


```
# Libraries for EDA
import pandas as pd
import missingno as msno
import seaborn as sns
import numpy as np
import matplotlib.pyplot as plt
import xgboost as xgb
import plotly.express as px
import plotly.graph_objects as go
from plotly.offline import init_notebook_mode
init_notebook_mode(connected=True)

# Libraries for MLA
from sklearn.model_selection import train_test_split, cross_val_score
from sklearn.preprocessing import StandardScaler
from sklearn.metrics import accuracy_score

from sklearn import ensemble, tree, linear_model
from xgboost import XGBClassifier
from catboost import CatBoostRegressor
from catboost import CatBoostClassifier
from sklearn.ensemble import VotingClassifier
```



```
# Upload the dataset and viewing the pandas
df = pd.read_csv('/content/drive/MyDrive/Colab Datasets/Maternal_Health_Risk_DataSet.csv')
df.head()
```

	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	

```
# Variables Dtype
df.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

```

```

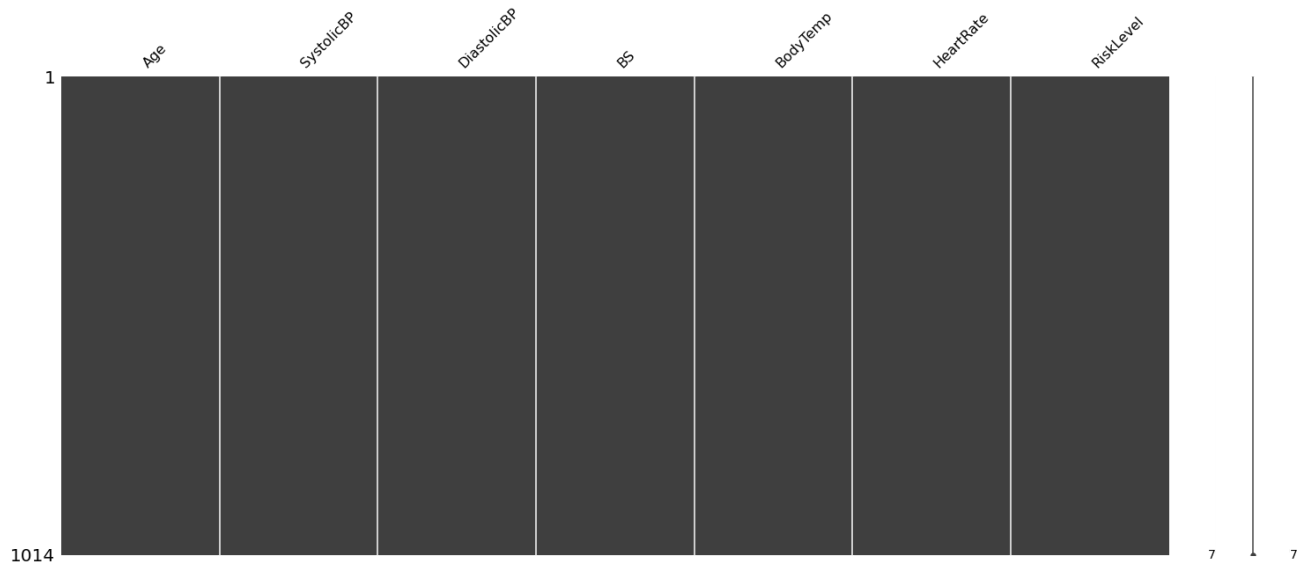
# Missing data with missing no visualization
msno.matrix(df)

```

```

<matplotlib.axes._subplots.AxesSubplot at 0x7f7afe158c90>

```



```

# Risk level values (only for object dtype in df)
df.RiskLevel.value_counts()

```

```

low risk      406
mid risk      336
high risk     272
Name: RiskLevel, dtype: int64

```

```

# Replace RiskLevel column values with integers to make a pairplot visualization
df['RiskLevel'] = df['RiskLevel'].replace({'low risk':1, 'mid risk': 2, 'high risk': 3})
df['RiskLevel']= df['RiskLevel'].astype('int')

```

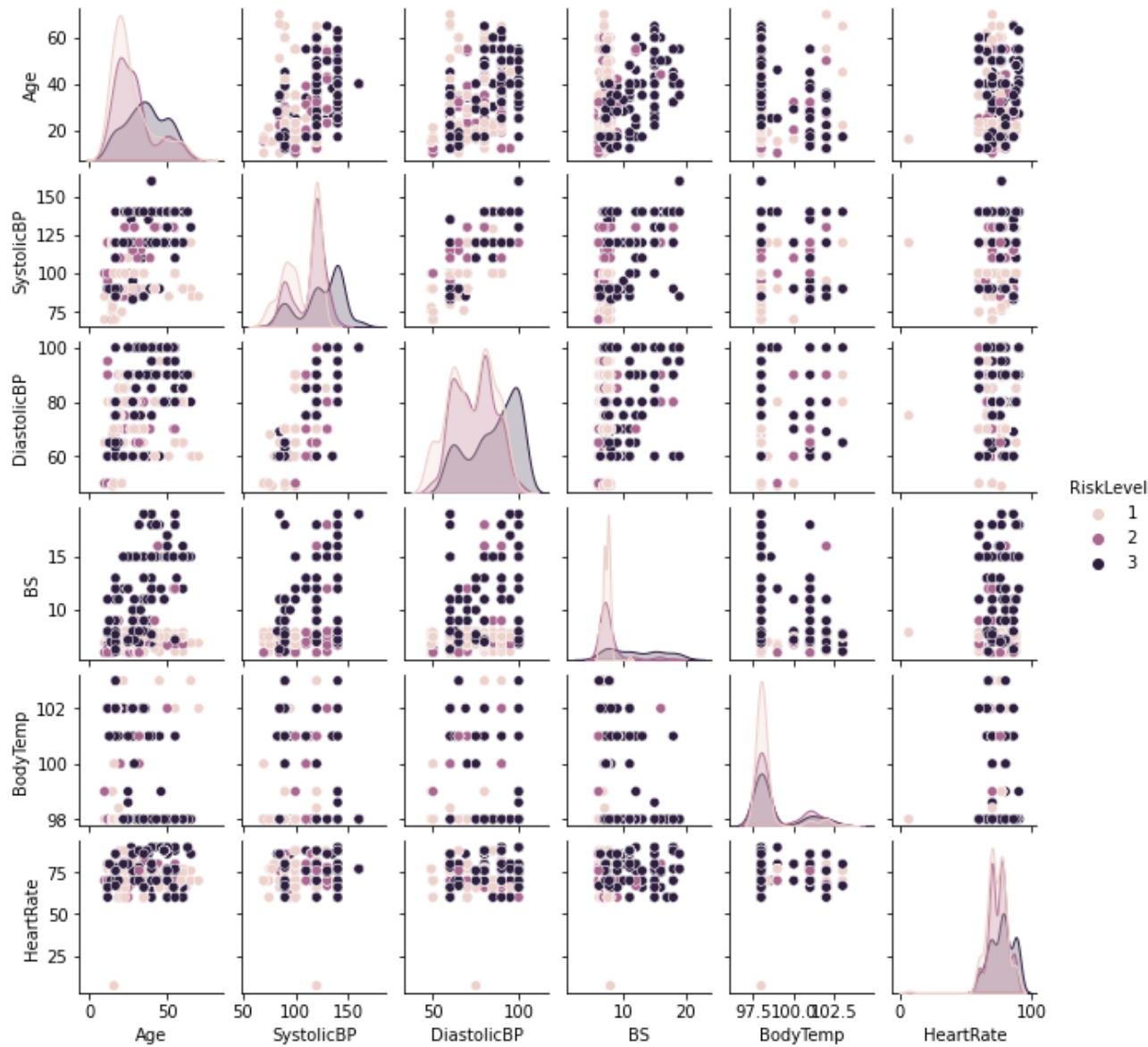
```
df.head()
# df.RiskLevel.value_counts()
```

	Age	SystolicBP	DiastolicBP	BS	BodyTemp	HeartRate	RiskLevel
0	25	130	80	15.0	98.0	86	3
1	35	140	90	13.0	98.0	70	3
2	29	90	70	8.0	100.0	80	3
3	30	140	85	7.0	98.0	70	3
4	35	120	60	6.1	98.0	76	1



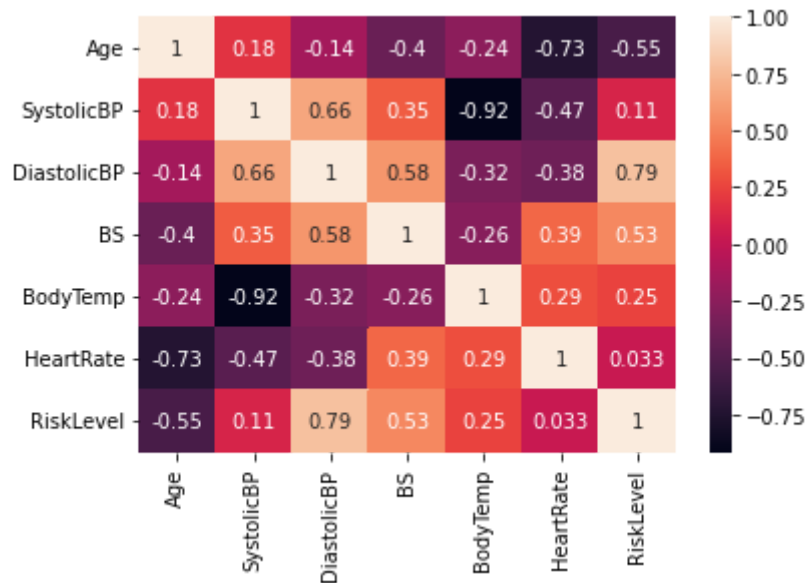
```
# Pairplot visualization with RiskLevel as hue
sns.pairplot(df,height=1.5,hue='RiskLevel')
```

<seaborn.axisgrid.PairGrid at 0x7f7afdc92b90>



```
# Correlation between variables with a heatmap
sns.heatmap(df[:5].corr(method = 'pearson'), annot=True)
```

<matplotlib.axes.\_subplots.AxesSubplot at 0x7f7afdb68c10>



The dataset is complete and does not have missing values

Heatmap correlation gives us insights as:

Age - Risk Level: -55%

Age - Heart Rate: -73%

Systolic BP - Body Temp: -92%

Systolic BP - Diastolic BP: 66%

Diastolic BP - Risk Level: 79%

Diastolic BP - BS: 58%

## ▼ Exploratory Data Analysis

### ▼ Age

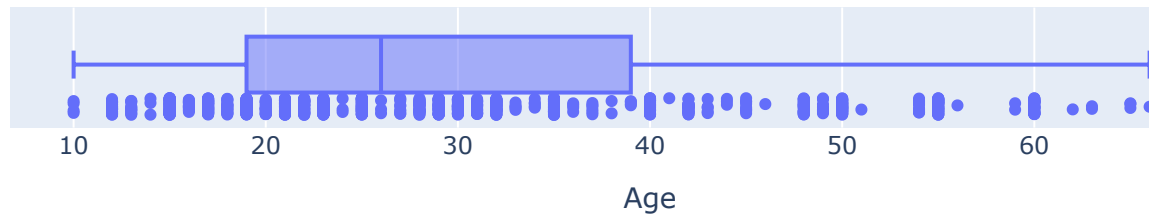
df.head()

	Age	SystolicBP	DiastolicBP	BS	BodyTemp	HeartRate	RiskLevel
0	25	130	80	15.0	98.0	86	3
1	35	140	90	13.0	98.0	70	3
2	29	90	70	8.0	100.0	80	3
3	30	140	85	7.0	98.0	70	3
4	35	120	60	6.1	98.0	76	1

# Age in boxplot

fig = px.box(df, x="Age", points="all", width=800, height=200)

```
fig = px.box(df, x=Age, points=True, width=800, height=400)
fig.show(renderer="colab")
```



```
# Age statistics
print('Age min: {age}'.format(age = df['Age'].min()))
print('Age max: {age}'.format(age = df['Age'].max()))
print('Age avg: {age}'.format(age = df['Age'].mean()))
print('Age median: {age}'.format(age = df['Age'].median()))
print('Age std: {age}'.format(age = df['Age'].std()))
```

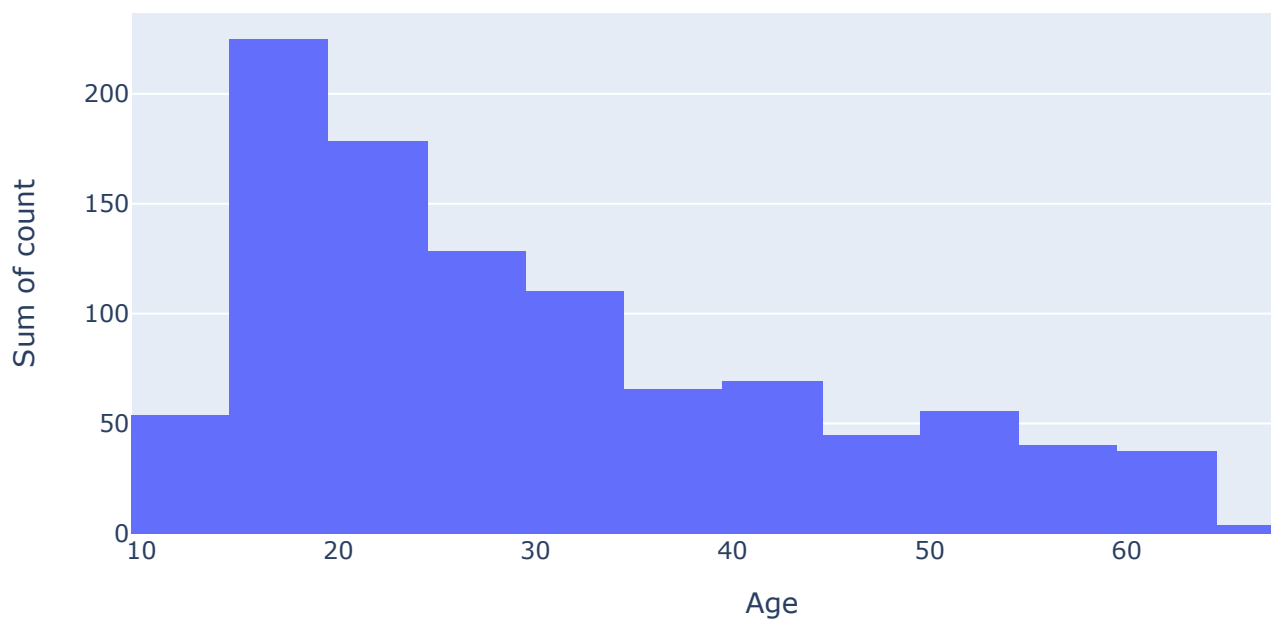
```
Age min: 10
Age max: 70
Age avg: 29.871794871794872
Age median: 26.0
Age std: 13.474385532634372
```

```
# Age value count
data = df[['Age']].value_counts().reset_index()
data.rename(columns={data.columns[1]: 'Count'}, inplace=True)
fig = px.bar(data, x='Age', y='Count', width=800, height=400)
fig.update_layout(
    title='Number of people by Age',
    yaxis_title="Count")
fig.show(renderer="colab")
```

## Number of people by Age

```
# Age in histogram
data = df[['Age']].value_counts().reset_index()
data.rename(columns={data.columns[1]:'Count'}, inplace=True)
data = data.sort_values(by='Age')
fig = px.histogram(data, x="Age", y="Count",nbins=20,width=800, height=400)
fig.update_layout(
    title='Age histogram',
    yaxis_title="Sum of count")
fig.show(renderer="colab")
```

Age histogram



```
# Using the age categories life cylce group by statistics department
```

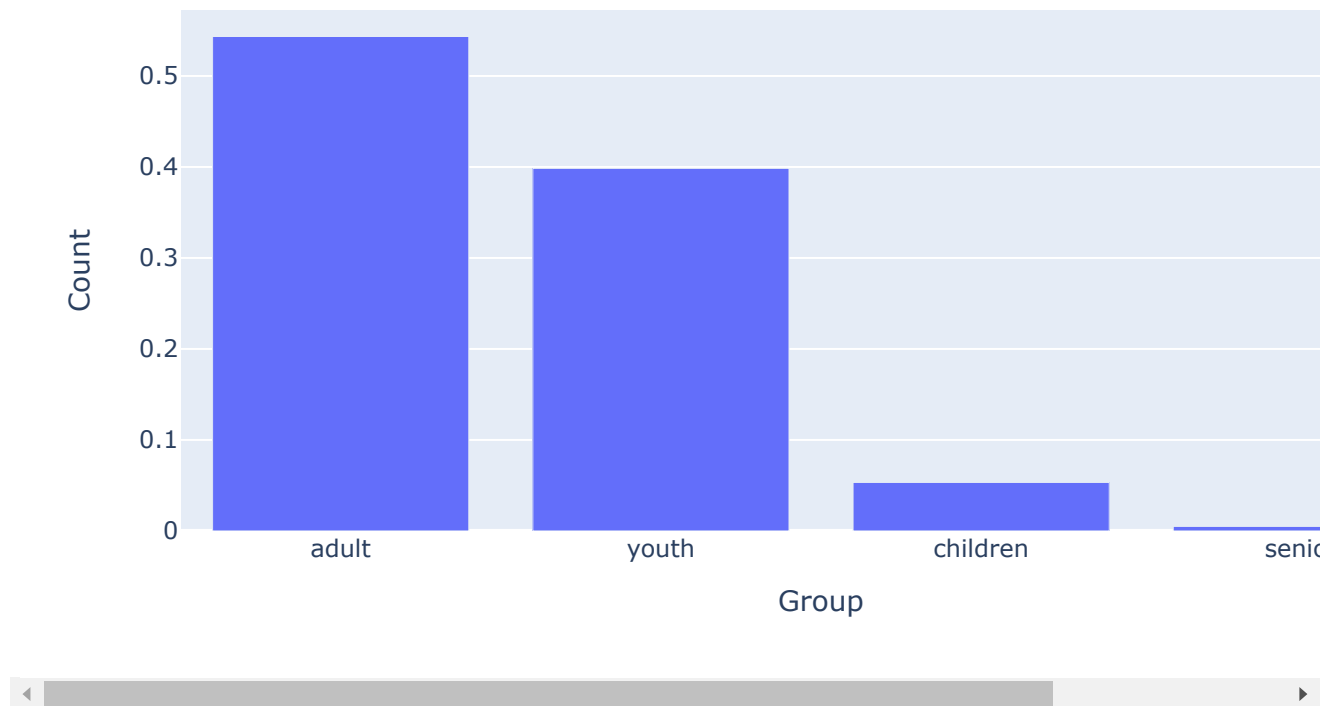
```
sections = [(df['Age'] <= 14 ),\
             (df['Age'] >= 15) & (df['Age'] <=24),\
             (df['Age'] >= 25) & (df['Age'] <=64),\
             (df['Age'] > 64)]
```

```
choice =['children','youth','adult','senior']
df['Group'] = np.select(sections, choice)
```

```
# Visualization by Group
```

```
data = df[['Group']].value_counts(normalize=True).reset_index()
data.rename(columns={data.columns[1]:'Count'}, inplace=True)
fig = px.bar(data, x='Group', y='Count',width=800, height=400)
fig.update_layout(
    title='Percent by Group',
    yaxis_title="Count")
fig.show(renderer="colab")
```

Percent by Group



#### Conclusion for Age:

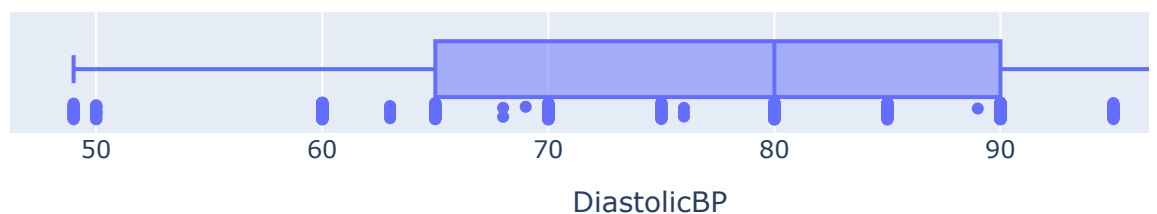
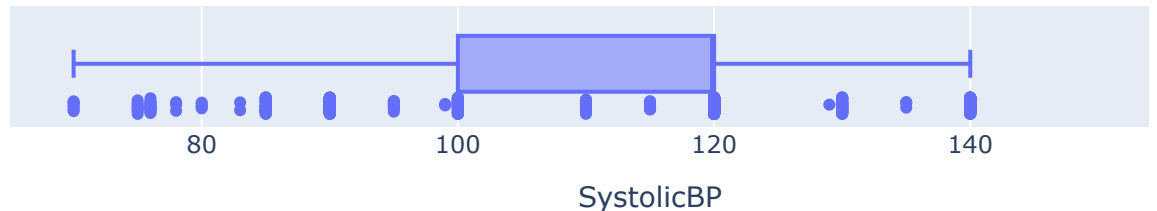
- The mean of the Age is 30
- The median of the column Age is 26
- Min Age is 10 and Max Age is 70.
- The standard deviation of the Age range is 13.5
- Higher number of people are below 35 having the count as 71 for 23 years, 67 for 19 years, 63 for 17 years and 60 for 15 years
- When we group the ages to attain the seniority level we get 54.3% of the group to be adults, 39.8% are youths, 5.3% are children and 0.4% are senior

## ▼ SystolicBP and DiastolicBP

```
# Top 5 values of SystolicBP and Diastolic BP
data = df[['SystolicBP', 'DiastolicBP']].value_counts().reset_index()
data.rename(columns={data.columns[2]: 'count'}, inplace=True)
data.head()
```

SystolicBP DiastolicBP count 

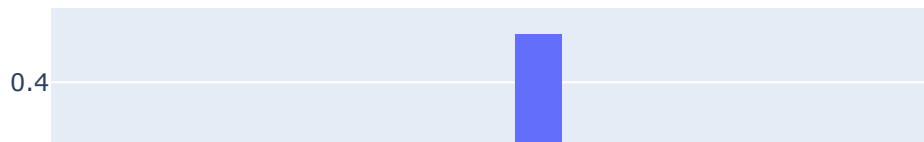
```
# Box plot distribution for SystolicBP and Diastolic BP
fig = px.box(df, x="SystolicBP", points='all',width=800, height=200)
fig.show(renderer="colab")
fig = px.box(df, x="DiastolicBP", points='all',width=800, height=200)
fig.show(renderer="colab")
```



```
# SystolicBP values
data = df[['SystolicBP']].value_counts(normalize =True).reset_index()
data.rename(columns={data.columns[1]:'Count'}, inplace=True)
fig = px.histogram(data, x='SystolicBP', y='Count',nbins=20,width=600, height=400)
fig.update_layout(
    title='Systolic BP count',
    yaxis_title="Count")
fig.show(renderer="colab")
```

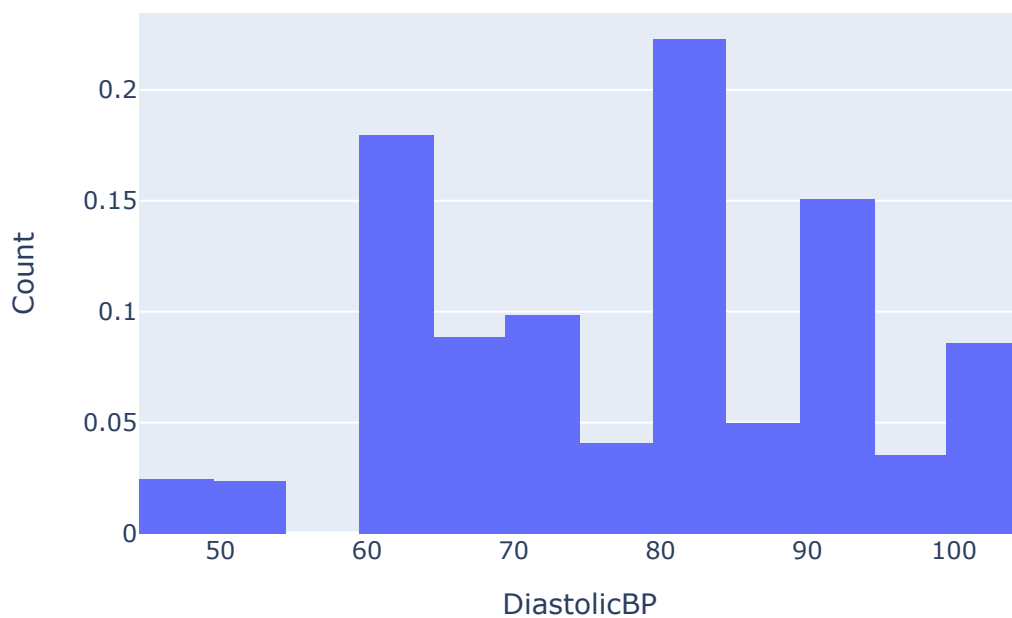


## Systolic BP count

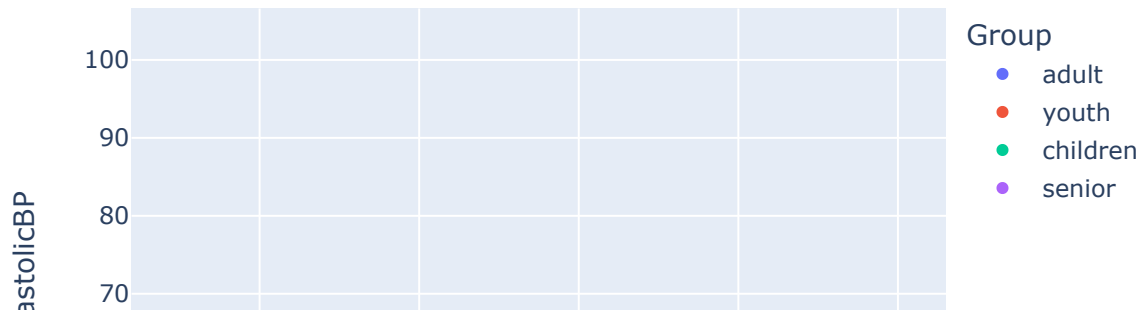


```
# Diastolic BP values
data = df[['DiastolicBP']].value_counts(normalize=True).reset_index()
data.rename(columns={data.columns[1]: 'Count'}, inplace=True)
fig = px.histogram(data, x='DiastolicBP', y='Count', nbins=20, width=600, height=400)
fig.update_layout(
    title='Diastolic BPcount',
    yaxis_title="Count")
fig.show(renderer="colab")
```

## Diastolic BPcount



```
# Scatter plot between Systolic and Diastolic Blood pressure by Group
data = df[['SystolicBP', 'DiastolicBP', 'Group']]
fig = px.scatter(df, x="SystolicBP", y="DiastolicBP", color="Group", trendline="ols", width=
fig.show(renderer="colab")
```



Use of Mayo Clinic categories for Systolic and Diastolic Blood Pressure [7] to categorize in sections

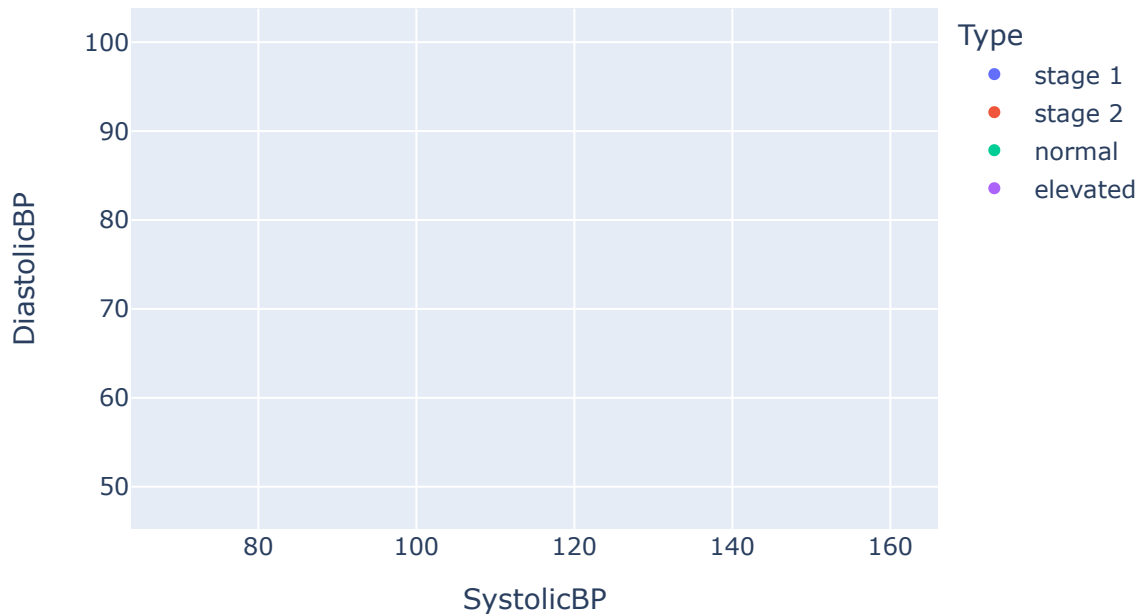


```
# Mayo clinic categories for SystolicBP
sections = [(df['SystolicBP'] < 120 ) & (df['DiastolicBP'] <80),\
            (df['SystolicBP'] >= 120) & (df['SystolicBP'] <=129) & (df['DiastolicBP'] < 80)
            (df['SystolicBP'] >= 130) & (df['SystolicBP'] <=139) | (df['DiastolicBP'] >= 80
            (df['SystolicBP'] >=140) | (df['DiastolicBP'] >= 90)]
choice =['normal','elevated','stage 1','stage 2']
df['Type'] = np.select(sections,choice)

data = df[['Type']].value_counts(normalize=True).reset_index()
data.rename(columns={data.columns[1]:'Count'}, inplace=True)
data = data.sort_values(by='Type')
fig = px.bar(data, x="Type", y="Count",width=800, height=400)
fig.update_layout(
    title='Histogram Representation',
    yaxis_title="Percent")
fig.show(renderer="colab")
```

```
# Scatter plot between Systolic and Diastolic Blood pressure by Group
data = df[['SystolicBP', 'DiastolicBP', 'Type']]
fig = px.scatter(data, x="SystolicBP", y="DiastolicBP", color="Type", trendline="ols", width
fig.show(renderer="colab")
```

☹



## Conclusion for Systolic and DyastolicBP

### Systolic BP

- 44% of the population are between 120 - 124 bp
- Min is 70 & Max is 160 bp
- Q1: 100, Q2: 120, Q3: NONE

### Diastolic BP

- 22% of the population are between 80 - 84 bp
- Min is 49 & Max is 100 bp
- Q1: 65, Q2: 80, Q3: 90

The systolic blood pressure measures the force of blood against the artery walls while the ventricles (the lower two chambers of your heart) squeezes resulting in pushing the blood to the rest of the body.

The diastolic blood pressure measures the force of blood against the artery walls as the heart relaxes and the ventricles are allowed to refill with blood.

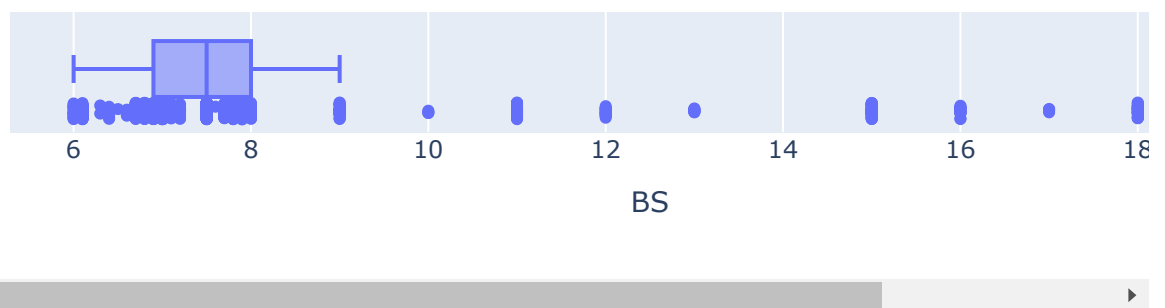
Diastole is this period of time when the heart relaxes between the beats (time taken by coronary artery to supply blood to your heart).

Between these two, there is a classification to find between a "normal" rate and an atypical one.

The Mayo clinic categories chart shows that 33% are normal, 32% are stage 1 hypertension, 26% are stage 2 hypertension and 7.6% are elevated.

## ▼ Blood Sugar level

```
# Boxplot distribution Blood sugar levels
fig = px.box(df, x="BS", points='all',width=800, height=200)
fig.show(renderer="colab")
```



```
# Histogram for BS-Level
data = df[['BS', 'Group']].value_counts().reset_index()
data.rename(columns={data.columns[2]: 'Count'}, inplace=True)
fig = px.histogram(data, x='BS', y='Count',width=1000, height=400,nbins=40,facet_col='Grou
fig.update_layout(
    title='BS histogram',
    yaxis_title="Count")
fig.show(renderer="colab")
```

## BS histogram

Group=vouth

Group=adult

Group=children

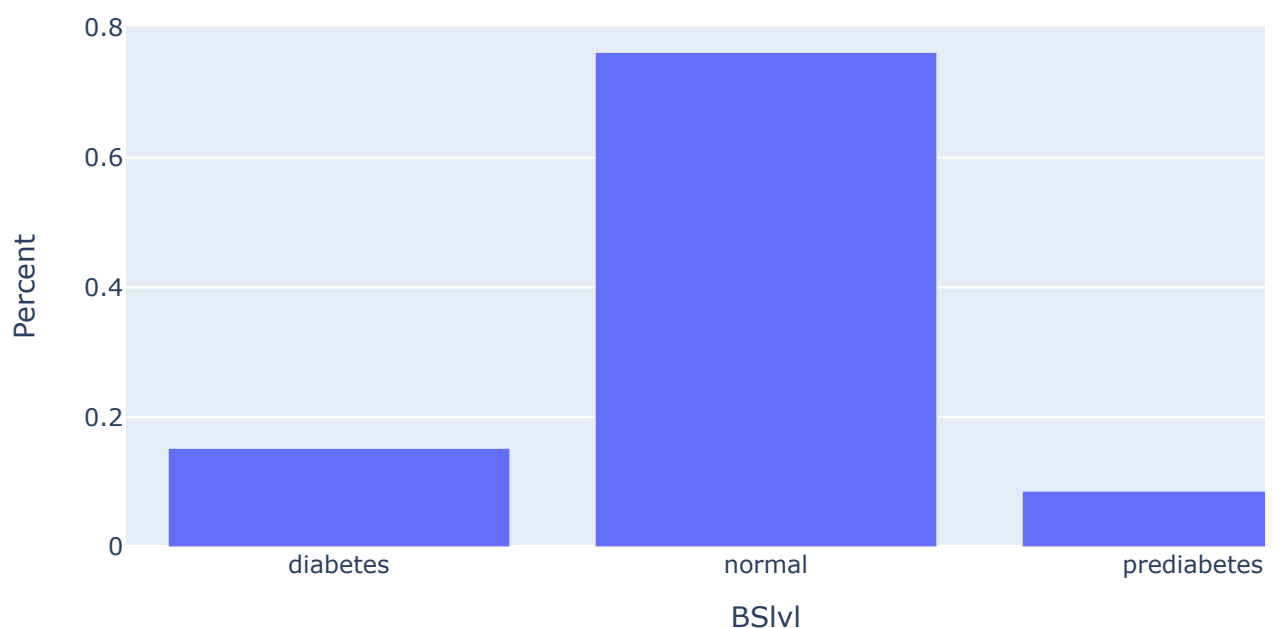
As per the clinical measure

A blood sugar level less than 140 mg/dL (7.8 mmol/L) is normal. A reading of more than 200 mg/dL (11.1 mmol/L) after two hours indicates diabetes. A reading between 140 and 199 mg/dL (7.8 mmol/L and 11.0 mmol/L) indicates prediabetes.

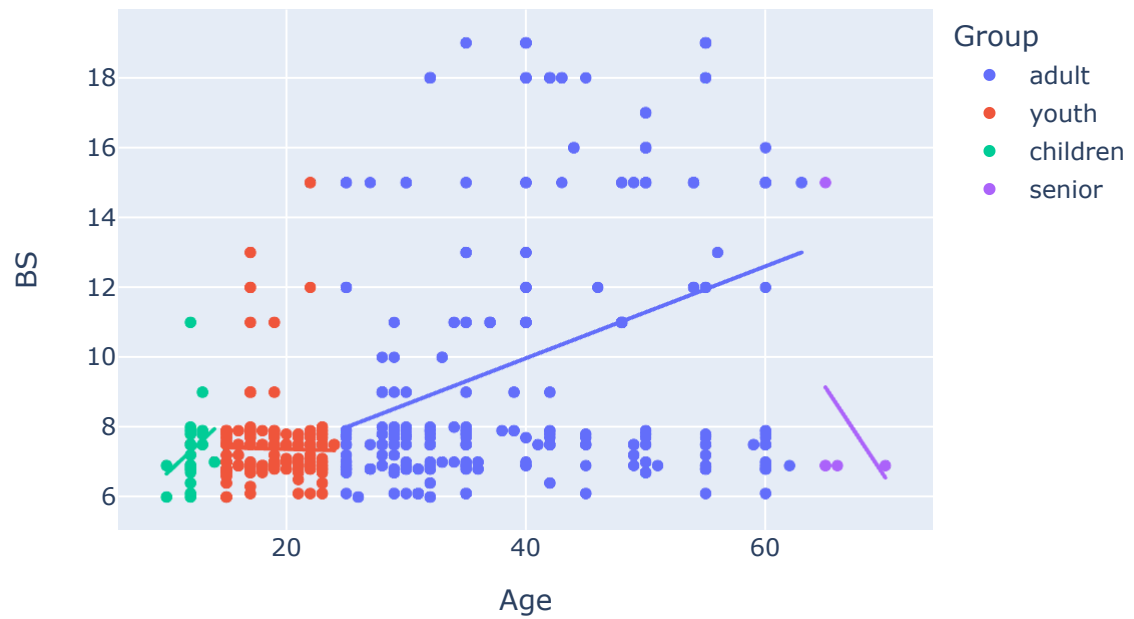
```
# Mayo clinic categories for Blood sugar levels
sections = [(df['BS'] <= 8),\
             (df['BS'] > 8) & (df['BS'] <=11),\
             (df['BS'] > 11)]
choice = ['normal','prediabetes','diabetes']
df['BSlvl'] = np.select(sections,choice)

data = df[['BSlvl']].value_counts(normalize=True).reset_index()
data.rename(columns={data.columns[1]:'Count'}, inplace=True)
data = data.sort_values(by='BSlvl')
fig = px.bar(data, x="BSlvl", y="Count",width=800, height=400)
fig.update_layout(
    title='Blood Sugar level as histogram',
    yaxis_title="Percent")
fig.show(renderer="colab")
```

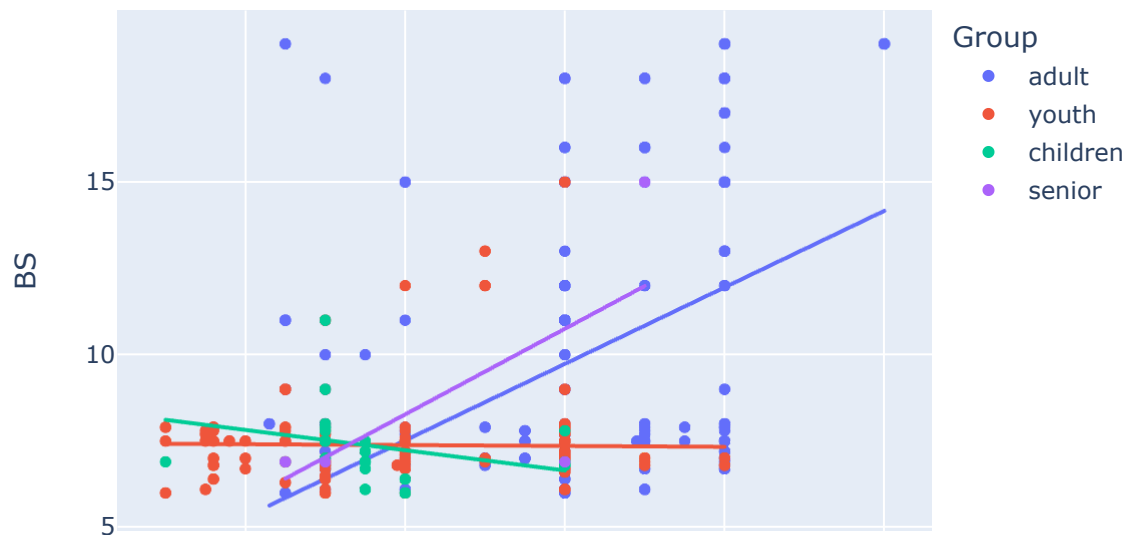
Blood Sugar level as histogram



```
# BS-Level and Age relationship
fig = px.scatter(df, x="Age", y="BS",color="Group", trendline="ols",width=600, height=400)
fig.show(renderer="colab")
```



```
# SystolicBP & DiastolicBP and BS-Level relationship
fig = px.scatter(df, x="SystolicBP", y="BS",color="Group", trendline="ols",width=600, height=400)
fig.show(renderer="colab")
fig = px.scatter(df, x="DiastolicBP", y="BS",color="Group", trendline="ols",width=600, height=400)
fig.show(renderer="colab")
```



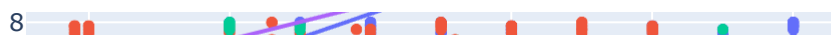
### Conclusion for Blood sugar level

- 44% of the population are between 120 - 124 SystolicBP
- Min is 6 & Max is 19
- Q1: 6.9, Q2: 7.5, Q3: 8
- 76% of the dataset have a normal Blood Sugar Level
- There is a 58% of correlation between BS-Levels and DiastolicBP & 35% between BS-Levels and SystolicBP

BS-Levels are related to Age, SystolicBP and DiastolicBP as the variables increase and the risk to have a high level of glucose in blood is related to lifestyle of different groups

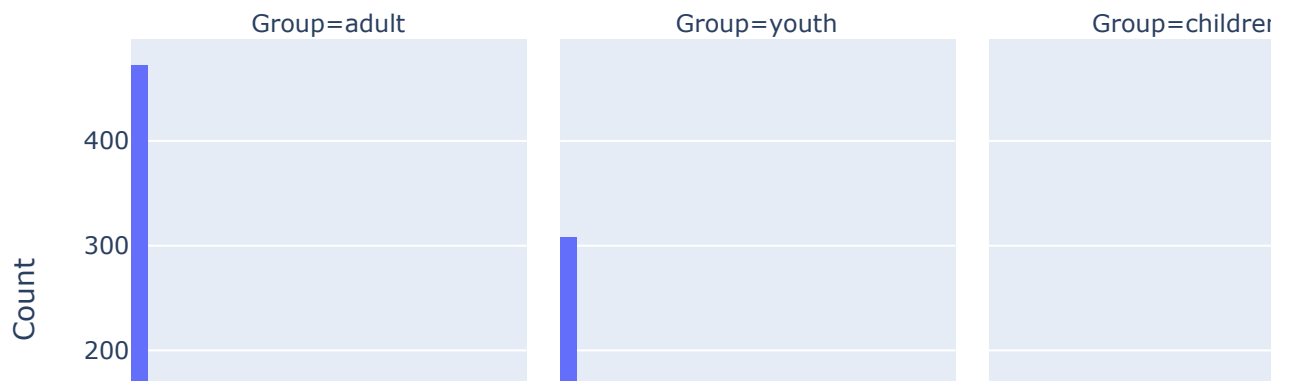


### ▼ Body temperature



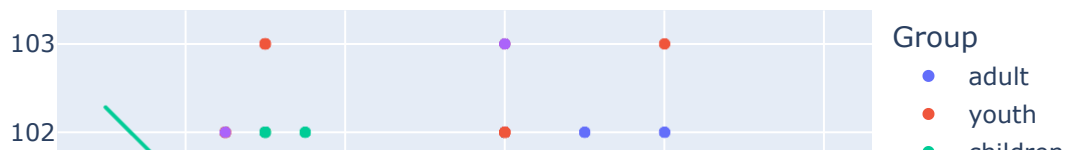
```
# Body Temperature in Histogram
data = df[['Group', 'BodyTemp']].value_counts().reset_index()
data.rename(columns={data.columns[2]: 'Count'}, inplace=True)
fig = px.histogram(data, x='BodyTemp', y='Count', width=1000, height=400, nbins=40, facet_col=0)
fig.update_layout(
    title='Body Temperature histogram',
    yaxis_title="Count")
fig.show(renderer="colab")
```

## Body Temperature histogram



```
# Decoding the relationship between SystolicBP & DiastolicBP to Body Temperature
fig = px.scatter(df, x="SystolicBP", y="BodyTemp",color="Group", trendline="ols",width=600
fig.show(renderer="colab")
fig = px.scatter(df, x="DiastolicBP", y="BodyTemp",color="Group", trendline="ols",width=60
fig.show(renderer="colab")
```





### Conclusion for Body Temperature

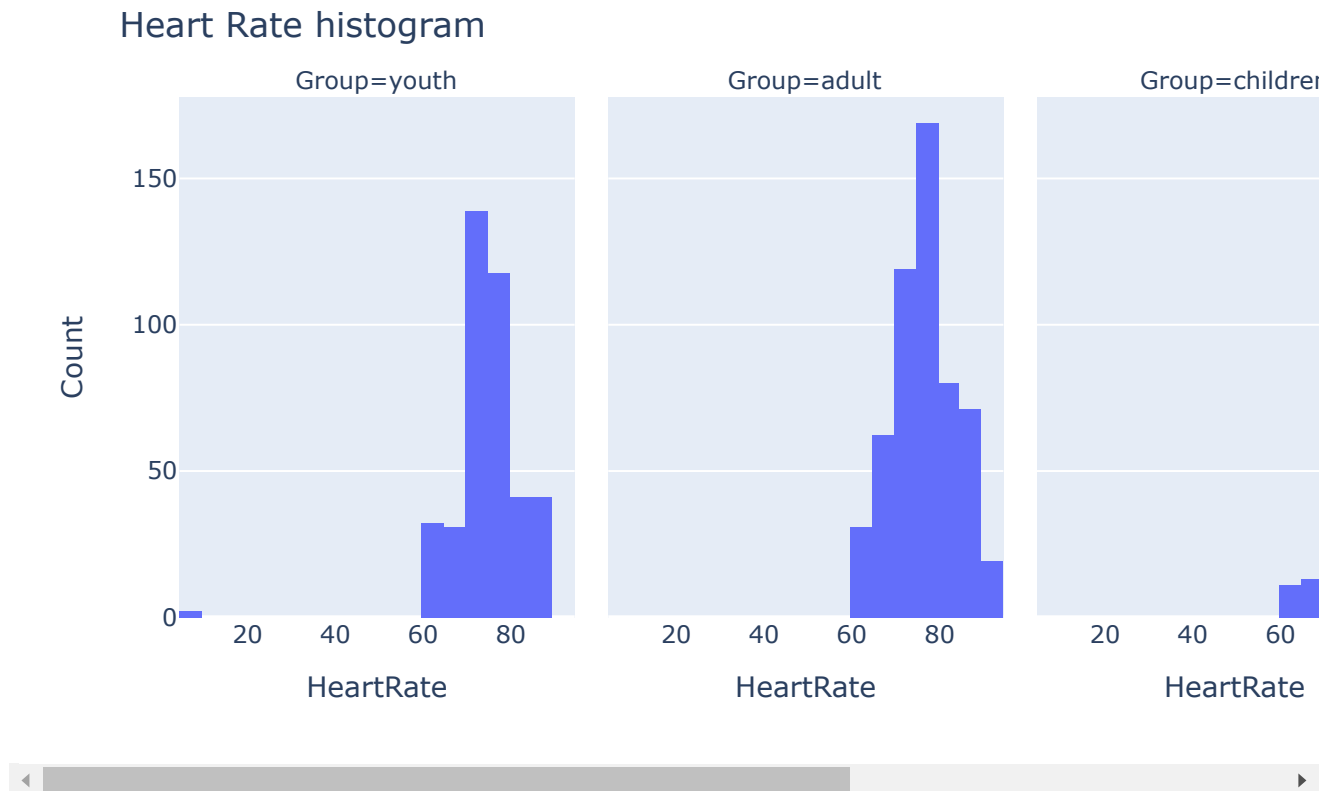
- In the youth and adult group almost the 80% of the count are between 98° - 99° (normal) while the children are around 40% and senior are around 60%
- Body temperature over 100° can be because of any infectious disease
- As systolic and diastolic blood pressure increases, body temperature also increases but due to the regulatory effects, the body begins to adapt to its original temperature and this can cause the body temperature to decrease.

This maybe the reason for -92% correlation between SystolicBP and Body Temperature

## ▼ Heart rate

```
# Heart Rate in Boxplot distribution
fig = px.box(df, x="HeartRate", points='all', facet_row='Group')
fig.show(renderer="colab")
```

```
# Heart Rate in Histogram
data = df[['HeartRate', 'Group']].value_counts().reset_index()
data.rename(columns={data.columns[2]: 'Count'}, inplace=True)
fig = px.histogram(data, x='HeartRate', y='Count', width=1000, height=400, nbins=40, facet_col='Group')
fig.update_layout(
    title='Heart Rate histogram',
    yaxis_title="Count")
fig.show(renderer="colab")
```

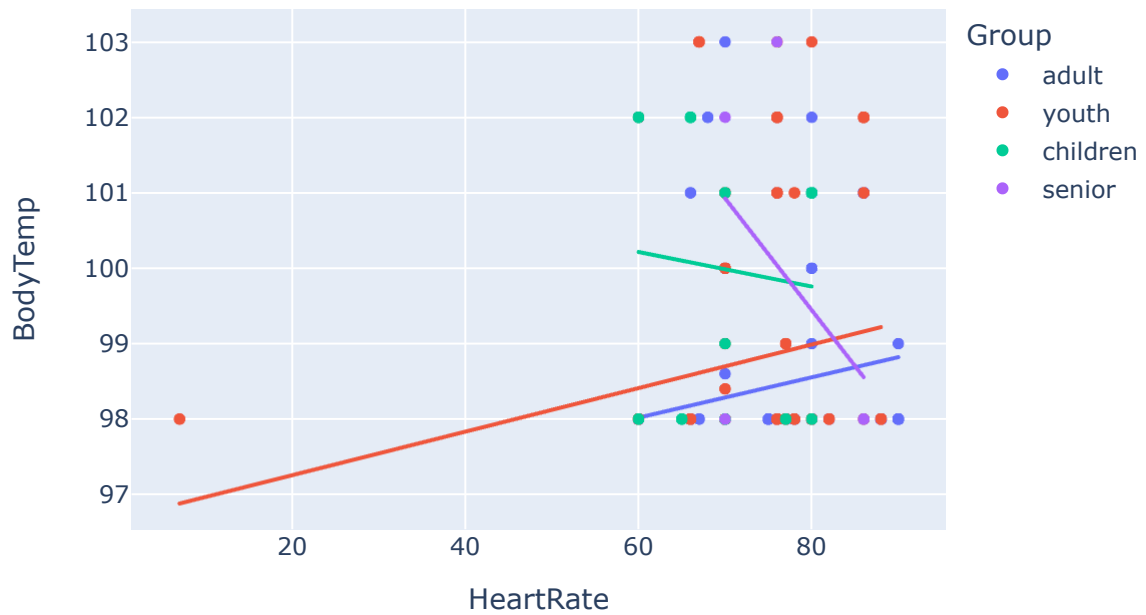


```
# Relationship between Heart Rate and Age
fig = px.scatter(df, x="Age", y="HeartRate", color="Group", trendline="ols", width=600, height=400)
fig.show(renderer="colab")
```



# Relationship between Heart Rate and Body Temperature

```
fig = px.scatter(df, x="HeartRate", y="BodyTemp", color="Group", trendline="ols", width=600,
fig.show(renderer="colab")
```



Conclusion for Heart rate

Heart rate for children:

- Q1: 65, Q2: 70, Q3: 80
- Min: 60, Max: NONE

Heart rate for youths:

- Q1: NONE, Q2: 70, Q3: 77
- Min: 7, Max: 88
- Atypical Heart rate: 7 bpm

Heart rate for adults:

- Q1: 70, Q2: 76, Q3: 80
- Min: 60, Max: 90

Heart rate for seniors:

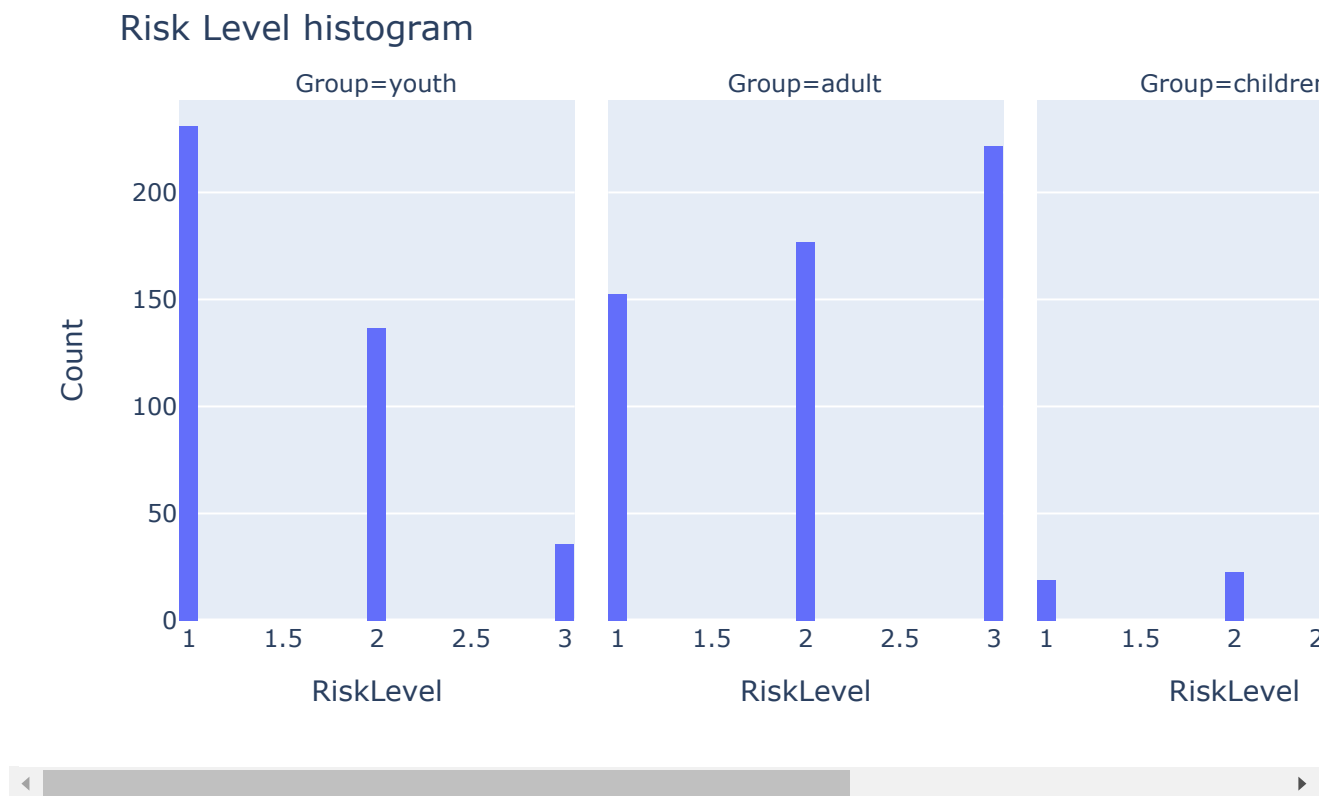
- Q1: 70, Q2: 76, Q3: 86

- Min: NONE, Max: NONE

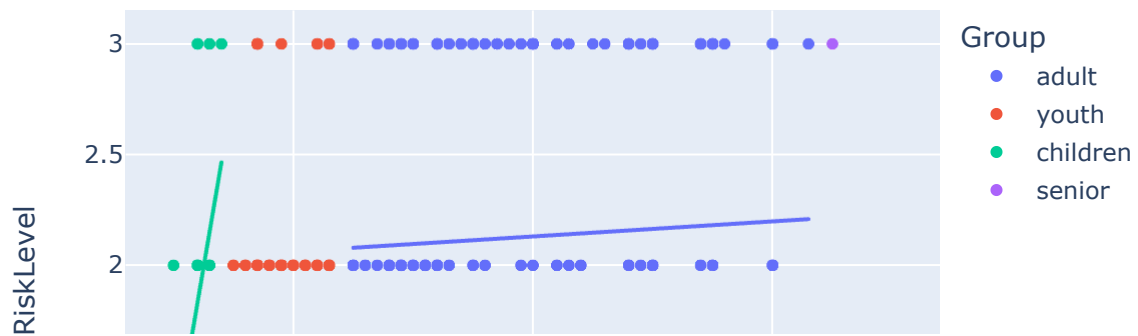
As Age increases in Youth, Adult and Senior the correlation between Heart Rate is negative whereas in the Children group as the Age increases the correlation is positive.

## ▼ Risk level

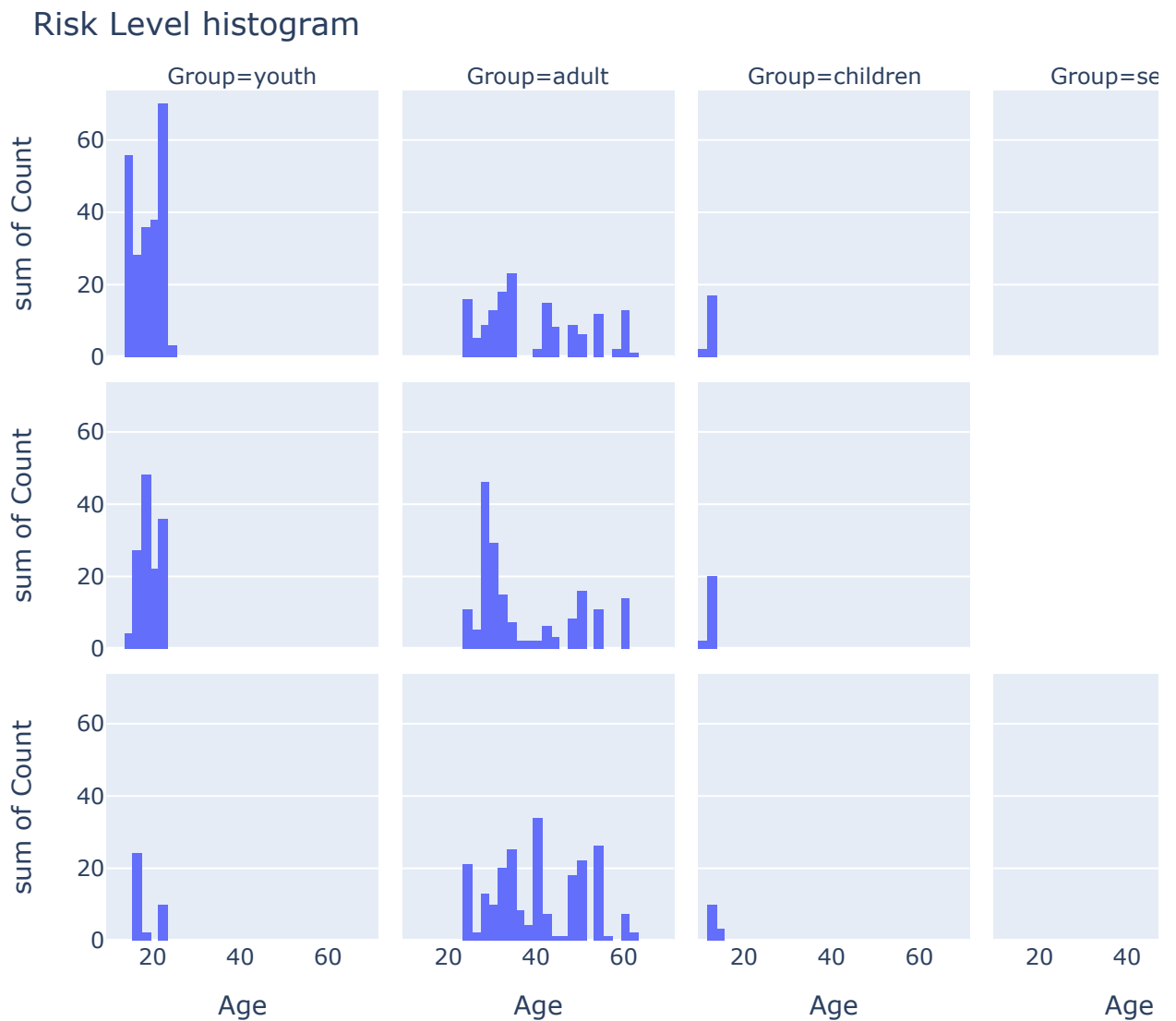
```
# Heart Rate in Histogram
data = df[['RiskLevel', 'Group']].value_counts().reset_index()
data.rename(columns={data.columns[2]: 'Count'}, inplace=True)
fig = px.histogram(data, x='RiskLevel', y='Count', width=1000, height=400, nbins=40, facet_col='Group')
fig.update_layout(
    title='Risk Level histogram',
    yaxis_title="Count")
fig.show(renderer="colab")
```



```
# Relationship between Risk Level and Age
fig = px.scatter(df, x="Age", y="RiskLevel", color="Group", trendline="ols", width=600, height=400)
fig.show(renderer="colab")
```



```
# Relationship between Heart Rate, Group & Age in Histogram
data = df[['RiskLevel', 'Group', 'Age']].value_counts().reset_index()
data.rename(columns={data.columns[3]: 'Count'}, inplace=True)
fig = px.histogram(data, x='Age', y='Count', width=800, height=600, nbins=40, facet_col='Group')
fig.update_layout(
    title='Risk Level histogram')
fig.show(renderer="colab")
```



Conclusion for Risk Level

No of children in each risk level

- Risk level 1: 231
- Risk level 2: 137
- Risk level 3: 36

No of youths in each risk level

- Risk level 1: 152
- Risk level 2: 177
- Risk level 3: 222

No of adults in each risk level

- Risk level 1: 19
- Risk level 2: 22
- Risk level 3: 13

No of seniors in each risk level

- Risk level 1: 4
- Risk level 2: NONE
- Risk level 3: 1

As per the medical conditions and our analysis,

By looking at the Age and Risk Level scatter plot, the correlation between the Youth and Adult is positive while for the Senior is negative and Youth is none.

This can be explained as "Early childbearing can increase the risk for newborns as well as the young mothers. Babies born to the mothers under 20 years of age face higher risks of low birth weight, preterm delivery and severe neonatal disorders.

Babies born to the elder mothers have a higher risk of certain chromosome problems like Down syndrome. The risk of pregnancy loss is higher by miscarriage and stillbirth increases as they get older. This is due to the pre-existing medical conditions or fetal chromosomal abnormalities.

## ▼ Machine Learning Analysis

```
# Create X and y variables
X = df.drop(['RiskLevel', 'Group', 'Type', 'BSlvl'], axis=1)
y = df.RiskLevel
SEED = 1
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=SEED)
X_train.shape, X_test.shape

((811, 6), (203, 6))
```

```

# Scale the X dataset
ss = StandardScaler()

X_train_scaled = ss.fit_transform(X_train)
X_test_scaled = ss.transform(X_test)

# Using Machine Learning Algorithms listed below
MLA = [
    #Ensemble Methods
    ensemble.GradientBoostingClassifier(random_state=SEED),
    ensemble.RandomForestClassifier(random_state=SEED),

    #GLM
    linear_model.SGDClassifier(random_state=SEED),
    linear_model.LogisticRegression(random_state=SEED),

    #Trees
    tree.DecisionTreeClassifier(random_state=SEED),
    tree.ExtraTreeClassifier(random_state=SEED),

    XGBClassifier(eval_metric="mlogloss"),
    CatBoostClassifier(silent=True, random_state=SEED)
]

# Create a dataframe
MLA_compare = pd.DataFrame()

# Function for MLA to append to dataframe
def MLA_testing(MLA, X_train, X_test):
    row_index = 0
    for classifier in MLA:

        classifier.fit(X_train, y_train)
        y_pred = classifier.predict(X_test_scaled)
        classifier_accuracy_score = accuracy_score(y_test, y_pred)

        kfold_accuracy = cross_val_score(estimator = classifier, X = X_train, y = y_train,

        MLA_name = classifier.__class__.__name__
        MLA_compare.loc[row_index, 'MLA Name'] = MLA_name
        MLA_compare.loc[row_index, 'Accuracy Score'] = classifier_accuracy_score*100
        MLA_compare.loc[row_index, 'K-Fold Accuracy'] = kfold_accuracy.mean()*100

    # Print(MLA_name, "Done")
    row_index+=1

# Determining the accuracy for each MLA
MLA_testing(MLA=MLA, X_train=X_train_scaled, X_test=X_test)

MLA_compare = MLA_compare.sort_values(by="Accuracy Score", ascending=False).reset_index(drop=True)
MLA_compare

```

	MLA Name	Accuracy Score	K-Fold Accuracy
0	RandomForestClassifier	87.192118	82.494731
1	DecisionTreeClassifier	86.699507	82.121349
2	CatBoostClassifier	86.699507	82.738633
3	ExtraTreeClassifier	83.251232	80.271003
4	GradientBoostingClassifier	80.295567	78.297200
5	XGBClassifier	76.847291	74.846432
6	LogisticRegression	60.098522	63.250527
7	SGDClassifier	57.142857	59.302921



# Machine Learning Algorithm for Voting classifier using MLA selected algorithms

```
MLA = [
    # Ensemble Methods
    ('Random Forest',ensemble.RandomForestClassifier(random_state=SEED)),
    # Trees
    ('Decision Tree',tree.DecisionTreeClassifier(random_state=SEED)),
    ('Extra Tree',tree.ExtraTreeClassifier(random_state=SEED)),

    ('XGB Classifier',XGBClassifier(eval_metric="mlogloss"))

]
```

```
# Initiate a VotingClassifier vc
vc = VotingClassifier(estimators=MLA)
```

```
# Fit vc to the training set
vc.fit(X_train, y_train)
```

```
# Evaluate the test set predictions
y_pred = vc.predict(X_test)
```

```
# Calculate accuracy score
accuracy = accuracy_score(y_test, y_pred)
print('Voting Classifier: {:.3f} %'.format(accuracy*100))
```

Voting Classifier: 86.700 %

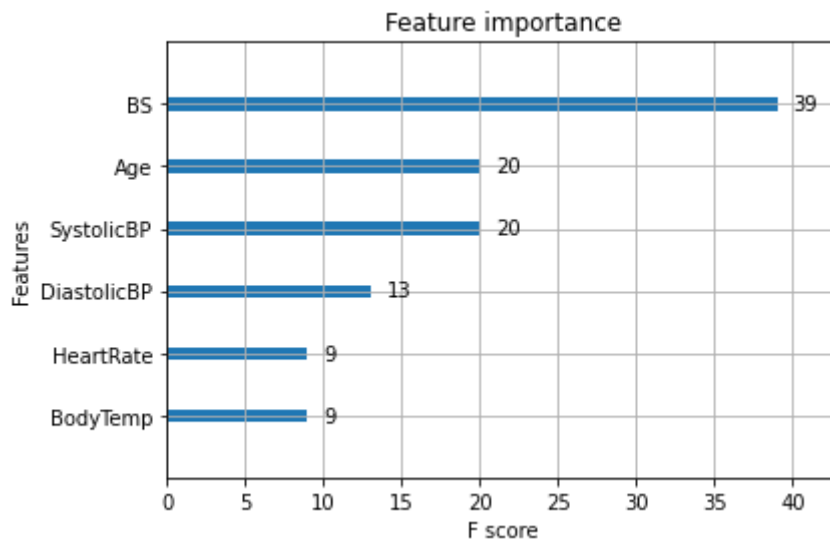
```
# Create the DMatrix
maternal_dmatrix = xgb.DMatrix(data = X, label = y)
```

```
params = {'eval_metric':"mlogloss"}
```

```
# Train the model: xg_reg
xg_reg = xgb.train(dtrain=maternal_dmatrix,params=params,num_boost_round=5)
```

```
# Plot the feature importances
xgb.plot_importance(xg_reg)
plt.show()
```





## ▼ Conclusion

As we review the data collected from the prediction, most of the information are for women around 30 years old with a standard deviation of 13.5 being the top count among the ages in the children and youth categories.

About the SystolicBP and DiastolicBP, looking at the Feature importance table we could not conclude that SystolicBP have more impact in the risk level prediction than the DiastolicBP but we can say that the SystolicBP has a 44% of the population around 120 - 124 bp while the Diastolic distribution being only 22% of the population between 80 - 84 bp (Mayo clinic "common" values").

The Blood Sugar Levels (BS-Levels) being the top one in Feature importance table would be an important factor for risk level. 76% of the dataset have normal Blood Sugar Level but only 44% of the population are between 120 - 124 bp (SystolicBP). BS-Levels are related to Age, SystolicBP and DiastolicBP as the variables increase.

The risk to have a high level of glucose in blood is related to the lifestyle of different groups. The Body Temperature and Heart Rate in the Feature importance need more information to reduce the feature selection. For Body Temperature, the youth and adult groups have 80% (normal) while children only have 40% and seniors having 60%. We also need more information about the disease existence and to do more research on the correlation between the SystolicBP and Body Temperature.

Heart rate could have an effect in Age and risk level but we need still more data to make the exact prediction. We are close to the perfect accuracy now.

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