

Data Analysis Report

for Molecular Biology Splice Junction gene sequences

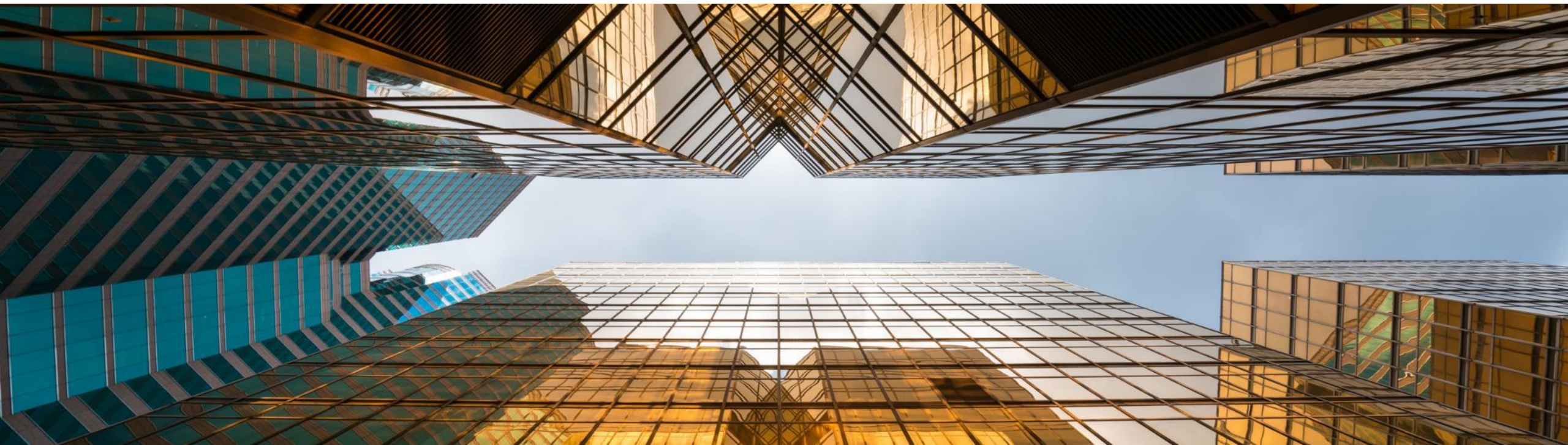
Speaker's Name, Abhinav Dogra
16-03-2023

Molecular Biology_Splice_Junction_Gene_Sequences review Analysis

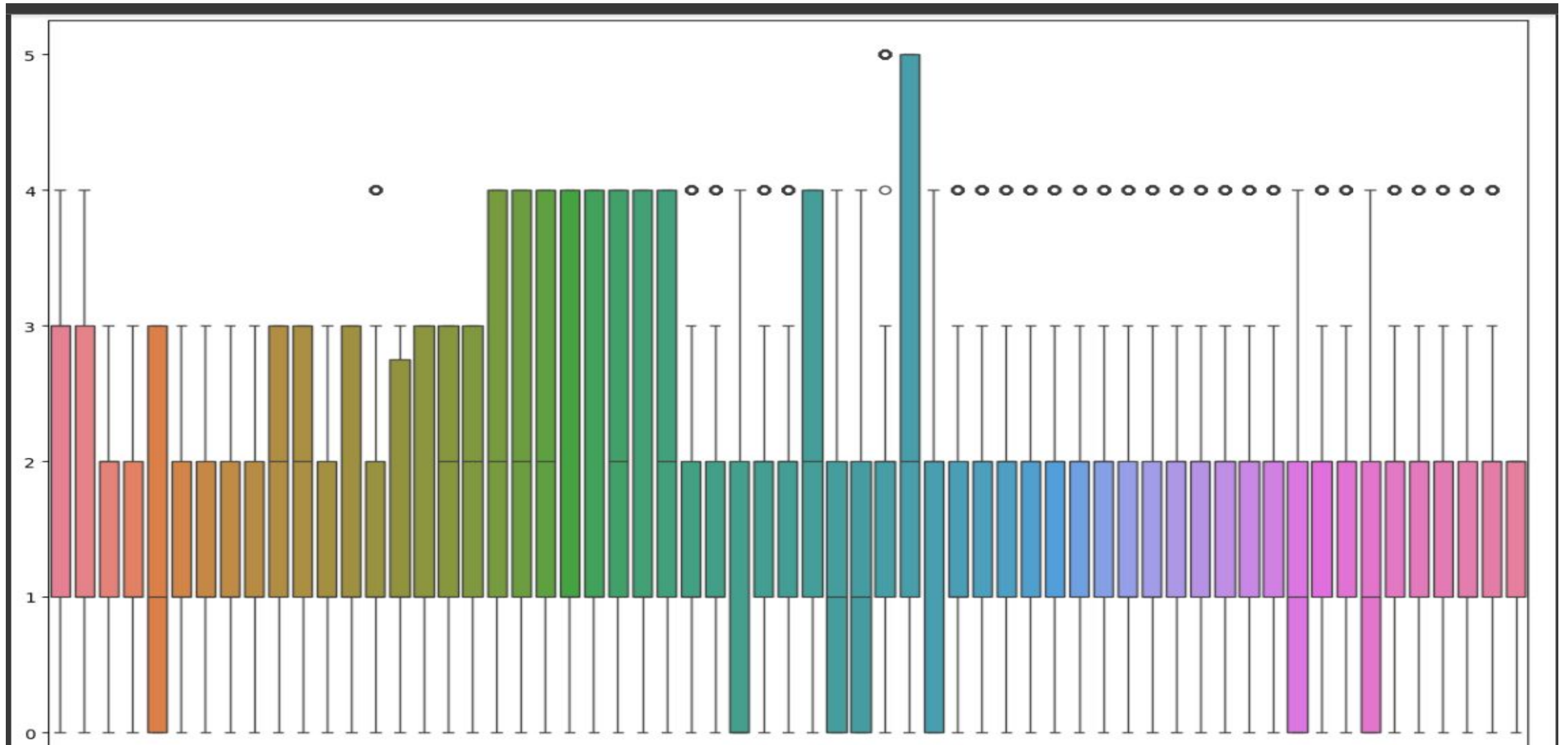
- Dataset Information
 - RangeIndex: 3190 entries
 - Columns: 61 { 0-59 Feature, 1 Target}
 - Null values: 0
 - Duplicated Rows: 10
- Unique Target Category
 - ['EI', 'IE', 'N']

```
N      1655
IE      768
EI      767
Name: Target, dtype: int64
```

Features per Target



Box Plot: Dimensionality of data

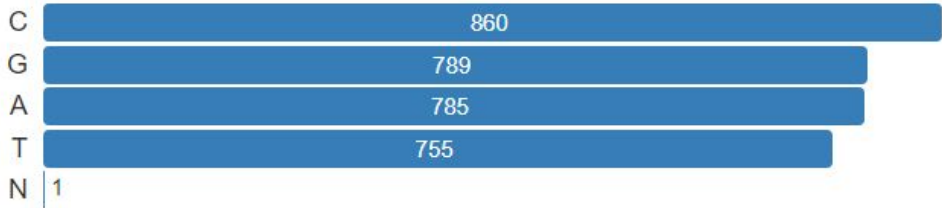


Base59

Categorical

HIGH..CORRELATION

Distinct	5
Distinct (%)	0.2%
Missing	0
Missing (%)	0.0%
Memory size	25.0 KiB



More details

OverviewCategoriesWordsCharacters

Common Values

Value	Count	Frequency (%)
C	860	27.0%
G	789	24.7%
A	785	24.6%
T	755	23.7%
N	1	< 0.1%

Length

Sum of Target by Base1



Sum of Target by Base20



Sum of Target by Base21



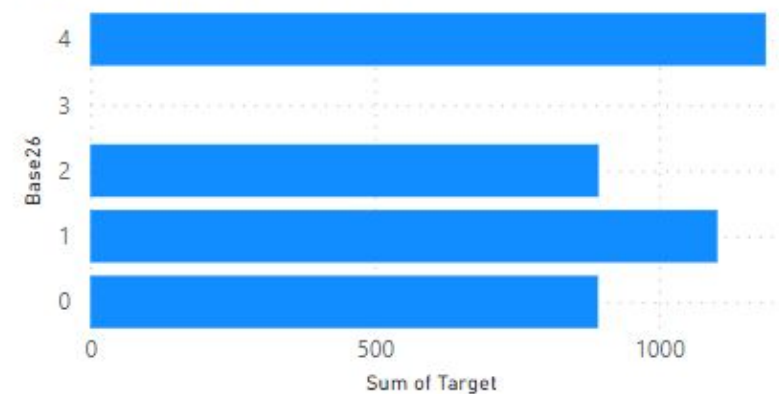
Sum of Target by Base23



Sum of Target by Base24



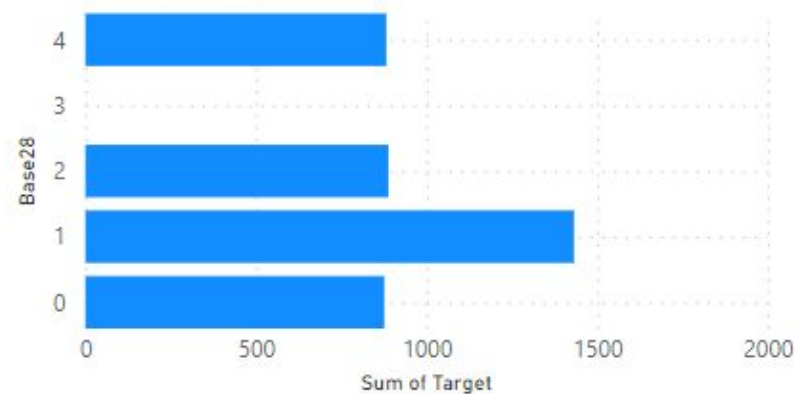
Sum of Target by Base26



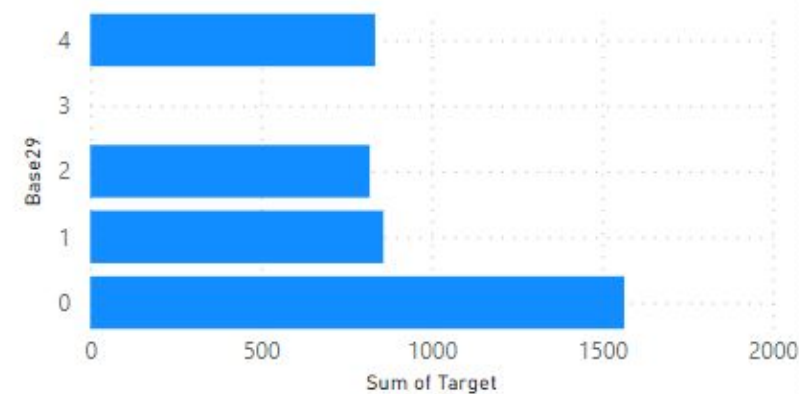
Sum of Target by Base27



Sum of Target by Base28



Sum of Target by Base29



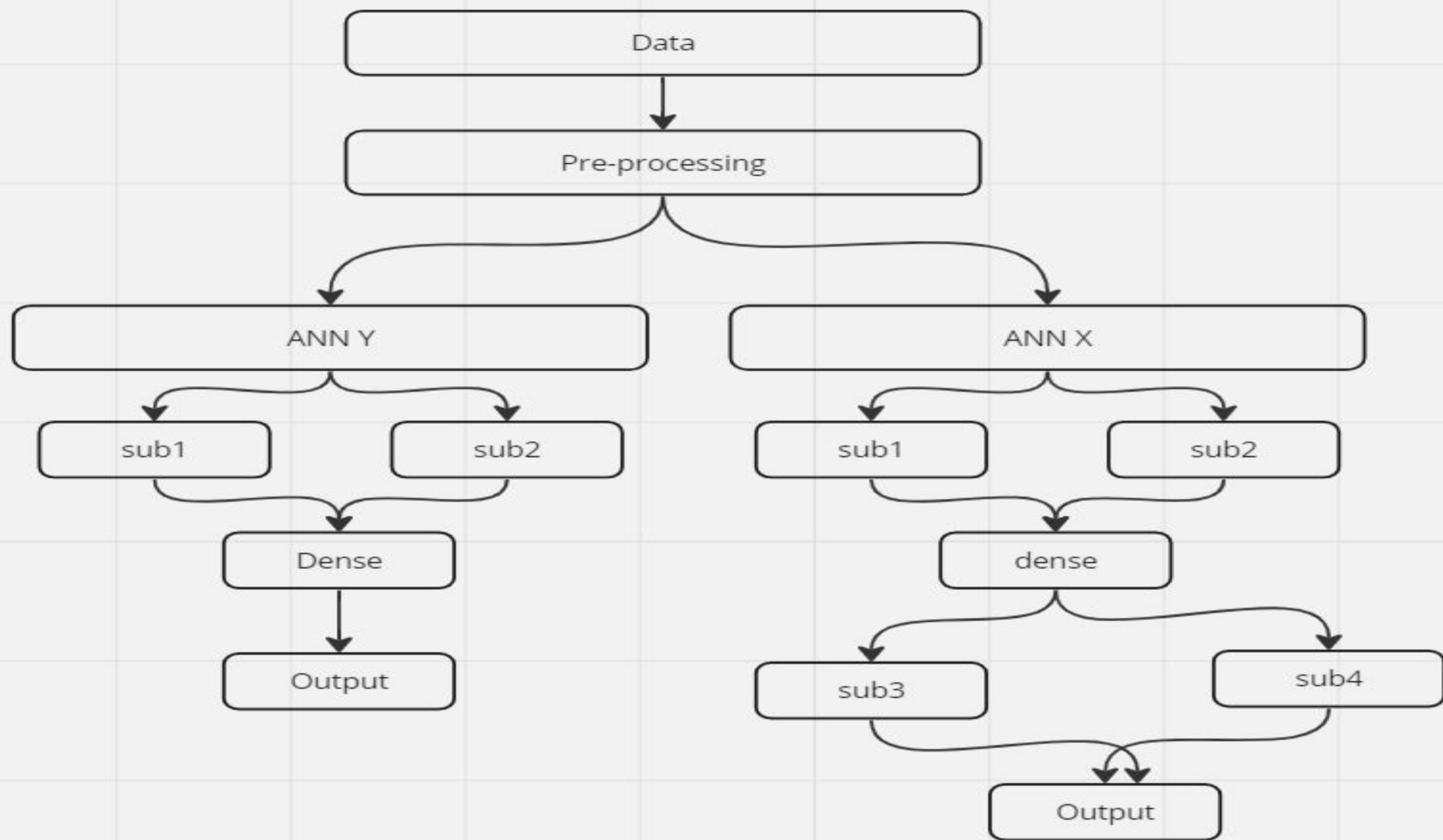
Preprocessing

✓ Preprocessing the data

```
[ ] def preproc_data(df, train_sample: float, pca_dim=31):  
  
    # Label encode  
    categorical_cols = df.select_dtypes(include=['object']).columns  
  
    # If there are categorical columns, encode them  
    if len(categorical_cols) > 0:  
        label_encoder = LabelEncoder()  
        for col in categorical_cols:  
            df[col] = label_encoder.fit_transform(df[col])  
  
    # Train test split  
    x_train, x_test, y_train, y_test = train_test_split(df.iloc[:, :-1],  
                                                        df['Target'],  
                                                        test_size=1-train_sample,  
                                                        random_state=0)  
  
    # Standard scaling  
    ss = StandardScaler().fit(x_train)  
  
    x_train = ss.transform(x_train)  
    x_test = ss.transform(x_test)  
  
    # PCA  
    pca = PCA(n_components=0.99).fit(x_train)  
  
    x_train = pca.transform(x_train)  
    x_test = pca.transform(x_test)  
  
    # Normalization  
    norm = Normalizer().fit(x_train)  
  
    x_train = norm.transform(x_train)  
    x_test = norm.transform(x_test)  
  
    # Reshaping  
    y_train = y_train.values.reshape(-1,1)  
    y_test = y_test.values.reshape(-1,1)  
  
    return x_train, x_test, y_train, y_test
```

✓ data divided in 75/25 split

```
[ ] x_train, x_test, y_train, y_test = preproc_data(df, train_sample=0.75)# data - clean
```

ANN Model Pre

```
# Assuming you have x_train, y_train, x_test, y_test
unique_labels = len(np.unique(y_train))

y_train1_encoded = to_categorical(y_train, num_classes=unique_labels)

y_test_encoded = to_categorical(y_test, num_classes=unique_labels)

# Define the first sub-model
def sub_model1(inputs):
    x = Dense(128, activation='relu')(inputs)
    x = Dense(512, activation='relu')(x)
    x = Dense(1024, activation='relu')(x)
    x = Dense(256, activation='relu')(x)
    x = Dense(64, activation='relu')(x)
    return x

# Define the second sub-model
def sub_model2(inputs):
    x = Dense(256, activation='relu')(inputs)
    x = Dense(1024, activation='relu')(x)
    x = Dense(2048, activation='relu')(x)
    x = Dense(512, activation='relu')(x)
    x = Dense(128, activation='relu')(x)
    x = Dense(64, activation='relu')(x)
    return x

input_layer = Input(shape=(x_train.shape[1],))

sub_model1_output = sub_model1(input_layer)

sub_model2_output = sub_model2(input_layer)

concatenated_output = Concatenate()([sub_model1_output, sub_model2_output])
x = Dense(32, activation='relu')(concatenated_output)
output_layer = Dense(unique_labels, activation='softmax')(x)

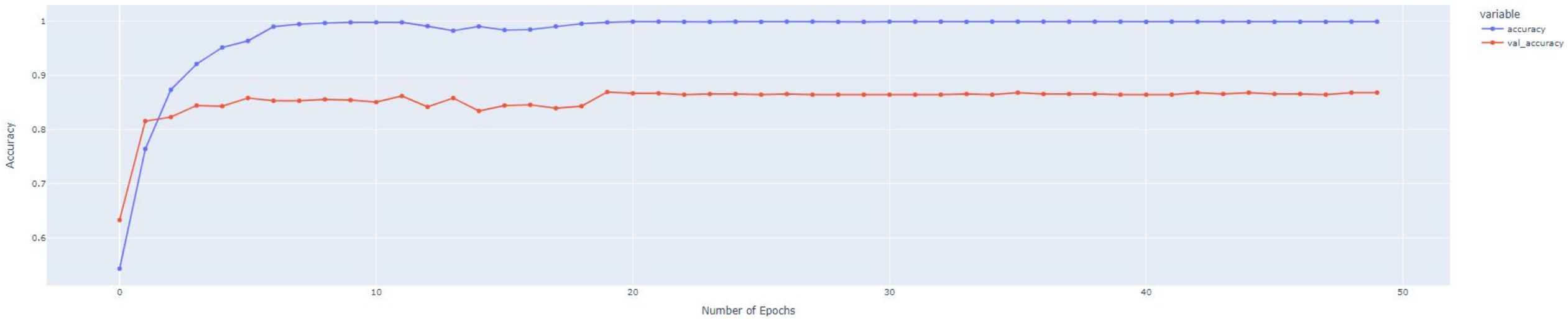
model = Model(inputs=input_layer, outputs=output_layer)

model.compile(optimizer='adam', loss='categorical_crossentropy', metrics=['accuracy'])

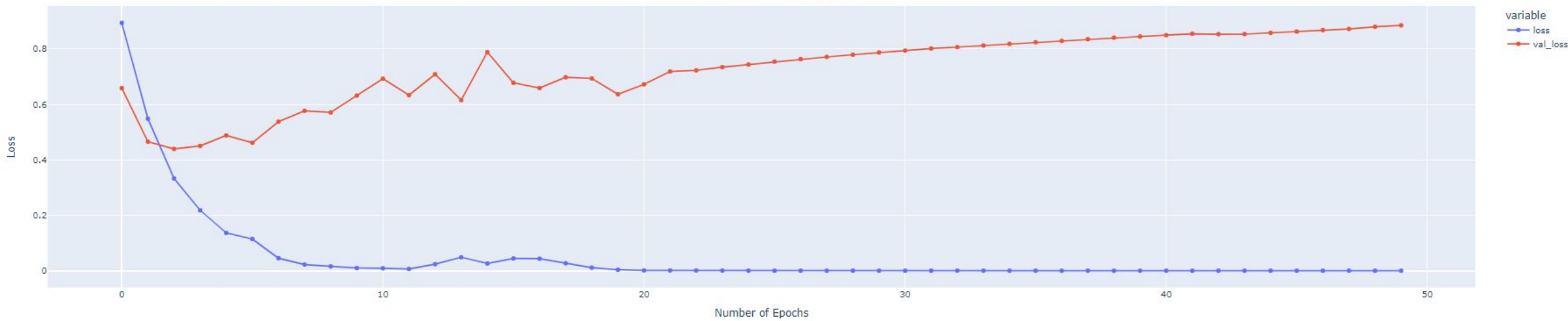
# Train the model
# model.fit(X_train2, y_train1, epochs=10, batch_size=32, validation_data=(x_test, y_test))
```

Accuracy and loss

Accuracy vs Number of Epochs



Loss vs Number of Epochs



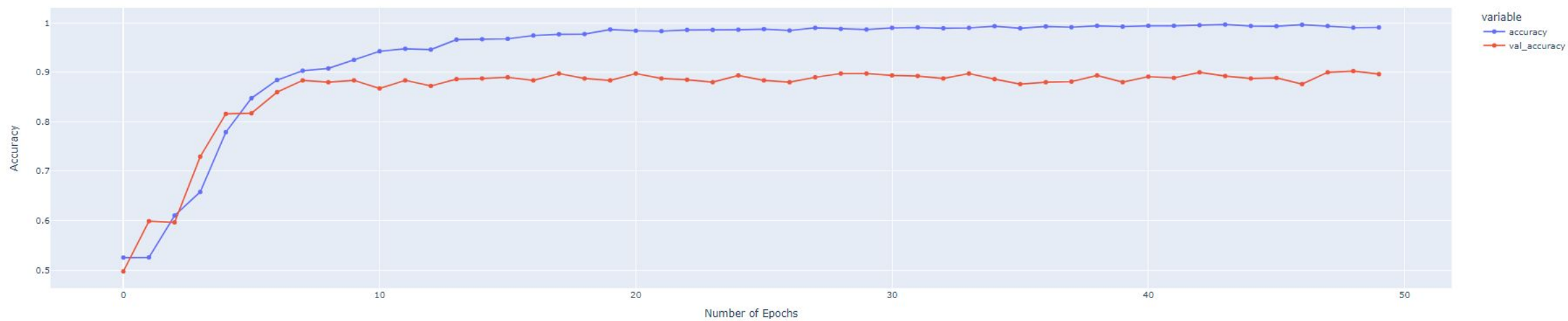
ANN model 2

```
def sub_model1(inputs):  
    x = Dense(256, activation='relu')(inputs)  
    x = Dropout(0.3)(x)  
    x = Dense(512, activation='relu')(x)  
    x = Dropout(0.3)(x)  
    x = Dense(128, activation='relu')(x)  
    x = Dropout(0.3)(x)  
    return x
```

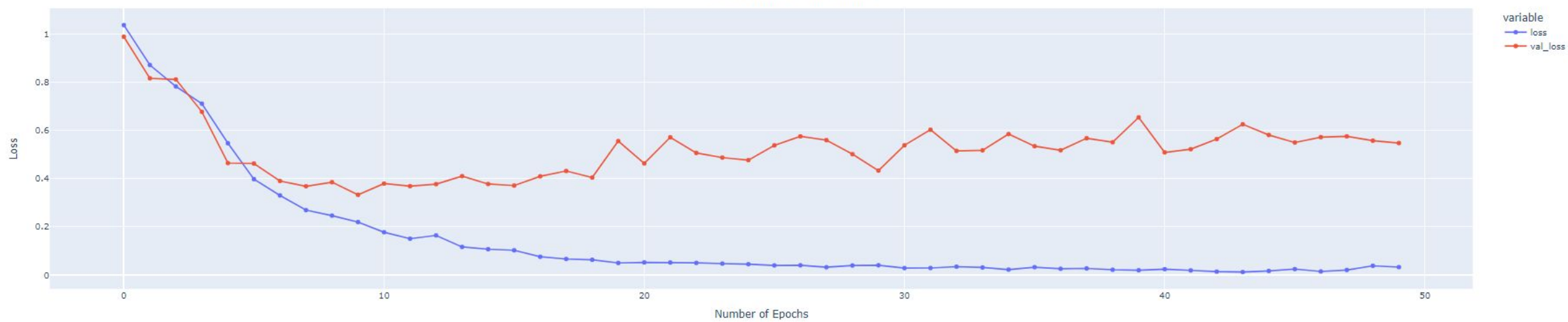
```
def sub_model2(inputs):  
    x = Dense(256, activation='relu')(inputs)  
    x = Dropout(0.3)(x)  
    x = Dense(1024, activation='relu')(x)  
    x = Dropout(0.3)(x)  
    x = Dense(2048, activation='relu')(x)  
    x = Dropout(0.2)(x)  
    x = Dense(512, activation='relu')(x)  
    x = Dropout(0.2)(x)  
    x = Dense(128, activation='relu')(x)  
    x = Dropout(0.2)(x)  
    return x
```

```
def sub_model3(inputs):  
    x = Dense(64, activation='relu')(inputs)  
    x = Dense(512, activation='relu')(x)
```


Accuracy vs Number of Epochs



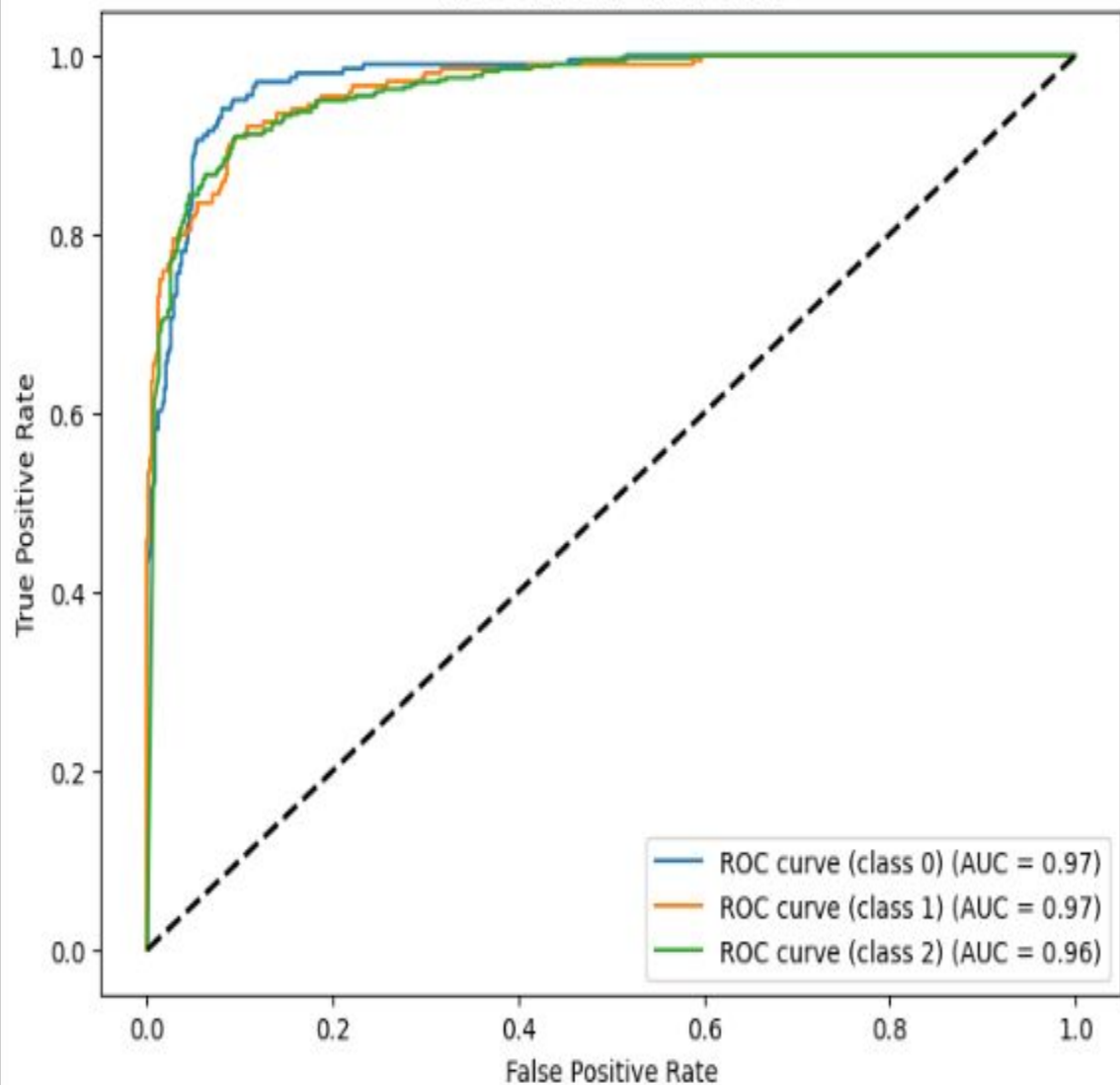
Loss vs Number of Epochs



model1

25/25 [=====] - 1s 20ms/step

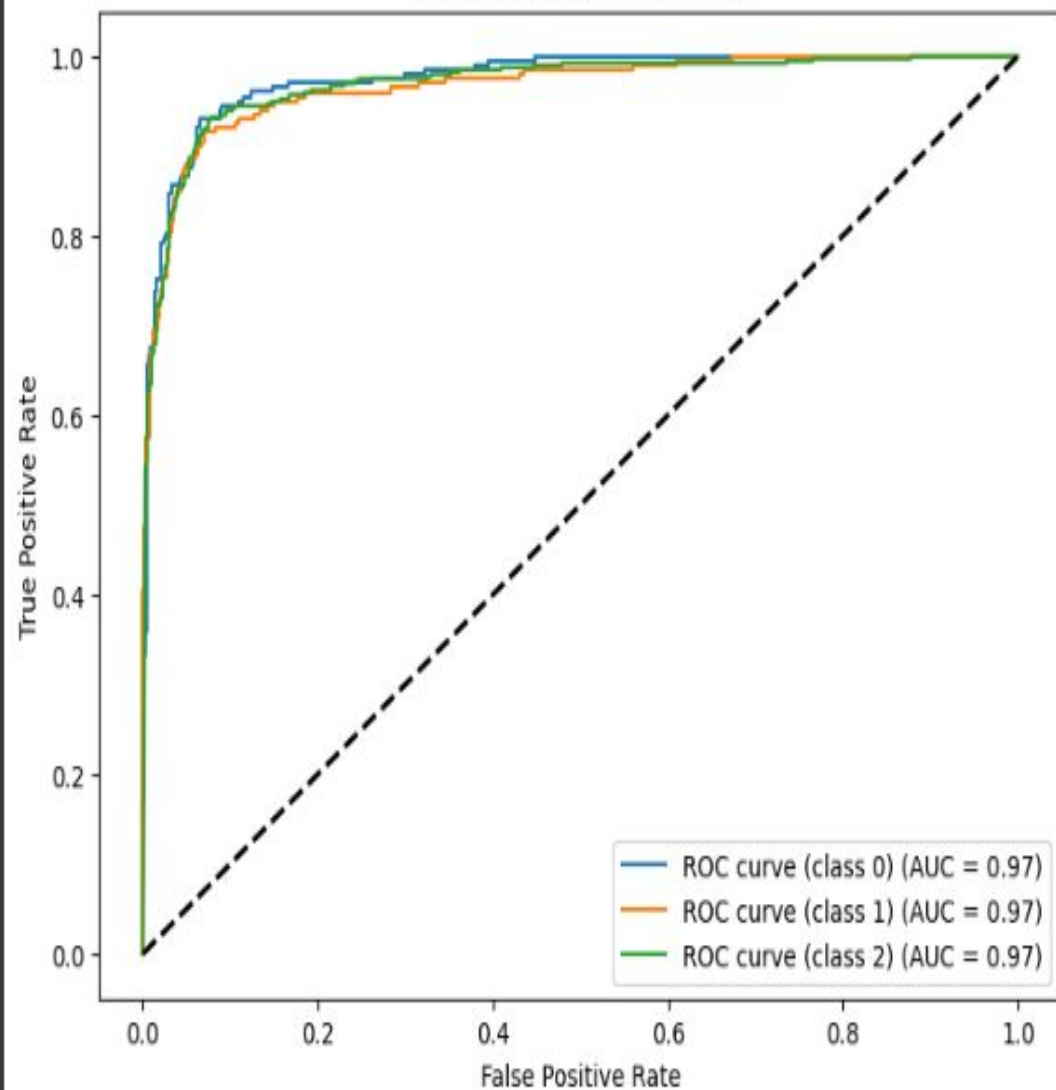
ROC Curve for Each Class



model2

25/25 [=====] - 1s 18ms/step

ROC Curve for Each Class



ML + Voting Classifier + Cross validation



```
svm_classifier = SVC(C=10, kernel='rbf', gamma='auto', probability=True)
rf_classifier = RandomForestClassifier(n_estimators=100, random_state=42)
lr_classifier = LogisticRegression(random_state=42)

voting_classifier = VotingClassifier(estimators=[
    ('svm', svm_classifier),
    ('rf', rf_classifier),
    ('lr', lr_classifier)
], voting='soft')

k_fold = StratifiedKFold(n_splits=5, shuffle=True, random_state=42)

scores = cross_val_score(voting_classifier, x_train, y_train, cv=k_fold, scoring='accuracy')

print("Average Accuracy:", scores.mean())

voting_classifier.fit(x_train, y_train)

y_pred_ensemble = voting_classifier.predict(x_test)

accuracy_ensemble = accuracy_score(y_test, y_pred_ensemble)
print("Ensemble Accuracy on Test Dataset:", accuracy_ensemble)
```

ML Model processed

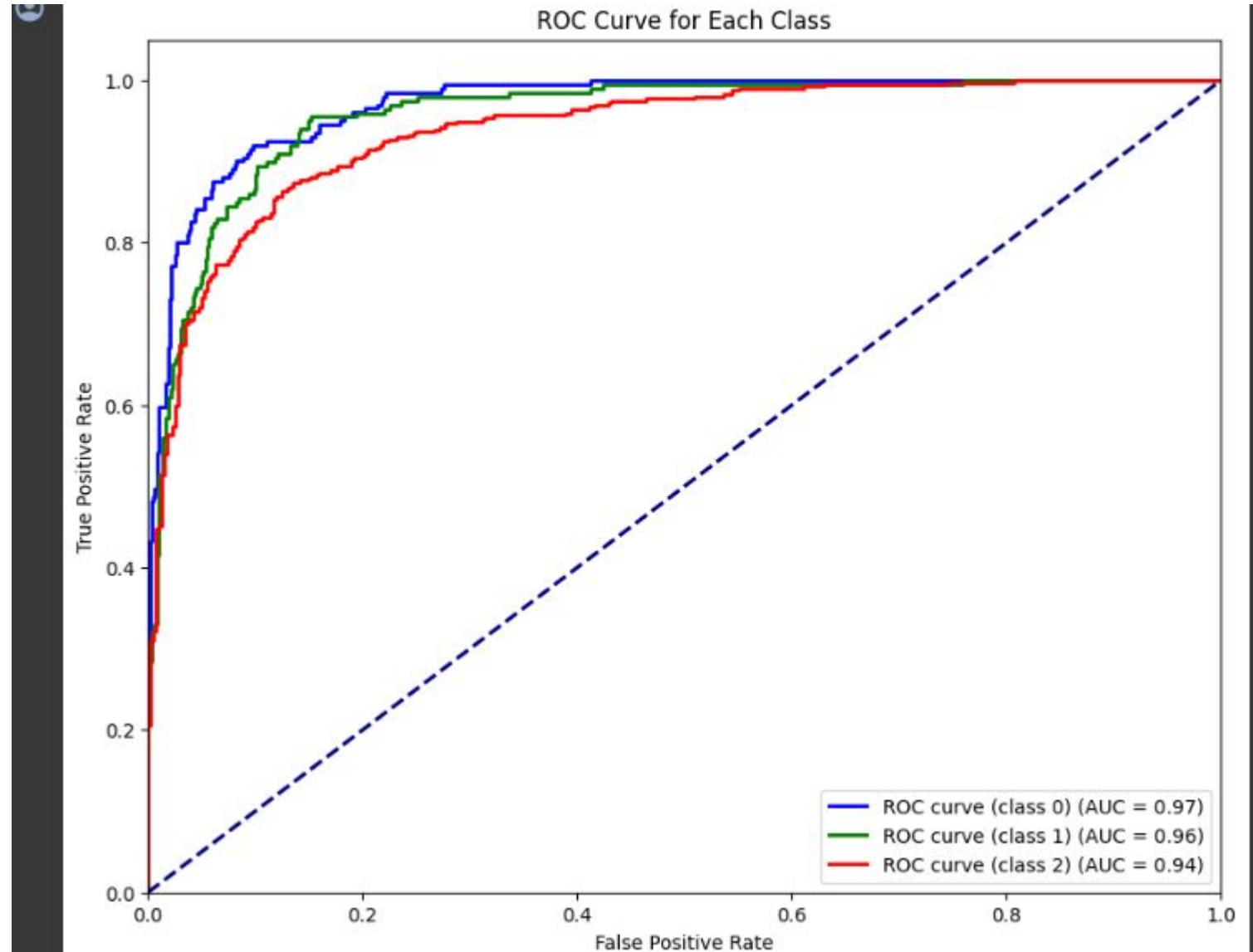
Creating the complex voting classifier with input model logistic regression, SVM, Random Forest with cross validation,

Average Accuracy:

0.818551550038871

Ensemble Accuracy on Test Dataset:

0.8521303258145363



H2O Model

H2o with cross validation,
MSE 0.35 for cv-4

		mean	sd	cv_1_valid	cv_2_valid	\
0	aic	NaN	0.000000	NaN	NaN	
1	loglikelihood	NaN	0.000000	NaN	NaN	
2	mae	0.510577	0.013617	0.502544	0.523485	
3	mean_residual_deviance	0.384992	0.022916	0.374499	0.393836	
4	mse	0.384992	0.022916	0.374499	0.393836	
5	r2	0.432125	0.031040	0.418246	0.453587	
6	residual_deviance	0.384992	0.022916	0.374499	0.393836	
7	rmse	0.620255	0.018574	0.611963	0.627563	
8	rmsle	0.345565	0.014374	0.330114	0.357405	

	cv_3_valid	cv_4_valid	cv_5_valid
0	NaN	NaN	NaN
1	NaN	NaN	NaN
2	0.510404	0.492423	0.524029
3	0.392496	0.351744	0.412386
4	0.392496	0.351744	0.412386
5	0.413210	0.475065	0.400519
6	0.392496	0.351744	0.412386
7	0.626495	0.593080	0.642173
8	0.353712	0.329680	0.356914

H2O session - cid 0064 - closed

conclusion

As After going around with dataset we concluded that the there 34 high correlation set which effect the model highly like 23,40, 41 etc.

The variation in data is high causing the model prediction loss to high after some time. So, require more data for better model.

The data predictability for target after optimization goes to, accuracy: 0.9904 - val_accuracy: 0.8960

After the pre process we have optimize both time and accuracy of model for ML ~78 - > ~85%

After the pre process we have loss reduce from ~0.8 -> ~0.5

and predicting efficiency of ~ 97% Achieved.

Thank you.

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