→ Predicting Antibiotic Resistance Genes | Proof Of Concept

The situation is a simple binary classification on sequence data. The Dataset was original gathered from kaggle, but the author privated the dataset soon after I downloaded (not kidding).

Results:

all models consistantly get above 90% accuracy with little optimization

- MLP = 94%
- GRU = 97%
- CNN = 98%

In summary, resistance is easily identified through genes, predicting based off Pan / meta genomes will be less simple. Many improvements could have been made in light of future models.

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt

import tensorflow as tf
from tensorflow import keras
from keras import layers

from functools import partial
from sklearn.metrics import ConfusionMatrixDisplay, accuracy_score
```

Setup

```
from google.colab import drive
drive.mount('/content/drive')
!cd /content/drive/MyDrive/
!ls

Drive already mounted at /content/drive; to attempt to forcibly remount, call drive.moundrive sample_data

***

**Np_data = np.load('/content/drive/MyDrive/datasets/dataset.npy', allow_pickle=True)
np_data
**True**

**Provided to the provided to
```

array(['ATGCACTACCGTATGATCCCCCTTCACTGGATGATGGAAATTGACTGCAATGGCTGCGCTAATAATACTTTGTCTCGTC

array({'resistant': array([False, False, False, ..., True,

True, False]), 'genes':

- 'ATGCACTACCGTATGATTCACTGGATGATGGAAATTGACTGCAATGGCTGCGCTAATAATACTTTGTCTCGTCGTTGGAATTACGA
- 'ATGCACTACCGTATGATTCACTGGATCGTGATGGAAATTGACTGCAATGGCTGCGCTAATAATACTTTGTCTCGTCGTTGGAATTA
- 'ATGCACTACCGTATGATTCACTGGATGATGGAAACTGCAATGGCTGCGCTAATAATACTTTGTCTCGTCGTTGGAATTACGACTTC
- 'ATGCACTACCGTATGATTCACTGGATGATGGAAATTGACTTGCAATGGCTGCGCTAATAATACTTTGTCTCGTCGTTGGAATTACG
- 'ATGCACTACCGTATGATTCACTGGATGATGGAAATTGACTGCAATGGCTGCGCTAATAATACTTTGTCTCGTCGTTGGAATTACGA dtype=object)}, dtype=object)

```
# thanks to Alexander Scarlat .MD for the pandas dataframe convertion
Datadict = np_data[()]
df = pd.DataFrame.from_dict(Datadict)
print(df.shape)
df
```

(100000, 2)

	resistant	ge ge
0	False	ATGCACTACCGTATGATCCCCCTTCACTGGATGATGGAAATTGA
1	False	ATGCACTACCGTATGATTCACTGGATGATGGAAATTGACTGCAAT
2	False	ATGCACTACCGTATGATTCACTGGATCGTGATGGAAATTGACTG
3	False	ATGCACTACCGTATGATTCACTGGGTGATGGAAATTGACTGCAAT
4	False	ATGCACGACCGTATCATTCACTGGATGATGGAAATTGACTGCAAT
99995	False	ATGCACTACCGTATGATTCACTGGATGATGGAAACTCTCTTTGA
99996	False	ATGCACTACCGTATGATTCACTGGATGATGGAAATTGACTGCAAT
99997	True	ATGCACTACCGTATGATTCACTGGATGATGGAAACTGCAATGGC
99998	True	ATGCACTACCGTATGATTCACTGGATGATGGAAATTGACTTGCA
←		···

```
# gene
X = df['genes'].iloc[0]
print(len(X), X)
```

156 ATGCACTACCGTATGATCCCCCTTCACTGGATGATGGAAATTGACTGCAATGGCTGCGCTAATAATACTTTGTCTCGTCGTTG

```
df.info()
```

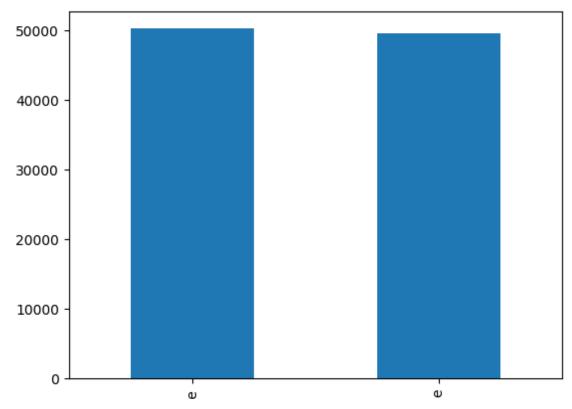
```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 100000 entries, 0 to 99999
Data columns (total 2 columns):
    # Column Non-Null Count Dtype
--- 0 resistant 100000 non-null bool
    1 genes 100000 non-null object
dtypes: bool(1), object(1)
memory usage: 879.0+ KB
```

```
val_counts = df["resistant"].value_counts()
print(val_counts)
val_counts.plot(kind="bar")
```

```
False 50297
True 49703
```

Name: resistant, dtype: int64

<Axes: >



```
from keras.utils import pad_sequences

vocab = ['A', 'C', 'G', 'T']
char2idx = {
  char: (idx+1) for idx, char in enumerate(vocab)
}
```

```
# tokenize (convert to ATGC to 1-4)
def tokenize(sequence):
  return [char2idx[char] for char in sequence]
# one hot encode (convert to sparse vector)
def encode(tokens):
 tensor = tf.constant(tokens)
  one_hot = np.asarray(tf.one_hot(tensor, len(vocab)))
  return one hot.astype("int32")
df['genes tokenized'] = df['genes'].apply(tokenize)
# pad right with 0's for the tokenized column
X token = pad sequences(df['genes tokenized'], maxlen=160, padding='post', truncating='post',
X enc = np.array([encode(tokens) for tokens in X token])
print(df.head(3))
print("OHE:\n ", X enc[0][0][:5], "\n .... ")
        resistant
                                                                genes \
     0
            False ATGCACTACCGTATGATCCCCCTTCACTGGATGATGGAAATTGACT...
            False ATGCACTACCGTATGATTCACTGGATGATGGAAATTGACTGCAATG...
     2
            False ATGCACTACCGTATGATTCACTGGATCGTGATGGAAATTGACTGCA...
                                          genes tokenized
     0 [1, 4, 3, 2, 1, 2, 4, 1, 2, 2, 3, 4, 1, 4, 3, ...
     1 [1, 4, 3, 2, 1, 2, 4, 1, 2, 2, 3, 4, 1, 4, 3, ...
     2 [1, 4, 3, 2, 1, 2, 4, 1, 2, 2, 3, 4, 1, 4, 3, ...
     OHE:
       [0 1 0 0]
y = np.array(df['resistant']).astype('int32')
def split(X, ratio=0.8):
 # take out test set (top 20%)
 test split = int(len(X) * ratio)
 full_train, test = X[:test_split], X[test_split:]
 # hold out top 20% of training for per epoch validation
  validation split = int(len(full train) * ratio)
  train, validation = full train[:validation split], full train[validation split:]
  return train, validation, test
y_train, y_valid, y_test = split(y)
X enc train, X enc valid, X enc test = split(X enc)
X_token_train, X_token_valid, X_token_test = split(X_token)
```

- SVM

```
''' from sklearn.metrics import ConfusionMatrixDisplay, accuracy_score
from sklearn.svm import SVC

svm = SVC(kernel='linear')
svm.fit(X_token_train, y_train)

y_pred = svm.predict(X_token_test)

accuracy = accuracy_score(y_test, y_pred)
print("Accuracy: ", accuracy)

ConfusionMatrixDisplay.from_predictions(y_test, y_pred) '''

# colab dies -> to much data for non parametric
```

' from sklearn.metrics import ConfusionMatrixDisplay, accuracy_score\nfro
m sklearn.svm import SVC\n\nsvm = SVC(kernel=\'linear\')\nsvm.fit(X_token
thain \(\text{token} \) \(\te

MLP

```
DefaultDense = partial(
  layers.Dense,
  activation='relu',
  kernel initializer="he uniform",
  kernel regularizer= keras.regularizers.12(0.01)
)
mlp model = keras.Sequential([
    keras.Input(160),
    DefaultDense(20), # technically not a MLP cos 2 hidden layers but who cares
    DefaultDense(10),
    layers.Dense(1, activation='sigmoid')
1)
mlp_model.compile(
  loss='binary crossentropy',
  optimizer='adam',
  metrics=['accuracy']
mlp_model.summary()
```

Model: "sequential_5"

Layer (type)	Output Shape	Param #
	···	
dense_5 (Dense)	(None, 20)	3220

Non-trainable params: 0

```
      dense_6 (Dense)
      (None, 10)
      210

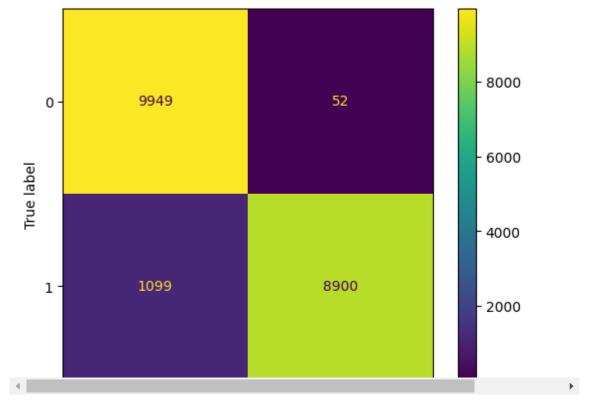
      dense_7 (Dense)
      (None, 1)
      11

      Total params: 3,441

      Trainable params: 3,441
```

```
pd.DataFrame(mlp_history.history)[['accuracy', 'val_accuracy']].plot()
```

Accuracy: 0.94245 <sklearn.metrics._plot.confusion_matrix.ConfusionMatrixDisplay object at @



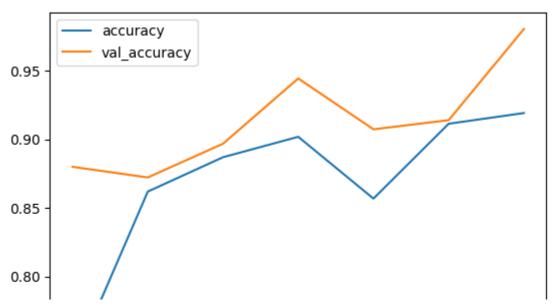
- GRU

```
input_shape=(160, 4)
),
    # add another dense?
    layers.Dense(1, activation='sigmoid')
])
gru_model.compile(optimizer='adam', loss='binary_crossentropy', metrics=['accuracy'])
gru_model.summary()
```

Model: "sequential_4"

```
pd.DataFrame(gru_history.history)[['accuracy', 'val_accuracy']].plot()
```

<Axes: >



overfits; should re-add dropout/regularization

```
y_pred = gru_model.predict(X_enc_test)
y_pred = (y_pred > 0.5).astype("int32")
gru_accuracy = accuracy_score(y_test, y_pred)

print("Accuracy: ", gru_accuracy)
print(ConfusionMatrixDisplay.from_predictions(y_test, y_pred))
```

```
625/625 [==========] - 5s 6ms/step Accuracy: 0.9799
```

- CNN

```
DefaultConv = partial(layers.Conv1D, kernel size=3, strides=1, use bias=False,
                        padding='same', kernel_initializer='he_normal')
cnn model = keras.Sequential([
  DefaultConv(32, strides=1, input shape=(160, 4)),
  layers.Dropout(0.4),
  layers.MaxPooling1D(3, strides=2),
  DefaultConv(64),
  layers.MaxPooling1D(2, strides=2),
  layers.Flatten(),
  layers.Dropout(0.4),
  layers.Dense(64, activation="relu"),
  layers.Dense(1, activation="sigmoid")
])
cnn model.compile(optimizer='adam', loss='binary crossentropy', metrics=['accuracy'])
cnn_model.summary()
```

Model: "sequential 7"

Layer (type)	Output Shape	Param #
conv1d_6 (Conv1D)	(None, 160, 32)	384
dropout_6 (Dropout)	(None, 160, 32)	0
<pre>max_pooling1d_2 (MaxPooling 1D)</pre>	(None, 79, 32)	0
conv1d_7 (Conv1D)	(None, 79, 64)	6144
<pre>max_pooling1d_3 (MaxPooling 1D)</pre>	(None, 39, 64)	0
flatten_4 (Flatten)	(None, 2496)	0

```
      dropout_7 (Dropout)
      (None, 2496)
      0

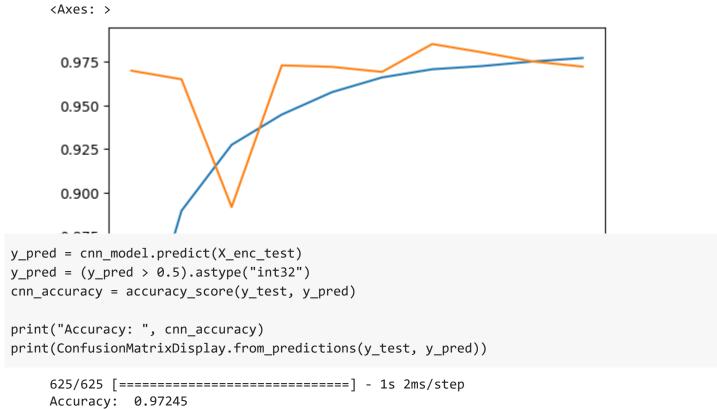
      dense_11 (Dense)
      (None, 64)
      159808

      dense_12 (Dense)
      (None, 1)
      65
```

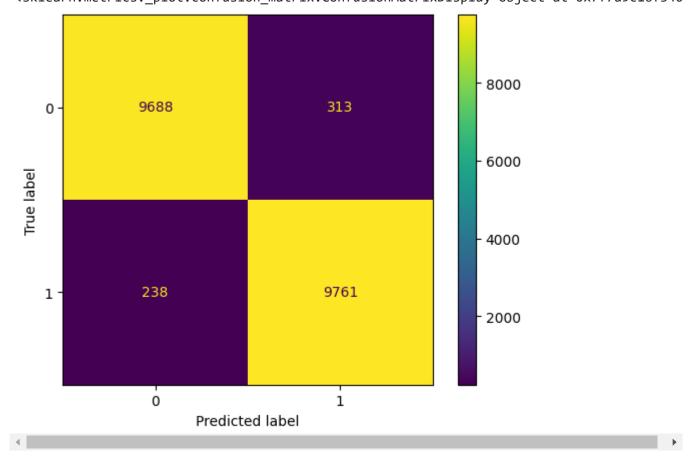
Total params: 166,401 Trainable params: 166,401 Non-trainable params: 0

```
Epoch 1/15
Epoch 2/15
2000/2000 [========================= ] - 9s 4ms/step - loss: 0.2311 - accuracy: 0.8
Epoch 3/15
2000/2000 [========================] - 8s 4ms/step - loss: 0.1686 - accuracy: 0.9
Epoch 4/15
Epoch 5/15
Epoch 6/15
2000/2000 [========================] - 8s 4ms/step - loss: 0.0960 - accuracy: 0.9
Epoch 7/15
2000/2000 [========================] - 9s 4ms/step - loss: 0.0875 - accuracy: 0.9
Epoch 8/15
2000/2000 [========================] - 8s 4ms/step - loss: 0.0834 - accuracy: 0.9
Epoch 9/15
2000/2000 [=================== ] - 8s 4ms/step - loss: 0.0774 - accuracy: 0.9
Epoch 10/15
```

```
pd.DataFrame(cnn_history.history)[['accuracy', 'val_accuracy']].plot()
```



<sklearn.metrics._plot.confusion_matrix.ConfusionMatrixDisplay object at 0x7f7a9c16f340</pre>



Improvements that could have been made

- padding sequences is lazy and not sutable for GRU; real scenario would make use of variable length sequences
- Hyper params werent optimized
- didnt use codons

X