Developing a fetal classifier.

A data science project by Kenneth Imade

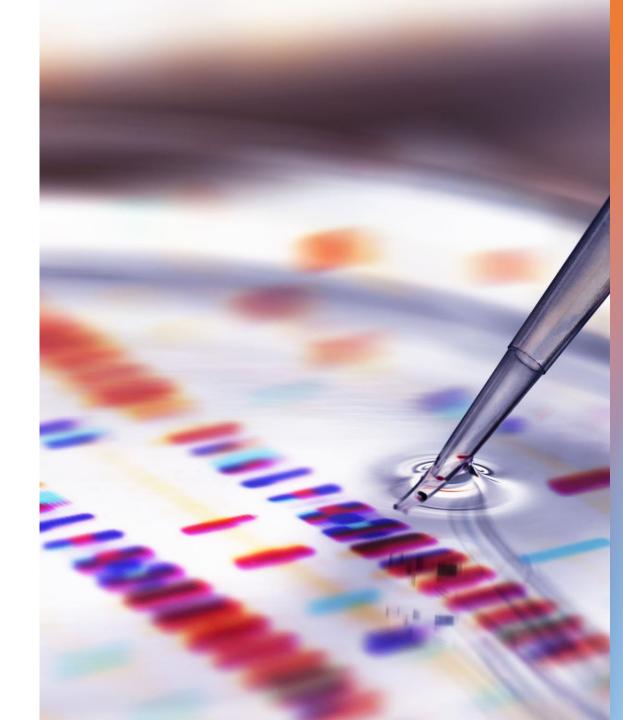




Objectives

- To understand the features that determine the health status of a fetus
- To develop a machine learning model capable of classifying fetus health into three categories; normal, suspect, or pathological

Exploratory Data Analysis



What is the distribution of the target variable?

Most Fetuses are classified as normal Number of observations 1600 1400 1200 1000 800 600 400 200

Suspect

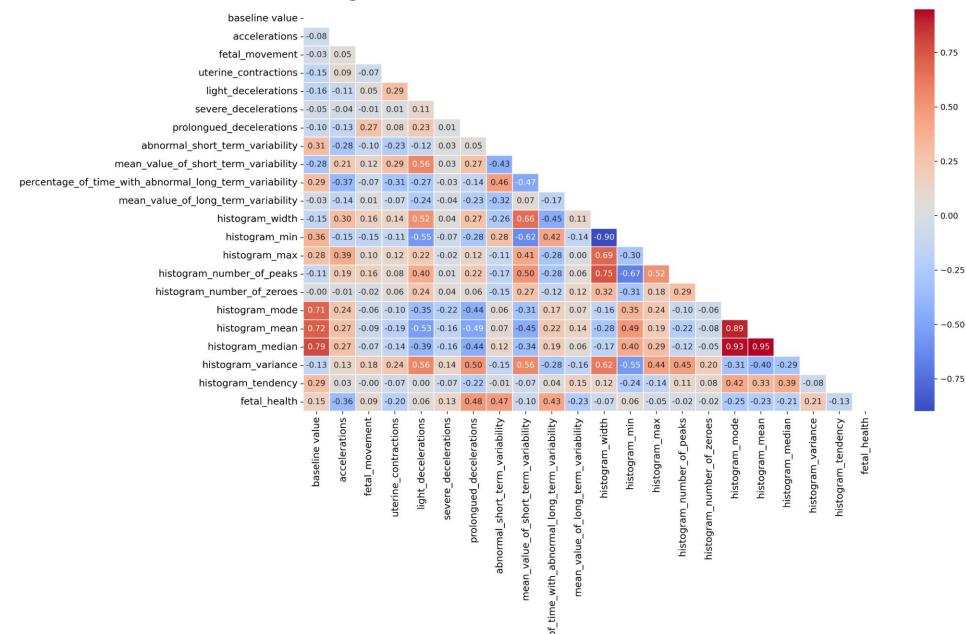
0

Normal

Pathological

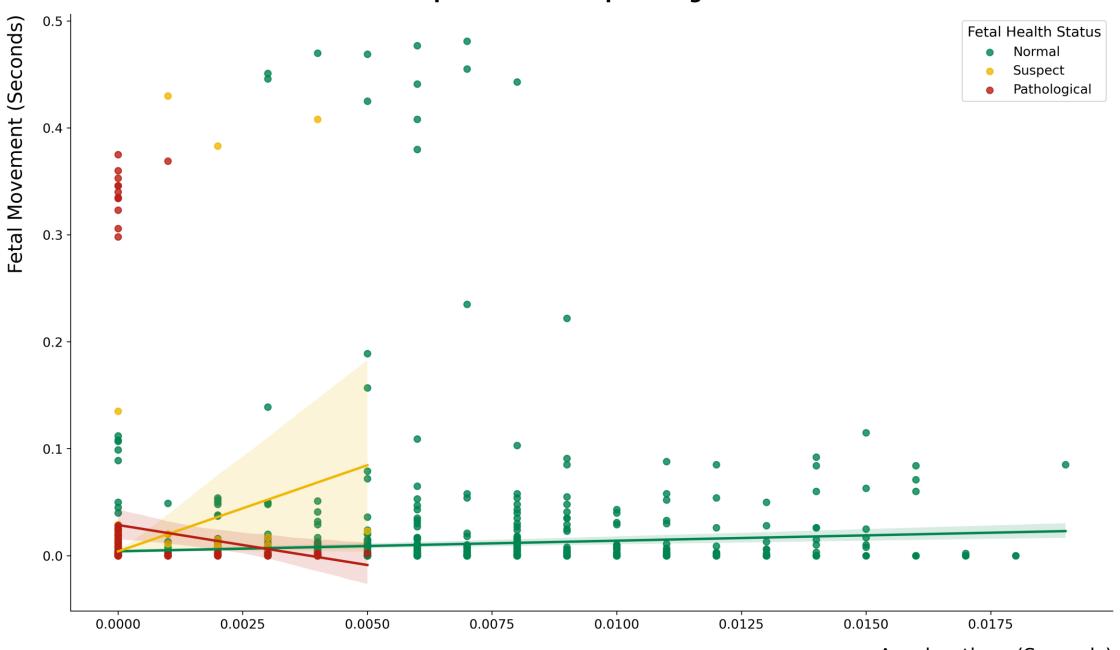
What is the relationship between the target variable and other variables?

Strong correlation exists between fetal health and other factors



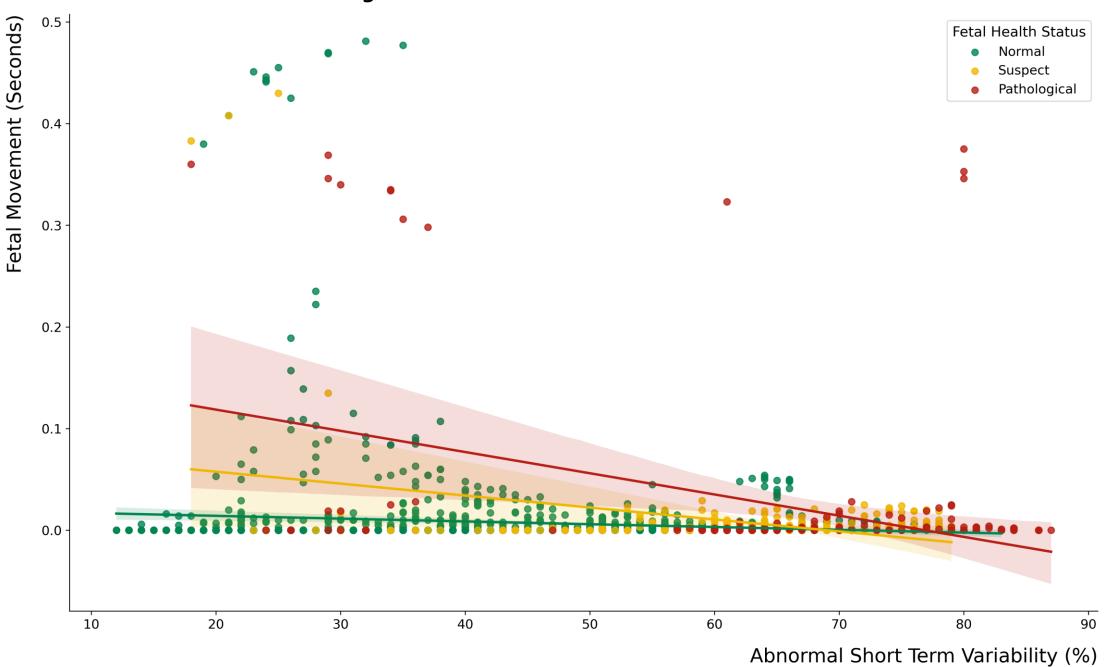
How does Fetal health change with respect to these variables?

Tendency for both normal and suspect fetuses movement to slightly increase in tandem with their acceleration but relationship flatlines with pathological fetuses



Accelerations (Seconds)

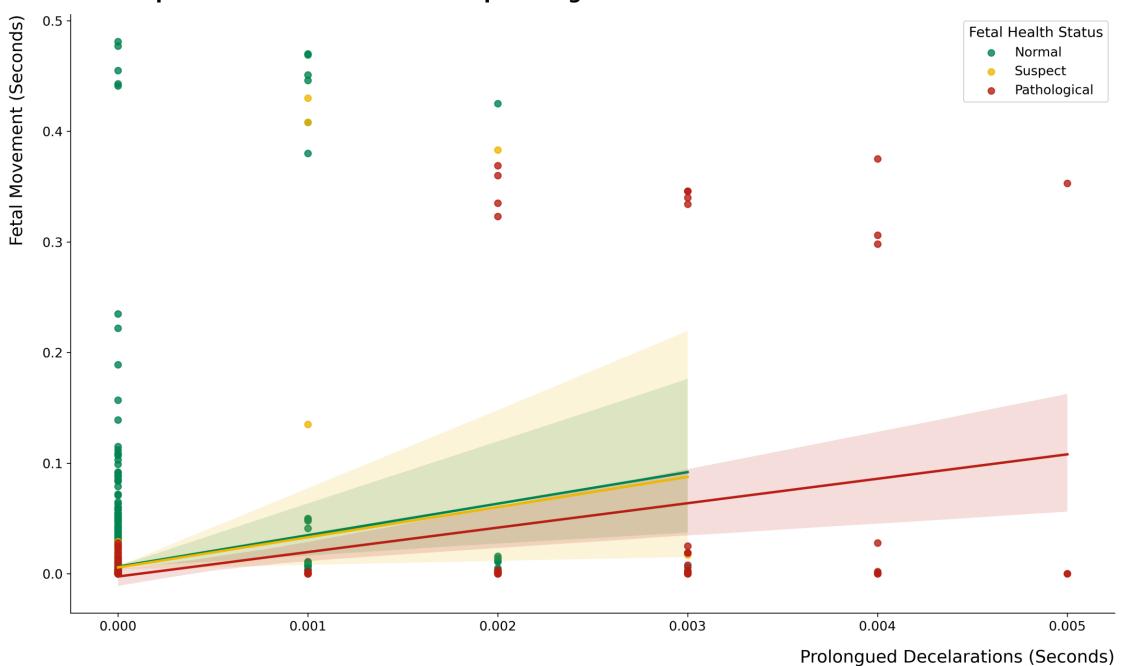
Increased short term fetal heart rate suggests a decrease in fetal movement across all fetal health categories

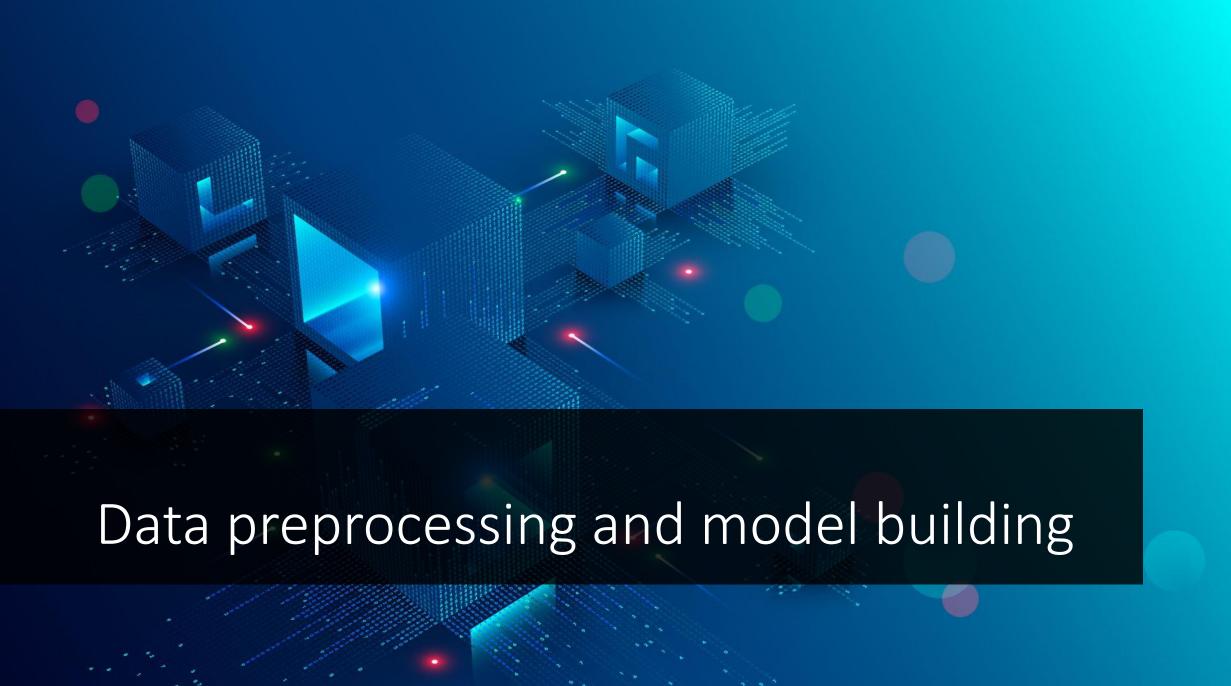


Strong relationship between long term variability and fetal movement in pathological fetuses but relationship is weaker in suspect fetuses and insignificant in normal fetuses

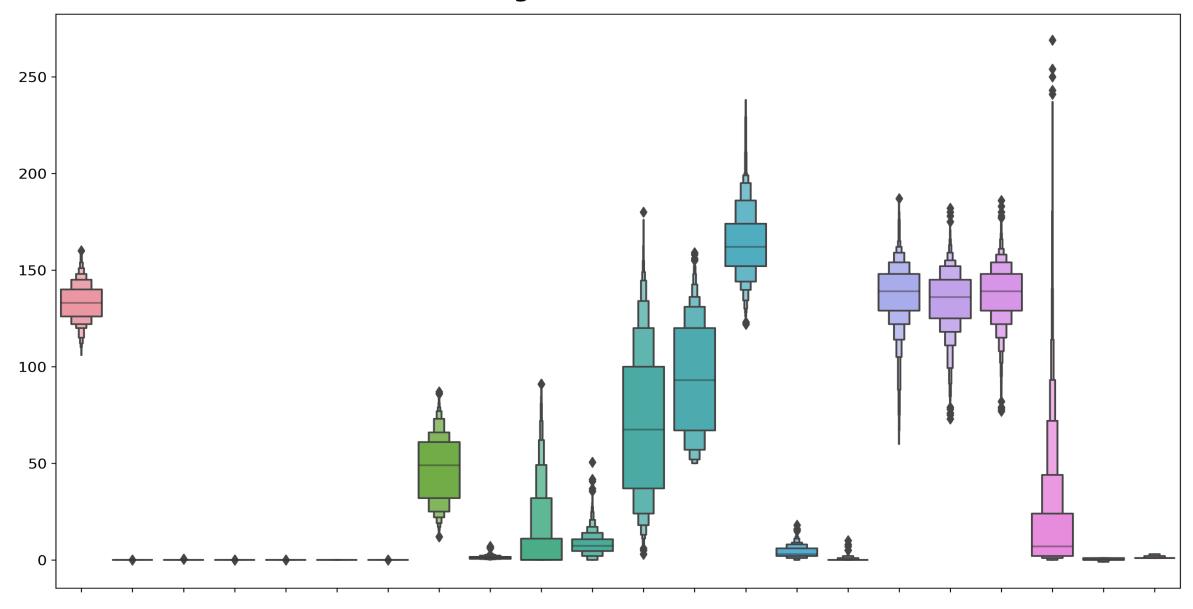


Fetal movement increases alongside prolongued decelerations in both normal and suspect fetuses but does not for pathological fetuses

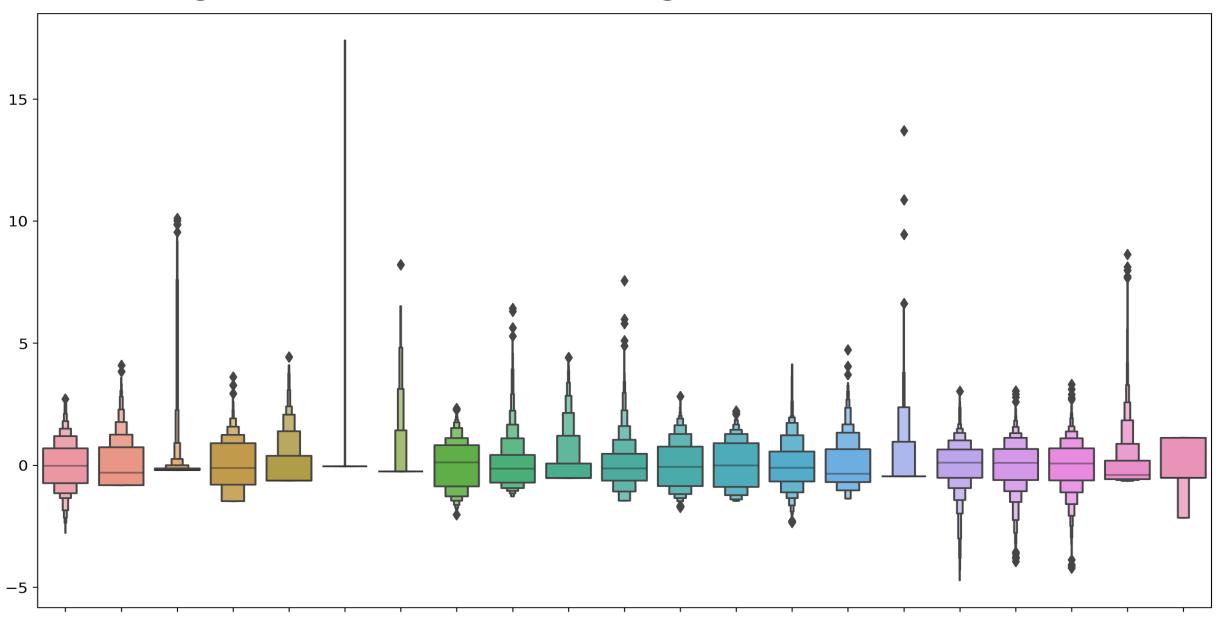




Features in dataset have varied ranges



Feature ranges standardised for model building



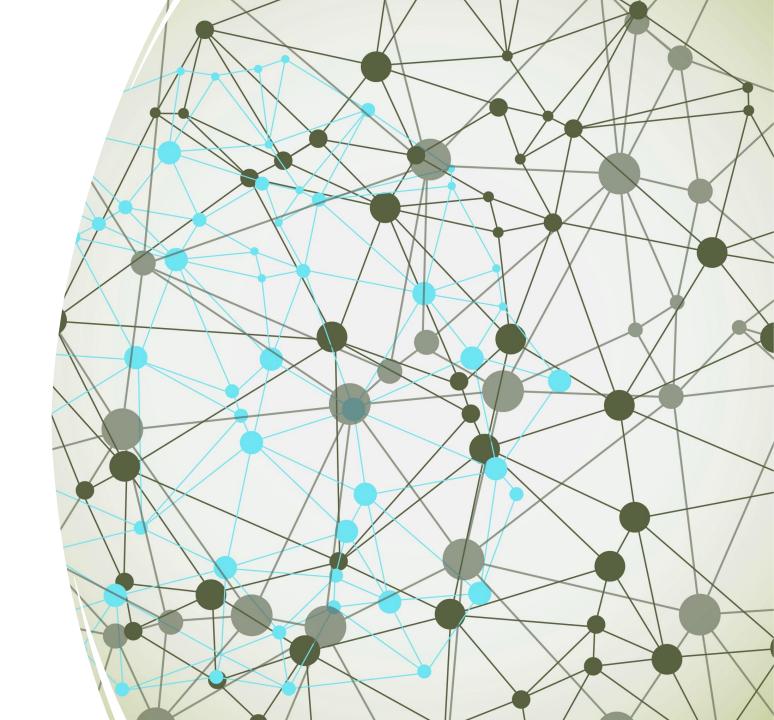
Choosing the best model

```
lr_model = Pipeline([('lr_classifier', LogisticRegression(random_state=42))])
dt_model = Pipeline([('dt_classifier', DecisionTreeClassifier(random_state=42))])
rf_model = Pipeline([('rf_classifier', RandomForestClassifier(random_state=42))])
knn_model = Pipeline([('knn_classifier', KNeighborsClassifier())])
svc_model = Pipeline([('svc_classifier', SVC())])
pipelines = [lr_model, dt_model, rf_model, knn_model, svc_model]
pipe_dict = {0: 'Logistic Regression', 1: 'Decision Tree', 2: 'Random Forest', 3: 'KNN', 4: 'SVC'}
for pipe in pipelines:
    pipe.fit(X_train, y_train)
cv_results_accuracy = []
for i, model in enumerate(pipelines):
    cv score = cross_val_score(model, X_train,y_train, cv=10 )
    cv_results_accuracy.append(cv_score)
    print("%s: %f " % (pipe_dict[i], cv_score.mean()))
```

Hyper-parameter tuning.

```
parameters = {
    'n_estimators': [100, 150, 200, 500, 700, 900],
    'max_features': ['auto', 'sqrt', 'log2'],
    'max_depth': [4,6,8,12,14,16],
    'criterion': ['gini', 'entropy'],
rfc_cv = GridSearchCV(estimator=RandomForestClassifier(), param_grid=parameters, cv= 5)
rfc_cv.fit(X_train, y_train)
rfc_cv.best_params_
```

Results



Classification Metrics

	Precision	Recall	F1-Score	Support
Normal (1.0)	0.96	0.98	0.97	496
Suspect (2.0)	0.92	0.78	0.84	101
Pathological (3.0)	0.88	0.93	0.90	41
Accuracy			0.95	638
Macro Avg	0.92	0.90	0.91	638
Weighted Avg	0.95	0.95	0.95	638

Confusion Matrix True 488 6 - 400 - 300 19 79 3 - 200 Pathological - 100 2 38 Pathological Normal Suspect

Predicted