Predicting risk factors for maternal mortality

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In [1]:
```
import numpy as np
import pandas as pd
import requests
import zipfile
import json
import logging
import pandera.pandas as pa
import altair as alt
import matplotlib.pyplot as plt
import seaborn as sns
from pandera import Column, Check
from deepchecks.tabular import Dataset
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, Confusic
```

```
/opt/conda/envs/dockerlock/lib/python3.12/site-packages/deepchecks/core/seri
alization/dataframe/html.py:16: UserWarning:

pkg_resources is deprecated as an API. See https://setuptools.pypa.io/en/lat
est/pkg_resources.html. The pkg_resources package is slated for removal as e
arly as 2025-11-30. Refrain from using this package or pin to Setuptools<81.
```

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.

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.

Methods

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.

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

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.

Results & Discussion

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 distibutions were visually distinct across risk levels. Thus, we continued to fit our model with the remaining features.

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

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")
```

In [3]:
```
health_data = pd.read_csv("../data/raw/Maternal Health Risk Data Set.csv", h
health_data
```

Out[3]:

	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 × 7 columns

Data Validation

Validation Ranges

For `Age`, we chose a validation range of 10-65 years. The lower limit of 10 accounts for rare cases of very early pregnancy, though pregnancies below the age of 15 are generally medically concerning. The upper limit of 65 represents the maximum biologically feasible range for pregnancy, though pregnancies beyond menopause are extremely rare and would usually require medical intervention. In very rare cases, values outside this range may occur but we can consider them extreme outliers, not suitable for our prediction task.

For `SystolicBP`, we chose a validation range of 60-200 mmHg. Systolic blood pressure below 60 mmHg indicates severe hypotension, whereas systolic blood pressure above 200 mmHg indicates severe hypertension, both of which are life-threatening emergencies requiring immediate medical intervention. Since our model aims to classify routine maternal health risk levels, values outside the validation range are outside the scope of our classification model and would be considered outliers.

For `DiastolicBP`, we chose a validation range of 40-140 mmHg. Diastolic blood pressure below 40 mmHg indicates severe hypotension, whereas diastolic blood pressure above 140 mmHg indicates severe hypertension, both of which are life-threatening emergencies requiring immediate medical intervention. Since our model aims to classify routine maternal health risk levels, values outside the validation range are outside the scope of our classification model and would be considered outliers.

For `BS`, we chose a validation range of 1-25 mmol/L. Blood sugar below 1 mmol/L indicates severe hypoglycemia, whereas blood sugar above 25 mmol/L indicates severe hyperglycemia. Both of these are life-threatening emergencies requiring immediate hospitalization and can therefore be considered unsuitable for our predictive model.

For `BodyTemp`, we chose a validation range of 95.0-105.0°F. Body temperature below 95.0°F indicates severe hypothermia, whereas body temperature above 105.0°F indicates severe hyperthermia. Both of these are life-threatening emergencies requiring immediate hospitalization and can therefore be considered as unsuitable for our predictive model.

For `HeartRate`, we chose a validation range of 50-150 bpm. A resting heart rate below 50 bpm or above 150 bpm suggests potential cardiovascular problems requiring immediate medical intervention. Neither of the extreme values is compatible with normal maternal health assessment, and such values can be considered outliers.

The target variable `RiskLevel` is a categorical variable representing the maternal health risk classification based on clinical assessment. Each observation must contain exactly one of these three risk levels: `low risk`, `mid risk` and `high risk`.

In [4]:
```
def validate_file_format(file_path, expected_file_extension):
    """
    Function to check if the file has the correct format,
    given the file path and expected file extension.
    """
    if not file_path.endswith(expected_file_extension):
        error_msg = "Invalid file format."
        raise ValueError(error_msg)

expected_file_extension = ".csv"
file_path = "data/raw/Maternal Health Risk Data Set.csv"
```

In [5]:
```
def validate_column_names(data, expected_columns):
    """
    Function to check if the DataFrame has the correct column names,
    given the DataFrame and the expected column names.
    """
    actual_columns = data.columns.tolist()

    missing_columns = set(expected_columns) - set(actual_columns)
    if missing_columns:
        error_msg = "Missing required columns."
        raise ValueError(error_msg)

    extra_columns = set(actual_columns) - set(expected_columns)
    if extra_columns:
        error_msg = "Unexpected extra columns found."
        raise ValueError(error_msg)

expected_columns = ["Age", "SystolicBP", "DiastolicBP", "BS", "BodyTemp", "H
```

In [6]:

```
# Code reference: https://github.com/skysheng7/DSCI522_data_validation_demo/

# Configure logging
logging.basicConfig(
    filename="validation_errors.log",
    filemode="w",
    format="%(asctime)s - %(message)s",
    level=logging.INFO,
)

# Define the schema
schema = pa.DataFrameSchema(
    {
        # check for correct category labels
        "RiskLevel": pa.Column(str, pa.Check.isin(["low risk", "mid risk", "
        # check for outliers and anomalous values
        "Age": pa.Column(int, pa.Check.between(10, 65), nullable=True),
        "SystolicBP": pa.Column(int, pa.Check.between(60, 200), nullable=Tru
        "DiastolicBP": pa.Column(int, pa.Check.between(40, 140), nullable=Tr
        "BS": pa.Column(float, pa.Check.between(1.0, 25.0), nullable=True),
        "BodyTemp": pa.Column(float, pa.Check.between(95.0, 105.0), nullable
        "HeartRate": pa.Column(int, pa.Check.between(50, 150), nullable=True
    },
    checks=[
        # check for duplicate rows and empty rows
        pa.Check(lambda df: ~df.duplicated().any(), error="Duplicate rows fo
        pa.Check(lambda df: ~(df.isna().all(axis=1)).any(), error="Empty row
        # check for Missingness not beyond expected threshold
        pa.Check(lambda df: (df.isna().mean() <= 0.05).all(), error="Some co
        # check for label imbalance in target variable
        pa.Check(
            lambda df: (df["RiskLevel"].value_counts(normalize=True) >= 0.05
            error="One or more RiskLevel categories have <5% of observations
        ),

        # make sure there is no column with constant values
        pa.Check(
            lambda df: df[["Age", "SystolicBP", "DiastolicBP", "BS",
                          "BodyTemp", "HeartRate"]].nunique().min() > 1,
            error="One or more features have no variation.",
        ),
    ],
    drop_invalid_rows=False,
)

# Initialize error cases DataFrame
error_cases = pd.DataFrame()
data = health_data.copy()

# Validate data and handle errors: correct file format, correct column names
try:
    validate_file_format(file_path, expected_file_extension)
    validate_column_names(data, expected_columns)
except ValueError as e:
    # Convert the error message to a JSON string
    error_message = json.dumps(str(e), indent=2)
    logging.error("\n" + error_message)

# Validate data and handle errors: no empty observations, missingness not be
# correct data types for columns, no outliers, correct category levels
try:
    validated_data = schema.validate(data, lazy=True)
except pa.errors.SchemaErrors as e:
    error_cases = e.failure_cases

    # Convert the error message to a JSON string
    error_message = json.dumps(e.message, indent=2)
    logging.error("\n" + error_message)

# Filter out invalid rows based on the error cases: keep the duplicate rows
if not error_cases.empty:
    invalid_indices = error_cases["index"].dropna().unique()
    validated_data = (
        data.drop(index=invalid_indices)
        .reset_index(drop=True)
        .dropna(how="all")
    )
else:
    validated_data = data
```

To ensure that the target variable is not severely imbalanced, we applied a minimum class frequency check (at least 5% per class). This avoids situations where certain risk levels are too rare for the model to learn meaningful patterns, which could lead to biased predictions.

In [7]:
```
print("Data shape before validation:")
print(data.shape)

print("Data shape after validation:")
print(validated_data.shape)
```

```
Data shape before validation:
(1014, 7)
Data shape after validation:
(1010, 7)
```

Data Validation Results

We dropped 4 observations during our preliminary data validation, as these rows contain invalid data entires that would introduce noise into our model. More details about which observations have been dropped can be found under `validation_errors.log` in the `notebooks` folder.

The validation log shows that the dropped observations include:

- 2 rows with `Age` outside the expected range (10-65 years): ages 66 and 70
- 2 rows with `HeartRate` of 7 bpm, which seems an impossibility for living people

Duplicate Observations

We have retained the 562 duplicate rows found in our data validation checks. Since the original data set lacks unique patient identifiers (no patient ID or timestamp), we cannot definitely determine whether these duplicates represent the same patient measured multiple times or different patients with identical measurements. Given this uncertainty and the substantial dataset reduction that would result from removing the duplicates, we opted to keep all duplicate rows and only remove observations that clearly fail other data validation checks.

The dataset passed all other validation checks, namely:

- Correct data file format
- Correct column names
- No empty observations
- Missingness not beyond expected threshold: all columns have <5% missing values (threshold = 0.05)
- Correct data types in each column
- Correct category levels: all categorical values match expected levels
- No outliers: all numeric values fall within reasonable ranges (with the exception of the 4 dropped rows)
- Target/response variable follows expected distribution

Our final validated dataset `validated_data` contains 1,010 observations.

In [8]:
```
health_data.describe()
```

Out[8]:

	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	76.000000
75%	39.000000	120.000000	90.000000	8.000000	98.000000	80.000000
max	70.000000	160.000000	100.000000	19.000000	103.000000	90.000000

In [9]:
```
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
```

Split Data

In [10]:
```
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")
```

In [11]:
```
train_df
```

Out[11]:

	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 × 7 columns

In [12]:
```
test_df
```

Out[12]:

	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

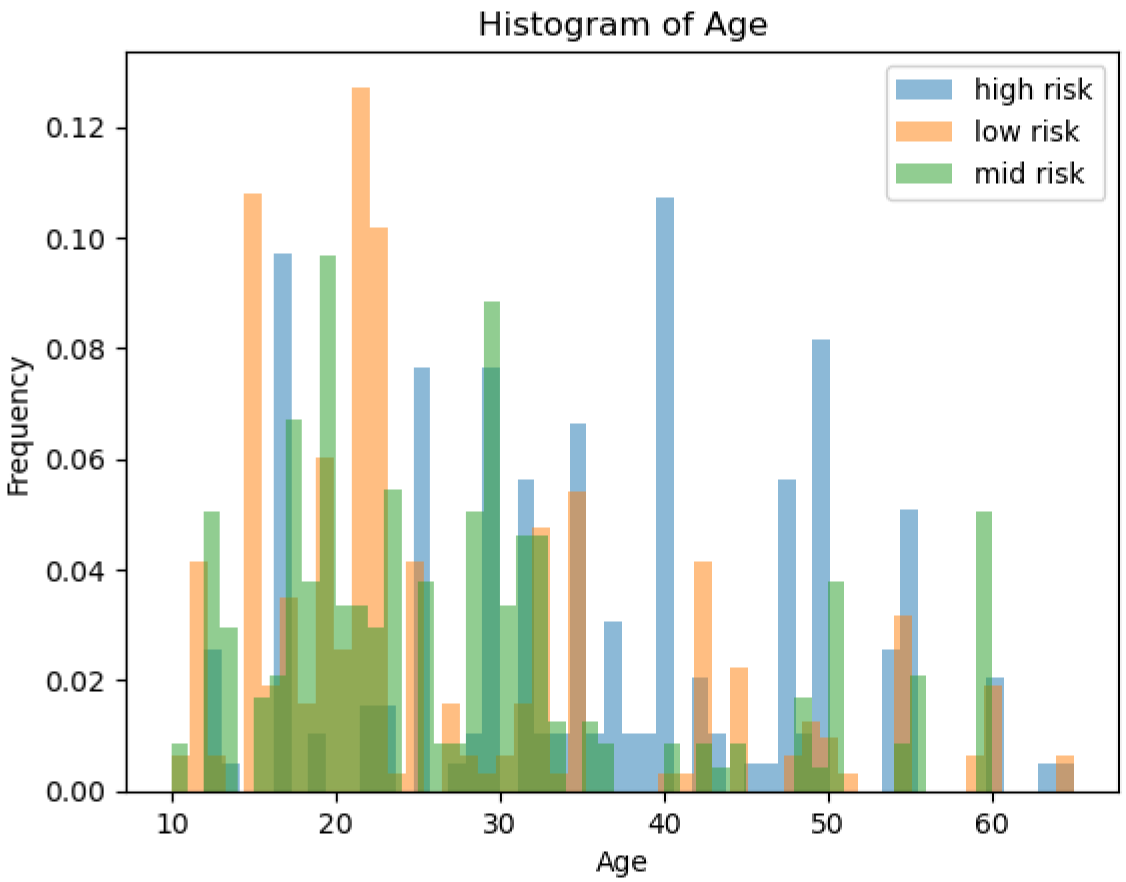
305 rows × 7 columns

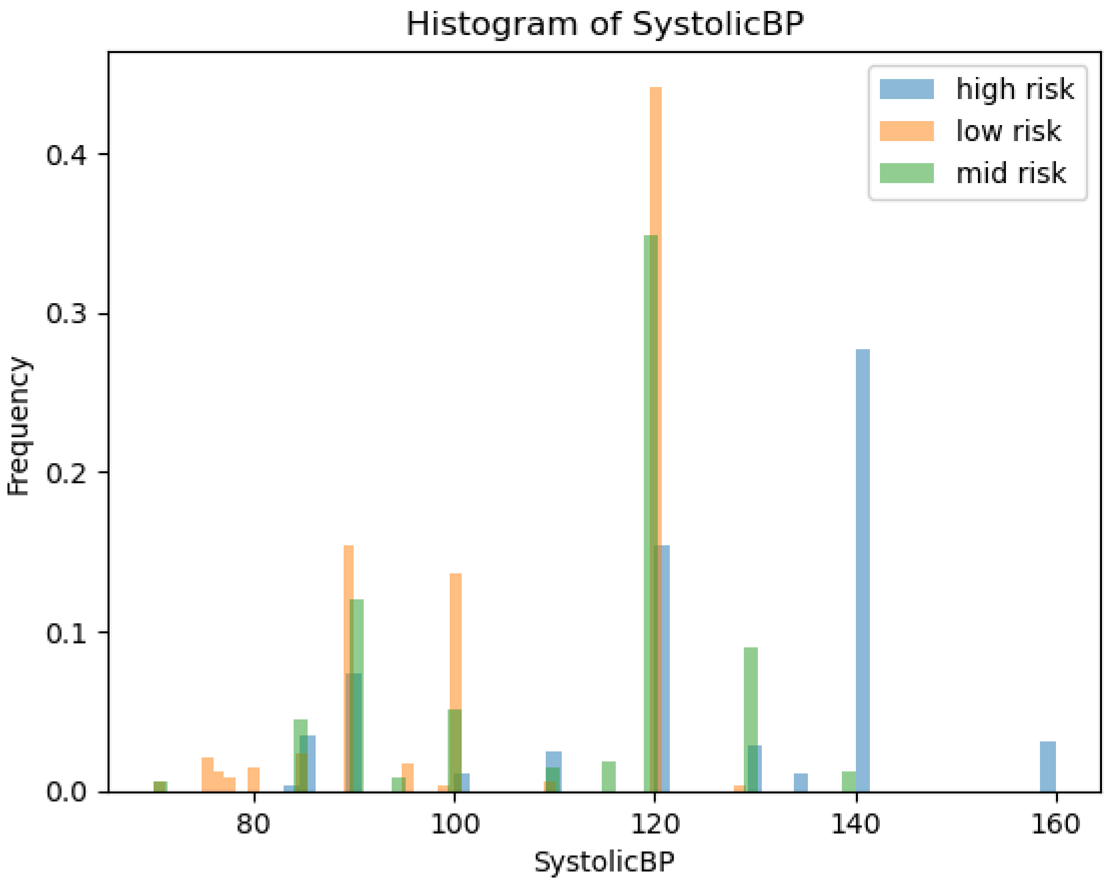
In [13]:
```
y_train.value_counts()
```

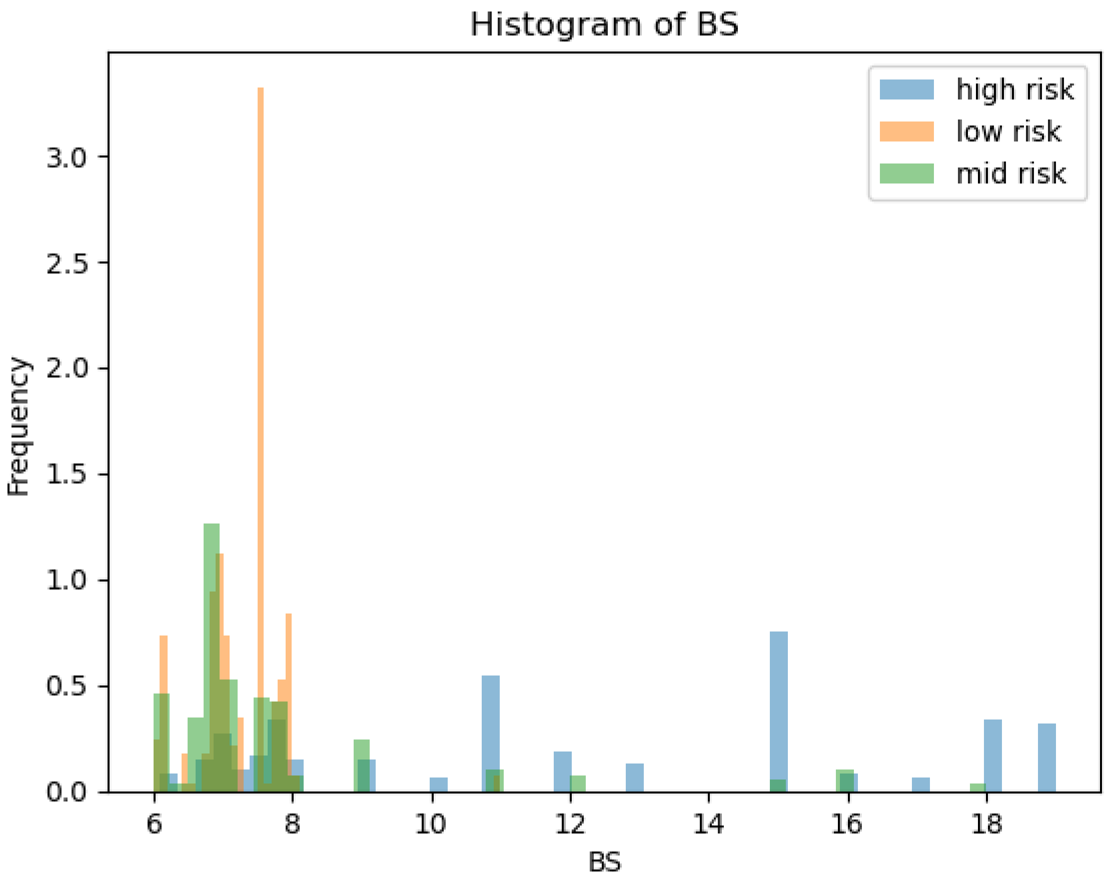
Out[13]:
```
RiskLevel
low risk     286
mid risk     238
high risk    185
Name: count, dtype: int64
```

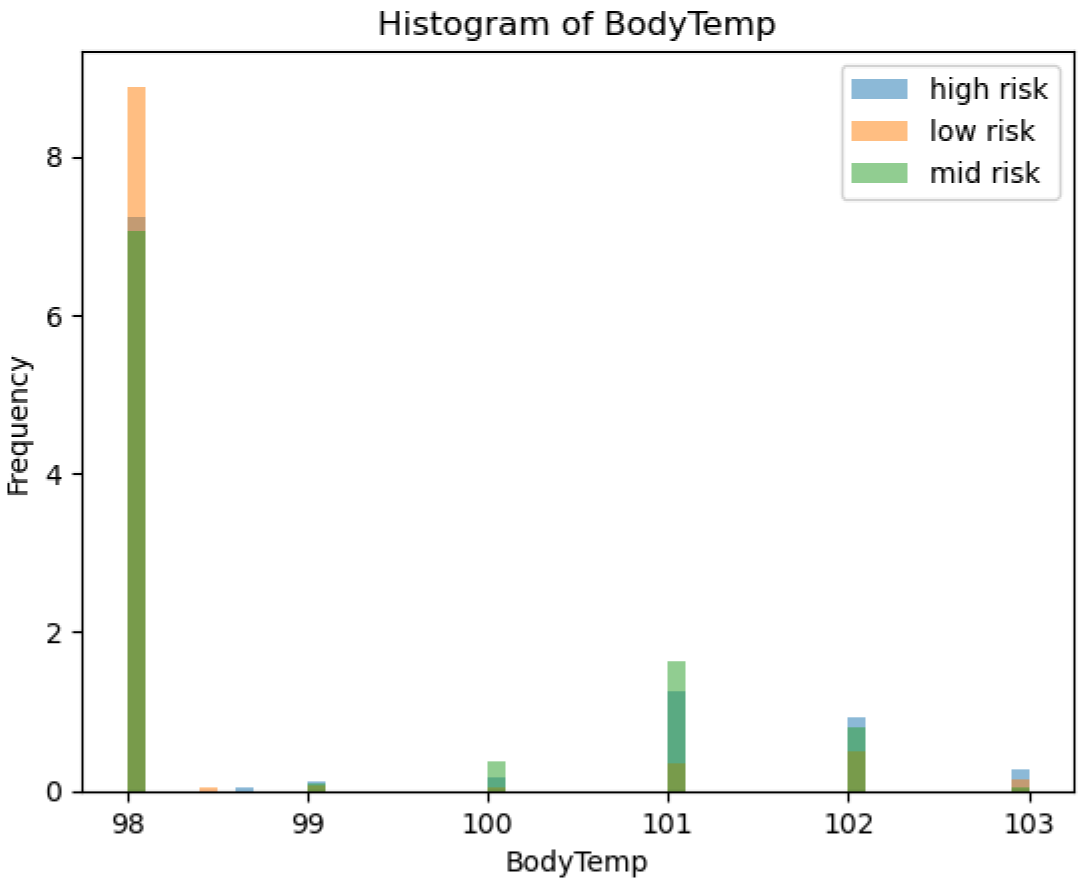
In [14]:
```
feature_cols = ["Age", "SystolicBP", "BS", "BodyTemp", "HeartRate"]

for feature in feature_cols:
    train_df.groupby("RiskLevel")[feature].plot.hist(bins=50, alpha=0.5, leg
    plt.xlabel(feature);
    plt.show()
```


Histogram of Age
high risk
low risk
mid risk
Frequency
0.00
0.02
0.04
0.06
0.08
0.10
0.12
10
20
30
40
50
60
Age


Histogram of SystolicBP
high risk
low risk
mid risk
Frequency
0.0
0.1
0.2
0.3
0.4
80
100
120
140
160
SystolicBP


Histogram of BS
high risk
low risk
mid risk
Frequency
0.0
0.5
1.0
1.5
2.0
2.5
3.0
6
8
10
12
14
16
18
BS


Histogram of BodyTemp
high risk
low risk
mid risk
Frequency
0
2
4
6
8
98
99
100
101
102
103
BodyTemp

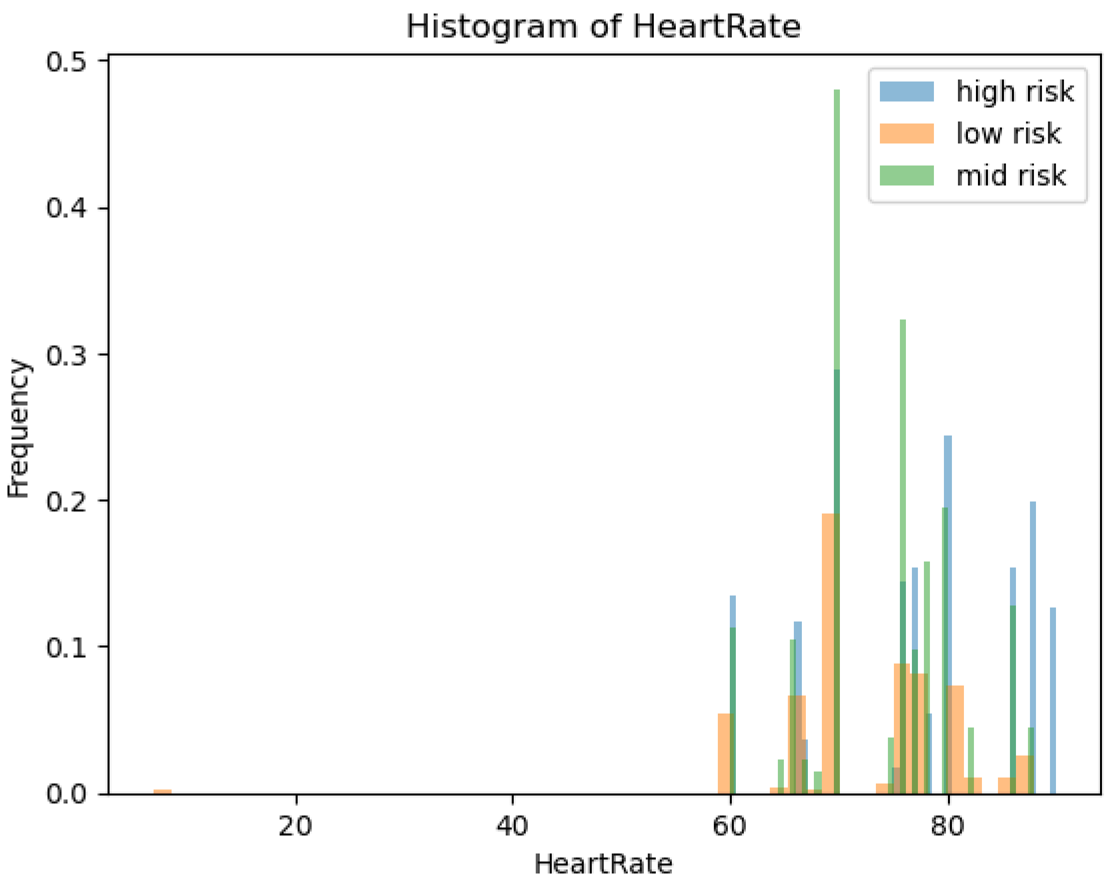


Figure 1. Comparison of the distributions of features contributing to the risk intensity level during pregnancy of an individual.

Data Validation - Correlations

In [15]:
```
# Code reference: https://ubc-dsci.github.io/reproducible-and-trustworthy-wo
from deepchecks.tabular import Dataset

mh_train_ds = Dataset(train_df, label="RiskLevel", cat_features=[])
```

Target-Feature Correlation

In [16]:
```
from deepchecks.tabular.checks import FeatureLabelCorrelation


check_feat_lab_corr = FeatureLabelCorrelation().add_condition_feature_pps_le
check_feat_lab_corr_result = check_feat_lab_corr.run(dataset=mh_train_ds)
```

In [17]:
```
# if deepchecks can not be use, use pandera for a similar but simplified tes
RISK_MAP = {"low risk": 0, "mid risk": 1, "high risk": 2}

corr_schema = pa.DataFrameSchema(
    {
        "Age": pa.Column(int),
        "SystolicBP": pa.Column(int),
        "DiastolicBP": pa.Column(int),
        "BS": pa.Column(float),
        "BodyTemp": pa.Column(float),
        "HeartRate": pa.Column(int),
        "RiskLevel": pa.Column(str),
    },
    checks=[
        # Feature–Label correlation check
        Check(
            lambda df: (
                # convert RiskLevel to integers(0–2)
                df.assign(
                    RiskNum=df["RiskLevel"].map(RISK_MAP)
                )
                # Compute correlations with all numeric features, Find the h
                # Fail validation if any feature has absolute correlation la
                .corr(numeric_only=True)["RiskNum"]
                .drop("RiskNum")
                .abs()
                .max()
                < 0.9
            ),
            error="One or more features have correlation ≥ 0.9 with the targ
        )
    ]
)
validated_df = corr_schema.validate(train_df, lazy=True)
```

Feature-Feature Correlation

In [18]:
```
from deepchecks.tabular.checks.data_integrity import FeatureFeatureCorrelati

feat_feat_check = (
    FeatureFeatureCorrelation()
    .add_condition_max_number_of_pairs_above_threshold(
        0.9,
        0
    )
)

feat_feat_result = feat_feat_check.run(dataset=mh_train_ds)

if not feat_feat_result.passed_conditions():
    raise ValueError(
        "Too many highly correlated feature pairs (possible redundancy or le
    )
```

Data Validation Results

To ensure that our predictive modeling process does not rely on spurious or overly strong relationships, we performed two correlation-based data validation checks on the training split only (to avoid test-set leakage):

1. Target–Feature Correlation Check

We applied the FeatureLabelCorrelation check from Deepchecks (used Pandera for a similar test if Deepchecks can't be used). This check evaluates whether any feature has an strong relationship with the target variable (RiskLevel), which could be a sign of target leakage. Threshold used: correlation < 0.9

Result: All features met the threshold. No anomalous or suspiciously high correlations were detected between features and the target.

2. Feature–Feature Correlation Check

We also used Deepchecks' FeatureFeatureCorrelation` to check for unusually high correlations between pairs of features, which may indicate redundancy or multicolinearity in modeling.

Result: Feature–feature correlations met the threshold. No pairs of features exhibited extremely high correlation that would require removal or special handling.

Overall Conclusion

Both correlation checks passed. There were no failing rows, and no features required modification or exclusion based on these validation steps. This suggests that the dataset has no correlation-based anomalies, and is appropriate for next step of model training.

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.

In [19]:
```
preprocessor = make_column_transformer(
    (StandardScaler(), feature_cols)
)
```

In [20]:
```
preprocessor.fit(X_train)
```

Out[20]:
```
▸ ColumnTransformer

▸ standardscaler

  ▸ StandardScaler
```

In [21]:
```
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
```

Out[21]:

	standardscaler__Age	standardscaler__SystolicBP	standardscaler__BS	standard
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	

709 rows × 5 columns

In [22]:
```
dc = DummyClassifier()
```

In [23]:
```
dc_score = pd.DataFrame(cross_validate(dc, X_train, y_train, cv=5, return_tr
```

In [24]:
```
dc_score
```

Out[24]:

	fit_time	score_time	test_score	train_score
0	0.000626	0.000955	0.401408	0.403880
1	0.000643	0.000422	0.401408	0.403880
2	0.001160	0.000690	0.401408	0.403880
3	0.000555	0.000367	0.408451	0.402116
4	0.000573	0.000357	0.404255	0.403169

In [25]:
```
svc = make_pipeline(preprocessor, SVC())
```

In [26]:
```
svc_score = pd.DataFrame(cross_validate(svc, X_train, y_train, cv=5, return_
```

In [27]:
```
svc_score
```

Out[27]:

	fit_time	score_time	test_score	train_score
0	0.013078	0.005012	0.725352	0.707231
1	0.007420	0.002907	0.676056	0.719577
2	0.008188	0.002903	0.718310	0.719577
3	0.007219	0.002766	0.711268	0.708995
4	0.007020	0.002792	0.659574	0.727113

Hyperparameter tuning

Because we are attempting to classify clincal 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.

In [28]:
```
svc_score = pd.DataFrame(cross_validate(svc, X_train, y_train, cv=5, return_
```

In [29]:
```
svc_score
```

Out[29]:

	fit_time	score_time	test_score	train_score
0	0.008980	0.004968	0.725352	0.707231
1	0.007323	0.004081	0.676056	0.719577
2	0.007280	0.003856	0.718310	0.719577
3	0.007394	0.003653	0.711268	0.708995
4	0.006839	0.003526	0.659574	0.727113

In [30]:
```
param_grid = {
    "svc__C": loguniform(1e-2, 1e3),
    "svc__gamma": loguniform(1e-4, 1e1)
}
```

In [31]:
```
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)
```

```
/opt/conda/envs/dockerlock/lib/python3.12/multiprocessing/queues.py:122: Use
rWarning: pkg_resources is deprecated as an API. See https://setuptools.pyp
a.io/en/latest/pkg_resources.html. The pkg_resources package is slated for r
emoval as early as 2025-11-30. Refrain from using this package or pin to Set
uptools<81.
  return _ForkingPickler.loads(res)
/opt/conda/envs/dockerlock/lib/python3.12/multiprocessing/queues.py:122: Use
rWarning: pkg_resources is deprecated as an API. See https://setuptools.pyp
a.io/en/latest/pkg_resources.html. The pkg_resources package is slated for r
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  return _ForkingPickler.loads(res)
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rWarning: pkg_resources is deprecated as an API. See https://setuptools.pyp
a.io/en/latest/pkg_resources.html. The pkg_resources package is slated for r
emoval as early as 2025-11-30. Refrain from using this package or pin to Set
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/opt/conda/envs/dockerlock/lib/python3.12/multiprocessing/queues.py:122: Use
rWarning: pkg_resources is deprecated as an API. See https://setuptools.pyp
a.io/en/latest/pkg_resources.html. The pkg_resources package is slated for r
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```
a.io/en/latest/pkg_resources.html. The pkg_resources package is slated for r
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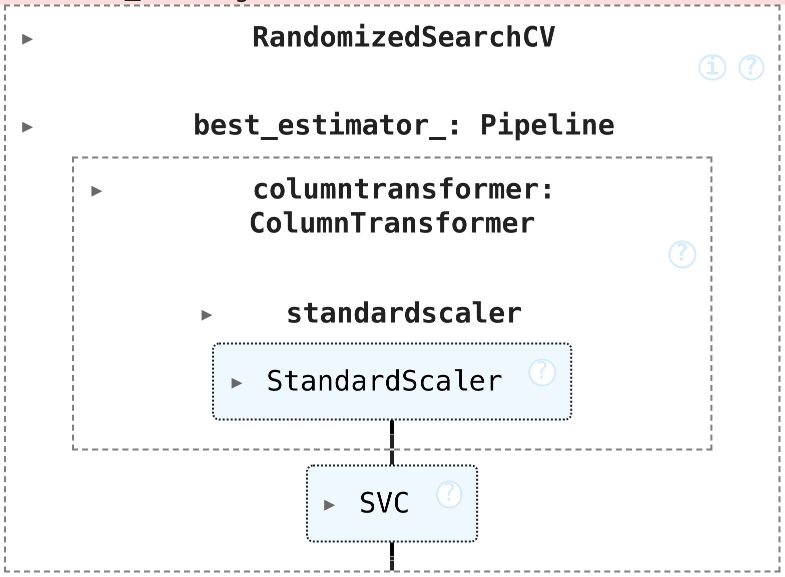
/opt/conda/envs/dockerlock/lib/python3.12/multiprocessing/queues.py:122: Use
rWarning: pkg_resources is deprecated as an API. See https://setuptools.pyp
a.io/en/latest/pkg_resources.html. The pkg_resources package is slated for r
emoval as early as 2025-11-30. Refrain from using this package or pin to Set
uptools<81.
  return _ForkingPickler.loads(res)
```

Out[31]:


▸ RandomizedSearchCV
▸ best_estimator_: Pipeline
▸ columntransformer: ColumnTransformer
▸ standardscaler
▸ StandardScaler
▸ SVC

In [32]:
```
random_search.best_score_
```

Out[32]:
```
0.7615895372233401
```

In [33]:
```
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
```

Out[33]:

rank_test_score	1	2	3	4	5	
mean_test_score	0.761590	0.760221	0.755956	0.753159	0.751771	0.73
param_svc__gamma	1.615660	8.282366	1.280916	2.749691	9.479652	1.5
param_svc__C	422.340226	323.263643	198.127782	21.103877	33.480671	34.95
mean_fit_time	0.017653	0.017338	0.016569	0.013986	0.017619	0.0

In [34]:

```
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()
```

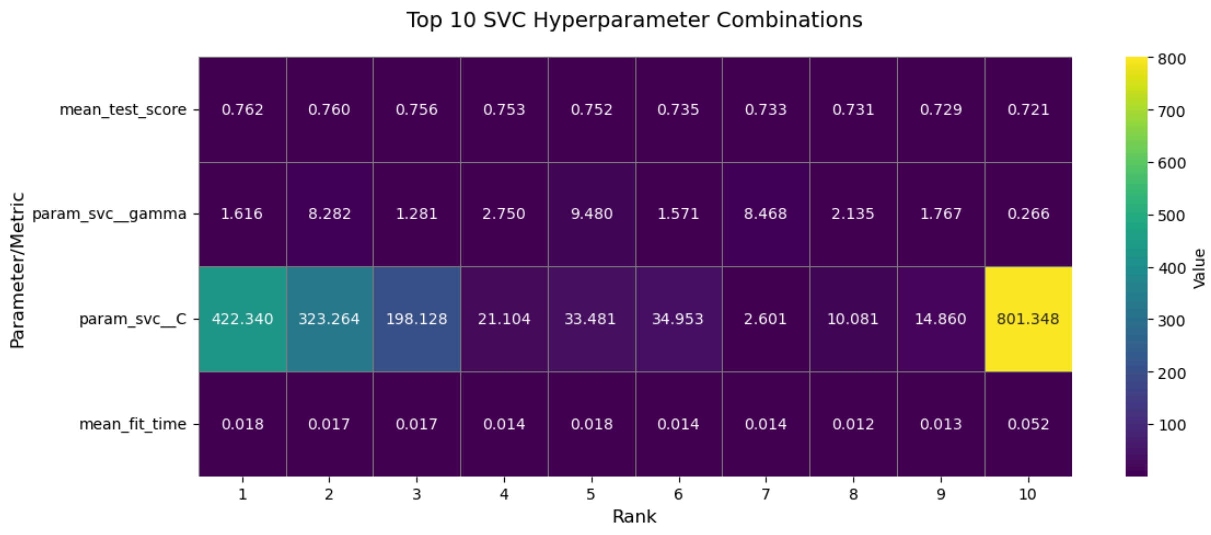


Figure 2. Results from hyperparameter optimization and 10-fold cross validation to choose gamma and C. Recall score was used as the classification metric as gamma and C was varied.

In [35]:
```
accuracy_score = random_search.score(
    X_test, y_test
)
```

In [36]:
```
accuracy_score
```

Out[36]:
```
0.7836065573770492
```

In [37]:
```
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'
)
```

In [38]:
```
recall
```

Out[38]:
```
0.7836065573770492
```

In [39]:
```
pd.crosstab(
    maternal_preds["actual"],
    maternal_preds["predicted"],
)
```

Out[39]:

predicted	high risk	low risk	mid risk
actual			
high risk	74	2	11
low risk	4	95	21
mid risk	9	19	70

In [40]:
```
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
```

Out[40]:
```
Text(0.5, 1.0, 'Confusion Matrix - Test Data')
```

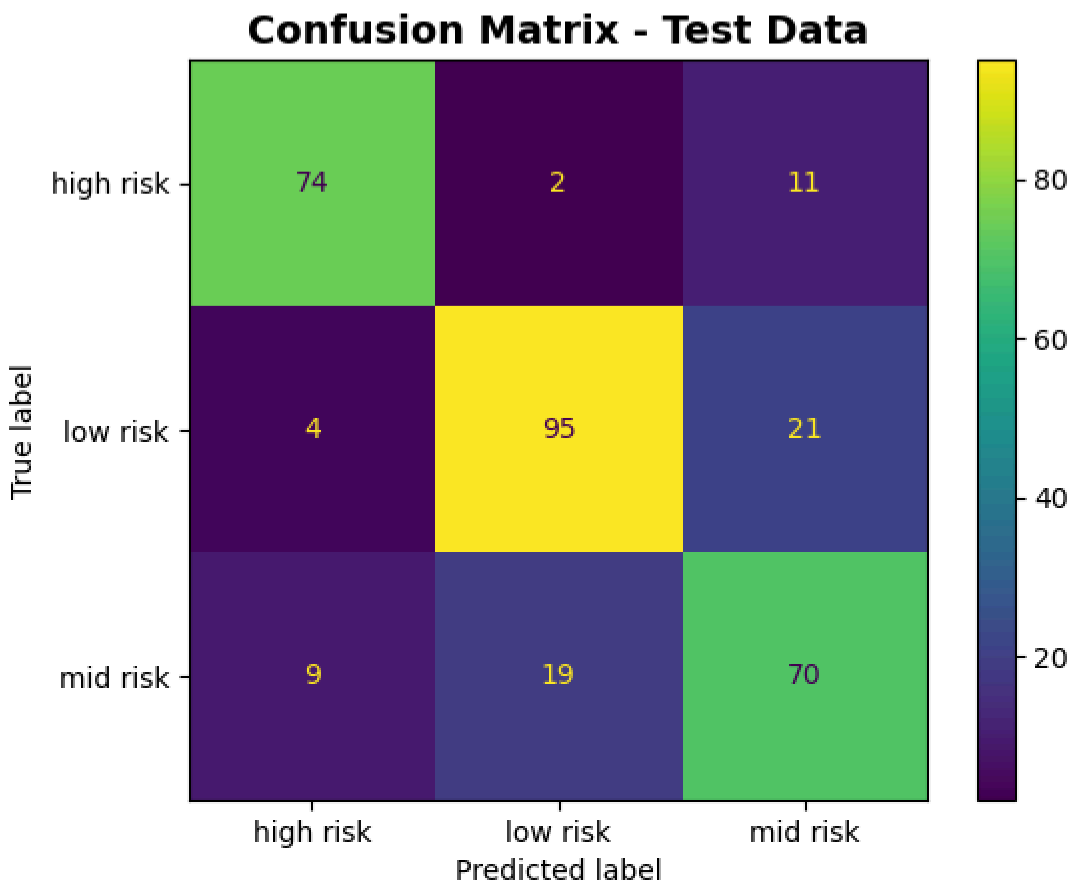


Figure 3. Confusion matrix of model performance on test data.

```
In [41]: 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 = 0.953
low risk: AUC = 0.884
mid risk: AUC = 0.858
```

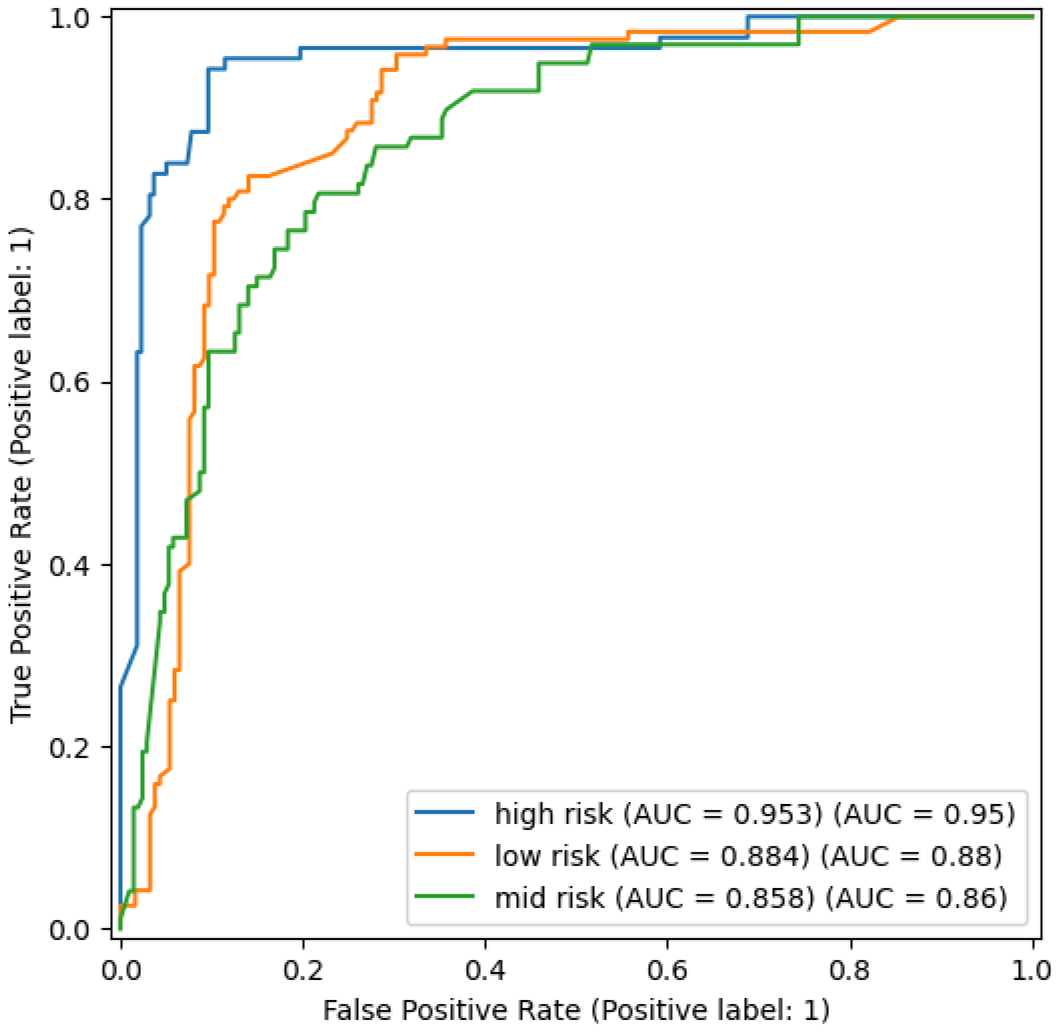


Figure 4. ROC curve of model performance on test data.

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.

References

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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, Ö., 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

```
In [ ]:
```