

**Survey on Algorithms for Personalized Patient Health Informatics and Diagnosis**

**CS 6045**

**Advanced Algorithms**

**Spring 2025**

**Michael Rizig**

Instructor – Dr. Michail Alexiou

1. Abstract

The goal of this research is to provide an analysis on the current algorithms used for detection and diagnosis of disease or illness. This research includes discussing the 4 primary approaches to the development of these type algorithms: Supervised Learning, Unsupervised Learning, Statistical Modeling, and custom-made algorithms that utilize some combination of both. We will discuss their strengths and weaknesses, and how they fit into the larger scheme of overall patient diagnosis. This research also covers the primary data sources for collecting anonymous patient data for developing and training machine learning classification algorithms, the use and considerations of this data, and results of each approach.

1. DATA COLLECTION

Collecting high quality data to train models on is the first step to any approach. There are several sources that one can use to collect data ethically. Here are 3 common sources:

MEDICAL IMAGING ARCHIVES (PACS): These archives contain anonymous medical images such as x-rays, scans, MRIS, and other digital medical images. This source would be useful for training a model in machine vision to detect anomalies or cancers in a radiology environment.

EXAMPLES:

<https://www.cancerimagingarchive.net/>

<https://grand-challenge.org/>

<https://www.cancerimagingarchive.net/browse-collections/>

ELECTRONIC HEALTH RECORDS (EHRs): Electronic health records databases incluse both structured and unstructured data and can vary by source. Some form of normalization is probably required.

EXAMPLES:

<https://starr.stanford.edu/data-types/electronic-health-record>

<https://www.nature.com/articles/s41597-022-01899-x>

LAB RESULTS DATABSES: This type of data consists of lab results from blood tests, stool tests, urine tests, etc. From my experience these are the hardest to get reliable data from as labs are often private organizations.

<https://pmc.ncbi.nlm.nih.gov/articles/PMC2929542/>

SKLEARN: The algorithms in this paper will utilize SKLearn’s openly available datasets for training models. This is simply the easiest and most compatible data for the small scale examples in this paper.

<https://scikit-learn.org/stable/datasets.html#datasets>

**Feature reduction Algorithm:**

This algorithm utilizes a divide and conquer approach to reduce the number of features while maintain accuracy. This allows for the model to run more efferently as it no longer has to process a high dimensionality of data. The time complexity of the feature reduction can be considered m (log reg model epochs) \* n (size of data) \* log(n) (reduction) or **O(m\*n\*log(n))**

**NOTE: While this was implemented for demonstration purposes, all results show model outputs when trained on the full feature set to ensure consistency and accuracy in the results and comparisons. This section is just to provide an alternative more streamlined dataset with reduced features.**

def divide\_and\_conquer\_feature\_selection(X\_train, y\_train, X\_test, y\_test, features, target\_num\_features):

if len(features) <= target\_num\_features:

return features

# Divide the features into two

mid = len(features) // 2

left = features[:mid]

right = features[mid:]

# Evaluate

aleft = helper(X\_train, y\_train, X\_test, y\_test, left)

aright = helper(X\_train, y\_train, X\_test, y\_test, right)

# Keep the better half

selected = left if aleft > aright else right

# Recurse

return divide\_and\_conquer\_feature\_selection(X\_train, y\_train, X\_test, y\_test, selected, target\_num\_features)

def helper(X\_train, y\_train, X\_test, y\_test, feature\_subset):

model = LogisticRegression(max\_iter=10000, solver='liblinear')

model.fit(X\_train[feature\_subset], y\_train)

y\_pred = model.predict(X\_test[feature\_subset])

return accuracy\_score(y\_test, y\_pred)

END OF ALGORITHM

1. APPROACH

There are 4 general approaches that will be covered in this paper. These include Supervised Learning, Unsupervised Learning, Deep Learning, Statistical Modeling, and Custom Algorithms.

1. SUPERVISED LEARNING:

Supervised learning algorithms utilize datasets with the correct output each data point labeled. By utilizing labeled data, the model can be trained Via backpropagation and can be used on new unseen patient data. Some applications of this type of model include image analysis, radiology, analyzing lab results, and suggesting treatments to certain ailments. Some examples of supervised learning include logistical regression state vector machines and neural networks. By setting the output classes of a neural network to all the possible diseases being tested for, a sufficiently deep neural network utilizing logistical regression may be able to predict diagnosis once trained.

2. UNSUPERVISED LEARNING:

Unsupervised learning is similar to supervised learning with the difference being that data points are not labeled. In this way the model must group data and generate classes based on similarity this type of model can be used to detect anomalies and also classify results with predefined groups. An example of this type of algorithm is a K-Means algorithm. With sufficient generated groups, the model could predict the output of a given datapoint by finding its closest group. It could also detect new groups based on previously unseen trends period

3. STATISTICAL MODELING:

Statistical modeling is a more classical approach to medical diagnosis. These types of models take into account the patients age, symptoms, and medical history to make predictions of what the diagnosis may be via probability. By asking the patient a series of questions, and having storing the conditional probability of each, the model can predict with some accuracy the general diagnosis of a patients illness.

4. CUSTOM ALGORITHMS:

In most cases, when trying to create a system that can reliably predict the diagnosis, a combination of the previous 3 approaches is used. By integrating the three approaches, we can reliably predict the diagnosis of a patient to aid in medical treatment. The tradeoff of this approach is it is the most computationally / time demanding as it would require the use of 3 or more models. These algorithms will not be covered in this paper as they encompass a wide range of solutions.

1. SUPERVISED LEARNING ALGORITHM

This section contains an example of a basic supervised learning algorithm that could be used to predict if a sample is malignant. The dataset used contains 569 samples classed as either Malignant or Benign, with 212 samples the former and 357 the latter. This algorithm trains a neural network classifier on the data logs the accuracy of the algorithm.

**Complexity:**

Determining the complexity of a supervised learning algorithm is not very straight forward depending on the type of algorithm. For this implementation, we can consider training and testing as 2 separate events and thus their complexities are distinct.

Training: Training the algorithm consists of passing the dataset through the network and back-progating to update weights. (2n). We do this on all features (k) and repeat this as many times as we need to reach our target epochs (m). Thus, the time complexity of **training** this supervised algorithm is O(m(n\*k)) where n = len(dataset), k = len(features), and m = len(epochs).

Prediction: Predicting if a sample is malignant or not does not require any use of the dataset n. The algorithm utilizes the learned weights to pass the data once through the network and arrive at a result.

Thus the time complexity of **prediction** is linear, at O(1).

Dataset:

<https://scikit-learn.org/stable/modules/generated/sklearn.datasets.load_breast_cancer.html>

Guides used:

<https://www.youtube.com/watch?v=z1oDlzngvI0>

<https://www.youtube.com/watch?v=EAGeDyygilM>

class BinaryClassifier(nn.Module):

def \_\_init\_\_(self, input\_size):

super(BinaryClassifier, self).\_\_init\_\_()

self.fc1 = nn.Linear(input\_size, 64) # layer 1

self.relu1 = nn.ReLU()

self.fc2 = nn.Linear(64, 32) # layer 2

self.relu2 = nn.ReLU()

self.fc3 = nn.Linear(32, 1) # layer 3 (output layer)

self.sigmoid = nn.Sigmoid() # map to value between 0 and 1

def forward(self, x):

# forward propigate through network

out = self.fc1(x)

out = self.relu1(out)

out = self.fc2(out)

out = self.relu2(out)

out = self.fc3(out)

out = self.sigmoid(out)

return out

class Supervised:

def \_\_init\_\_(self):

self.classifier = BinaryClassifier(30)

self.load\_data()

self.train\_model()

def load\_data(self):

# Load the dataset

cancer = load\_breast\_cancer()

X = pd.DataFrame(cancer.data, columns=cancer.feature\_names)

y = cancer.target

# grab features

self.features = list(X.columns)

# Split the data into train, test, adn validation sets

# lines 19 and 20 borrowed from sklearn website

xtrain, xtest, ytrain, y\_test = train\_test\_split(X, y, test\_size=0.2, random\_state=42)

xtrain, xvalidation, ytrain, yvalidation = train\_test\_split(xtrain, ytrain, test\_size=0.25, random\_state=42) # 0.25 of 0.8 is 0.2

# normalize the data

# https://scikit-learn.org/stable/modules/generated/sklearn.preprocessing.StandardScaler

self.scaler = StandardScaler()

xtrain = self.scaler.fit\_transform(xtrain)

xvalidation = self.scaler.transform(xvalidation)

xtest = self.scaler.transform(xtest)

# Convert data to tensors

self.xtrain = torch.tensor(xtrain, dtype=torch.float32)

self.xvalidation = torch.tensor(xvalidation, dtype=torch.float32)

self.xtest = torch.tensor(xtest, dtype=torch.float32)

self.ytrain = torch.tensor(ytrain, dtype=torch.long)

self.yvalidation = torch.tensor(yvalidation, dtype=torch.long)

self.y\_test = torch.tensor(y\_test, dtype=torch.long)

return self.xtrain, self.xvalidation, self.xtest, self.ytrain, self.yvalidation, y\_test, self.scaler, self.features

# divde and conquer reduce:

def divide\_and\_conquer\_feature\_selection(self,xtrain, ytrain, xtest, ytest, features, num\_features):

if len(features) <= num\_features:

return features

# Divide the features into two

mid = len(features) // 2

left = features[:mid]

right = features[mid:]

# Evaluate

aleft = self.helper(xtrain, ytrain, xtest, ytest, left)

aright = self.helper(xtrain, ytrain, xtest, ytest, right)

# Keep the better half

selected = left if aleft > aright else right

# Recurse

return self.divide\_and\_conquer\_feature\_selection(xtrain, ytrain, xtest, ytest, selected, num\_features)

def helper(self,xtrain, ytrain, xtest, ytest, feature\_subset):

model = LogisticRegression(max\_iter=10000, solver='liblinear')

model.fit(xtrain[feature\_subset], ytrain)

y\_pred = model.predict(xtest[feature\_subset])

return accuracy\_score(ytest, y\_pred)

def train\_model(self, epochs=100, learning\_rate=0.001):

lossc = nn.BCELoss()

optimizer = optim.Adam(self.classifier.parameters(), lr=learning\_rate)

# Train the model

val\_accuracies = []

for epoch in range(epochs):

# Forward propagation

pred = self.classifier(self.xtrain)

loss = lossc(pred, self.ytrain.float().view(-1, 1))

# Backward propagation and optimization

optimizer.zero\_grad()

loss.backward()

optimizer.step()

# Evaluate on validation set

with torch.no\_grad():

y\_pred\_val = self.classifier(self.xvalidation)

y\_pred\_val\_binary = (y\_pred\_val > 0.5).long() # Threshold at 0.5

val\_accuracy = accuracy\_score(self.yvalidation.numpy(), y\_pred\_val\_binary.numpy())

val\_accuracies.append(val\_accuracy)

return val\_accuracies

def predict(self, data):

pred = self.classifier(data)

pred = (pred>0.5).int().tolist()

return sum(pred,[])

def evaluate\_model(self):

# Evaluate the model on the test set

with torch.no\_grad():

y\_pred\_test = self.classifier(self.xtest)

y\_pred\_test\_binary = (y\_pred\_test > 0.5).long() # Threshold at 0.5

#test\_accuracy = accuracy\_score(self.y\_test, y\_pred\_test\_binary.numpy())

# variables for confusion matrix

tp =0

fp= 0

fn=0

tn=0

for i in range(len(y\_pred\_test\_binary)):

if y\_pred\_test\_binary[i] == 1:

if self.y\_test[i] == 1:

tp+=1

else:

fp+=1

else:

if self.y\_test[i] == 1:

fn+=1

else:

tn+=1

#print("fn", fn ," fp ", fp , " tn " , tn , " tp ", tp)

return classification\_report(self.y\_test, y\_pred\_test\_binary.numpy())

if \_\_name\_\_ == "\_\_main\_\_":

supervised = Supervised()

supervised.predict(supervised.xtest)

# Evaluate the model

print(supervised.evaluate\_model())

**END OF ALGORITHM**

**RESULTS:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Metric** | **Benign** | **Malignant** | **Accuracy** | **Macro F1** | **Weighted F1** |
| Precision | 0.9855 | 0.9333 | 0.9649 | 0.9630 | 0.9651 |
| Recall | 0.9577 | 0.9767 |
| F1-Score | 0.9714 | 0.9545 |
| Count | 43 | 71 |

Figure 1. Supervised Learning Results

**CONFUSION MATRIX:**

**Note: All confusion matrices in this report were generated via** [**https://www.damianoperri.it/public/confusionMatrix/**](https://www.damianoperri.it/public/confusionMatrix/)

A graph with numbers and a red square

Description automatically generated with medium confidence

Figure 2. Supervised Learning Confusion Matrix

1. UNSUPERVISED LEARNING ALGORITHM

This section contains an example of a basic unsupervised learning algorithm that could be used to predict if a sample is malignant. This algorithm utilizes the same exact dataset as before, but the algorithm does not utilize the labels for training. This algorithm (K-MEANS) creates cluster centers, assigns data based on how close the datapoint is to a given cluster, then re-averages the cluster centers and re-assigns the data again. This way the clusters become more and more fitting of the data it represents. The clusters are then matched with their actual values.

**Complexity**:

As with Supervised, Unsupervised learning is also broken down into training and testing complexities.

Training: For training, we are passing each datapoint (n) into our graph checking each cluster (2) based on the number of features (m), and we are doing this as many times as we need until our clusters stop changing (for sklearn this runs 10 times, but for demonstration purposeless we will call this k). Thus our **training** complexity is n \* 2 \* m \* k, or simply O(n\*m\*k)

Prediction: Predicting our datapoint in this unsupervised algorithm is not linear as it was in our supervised algorithm. It checks each cluster (2) by the number of features in the sample (n), this for our **prediction** approach our complexity is 2n or O(n), but in cases where the number of clusters is not simple, we can cay O(n\*m)

Dataset:

<https://scikit-learn.org/stable/modules/generated/sklearn.datasets.load_breast_cancer.html>

class Unsupervised:

def \_\_init\_\_(self):

self.load\_data()

self.train\_kmeans\_model()

self.assigned\_clusters = self.assign\_clusters\_to\_labels()

# load the data the same way as the supervised data but without labels

def load\_data(self):

# Load the dataset

cancer = load\_breast\_cancer()

X = cancer.data

y = cancer.target #useful for comparing the clusters to the actual labels

# note that this alg only loads the X values, not the Y values (no labels)

self.xtrain, self.xtest, self.ytrain, self.ytest = train\_test\_split(X, y, test\_size=0.2, random\_state=42)

scaler = StandardScaler()

self.xtrain = scaler.fit\_transform(self.xtrain)

self.xtest = scaler.transform(self.xtest)

return self.xtrain, self.xtest, self.ytrain, self.ytest, scaler

# train a k-means model (creates clusters and matches each datapoint to the cluster it is closest to)

def train\_kmeans\_model(self, n\_clusters=2):

self.kmeans = KMeans(n\_clusters=n\_clusters, random\_state=42, n\_init='auto')

# Train the model

self.kmeans.fit(self.xtrain)

return self.kmeans

def evaluate(self):

# Predict the clusters for the test data

cluster\_labels =self.kmeans.predict(self.xtest)

if self.assigned\_clusters[0] == 1: # if the labels are flipped, flip the labels of each

for i in range(len(cluster\_labels)):

if cluster\_labels[i] == 1:

cluster\_labels[i] = 0

else :

cluster\_labels[i] = 1

# generate variables for confusion matrix (same as before)

tp =0

fp= 0

fn=0

tn=0

for i in range(len(cluster\_labels)):

if cluster\_labels[i] == 1:

if self.ytest[i] == 1:

tp+=1

else:

fp+=1

else:

if self.ytest[i] == 1:

fn+=1

else:

tn+=1

#print("fn", fn ," fp ", fp , " tn " , tn , " tp ", tp)

#print(cluster\_labels, self.ytest, assigned\_clusers)

return classification\_report(self.ytest,cluster\_labels)

# goes through each cluster and finds the majority value (0 or 1) then assigns that cluster that valeu

def assign\_clusters\_to\_labels(self):

clusters = self.kmeans.predict(self.xtrain)

cluster\_labels = {}

for cluster\_id in range(self.kmeans.n\_clusters):

cluster\_indices = np.where(clusters == cluster\_id)[0]

cluster\_true\_labels = self.ytrain[cluster\_indices]

# Find the most frequent label in this cluster

if cluster\_true\_labels.size > 0:

most\_common\_label = np.bincount(cluster\_true\_labels).argmax()

else:

most\_common\_label = 0

cluster\_labels[cluster\_id] = most\_common\_label

return cluster\_labels

def predict(self, data):

pred = self.kmeans.predict(data)

if self.assigned\_clusters[0] == 1: # if the labels are flipped, flip the labels of each

for i in range(len(pred)):

if pred[i] == 1:

pred[i] = 0

else :

pred[i] = 1

return pred

if \_\_name\_\_ == "\_\_main\_\_":

unsupervised = Unsupervised()

# Evaluate the model

print(unsupervised.evaluate())

# Assign labels to clusters

#print(f"Cluster to label mapping: {unsupervised.assign\_clusters\_to\_labels()}")

**END OF ALGORITHM**

**RESULTS:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Metric** | **Benign** | **Malignant** | **Accuracy** | **Macro F1** | **Weighted F1** |
| Precision | 0.9091 | 0.9730 | 0.9298 | 0.9230 | 0.9286 |
| Recall | 0.9859 | 0.8372 |
| F1-Score | 0.9459 | 0.9000 |
| Count | 43 | 71 |

Figure 3. Unsupervised Learning Results

**CONFUSION MATRIX:**

**A graph with numbers and a red square

Description automatically generated with medium confidence**

Figure 4. Unsupervised Learning Confusion Matrix

1. STATISTICAL MODELING

Statistical Modeling is another method of utilizing models to predict a diagnosis. Bayes Classifiers work by utilizing prior probabilities to calculate the probability that a data sample belongs in any given class. It does this by multiplying the probability that the data point is in the group (by using the groups frequency over N) then multiplies this by the likelihood of each feature of the example appearing in that group. When done for every group, we get a set of probabilities, and we choose the highest value as our prediction.

**Complexity**:

As before, we will split the complexity into training complexity and predicting complexity.

Training: For training, we utilize the number of datapoints (n) and for each we utilize each feature (m) and compute the statistics based on these. This we can claim that for our binary approach, the complexity to **train** the model would be O(n\*m). This is significantly faster training than our other two models.

Prediction: Predicting our datapoint in this unsupervised algorithm is not linear as it was in our supervised algorithm. It checks each cluster (2) by the number of features in the sample (n), this for our **prediction** approach our complexity is 2n or O(n), but in cases where the number of clusters is not simple, we can cay O(n\*m)

class BayesClassifier:

def \_\_init\_\_(self):

self.bayes = GaussianNB()

self.load\_data()

self.train()

def load\_data(self):

# Load the dataset

cancer = load\_breast\_cancer()

X = pd.DataFrame(cancer.data, columns=cancer.feature\_names)

y = cancer.target

# grab features

features = list(X.columns)

# Split the data into train, test, adn validation sets

# lines 19 and 20 borrowed from sklearn website

xtrain, xtest, ytrain, ytest = train\_test\_split(X, y, test\_size=0.2, random\_state=42)

xtrain, xvalidation, ytrain, yvalidation = train\_test\_split(xtrain, ytrain, test\_size=0.25, random\_state=42) # 0.25 of 0.8 is 0.2

# normalize the data

scaler = StandardScaler()

xtrain = scaler.fit\_transform(xtrain)

xvalidation = scaler.transform(xvalidation)

xtest = scaler.transform(xtest)

# Convert data to tensors

self.xtrain = torch.tensor(xtrain, dtype=torch.float32)

self.xvalidation = torch.tensor(xvalidation, dtype=torch.float32)

self.xtest = torch.tensor(xtest, dtype=torch.float32)

self.ytrain = torch.tensor(ytrain, dtype=torch.long)

self.yvalidation = torch.tensor(yvalidation, dtype=torch.long)

self.ytest = torch.tensor(ytest, dtype=torch.long)

self.scaler = scaler

self.features = features

return self.xtrain, self.xvalidation, self.xtest, self.ytrain, self.yvalidation, self.ytest, self.scaler, self.features

def train(self):

# https://scikit-learn.org/stable/modules/naive\_bayes.html

self.load\_data()

self.bayes.fit(self.xtrain,self.ytrain)

def predict(self,data):

pred = self.bayes.predict(data)

return pred

def evaluate\_model(self):

pred = self.predict(self.xtest)

output= classification\_report(self.ytest.numpy(),pred)

# variables for confusion matrix

tp =0

fp= 0

fn=0

tn=0

for i in range(len(pred)):

if pred[i] == 1:

if self.ytest[i] == 1:

tp+=1

else:

fp+=1

else:

if self.ytest[i] == 1:

fn+=1

else:

tn+=1

#print("fn", fn ," fp ", fp , " tn " , tn , " tp ", tp)

return output

if \_\_name\_\_ == "\_\_main\_\_":

bayes = BayesClassifier()

bayes.train()

bayes.predict(bayes.xtest)

print(bayes.evaluate\_model())

END OF ALGORITHM

**RESULTS:**

We can clearly see that of the three models, Statistical performed similar in some aspects and actually performed better in others on this dataset. This is impressive considering the training time for bayes is significantly smaller than that of our other algorithms.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Metric** | **Benign** | **Malignant** | **Accuracy** | **Macro F1** | **Weighted F1** |
| Precision | 0.9583 | 0.9756 | 0.9646 | 0.9621 | 0.9644 |
| Recall | 0.9857 | 0.9302 |
| F1-Score | 0. 0.9718 | 0.9524 |
| Count | 43 | 71 |

Figure 5. Bayes Classifier Results

**CONFUSION MATRIX:**

A chart with red and green squares

Description automatically generated

Figure 6. Bayes Classifier Confusion Matrix

1. CUSTOM ALGORITHMS

Custom algorithms can be utilized to cross reference the results of each model. For example, a custom algorithm could run several models and use a voting system to ensure the highest likelihood of having an accurate result. In this approach, we could utilize the previously trained Supervised and Unsupervised algorithms and put all three predictions as votes. If there is a disagreement (2 positives and 1 negative, 2 negatives and 1 positive, etc), the higher frequency result would be the overall output.

from BayesClassifier import BayesClassifier

from SupervisedDiagnosis import Supervised

from UnSupervisedDiagnosis import Unsupervised

from sklearn.metrics import accuracy\_score, classification\_report

import numpy as np

if \_\_name\_\_ == "\_\_main\_\_":

# init all 3 models

bayes = BayesClassifier()

supervised = Supervised()

unsupervised = Unsupervised()

print("--------------BAYES--------------")

print(bayes.evaluate\_model())

print("--------------SUPERVISED--------------")

print(supervised.evaluate\_model())

print("--------------UNSUPERVISED--------------")

print(unsupervised.evaluate())

bayes\_output = bayes.predict(bayes.xtest)

supervised\_output = supervised.predict(bayes.xtest)

unsupervised\_output = unsupervised.predict(bayes.xtest)

voted\_output = []

# variables for confusion matrix

tp =0

fp= 0

fn=0

tn=0

for i in range(len(bayes\_output)):

true\_count = 0

if bayes\_output[i] == 1:

true\_count += 1

if supervised\_output[i] == 1:

true\_count += 1

if unsupervised\_output[i] == 1:

true\_count += 1

if true\_count >= 2:

voted\_output.append(1)

else:

voted\_output.append(0)

if voted\_output[i] == 1:

if bayes.ytest[i] == 1:

tp+=1

else:

fp+=1

else:

if bayes.ytest[i] == 1:

fn+=1

else:

tn+=1

print("fn", fn ," fp ", fp , " tn " , tn , " tp ", tp)

print(classification\_report(bayes.ytest.tolist(),voted\_output))

END OF ALGORITHM

**RESULTS:**

We can clearly see from our results that our custom algorithm which utilizes a voting system has the highest average accuracy, Macro F1 and Weighted F1 scores. It is important to note that this result only slightly beats our Bayes Classifier, despite being the highest cost algorithm to run.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Metric** | **Benign** | **Malignant** | **Accuracy** | **Macro F1** | **Weighted F1** |
| Precision | 0.9589 | 0.9756 | 0.9649 | 0.9623 | 0.9647 |
| Recall | 0.9859 | 0.9302 |
| F1-Score | 0.9722 | 0.9524 |
| Count | 43 | 71 |

Figure 5. Custom Algorithm Results

**CONFUSION MATRIX:**

A screenshot of a graph

Description automatically generated

Figure 5. Custom Algorithm Confusion Matrix

1. Conclusion

When surveying the algorithms for patient diagnosis, we can conclude that Supervised Learning, Unsupervised Learning, and Statistical Modeling algorithms can accurately and consistently detect and diagnose diseases in patients. The implications of these algorithms can be seen in online AI based wellness applications, as well as in the medical field. This technology has already begun testing in radiology and cancer detection applications in the modern medical field. While some algorithms are more accurate than others, there is an increased benefit when using multiple algorithms in collaboration to increase overall accuracy. This technology will likely change the medical landscape and allow for faster, cheaper, and more accurate diagnosis, ultimately making healthcare more accessible and affordable.

While we saw that our combination algorithm performed the best in terms of average accuracy, we must take into consideration the cost to accuracy ratio to determine a winner. As expected, picking the ‘best’ algorithm requires factoring in a project’s specific priorities. Based on this, below are the winners based on the three different criteria.

**Training Cost:**

The algorithm that wins in terms of training cost is the **Bayes Classifier**, due to it having the lowest training cost of the 3 models. This is because Bayes Classifier does not need to back-propagate like Supervised does, and does not need to repeatedly recalculate clusters like Unsupervised does. Thus, when picking a result that would be the most cost effective in training, Bayes Classifier wins.

**Prediction Cost:**

In situations where prediction cost is most important, then the **Supervised Learning** algorithm wins. This is because it not only performed well in accuracy, but has the lowest overall prediction cost (by far) with a linear prediction cost O(1). This means that in applications where training is one and done, or a pretrained model is used, Supervised Learning is the best option.

**Accuracy:**

When accuracy is the foremost concern, and cost is must less important, the **Custom Algorithm** wins as it gives the highest accuracy with this dataset. Which all the models were fairly accurate, the Custom Algorithm can truly shine when the dataset results in less accurate models overall. This would increase the need for a “highest voted solution”.

While there is no such thing as a one size fits all approach, adequate research and testing should lead the project to the best approach for its goal and dataset.

1. References

SUPERVISED LEARNING

1. Buch, V. H., Ahmed, I., & Maruthappu, M. (2018). Artificial intelligence in medicine: current trends and future possibilities. *The British journal of general practice : the journal of the Royal College of General Practitioners*, *68*(668), 143–144. https://doi.org/10.3399/bjgp18X695213

2. Lei Wang, Qing Qian, Qiang Zhang, Jishuai Wang, Wenbo Cheng, Wei Yan, Classification Model on Big Data in Medical Diagnosis Based on Semi-Supervised Learning, *The Computer Journal*, Volume 65, Issue 2, February 2022, Pages 177–191, <https://doi.org/10.1093/comjnl/bxaa006>

3 .A. Chebli, A. Djebbar and H. F. Marouani, "Semi-Supervised Learning for Medical Application: A Survey," *2018 International Conference on Applied Smart Systems (ICASS)*, Medea, Algeria, 2018, pp. 1-9, doi: 10.1109/ICASS.2018.8651980. <https://www.sciencedirect.com/science/article/abs/pii/S0933365715000482>

4 . Ramakanth Kavuluru, Anthony Rios, Yuan Lu,

An empirical evaluation of supervised learning approaches in assigning diagnosis codes to electronic medical records, <https://www.sciencedirect.com/science/article/abs/pii/S0933365715000482>

5. Roy, S., Meena, T., & Lim, S.-J. (2022). Demystifying Supervised Learning in Healthcare 4.0: A New Reality of Transforming Diagnostic Medicine. *Diagnostics*, *12*(10), 2549. <https://doi.org/10.3390/diagnostics12102549>

6. Samriti Sharma, Gurvinder Singh, Manik Sharma, A comprehensive review and analysis of supervised-learning and soft computing techniques for stress diagnosis in humans. <https://www.sciencedirect.com/science/article/abs/pii/S0010482521002444>

7. Eckardt Jan-Niklas , Bornhäuser Martin , Wendt Karsten , Middeke Jan Moritz, Semi-supervised learning in cancer diagnostics, Volume 12 – 2022, <https://www.frontiersin.org/journals/oncology/articles/10.3389/fonc.2022.960984> DOI=10.3389/fonc.2022.960984

8. Aljuaid, A., Anwar, M. Survey of Supervised Learning for Medical Image Processing. *SN COMPUT. SCI.* **3**, 292 (2022).

9. S. Muthurajkumar, R. Praveen, A.A. Abd El-Aziz, R. Shangeeth, S. Anika Lakshmi, and R. Gaythrisr, Medical diagnosis of human heart diseases using supervised learning techniques, <https://digital-library.theiet.org/doi/abs/10.1049/PBHE058E_ch4>

10. M. Zhao, R. H. M. Chan, T. W. S. Chow and P. Tang, "Compact Graph based Semi-Supervised Learning for Medical Diagnosis in Alzheimer’s Disease," in *IEEE Signal Processing Letters*, vol. 21, no. 10, pp. 1192-1196, Oct. 2014

11. Oumaima Terrada1 , Soufiane Hamida1 , Bouchaib Cherradi1, 2, Abdelhadi Raihani1,\* , Omar Bouattane1, Supervised Machine Learning Based Medical Diagnosis Support System for Prediction of Patients with Heart Disease, <https://www.researchgate.net/profile/Omar-Bouattane/publication/345325800_Supervised_Machine_Learning_Based_Medical_Diagnosis_Support_System_for_Prediction_of_Patients_with_Heart_Disease/links/5fb660c9458515b797511e8d/Supervised-Machine-Learning-Based-Medical-Diagnosis-Support-System-for-Prediction-of-Patients-with-Heart-Disease.pdf>

12. Nosayba Al-Azzam, Ibrahem Shatnawi, Comparing supervised and semi-supervised Machine Learning Models on Diagnosing Breast Cancer, Annals of Medicine and Surgery, <https://academic.oup.com/comjnl/article-abstract/65/2/177/5808795>

13. M. Pechenizkiy, A. Tsymbal, S. Puuronen and O. Pechenizkiy, "Class Noise and Supervised Learning in Medical Domains: The Effect of Feature Extraction," 19th IEEE Symposium on Computer-Based Medical Systems (CBMS'06), Salt Lake City, UT, USA, 2006, pp. 708-713, doi: 10.1109/CBMS.2006.65. <https://ieeexplore.ieee.org/abstract/document/1647654>

14. De Asmundis, R., Guarracino, M.R. (2013). Mathematical Models of Supervised Learning and Application to Medical Diagnosis. In: Pardalos, P., Coleman, T., Xanthopoulos, P. (eds) Optimization and Data Analysis in Biomedical Informatics. Fields Institute Communications, vol 63. Springer, New York, NY. <https://doi.org/10.1007/978-1-4614-4133-5_3>

15. Haseeb Hassan, Zhaoyu Ren, Chengmin Zhou, Muazzam A. Khan, Yi Pan, Jian Zhao, Bingding Huang,

Supervised and weakly supervised deep learning models for COVID-19 CT diagnosis: A systematic review,

<https://www.sciencedirect.com/science/article/pii/S0169260722001171>

UNSUPERVISED LEARNING:

16. Khalid Raza and Nripendra K. Singh, A Tour of Unsupervised Deep Learning for Medical Image Analysis, <https://www.benthamdirect.com/content/journals/cmir/10.2174/1573405617666210127154257>

17. Xiuli Bi, Shutong Li, Bin Xiao, Yu Li, Guoyin Wang, Xu Ma,

Computer aided Alzheimer's disease diagnosis by an unsupervised deep learning technology. <https://www.sciencedirect.com/science/article/abs/pii/S0925231219304709>

18. H. P. Ng, S. H. Ong, K. W. C. Foong, P. S. Goh and W. L. Nowinski, "Medical Image Segmentation Using K-Means Clustering and Improved Watershed Algorithm," *2006 IEEE Southwest Symposium on Image Analysis and Interpretation*, Denver, CO, USA, 2006, pp. 61-65, doi: 10.1109/SSIAI.2006.1633722. <https://ieeexplore.ieee.org/abstract/document/1633722>

STATISTICAL MODELS:

19. Langarizadeh, M., & Moghbeli, F. (2016). Applying Naive Bayesian Networks to Disease Prediction: a Systematic Review. *Acta informatica medica : AIM : journal of the Society for Medical Informatics of Bosnia & Herzegovina : casopis Drustva za medicinsku informatiku BiH*, *24*(5), 364–369. <https://doi.org/10.5455/aim.2016.24.364-369>

20. Regnier-Coudert O, McCall J, Lothian R, Lam T, McClinton S, N'dow J. Machine learning for improved pathological staging of prostate cancer: a performance comparison on a range of classifiers. Artif Intell Med. 2012 May;55(1):25–35. doi: 10.1016 <https://www.sciencedirect.com/science/article/abs/pii/S0933365711001461>

21 .Kazmierska J, Malicki J. Application of the Naïve Bayesian Classifier to optimize treatment decisions. Radiother Oncol. 2008 Feb;86(2):211–6. doi: 10.1016/j.radonc.2007.10.019 <https://www.sciencedirect.com/science/article/abs/pii/S0167814007005221>

22. M. Wiggins , A. Saad , B. Litt , G. Vachtsevanos, Evolving a Bayesian classifier for ECG-based age classification in medical applications, <https://www.sciencedirect.com/science/article/abs/pii/S1568494607000452>

23. Beí¡ta Reiz, Lehel Csató, Bayesian Network Classifier for Medical Data Analysis, <https://www.univagora.ro/jour/index.php/ijccc/article/view/2414>

24. KONONENKO, I. (1993). INDUCTIVE AND BAYESIAN LEARNING IN MEDICAL DIAGNOSIS. Applied Artificial Intelligence, 7(4), 317–337. <https://doi.org/10.1080/08839519308949993>

25. A. F. M. Hani, H. A. Nugroho and H. Nugroho, "Gaussian Bayes classifier for medical diagnosis and grading: Application to diabetic retinopathy," 2010 IEEE EMBS Conference on Biomedical Engineering and Sciences (IECBES), Kuala Lumpur, Malaysia, 2010, pp. 52-56, doi: 10.1109/IECBES.2010.5742198. <https://ieeexplore.ieee.org/abstract/document/5742198>