

# health\_analysis

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## 1 Predicting risk factors for maternal mortality

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```
[1]: import numpy as np
import pandas as pd
import requests
import zipfile
import altair as alt
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.model_selection import train_test_split
from sklearn.compose import make_column_transformer
from sklearn.preprocessing import StandardScaler, label_binarize
from sklearn.dummy import DummyClassifier
from sklearn.linear_model import LogisticRegression
from sklearn.svm import SVC
from sklearn.model_selection import cross_validate
from sklearn.pipeline import make_pipeline
from scipy.stats import loguniform
from sklearn.model_selection import RandomizedSearchCV, cross_val_predict
from sklearn.metrics import fbeta_score, make_scorer, recall_score,
ConfusionMatrixDisplay, confusion_matrix, RocCurveDisplay, roc_auc_score
```

## 2 Summary

In this project, we built a Support Vector Classifier (SVC) that draws from maternal health measurements to predict the risk intensity levels (low, medium, or high) of pregnant women. Data was sourced from the “Maternal Health Risk” dataset from the UCI Machine Learning Repository and was originally collected by Marzia Ahmed and her team. Our final classifier performed fairly well on an unseen test data set, with a weighted recall score of 0.77 and an overall accuracy of 0.77. Out of the 305 test data cases, it correctly predicted 235 cases. The model showed particularly strong performance in identifying high-risk pregnancies, achieving an AUV of 0.943 for the high-risk class, compared to 0.820 for low-risk class and 0.814 for medium-risk class. However, the model made notable errors where 13 high-risk cases were misclassified as 11 medium-risk and 2 low-risk. These false negatives are gaps where high-risk individuals may not receive the necessary care.

We recommend further research to improve the model’s sensitivity to high-risk cases and better

differentiate between medium and low-risk categories before it is ready to be put into production in clinical settings. Additional feature engineering or exploring ensemble methods may help reduce these critical misclassifications. The implementation of refined classifiers would expand the capabilities of most healthcare systems and increase the efficacy of monitoring and interventions in underprivileged communities.

### 3 Introduction

Maternal mortality is a serious issue that predates human history and still affects many mothers today. Among women of reproductive age, 9% of global deaths are currently attributable to maternal causes such as hemorrhaging, hypertension, and unsafe abortion (Hassfurter, 2025). Fortunately, gradual improvements in medical understanding, policy, healthcare, and overall quality of life have led to steadily decreasing maternal mortality rates. Recent UNICEF reports from 2023 place the global maternal mortality ratio at 197 per 100,000 live births, which is approximately 40% less than the reported ratio from 2000. Despite these trends, many rural and underserved communities continue to experience higher rates of maternal mortality.

Bangladesh is a country that has an overall maternal mortality ratio of 196 per 100,000 live births; however, deeper investigation reveals significant differences in mortality rate between women of different socioeconomic backgrounds (Hossain et. al, 2023). Mortality rate was higher among women with no education, women in rural areas, and women in poor wealth categories. According to a paper published in *The Lancet*, focusing research on the biomedical causes of mortality is insufficient, and more attention should be directed towards needs such as “primary prevention, early identification, and adequate management of pregnancy, labour, and postpartum complications” (Souza et. al, 2024).

A welcome innovation has been the development of wearable technology and internet-enabled devices that have allowed patients and physicians to reliably monitor health conditions from their homes (Kashem et. al, 2020). Additionally, these devices enabled the collection of physiological data from otherwise underserved communities. We aim to predict maternal health risk levels using clinical measurements gathered from pregnant individuals in rural Bangladesh. The ability to accurately predict high-risk pregnancies would allow timely and focused medical interventions for vulnerable individuals.

## 4 Methods

### 4.1 Data

The data set used in this project is of health conditions of pregnant women from the rural areas of Bangladesh created by Marzia Ahmed at Daffodil International University. This dataset was sourced from the UC Irvine Machine Learning Repository and can be found [here](#). Each observation in the dataset corresponds to a pregnant individual’s health profile, comprising a risk intensity level (low, medium, or high risk) and associated clinical measurements including demographic information (age) and vital signs (systolic blood pressure, diastolic blood pressure, blood glucose concentration, body temperature, and resting heart rate). The data set was collected via an IoT-based risk monitoring system from hospitals, community clinics, and maternal health cares in rural Bangladesh.

#### 4.1.1 Data dictionary

Column Name	Role	Type	Description
Age	Feature	Integer	Age of the patient during pregnancy (in years)
SystolicBP	Feature	Integer	Systolic (upper) blood pressure measured in mmHg
DiastolicBP	Feature	Integer	Diastolic (lower) blood pressure measured in mmHg
BS	Feature	Integer	Blood sugar level measured in mmol/L
BodyTemp	Feature	Integer	Body temperature of the patient measured in °F
HeartRate	Feature	Integer	Patient's resting heart rate measured in bpm
RiskLevel	Target	Categorical	Predicted pregnancy risk level based on clinical features

## 4.2 Analysis

SVC was used to build a classification model to predict risk levels for pregnant women in rural Bangladesh. With the exception of diastolic blood pressure, all variables from the original dataset were included for analysis. The features used were age, systolic blood pressure, blood glucose level (BS), body temperature, and heart rate. Data was partitioned into a 70:30 train-test split and the random\_state was set to 123 for reproducibility. We performed hyperparameter tuning using randomized search with 10-fold cross-validation and recall score (weighted) as our evaluation metric to select the optimal values for C (regularization parameter), gamma (kernel coefficient). Recall score was selected to optimize the model for sensitivity in predicting high-risk cases. All explanatory variables were numerical and were standardized via StandardScalar prior to fitting. The Python programming language and the following Python packages were used to perform the analysis: requests, zipfile, numpy, Pandas, altair, seaborn, and scikit-learn.

## 4.3 Results & Discussion

### 4.3.1 EDA

Preliminary exploratory data analysis (EDA) was performed to briefly examine each explanatory variable. Previous research have described hypertension as a complication risk; therefore, we dropped diastolic BP for the more commonly significant systolic. Distributions of each explanatory variable were plotted using histograms and coloured according to risk levels (blue: high risk, green: medium risk, orange: low risk). The plotted distributions were visually distinct across risk levels. Thus, we continued to fit our model with the remaining features.

```
[2]: # download data as zip and extract
url = "https://archive.ics.uci.edu/static/public/863/maternal+health+risk.zip"

request = requests.get(url)
with open("../data/raw/maternal+health+risk.zip", 'wb') as f:
    f.write(request.content)

with zipfile.ZipFile("../data/raw/maternal+health+risk.zip", 'r') as zip_ref:
    zip_ref.extractall("../data/raw")
```

```
[3]: health_data = pd.read_csv("../data/raw/Maternal Health Risk Data Set.csv", ↴
                             header=0)
health_data
```

	Age	SystolicBP	DiastolicBP	BS	BodyTemp	HeartRate	RiskLevel
0	25	130	80	15.0	98.0	86	high risk
1	35	140	90	13.0	98.0	70	high risk
2	29	90	70	8.0	100.0	80	high risk
3	30	140	85	7.0	98.0	70	high risk
4	35	120	60	6.1	98.0	76	low risk
...	...	...	...	...	...	...	...
1009	22	120	60	15.0	98.0	80	high risk
1010	55	120	90	18.0	98.0	60	high risk
1011	35	85	60	19.0	98.0	86	high risk
1012	43	120	90	18.0	98.0	70	high risk
1013	32	120	65	6.0	101.0	76	mid risk

[1014 rows x 7 columns]

```
[4]: health_data.describe()
```

	Age	SystolicBP	DiastolicBP	BS	BodyTemp	HeartRate
count	1014.000000	1014.000000	1014.000000	1014.000000	1014.000000	1014.000000
mean	29.871795	113.198225	76.460552	8.725986	98.665089	74.301775
std	13.474386	18.403913	13.885796	3.293532	1.371384	8.088702
min	10.000000	70.000000	49.000000	6.000000	98.000000	7.000000
25%	19.000000	100.000000	65.000000	6.900000	98.000000	70.000000
50%	26.000000	120.000000	80.000000	7.500000	98.000000	74.301775
75%	39.000000	120.000000	90.000000	8.000000	98.000000	70.000000
max	70.000000	160.000000	100.000000	19.000000	103.000000	70.000000

```
50%      76.000000
75%      80.000000
max      90.000000
```

[5]: `health_data.info()`

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1014 entries, 0 to 1013
Data columns (total 7 columns):
 #   Column      Non-Null Count  Dtype  
--- 
 0   Age          1014 non-null    int64  
 1   SystolicBP   1014 non-null    int64  
 2   DiastolicBP  1014 non-null    int64  
 3   BS           1014 non-null    float64 
 4   BodyTemp     1014 non-null    float64 
 5   HeartRate    1014 non-null    int64  
 6   RiskLevel    1014 non-null    object  
dtypes: float64(2), int64(4), object(1)
memory usage: 55.6+ KB
```

[6]: `train_df, test_df = train_test_split(  
 health_data, test_size=0.3, random_state=123  
)  
X_train, y_train = train_df.drop(columns=['RiskLevel']), train_df["RiskLevel"]  
X_test, y_test = test_df.drop(columns=['RiskLevel']), test_df["RiskLevel"]  
  
train_df.to_csv("../data/processed/maternal_health_risk_train.csv")  
test_df.to_csv("../data/processed/maternal_health_risk_test.csv")`

[7]: `train_df`

```
Age  SystolicBP  DiastolicBP  BS  BodyTemp  HeartRate  RiskLevel
1003  50          130          100  16.0      98.0       76  high risk
243   32          120          65   6.0       101.0      76  mid risk
848   15          70           50   6.0       98.0       70  mid risk
202   23          90           60   7.5       98.0       76  low risk
300   15          75           49   7.7       98.0       77  low risk
...
988   25          120          90   12.0      101.0      80  high risk
322   65          90           60   6.9       98.0       70  low risk
382   17          90           65   7.8       103.0      67  high risk
365   22          120          90   7.8       98.0       82  mid risk
510   17          90           63   7.5       101.0      70  low risk
```

[709 rows x 7 columns]

[8]: `test_df`

```
[8]:      Age SystolicBP DiastolicBP    BS BodyTemp HeartRate RiskLevel
 50     25       120        80   7.0    98.0       66  low risk
784     35       100        70   6.8    98.0       60  mid risk
204     15        76        49   7.5    98.0       77  low risk
85      18        90        60   6.9    98.0       70  mid risk
802     42       130        80  18.0    98.0       70  mid risk
...     ...
619     29       130        70   7.5    98.0       78  mid risk
607     45       120        95   7.5    98.0       66  low risk
700     15       120        80   6.6    99.0       70  low risk
1005    17        90        65   7.7   103.0       67  high risk
178     40       120        95  11.0    98.0       80  high risk
```

[305 rows x 7 columns]

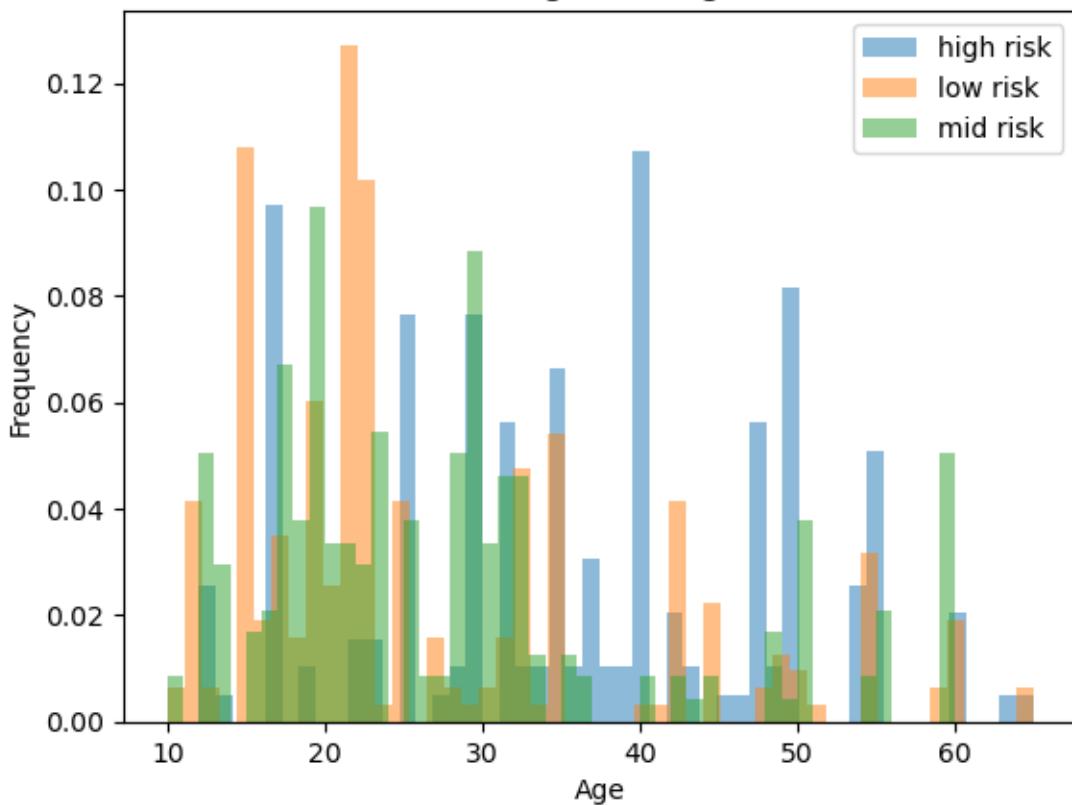
```
[9]: y_train.value_counts()
```

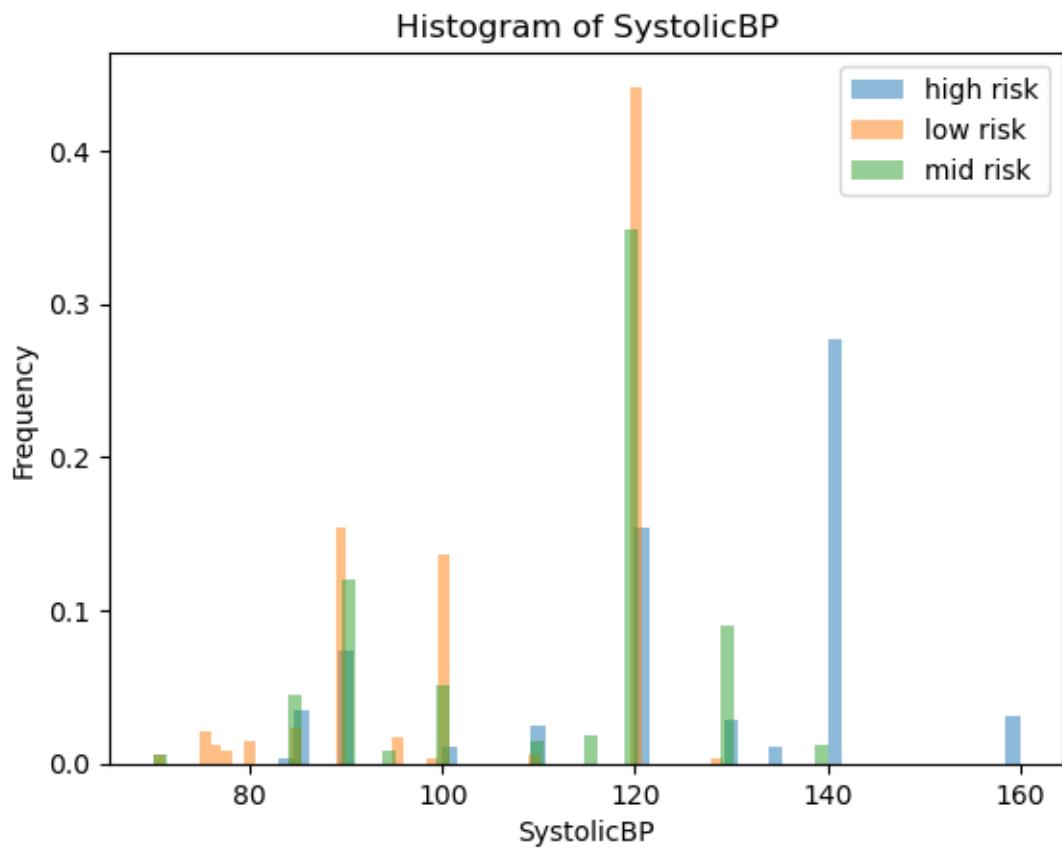
```
[9]: RiskLevel
low risk      286
mid risk     238
high risk    185
Name: count, dtype: int64
```

```
[10]: feature_cols = ["Age", "SystolicBP", "BS", "BodyTemp", "HeartRate"]

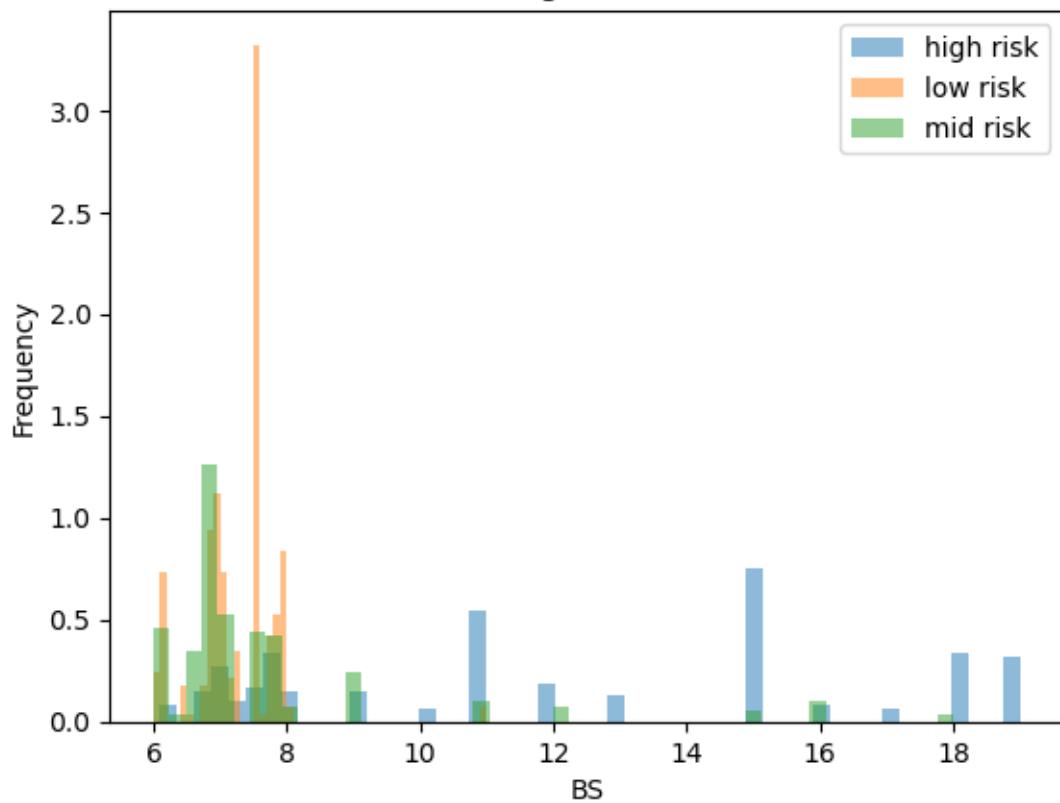
for feature in feature_cols:
    train_df.groupby("RiskLevel")[feature].plot.hist(bins=50, alpha=0.5, ↴
    legend=True, density = True, title = "Histogram of " + feature);
    plt.xlabel(feature);
    plt.show()
```

Histogram of Age

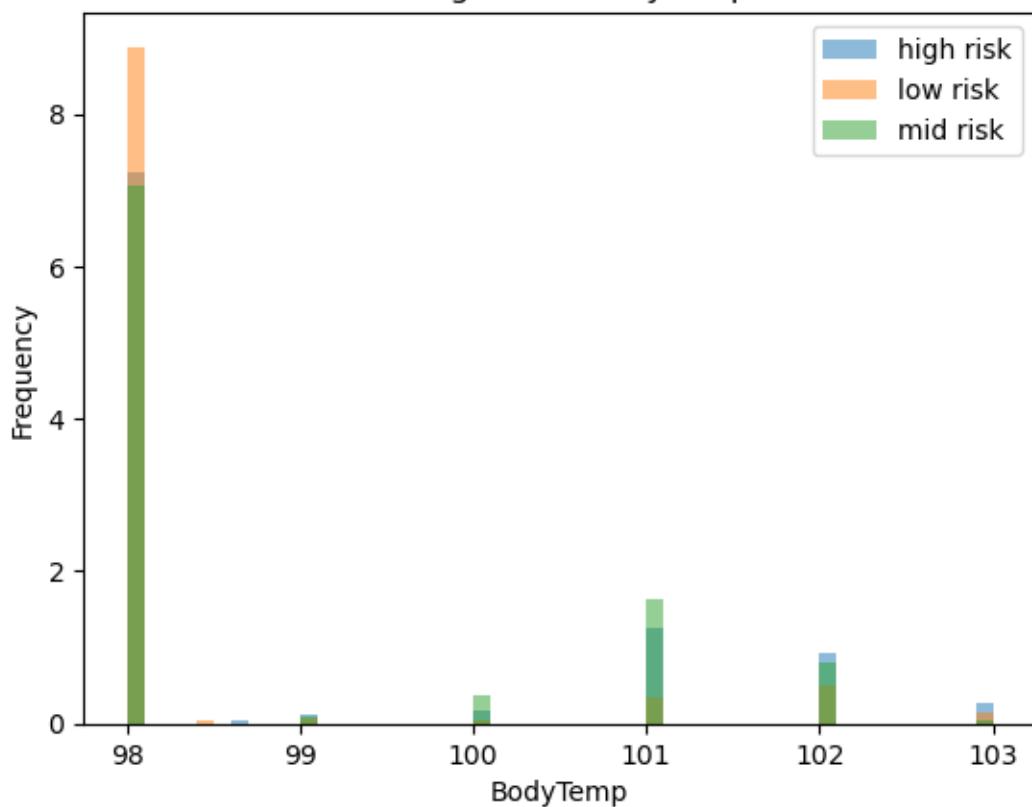




Histogram of BS



Histogram of BodyTemp



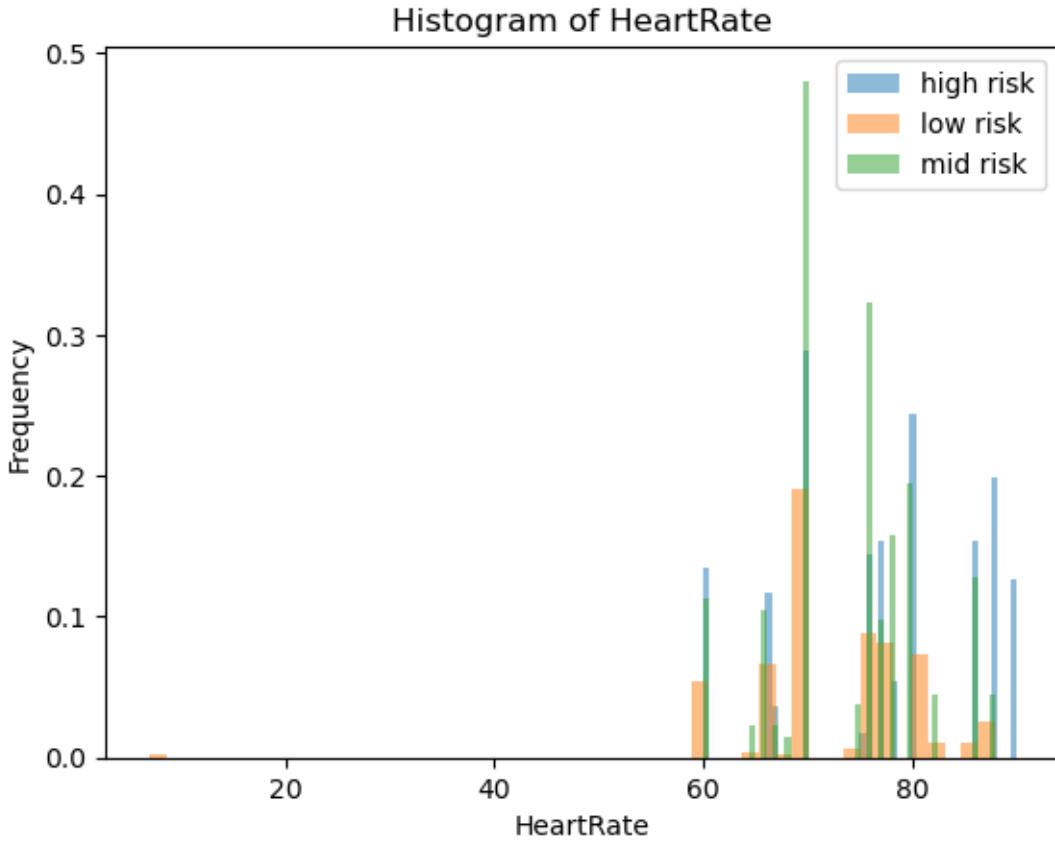


Figure 1. Comparison of the distributions of features contributing to the risk intensity level during pregnancy of an individual.

#### 4.3.2 Model construction

We selected a Support Vector Classifier (SVC) model for this classification task. To identify the model configuration that best predicted maternal health risk levels, we performed hyperparameter tuning using randomized search with 10-fold cross-validation and recall score (weighted) as our evaluation metric to select the optimal values for C (regularization parameter), gamma (kernel coefficient). We found that the optimal hyperparameters were 760 for C and 5.8 for gamma.

```
[11]: preprocessor = make_column_transformer(
    (StandardScaler(), feature_cols)
)
```

```
[12]: preprocessor.fit(X_train)
```

```
[12]: ColumnTransformer(transformers=[('standardscaler', StandardScaler(),
    ['Age', 'SystolicBP', 'BS', 'BodyTemp',
    'HeartRate'])])
```

```
[13]: X_train_enc = pd.DataFrame(
    preprocessor.transform(X_train),
    index=X_train.index,
    columns=preprocessor.get_feature_names_out()
)

# Show the transformed data
X_train_enc
```

	standardscaler__Age	standardscaler__SystolicBP	standardscaler__BS
1003	1.539667	0.915275	2.278454
243	0.182676	0.373190	-0.820502
848	-1.098927	-2.337235	-0.820502
202	-0.495820	-1.253065	-0.355659
300	-1.098927	-2.066193	-0.293680
...	...	...	...
988	-0.345043	0.373190	1.038872
322	2.670493	-1.253065	-0.541596
382	-0.948150	-1.253065	-0.262690
365	-0.571208	0.373190	-0.262690
510	-0.948150	-1.253065	-0.355659
	standardscaler__BodyTemp	standardscaler__HeartRate	
1003	-0.499908	0.209123	
243	1.630962	0.209123	
848	-0.499908	-0.543507	
202	-0.499908	0.209123	
300	-0.499908	0.334561	
...	...	...	
988	1.630962	0.710876	
322	-0.499908	-0.543507	
382	3.051541	-0.919822	
365	-0.499908	0.961753	
510	1.630962	-0.543507	

[709 rows x 5 columns]

```
[14]: dc = DummyClassifier()

[15]: dc_score = pd.DataFrame(cross_validate(dc, X_train, y_train, cv=5, return_train_score=True))

[16]: dc_score
```

	fit_time	score_time	test_score	train_score
0	0.000631	0.000400	0.401408	0.403880
1	0.000305	0.000305	0.401408	0.403880

```
2 0.000314    0.000233    0.401408    0.403880
3 0.000261    0.000215    0.408451    0.402116
4 0.000252    0.000210    0.404255    0.403169
```

```
[17]: svc = make_pipeline(preprocessor, SVC())
```

```
[18]: svc_score = pd.DataFrame(cross_validate(svc, X_train, y_train, cv=5,
                                             return_train_score=True))
```

```
[19]: svc_score
```

```
[19]:   fit_time  score_time  test_score  train_score
0  0.006774    0.002788    0.725352    0.707231
1  0.006165    0.002624    0.676056    0.719577
2  0.005901    0.002521    0.718310    0.719577
3  0.005892    0.002555    0.711268    0.708995
4  0.005446    0.002316    0.659574    0.727113
```

### 4.3.3 Hyperparameter tuning

Because we are attempting to classify clinical risk levels, we selected recall score as the preferred evaluation metric. This is because recall score measures the percentage correctly identified of actual high-risk pregnancies. This is critical for maternal health prediction where false negatives could result in missing high-risk, vulnerable individuals. Although prioritizing recall could increase the rate of false positive errors, it is the safer choice in this context.

```
[20]: svc_score = pd.DataFrame(cross_validate(svc, X_train, y_train, cv=5,
                                             return_train_score=True, scoring="recall_weighted"))
```

```
[21]: svc_score
```

```
[21]:   fit_time  score_time  test_score  train_score
0  0.006638    0.003394    0.725352    0.707231
1  0.005858    0.003036    0.676056    0.719577
2  0.005968    0.003039    0.718310    0.719577
3  0.005742    0.003326    0.711268    0.708995
4  0.005789    0.003167    0.659574    0.727113
```

```
[22]: param_grid = {
    "svc_C": loguniform(1e-2, 1e3),
    "svc_gamma": loguniform(1e-4, 1e1)
}
```

```
[23]: random_search = RandomizedSearchCV(svc,
                                         param_distributions=param_grid,
                                         n_iter=100,
                                         n_jobs=-1,
                                         return_train_score=True,
```

```

        cv=10,
        scoring='recall_weighted',
        random_state=123)

random_search.fit(X_train, y_train)

```

```

[23]: RandomizedSearchCV(cv=10,
                         estimator=Pipeline(steps=[('columntransformer',
                           ColumnTransformer(transformers=[('standardscaler',
                           StandardScaler(),
                           ['Age',
                           'SystolicBP',
                           'BS',
                           'BodyTemp',
                           'HeartRate'])])),
                           ('svc', SVC()))]),
                         n_iter=100, n_jobs=-1,
                         param_distributions={'svc__C':
<scipy.stats._distn_infrastructure.rv_continuous_frozen object at 0x3050b7380>,
                           'svc__gamma':
<scipy.stats._distn_infrastructure.rv_continuous_frozen object at 0x305a8ae90>},
                           random_state=123, return_train_score=True,
                           scoring='recall_weighted')

```

```
[24]: random_search.best_score_
```

```
[24]: np.float64(0.7629979879275655)
```

```

[25]: result_grid = pd.DataFrame(random_search.cv_results_)
result_grid = result_grid[
    [
        "mean_test_score",
        "param_svc__gamma",
        "param_svc__C",
        "mean_fit_time",
        "rank_test_score",
    ]
].set_index("rank_test_score").sort_index().T.iloc[:, :10]

result_grid

```

	1	2	3	4	5	\
rank_test_score						
mean_test_score	0.762998	0.760221	0.755956	0.753159	0.751771	
param_svc__gamma	1.615660	8.282366	1.280916	2.749691	9.479652	
param_svc__C	422.340226	323.263643	198.127782	21.103877	33.480671	
mean_fit_time	0.013005	0.012636	0.010105	0.008967	0.009363	

	6	7	8	9	10
rank_test_score	6	7	8	9	10
mean_test_score	0.734849	0.733400	0.730624	0.729215	0.720644
param_svc_gamma	1.571147	8.468353	2.134628	1.766684	0.265551
param_svc_C	34.953203	2.601185	10.080750	14.859520	801.347695
mean_fit_time	0.014226	0.012603	0.008903	0.012903	0.025342

```
[26]: plt.figure(figsize=(12, 5))
sns.heatmap(result_grid,
            annot=True,
            fmt='.3f',
            cmap='viridis',
            cbar_kws={'label': 'Value'},
            linewidths=0.5,
            linecolor='gray')

plt.title('Top 10 SVC Hyperparameter Combinations', fontsize=14, pad=20)
plt.xlabel('Rank', fontsize=12)
plt.ylabel('Parameter/Metric', fontsize=12)
plt.tight_layout()
plt.show()
```

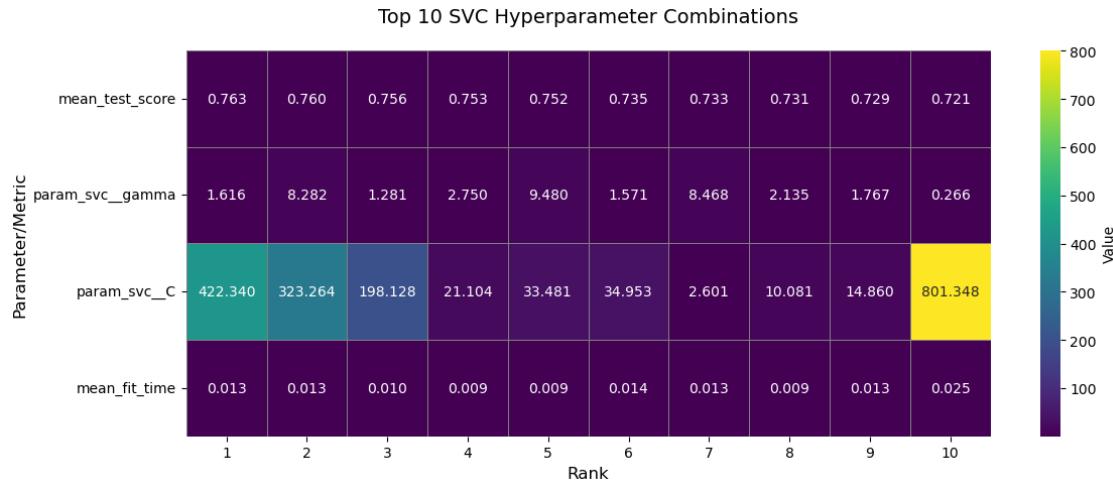


Figure 2. Results from hyperparameter optimization and 10-fold cross validation to choose gamma and C. Recall score was used as the classification metric as gamma and C was varied.

```
[27]: accuracy_score = random_search.score(
    X_test, y_test
)
```

```
[28]: accuracy_score
```

```
[28]: 0.7836065573770492
```

```
[29]: maternal_preds = X_test.assign(
    predicted=random_search.best_estimator_.predict(X_test)
)

# Add the actual labels
maternal_preds['actual'] = y_test.values

# Compute recall score (weighted for multi-class)
recall = recall_score(
    maternal_preds['actual'],
    maternal_preds['predicted'],
    average='weighted'
)
```

```
[30]: recall
```

```
[30]: 0.7836065573770492
```

```
[31]: pd.crosstab(
    maternal_preds["actual"],
    maternal_preds["predicted"],
)
```

```
[31]:   predicted    high risk   low risk   mid risk
  actual
  high risk        74         2        11
  low risk         4        95        21
  mid risk         9        19        70
```

```
[32]: confmat_logreg_bal = ConfusionMatrixDisplay.from_predictions(
    y_test,
    random_search.best_estimator_.predict(X_test),
    #normalize='all'
)
confmat_logreg_bal.ax_.set_title('Confusion Matrix - Test Data', fontsize=14, u
    ↪fontweight='bold')
```

```
[32]: Text(0.5, 1.0, 'Confusion Matrix - Test Data')
```

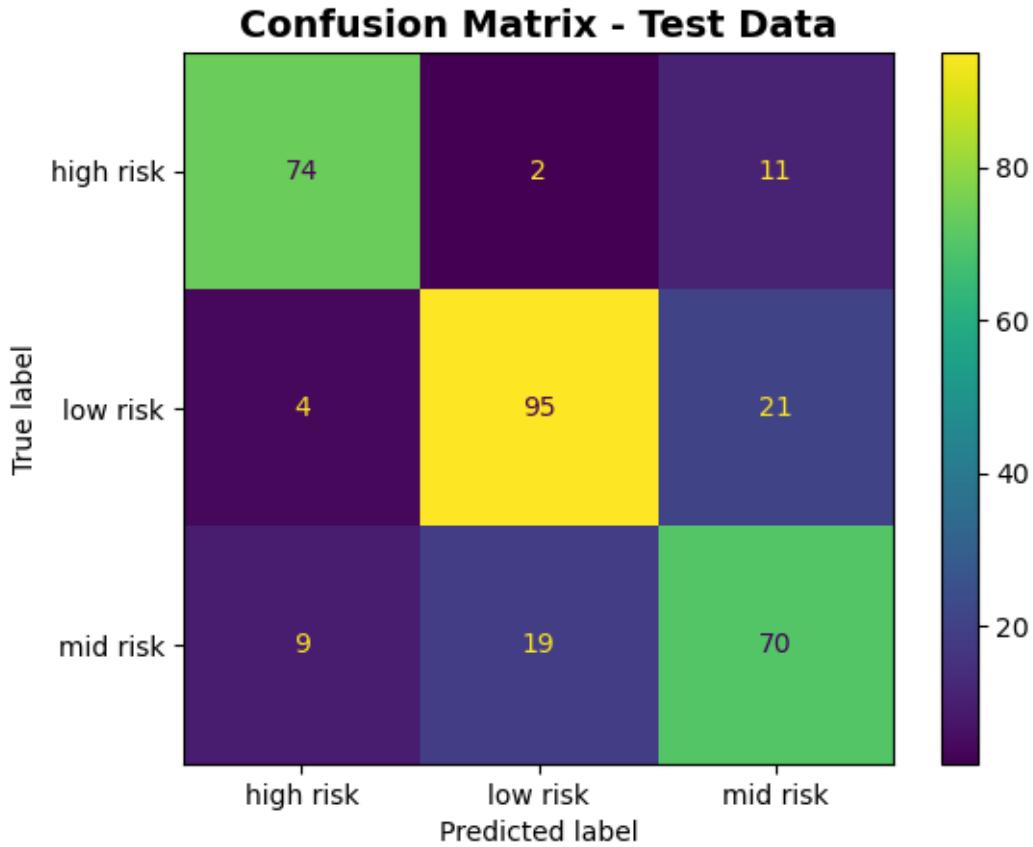


Figure 3. Confusion matrix of model performance on test data.

```
[33]: y_score = random_search.best_estimator_.decision_function(X_test)
svc_classes = random_search.best_estimator_.named_steps['svc'].classes_
y_test_bin = label_binarize(y_test, classes=svc_classes)
fig, ax = plt.subplots(figsize=(6, 8))

for i, class_name in enumerate(svc_classes):
    auc = roc_auc_score(y_test_bin[:, i], y_score[:, i])
    RocCurveDisplay.from_predictions(
        y_test_bin[:, i],
        y_score[:, i],
        name=f'{class_name} (AUC = {auc:.3f})',
        ax=ax
    )
    print(f'{class_name}: AUC = {auc:.3f}")
```

```
high risk: AUC = 0.952
low risk: AUC = 0.885
mid risk: AUC = 0.854
```

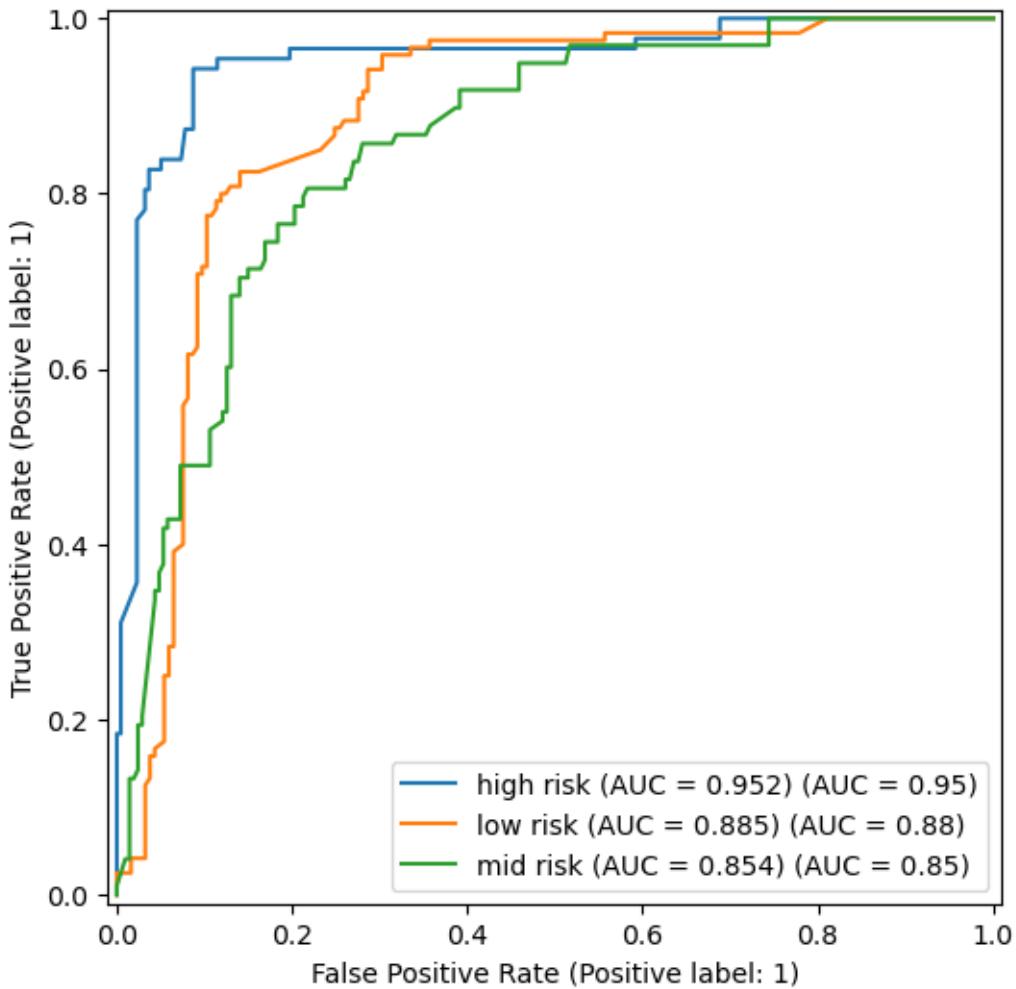


Figure 4. ROC curve of model performance on test data.

#### 4.3.4 Summary of Model Results

The final SVC classifier performed fairly well on an unseen test data set, with a weighted recall score of 0.77 and an overall accuracy of 0.77. Out of the 305 test data cases, it correctly predicted 235 cases. The model showed particularly strong performance in identifying high-risk pregnancies, achieving an AUV of 0.943 for the high-risk class, compared to 0.820 for low-risk class and 0.814 for medium-risk class. It correctly identifies 74 out of 87 actual high-risk pregnancies resulting in a 85% recall for high risk. The 13 notable errors were true high-risk cases were misclassified as 11 medium-risk and 2 low-risk. These false negatives are gaps where high-risk individuals may not receive the necessary care. We recommend further research to improve the model's sensitivity to high-risk cases and better differentiate between medium and low-risk categories before it is ready to be put into production in clinical settings.

#### 4.4 References

- A.B.M. Sharif Hossain, Siddique, A., Jabeen, S., Khan, S., M Moinuddin Haider, Ameen, S., Tazeen Tahsina, Chakraborty, N., Nahar, Q., Jamil, K., Shams El Arifeen, & Ahmed Ehsanur Rahman. (2023). Maternal mortality in Bangladesh: Who, when, why, and where? A national survey-based analysis. *Journal of Global Health*, 13. <https://doi.org/10.7189/jogh.13.07002>
- Ahmed, M., Kashem, M. A., Rahman, M., & Khatun, S. (2020). Review and Analysis of Risk Factor of Maternal Health in Remote Area Using the Internet of Things (IoT). *Lecture Notes in Electrical Engineering*, 357–365. [https://doi.org/10.1007/978-981-15-2317-5\\_30](https://doi.org/10.1007/978-981-15-2317-5_30)
- Hassfurter, K. (2025, April 6). Trends in maternal mortality 2000 to 2023 - UNICEF DATA. UNICEF DATA. <https://data.unicef.org/resources/trends-in-maternal-mortality-2000-to-2023/>
- Souza, J. P., Day, L., Rezende-Gomes, A. C., Zhang, J., Mori, R., Baguiya, A., Jayaratne, K., Osoti, A., Vogel, J. P., Campbell, R., Mugerwa, K., Lumbiganon, P., Tunçalp, ., Cresswell, J. A., Say, L., Moran, A. C., & Oladapo, O. T. (2023). A Global Analysis of the Determinants of Maternal Health and Transitions in Maternal Mortality. *The Lancet Global Health*, 12(2). [https://doi.org/10.1016/s2214-109x\(23\)00468-0](https://doi.org/10.1016/s2214-109x(23)00468-0)