55	0.0	0.0		
File 8	7.15	7.31	76.39	38.19	0.0	0.0		
File 9	7.32	7.32	99.86	49.93	0.0	0.0		
File 10	9.63	9.67	95.54	47.77	0.0	0.0		
AGGREGATE								
0	7.4	7.48	86.7	43.35	0.0	0.0		

See benchmarks for how penalised group accuracy is calculated