



# Machine Learning: Fetus Classification


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# Important Questions

**We had three questions we wanted to try and answer.**

1. Can we use machine learning to predict healthcare outcomes?
2. How many input columns will be needed to maintain a minimum of 90% accuracy?
3. Can we increase the accuracy of the model by tuning the parameters?

The group was originally interested in exploring machine learning in the medical field. We were able to find the data set on Kaggle that met some desired requirements including:

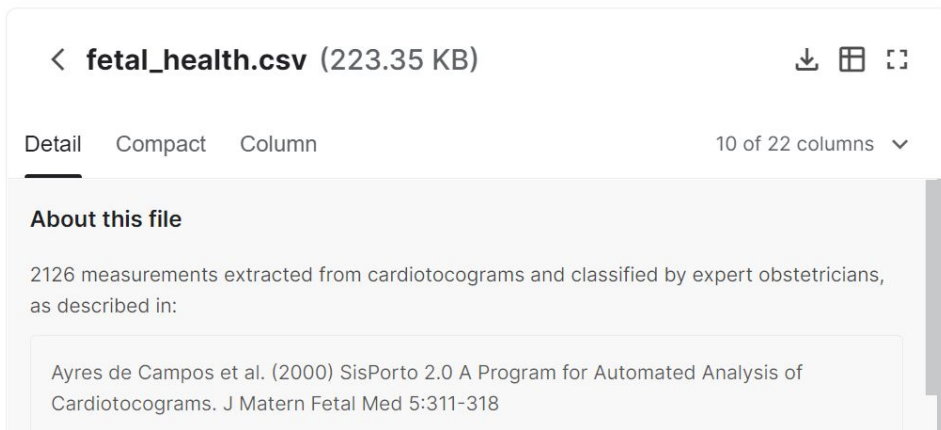
1. More than 1,000 data points
  2. Numerical Data
  3. Final classification into 3 or less categories
- 

# Our Data Sources

## The Following Data Source Was Utilized:

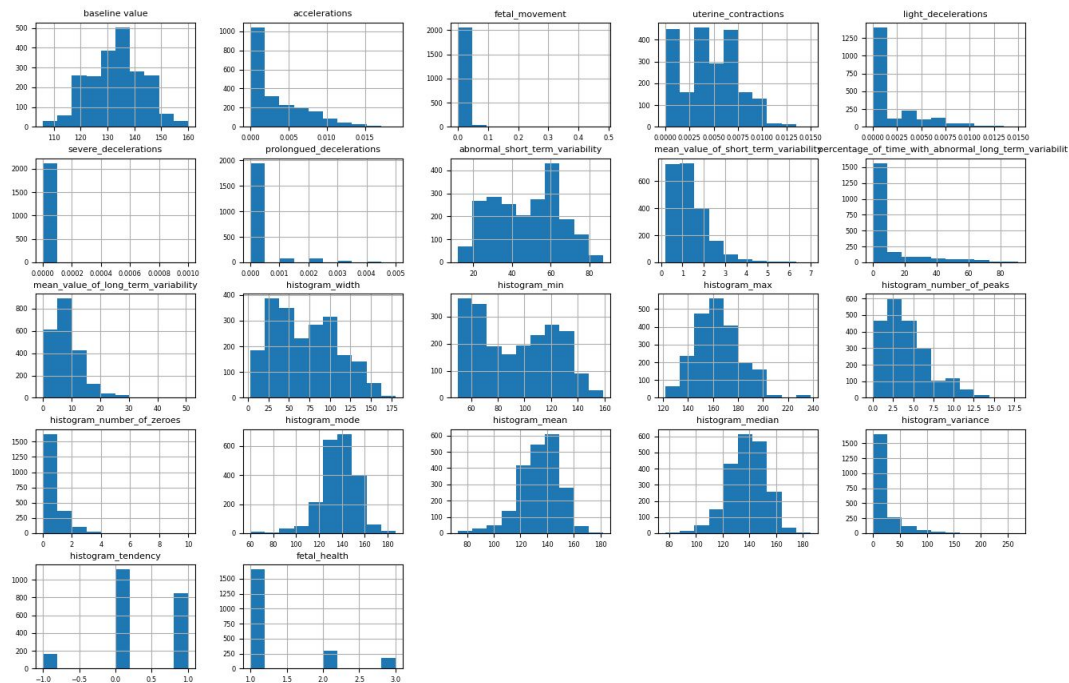
**Fetal Health Classification**- Ayres de Campos et al. (2000) SisPorto 2.0 A Program for Automated Analysis of Cardiotocograms. J Matern Fetal Med 5:311-318

<https://www.kaggle.com/andrewmvd/fetal-health-classification>



# Input Histograms:

Below are the histograms of the input data from the dataset.

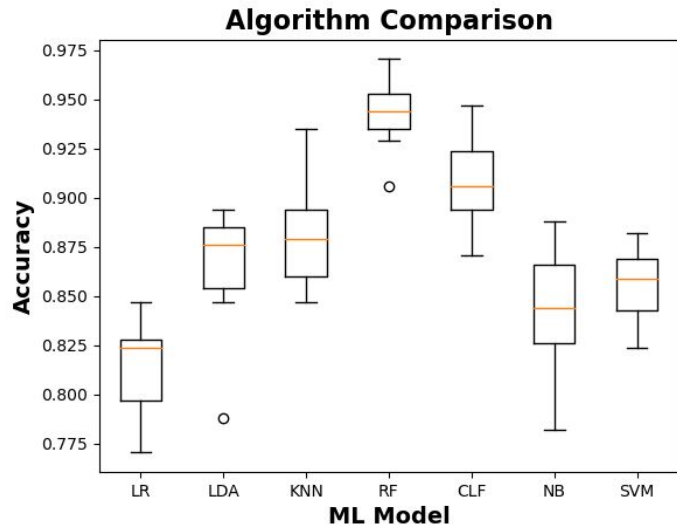


# Checking ML Algorithms

The following code was utilized to check which machine learning algorithm would give the highest accuracy to determine what would be used going forward.

```
ML

# Spot Check Algorithms
models = []
models.append(('LR', LogisticRegression(solver='liblinear', multi_class='ovr')))
models.append(('LDA', LinearDiscriminantAnalysis()))
models.append(('KNN', KNeighborsClassifier()))
models.append(('RF', RandomForestClassifier()))
models.append(('CLF', DecisionTreeClassifier()))
models.append(('NB', GaussianNB()))
models.append(('SVM', SVC(gamma='auto')))
# evaluate each model in turn
results = []
names = []
for name, model in models:
    kfold = StratifiedKfold(n_splits=10, random_state=1, shuffle=True)
    cv_results = cross_val_score(model, X_train, y_train, cv=kfold, scoring='accuracy')
    results.append(cv_results)
    names.append(name)
    print('%s: %f (%f)' % (name, cv_results.mean(), cv_results.std()))
```



# Parameter Tuning/Final Accuracy

```
▶ ML

# Number of trees in random forest
n_estimators = [int(x) for x in np.linspace(start = 200, stop = 1200, num = 11)]
# Number of features to consider at every split
max_features = ['auto', 'sqrt']
# Maximum number of levels in tree
max_depth = [int(x) for x in np.linspace(10, 110, num = 11)]
max_depth.append(None)
# Minimum number of samples required to split a node
min_samples_split = [2, 5, 10]
# Minimum number of samples required at each leaf node
min_samples_leaf = [1, 2, 4]
# Method of selecting samples for training each tree
bootstrap = [True, False]
# Create the random grid
random_grid = {'n_estimators': n_estimators,
               'max_features': max_features,
               'max_depth': max_depth,
               'min_samples_split': min_samples_split,
               'min_samples_leaf': min_samples_leaf,
               'bootstrap': bootstrap}
pprint(random_grid)
```

Code to set up the testing grid

```
▶ ML

# Use the random grid to search for best hyperparameters
# First create the base model to tune
rf1 = RandomForestRegressor()
# Random search of parameters, using 3 fold cross validation,
# search across 100 different combinations, and use all available
cores
rf_random = RandomizedSearchCV(estimator = rf1, param_distributions =
random_grid, n_iter = 100, cv = 3, verbose=2, random_state=42, n_jobs
= -1)
# Fit the random search model
rf_random.fit(X_train5, y_train)
```

Code to Test for best Parameters



# Outcomes of Hypertuning

```
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# Use hypertuning parameters to train random forest classifier (ran  
previously and these were the numbers that were obtained)  
final_model = RandomForestClassifier(n_estimators=200,  
min_samples_split=2, min_samples_leaf=1, max_features='sqrt',  
max_depth=20, bootstrap=True)  
final_model = final_model.fit(X_train5, y_train)  
final_model.score(X_test5, y_test)  
  
0.9295774647887324
```

93% Accuracy was Achieved with Tuned Model for Test Data

```
▶ ▶≡ M↓  
# load the model from disk  
loaded_model = pickle.load(open(filename, 'rb'))  
result = loaded_model.score(X_test5, y_test)  
print(result)  
  
0.9295774647887324
```

Confirmation of Loaded Model Accuracy

# Initial thoughts on Visualization

The data on Postgres with AWS  
server

```
[18] > % python3 m1

alchemyengine = create_engine('postgresql+psycopg2://postgres:' + password + '@final-project-chgprvrvy5u3.us-east-2.rds.amazonaws.com/postgres', pool_recycle=3600)

# Connect to PostgreSQL server
postgresSQLConnection = alchemyengine.connect()
postgresSQLTable = "fetal_upload"

try:

    frame = fetal_upload.to_sql(postgresSQLTable, postgresSQLConnection, if_exists='fail')

except ValueError as vx:

    print(vx)

except Exception as ex:

    print(ex)

else:

    print("PostgreSQL Table %s has been created successfully." % postgresSQLTable)

finally:

    postgresSQLConnection.close()

PostgreSQL Table fetal_upload has been created successfully.
```

The code uploading on Postgres  
AWS server



# From ML to Visualization - Flask App

```
# clf = load('finalized_model.sav')
@app.route('/predict', methods=['POST'])
def predict():
    # try out for code on Heroku
    clf = pickle.load(open('finalized_model.sav', 'rb'))
    print('clf')
    int_features = [float(x) for x in request.form.values()]
    query_df = [np.array(int_features)]
    print(query_df)
    # query = pd.get_dummies(query_df)

    # for col in model_columns:
    #     if col not in query.columns:
    #         query[col] = 0

    prediction = clf.predict(query_df)
    print(prediction)
    prediction_dictionary = {
        1: "The health of the fetus is likely normal.",
        2: "The health of the fetus is suspicious for possible pathology.",
        3: "The health of the fetus is likely pathological."
    }
    if int(prediction) in prediction_dictionary.keys():
        prediction_string = prediction_dictionary[int(prediction)]
    return render_template('fetal_health_predictor.html', prediction = prediction_string)
```

Flask app was used to build user interaction with the ML done. Predict route takes information from user and presents result.

# Deployment of app on the Internet

Heroku was used in deploying app noting

- its ease of use,
- ability to scale application
- suitable for web and python based applications

The screenshot shows the Heroku dashboard for a personal application named 'fetal-health'. The breadcrumb navigation at the top reads 'Personal > fetal-health'. Below this, it says 'GitHub Storkopolus/Final\_Project1'. The main navigation bar includes 'Overview', 'Resources', 'Deploy' (which is the active tab), 'Metrics', 'Activity', 'Access', and 'Settings'. In the 'Deploy' section, there are two main instructions: 'Add this app to a pipeline' and 'Add this app to a stage in a pipeline to enable additional features'. The first instruction suggests creating a new pipeline or choosing an existing one. The second instruction explains that pipelines can connect multiple apps to promote code and that connecting to GitHub can enable review apps. Below these instructions, a message states: 'Only the owner of this app (bstork@gmail.com) can add fetal-health to a pipeline.' At the bottom, the 'Deployment method' section shows three options: 'Heroku Git' (with a 'Use Heroku CLI' button), 'GitHub' (marked as 'Connected' with a green checkmark), and 'Container Registry' (with a 'Use Heroku CLI' button).

Personal > fetal-health

GitHub Storkopolus/Final\_Project1

Overview Resources **Deploy** Metrics Activity Access Settings

**Add this app to a pipeline**

Create a new pipeline or choose an existing one and add this app to a stage in it.

**Add this app to a stage in a pipeline to enable additional features**

Pipelines let you connect multiple apps together and **promote code** between them. [Learn more.](#)

Pipelines connected to GitHub can enable **review apps**, and create apps for new pull requests. [Learn more.](#)

Only the owner of this app (bstork@gmail.com) can add **fetal-health** to a pipeline.

**Deployment method**

Heroku Git Use Heroku CLI

GitHub **Connected**

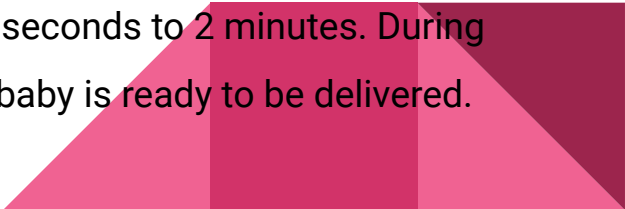
Container Registry Use Heroku CLI

# 6 User Inputs for Machine Learning

**Baseline Fetal Heart Rate:** the heart rate during a 10 minute segment rounded to the nearest 5 beats per minute. Normal baseline fetal heart rate is 110-160 beats per minute.

**Accelerations:** short term rises in the baseline fetal heart rate of at least 15 beats per minute and lasting at least 15 seconds. These are normal and healthy, and indicate the fetus has an adequate supply of oxygen.

**Uterine Contractions:** tightening of the muscles of the uterus. During the 2nd and 3rd trimester, occasional contractions called Braxton-Hicks are normal and may last 30 seconds to 2 minutes. During labor, contractions last 30-70 seconds and become more frequent as the baby is ready to be delivered.




# 6 User Inputs for Machine Learning

**Decelerations:** decelerations are temporary drops in the baseline fetal heart rate. A prolonged deceleration is a drop below baseline by 15 bpm for longer than 2 minutes but less than 10 minutes. Prolonged deceleration indicate the fetus isn't getting enough oxygen.

**Short Term Variability:** short term variability is the beat to beat variation in fetal heart rate. Normal variability is 6-25 beats per minute. Variability is normal after 32 weeks. Decreased variability may indicate lack of oxygen or a congenital heart anomaly.

**Long Term Variability:** long term variability is the fluctuation in fetal heart rate in one minute.

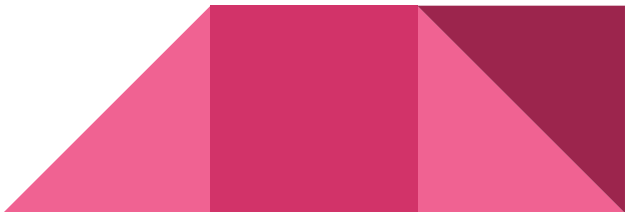


# Output Possibilities

**Machine Learning outputs a 1, 2 or 3 as the result**

**Created a dictionary in the Flask app to output a String related to the numerical output**

```
prediction_dictionary = {  
    1: "The health of the fetus is likely normal.",  
    2: "The health of the fetus is suspicious for possible pathology.",  
    3: "The health of the fetus is likely pathological."  
}
```



# Conclusions/Learning lessons

- To deploy to Heroku, need to make sure have all proper requirements
- Learned and experimented with Heroku--loading from github vs. terminal/bash
- Needed to confirm that machine learning model was in the correct folder location.
  - There were issues with Heroku finding our finalized\_model.sav
- When deploying Heroku app (from GitHub), make sure that the person hosting the repository is the one that launches the application. Otherwise there could be additional folders created inside the repository.

Storkopolus changed to fetal-health and now using pickle (#24) fd6043a 12 hours ago 71 commits		
📁 .ipynb_checkpoints	Started coding to figure out what Machine Learning Model would be best	22 days ago
📁 Data	Added the data CSV to the repository	24 days ago
📁 Database	Segs (#7)	11 days ago
📁 fetal-health	main	23 hours ago

Show Website

