Reading the Data

In [1]:

```
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
from matplotlib import rcParams
sns.set()
```

In [2]:

```
df=pd.read_csv("diabetes1.csv")
```

In [3]:

```
df.columns
```

Out[3]:

```
Index(['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'I
nsulin',
       'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome'],
      dtype='object')
```

In [4]:

```
df.shape
```

Out[4]:

```
(768, 9)
```

In [5]:

```
df.describe()
```

Out[5]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	Diabete
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	
mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578	
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	

It seems in the minumum there are values of zero which we need to deal with later

In [6]:

```
df.info(verbose=True)
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
 #   Column                    Non-Null Count  Dtype  
---  ------                    --------------  -----  
 0   Pregnancies               768 non-null    int64  
 1   Glucose                   768 non-null    int64  
 2   BloodPressure             768 non-null    int64  
 3   SkinThickness             768 non-null    int64  
 4   Insulin                   768 non-null    int64  
 5   BMI                       768 non-null    float64
 6   DiabetesPedigreeFunction  768 non-null    float64
 7   Age                       768 non-null    int64  
 8   Outcome                   768 non-null    int64  
dtypes: float64(2), int64(7)
memory usage: 54.1 KB
```

It seems that all features are continuous numbers/integers (no categorical)

In [7]:

```
df.rename(columns ={"DiabetesPedigreeFunction":"DPF"},inplace=True)
```

We rename the Diabetes Pedigree Function feature to DPF in order to shorten it for easier use

In [8]:

```
df.drop_duplicates().shape
```

Out[8]:

```
(768, 9)
```

It seems that there are no duplicates as number of observations of the data did not change

Statistical Distribution

In [9]:

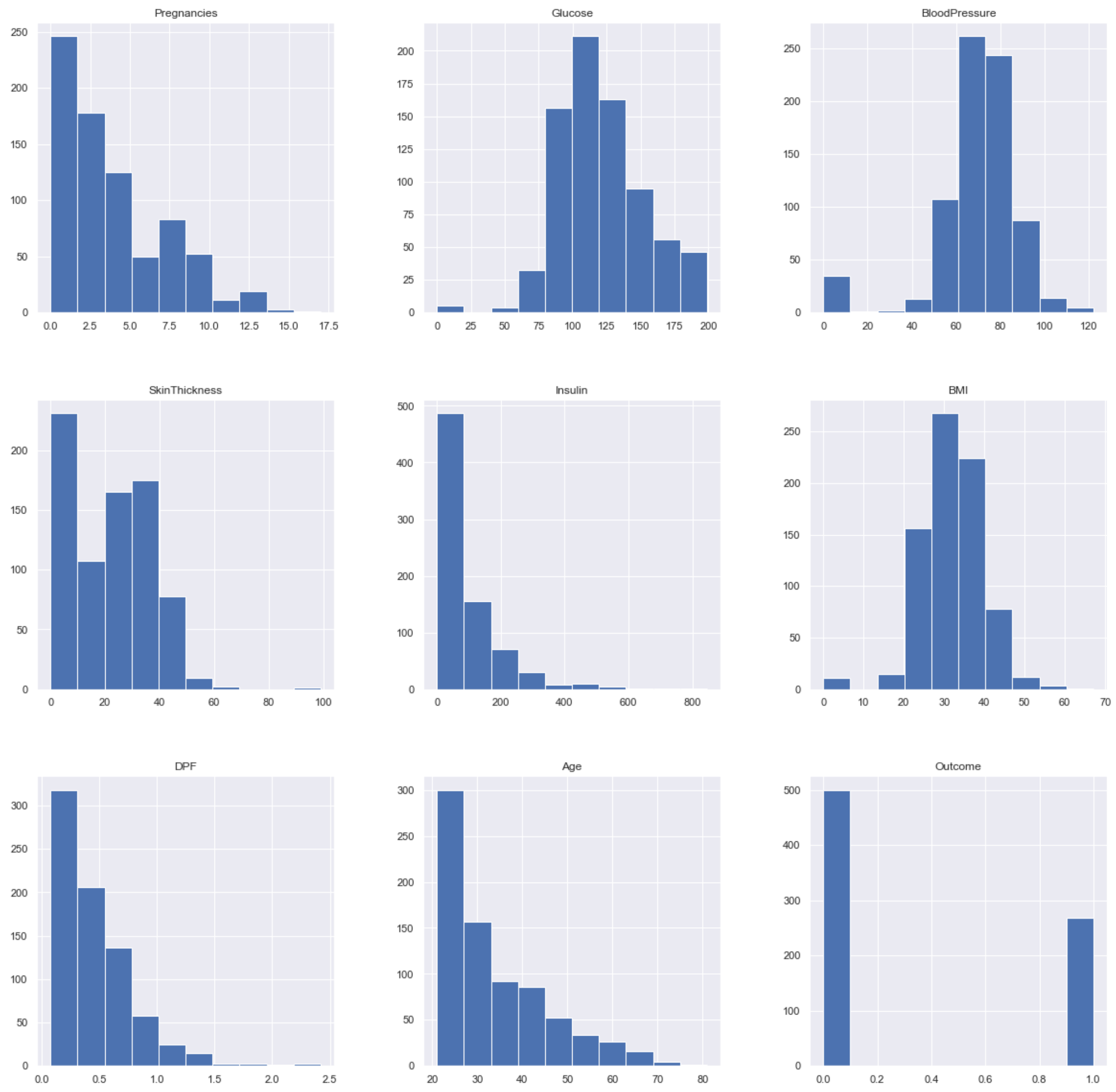
```
counts = df['Outcome'].value_counts()
counts
```

Out[9]:

```
0    500
1    268
Name: Outcome, dtype: int64
```

In [10]:

```
hist = df.hist(figsize = (20,20))
```



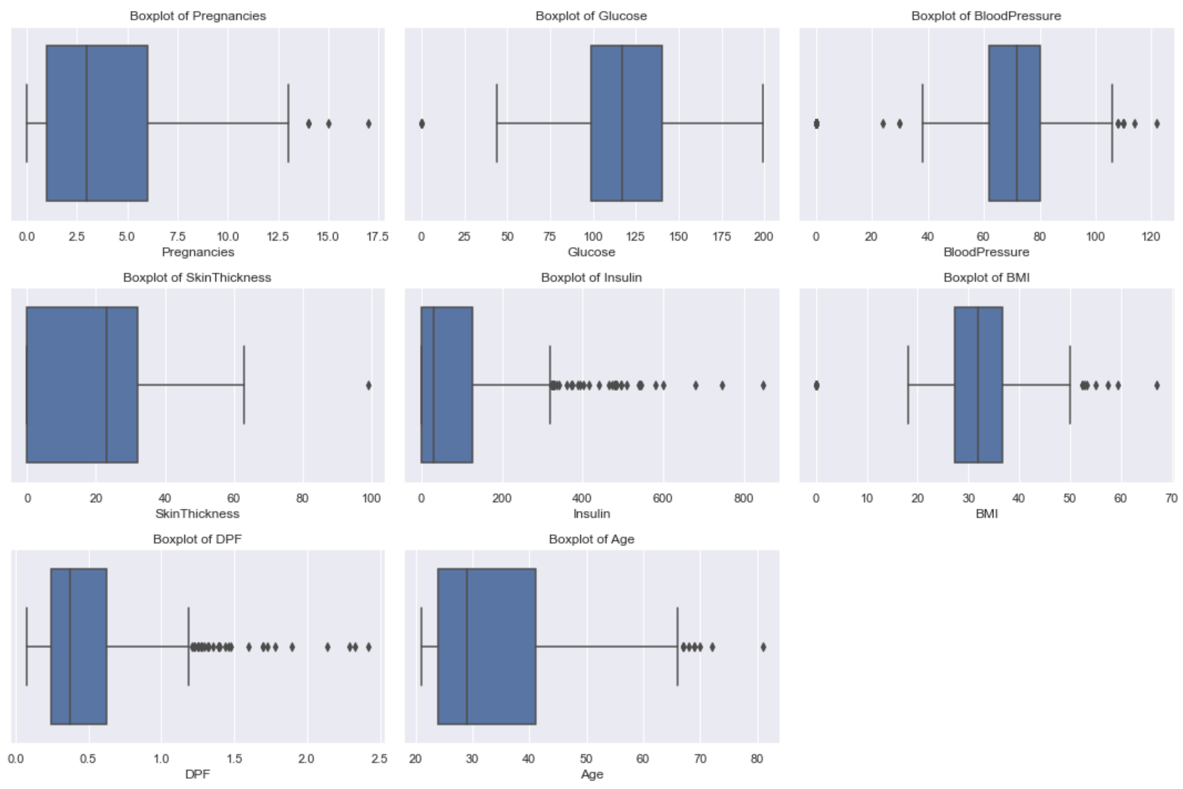
Glucose, Blood Pressure and BMI graphs are almost symmetric

Pregnancies, SkinThickness, Insulin, Age, and DPF are positively skewed

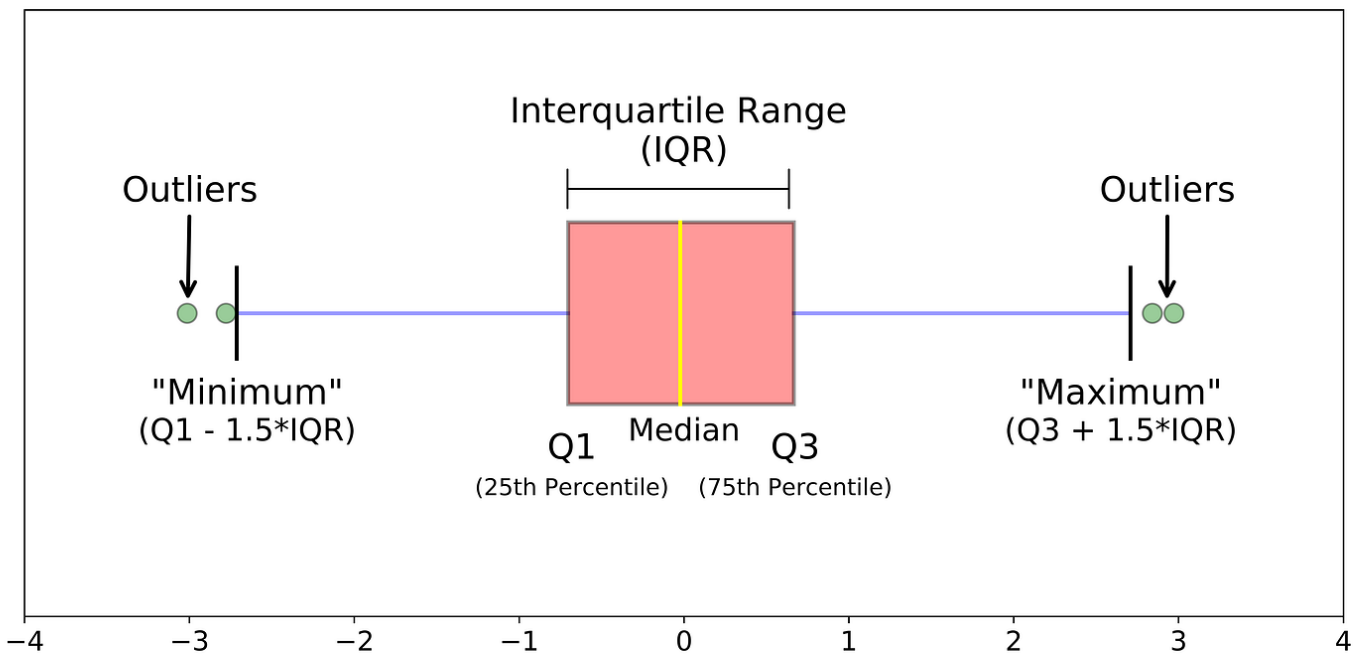
Box Plots for Numerical Variables

In [11]:

```
numerical_columns = df.columns[:-1]
plt.figure(figsize=(15, 10))
for i, column in enumerate(numerical_columns, 1):
    plt.subplot(3, 3, i)
    sns.boxplot(x=df[column])
    plt.title(f'Boxplot of {column}')

plt.tight_layout()
plt.show()
```



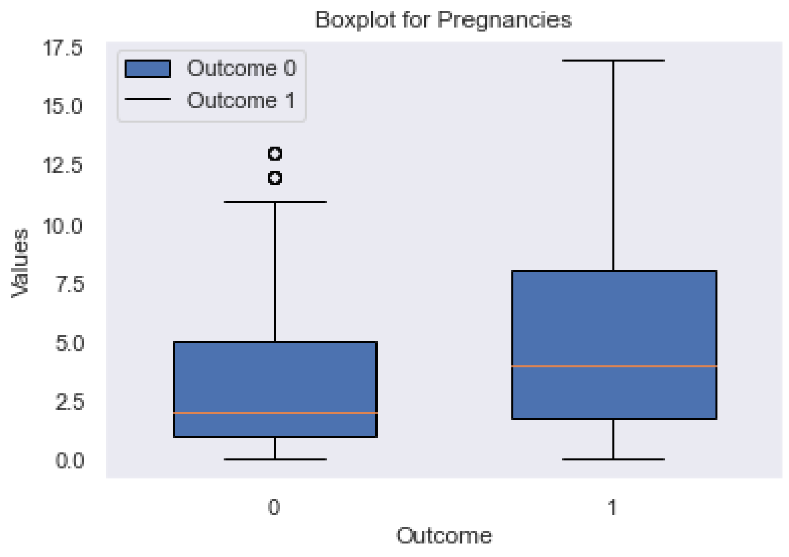
As shown from the Boxplots there are some outliers in each variable as any points below the minimum or above the maximum are considered outliers


Interquartile Range
(IQR)
Outliers
Outliers
"Minimum"
(Q1 - 1.5*IQR)
Median
Q1
(25th Percentile)
Q3
(75th Percentile)
"Maximum"
(Q3 + 1.5*IQR)
−4
−3
−2
−1
0
1
2
3
4

Boxplot by Outcome Variable

In [12]:

```
# Grouping DataFrame by outcome variable
groups = df.groupby('Outcome')

# Plotting boxplots for each variable
for variable in df.columns[:-1]:  # Exclude the outcome variable
    plt.figure(figsize=(6, 4))
    for outcome, group in groups:
        plt.boxplot(group[variable], positions=[outcome], widths=0.6, patch_artist=
    plt.title(f'Boxplot for {variable}')
    plt.xlabel('Outcome')
    plt.ylabel('Values')
    plt.xticks([0, 1], ['0', '1'])
    plt.grid(False)
    plt.legend(['Outcome 0', 'Outcome 1'])
    plt.show()
```



As shown from the Boxplots grouped by outcome, there are some outliers for both classes in each variable, but we can see that class with label zero has more outliers and this could be due to that this class has more observations than the other class.

Checking Class Imbalance for the Target Class "Outcome"

In [13]:

```
import plotly.graph_objects as go
colors = ['skyblue', 'orange']
labels = ['0','1']
values = df['Outcome'].value_counts()/df['Outcome'].shape[0]

fig = go.Figure(data=[go.Pie(labels=labels, values=values, hole=.3)])
fig.update_traces(hoverinfo='label+percent', textinfo='percent', textfont_size=20,
                  marker=dict(colors=colors, line=dict(color='#000000', width=2)))
fig.update_layout(
    title_text="Outcome")
fig.show()
```

As shown from the outcome variable distriution there is no major class imbalance as the class with label 0 has 500 observations which represents 65.1% from the data and the class with label 1 has 268 observations which represents 34.9% from the data.

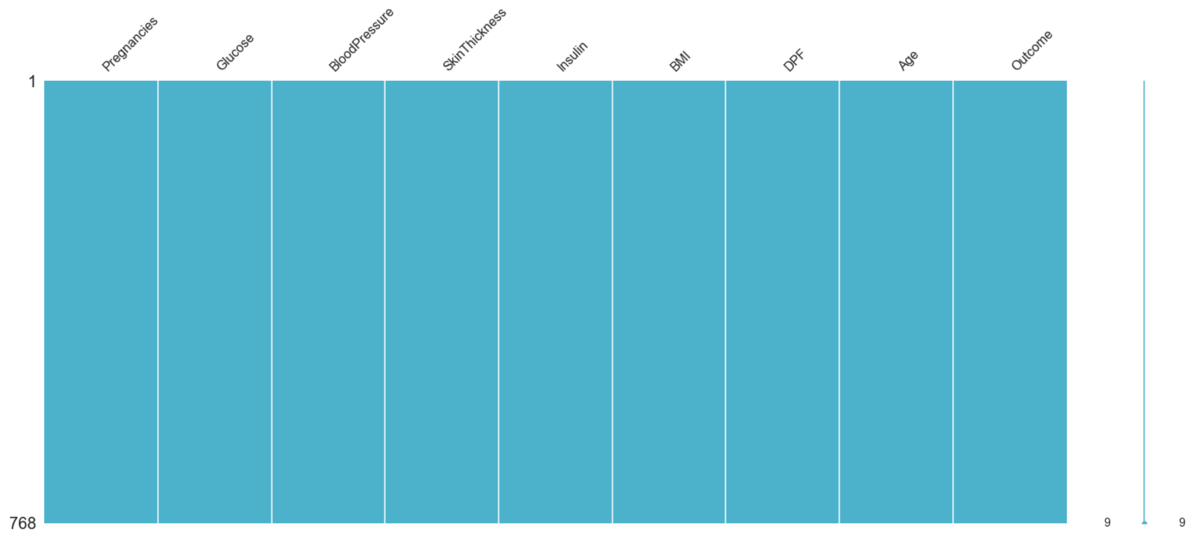
Missing Values

In [14]:

```
import missingno as msno
msno.matrix(df, color=(0.3, 0.7, 0.8))
```

Out[14]:

```
<AxesSubplot:>
```



In [15]:

```
df.isnull().sum()
```

Out[15]:

```
Pregnancies      0
Glucose          0
BloodPressure    0
SkinThickness    0
Insulin          0
BMI              0
DPF              0
Age              0
Outcome          0
dtype: int64
```

There are no missing values.

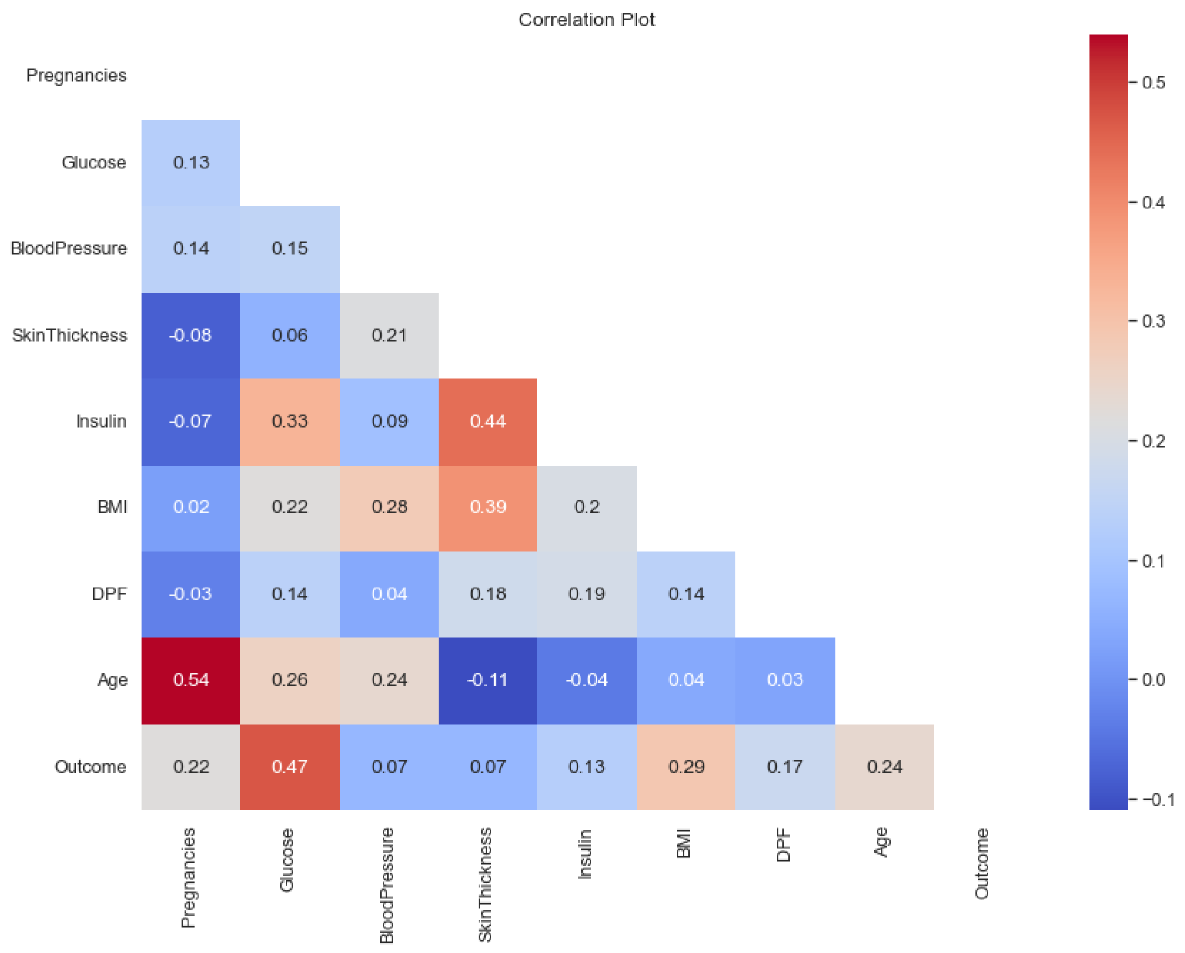
Correlation with Target Feature "Outcome"

In [16]:

```python
corr=df.corr().round(2)

sns.set(font_scale=1.15)
plt.figure(figsize=(14, 10))
sns.set_palette("bright")
sns.set_style("white")
mask = np.zeros_like(corr)
mask[np.triu_indices_from(mask)] = True
sns.heatmap(corr,annot=True,cmap='coolwarm',mask=mask,cbar=True)
plt.title('Correlation Plot')
```

Out[16]:

```
Text(0.5, 1.0, 'Correlation Plot')
```



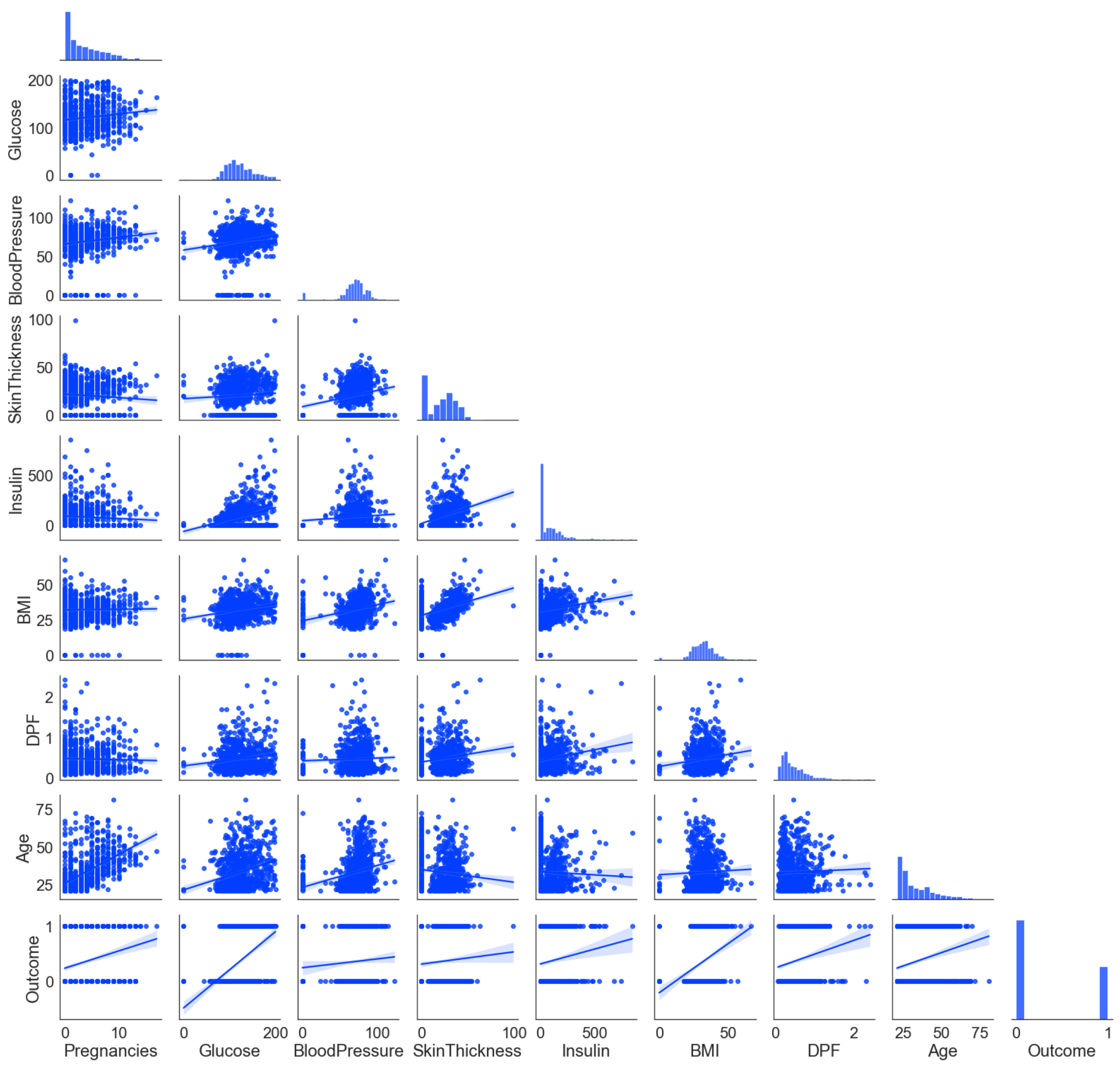
In [17]:

```
sns.set(font_scale=2)
plt.figure(figsize=(10, 8))
sns.set_style("white")
sns.set_palette("bright")
sns.pairplot(df,kind = 'reg',corner = True,palette ='YlGnBu' )
```

Out[17]:

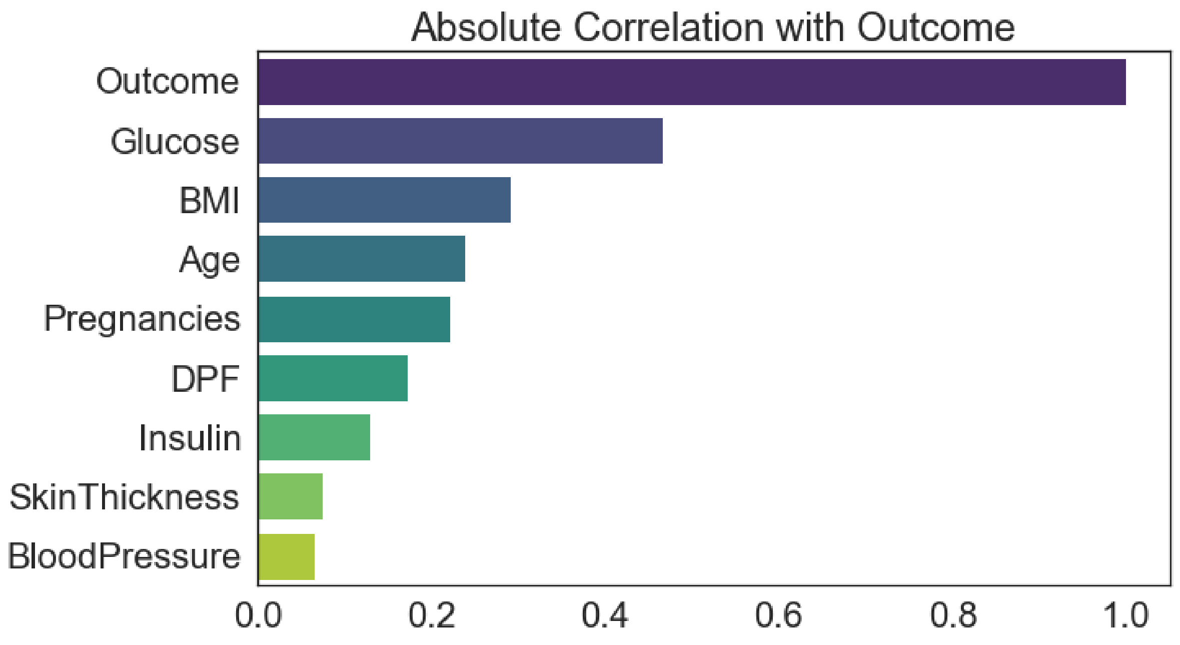
```
<seaborn.axisgrid.PairGrid at 0x28aee7fd3a0>
```

```
<Figure size 720x576 with 0 Axes>
```



In [18]:

```
correlation_matrix = df.corr()

sorted_corr_abs = correlation_matrix["Outcome"].abs().sort_values(ascending=False)

plt.figure(figsize=(10, 6))
sns.barplot(x=sorted_corr_abs.values, y=sorted_corr_abs.index, palette="viridis")
plt.title("Absolute Correlation with Outcome")
plt.show()
```



Observation:

- The correlation between Outcome and Glucose is high. Glucose seems to be the most important feature in model training.
- BMI, Pregnancies, and Age are also expected to be used as important features in model training.
- High correlation coefficient with SkinThickness and BMI. This might create a multicollinearity problem.

Checking and treating Outliers

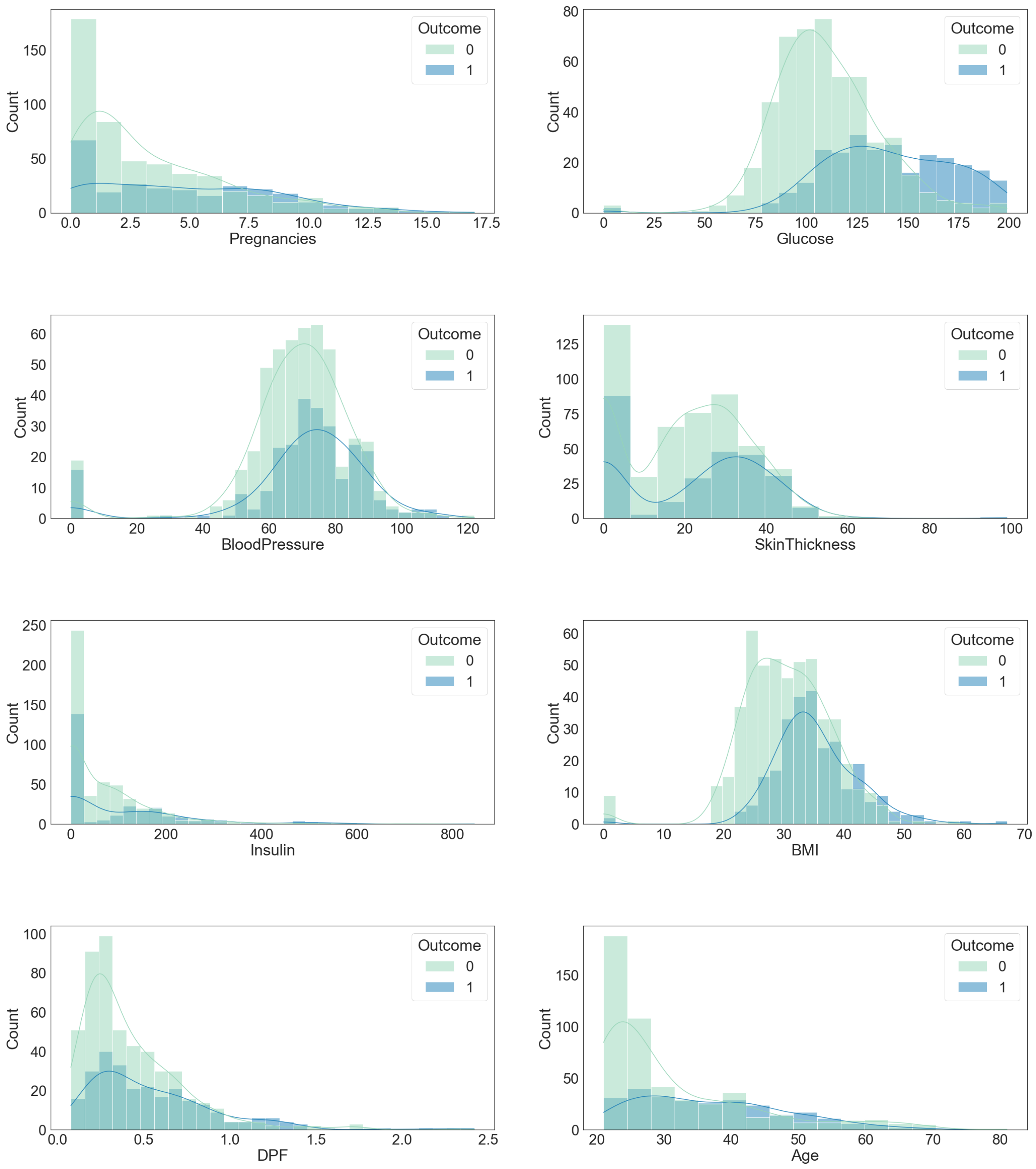
We plot our feautures without the target feauture (Outcome) to observe outliers

In [19]:

```
feature_names = [cname for cname in df.loc[:,:'Age'].columns]
```

In [20]:

```python
rcParams['figure.figsize'] = 40,60
sns.set(font_scale = 3)
sns.set_style("white")
sns.set_palette("bright")
plt.subplots_adjust(hspace=0.5)
i = 1;
for name in feature_names:
    plt.subplot(5,2,i)
    sns.histplot(data=df, x=name, hue="Outcome",kde=True,palette="YlGnBu")
    i = i + 1
```



It seems that there are a lot of features that have 0 values and these should be treated as outliers. Age & DiabetesPedigreeFunction do not have to have minimum 0 value so no need to replace , also no. of pregnancies as 0 is possible as observed.

Number of zero values in each column:

In [21]:

```
print(df[df['BloodPressure']==0].shape[0])
print(df[df['Glucose']==0].shape[0])
print(df[df['SkinThickness']==0].shape[0])
print(df[df['Insulin']==0].shape[0])
print(df[df['BMI']==0].shape[0])
```

```
35
5
227
374
11
```

It seems that there are zero values in the above 5 features, and since they do not make sense in our analysis they need to be treated. It isn't medically possible for these data records to have 0 value (such as Blood Pressure, Glucose levels, BMI). Hence we replace them with the mean/median value of that particular column.

We will treat the 5 features: Insulin, Glucose, Skin Thickness, Blood Pressure, and BMI

In [22]:

```
df[['Glucose','BloodPressure','SkinThickness','Insulin','BMI']] = df[['Glucose','Bl
                                                                      'SkinThicknes
```

all zero values are encoded with NaN value

In [23]:

```
def median_target(var):
    temp = df[df[var].notnull()]
    temp = temp[[var, 'Outcome']].groupby(['Outcome'])[[var]].median().reset_index(
    return temp
```

In [24]:

```
median_target('Insulin')
```

Out[24]:

	Outcome	Insulin
0	0	102.5
1	1	169.5

Insulin's medians by the target are really different, 102.5 for a healthy person and 169.5 for a diabetic person.

Therefore we need to replace the NaN values accordingly (and same for the next 4 features).

In [25]:

```
df.loc[(df['Outcome'] == 0 ) & (df['Insulin'].isnull()), 'Insulin'] = 102.5
df.loc[(df['Outcome'] == 1 ) & (df['Insulin'].isnull()), 'Insulin'] = 169.5
```

In [26]:

```
median_target('Glucose')
```

Out[26]:

	Outcome	Glucose
0	0	107.0
1	1	140.0

In [27]:

```
df.loc[(df['Outcome'] == 0 ) & (df['Glucose'].isnull()), 'Glucose'] = 107
df.loc[(df['Outcome'] == 1 ) & (df['Glucose'].isnull()), 'Glucose'] = 140
```

In [28]:

```
median_target('SkinThickness')
```

Out[28]:

	Outcome	SkinThickness
0	0	27.0
1	1	32.0

In [29]:

```
df.loc[(df['Outcome'] == 0 ) & (df['SkinThickness'].isnull()), 'SkinThickness'] = 2
df.loc[(df['Outcome'] == 1 ) & (df['SkinThickness'].isnull()), 'SkinThickness'] = 3
```

In [30]:

```
median_target('BloodPressure')
```

Out[30]:

	Outcome	BloodPressure
0	0	70.0
1	1	74.5

In [31]:

```
df.loc[(df['Outcome'] == 0 ) & (df['BloodPressure'].isnull()), 'BloodPressure'] = 7
df.loc[(df['Outcome'] == 1 ) & (df['BloodPressure'].isnull()), 'BloodPressure'] = 7
```

In [32]:

```
median_target('BMI')
```

Out[32]:

	Outcome	BMI
0	0	30.1
1	1	34.3

In [33]:

```
df.loc[(df['Outcome'] == 0 ) & (df['BMI'].isnull()), 'BMI'] = 30.1
df.loc[(df['Outcome'] == 1 ) & (df['BMI'].isnull()), 'BMI'] = 34.3
```

In [34]:

```
print(df[df['BloodPressure']==0].shape[0])
print(df[df['Glucose']==0].shape[0])
print(df[df['SkinThickness']==0].shape[0])
print(df[df['Insulin']==0].shape[0])
print(df[df['BMI']==0].shape[0])
```

```
0
0
0
0
0
```

Now we do not have zero values.

Adding New Features

In [35]:

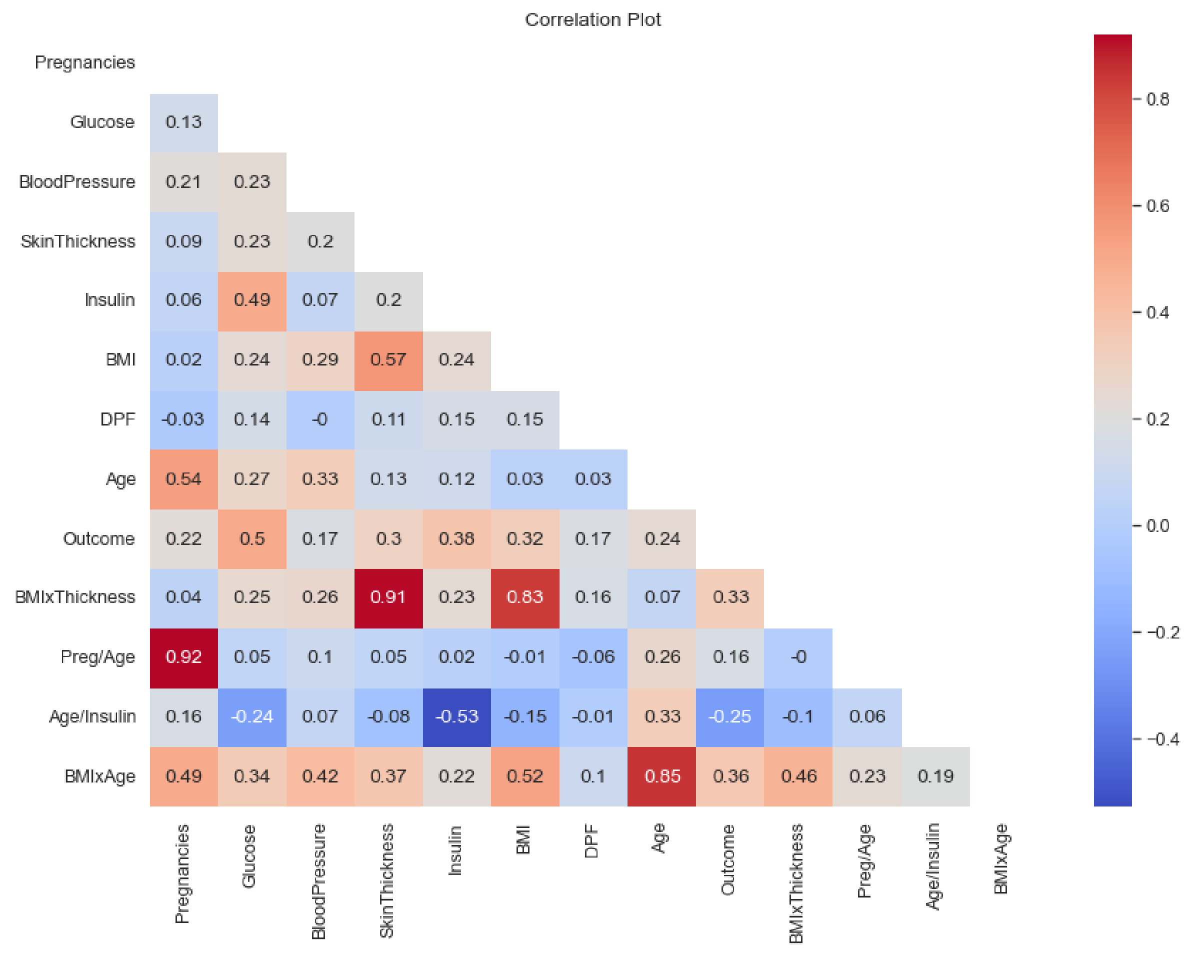
```
df['BMIxThickness'] = df['BMI'] * df['SkinThickness']

df['Preg/Age'] =  df['Pregnancies'] / df['Age']

df['Age/Insulin'] = df['Age'] / df['Insulin']

df['BMIxAge'] = df['BMI'] * df['Age']
```

In [36]:

```python
corr=df.corr().round(2)

sns.set(font_scale=1.15)
plt.figure(figsize=(14, 10))
sns.set_palette("bright")
sns.set_style("white")
mask = np.zeros_like(corr)
mask[np.triu_indices_from(mask)] = True
sns.heatmap(corr,annot=True,cmap='coolwarm',mask=mask,cbar=True)
plt.title('Correlation Plot')
```

Out[36]:

```
Text(0.5, 1.0, 'Correlation Plot')
```

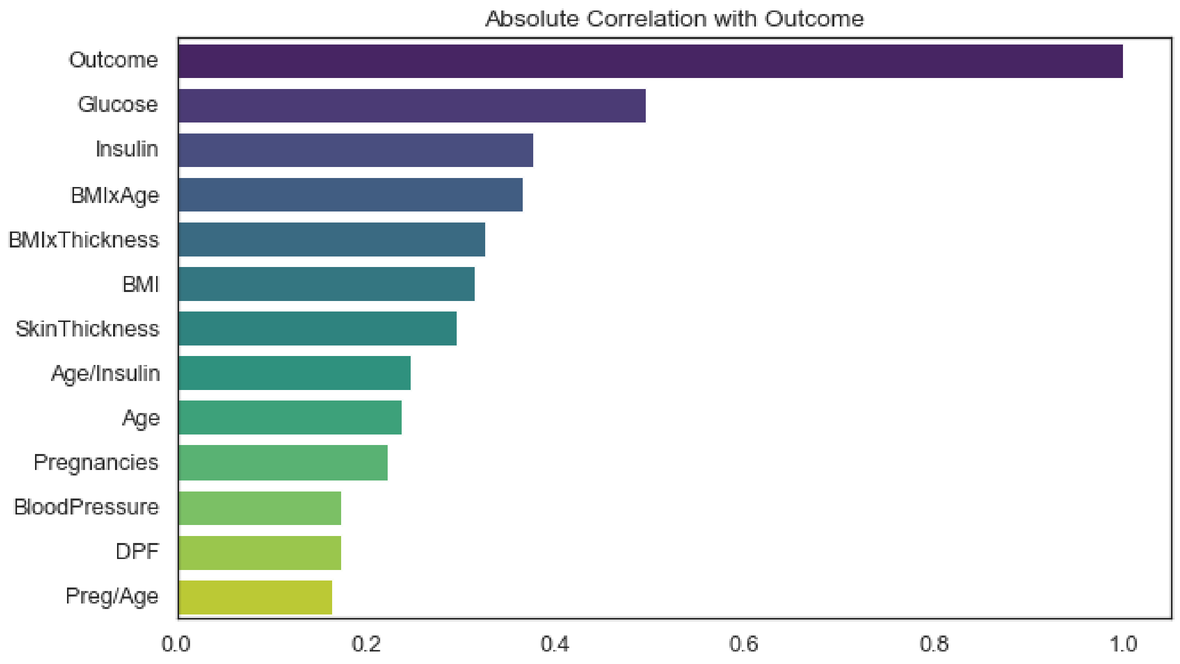


We inserted new features and they seem to have stronger correlations so they might be better used for prediction.

We will sort the correlation to observe which features have the strongest relation to Outcome:

In [37]:

```
correlation_matrix = df.corr()

sorted_corr_abs = correlation_matrix["Outcome"].abs().sort_values(ascending=False)

plt.figure(figsize=(10, 6))
sns.barplot(x=sorted_corr_abs.values, y=sorted_corr_abs.index, palette="viridis")
plt.title("Absolute Correlation with Outcome")
plt.show()
```



Features Selection according to semantic importance / relevance

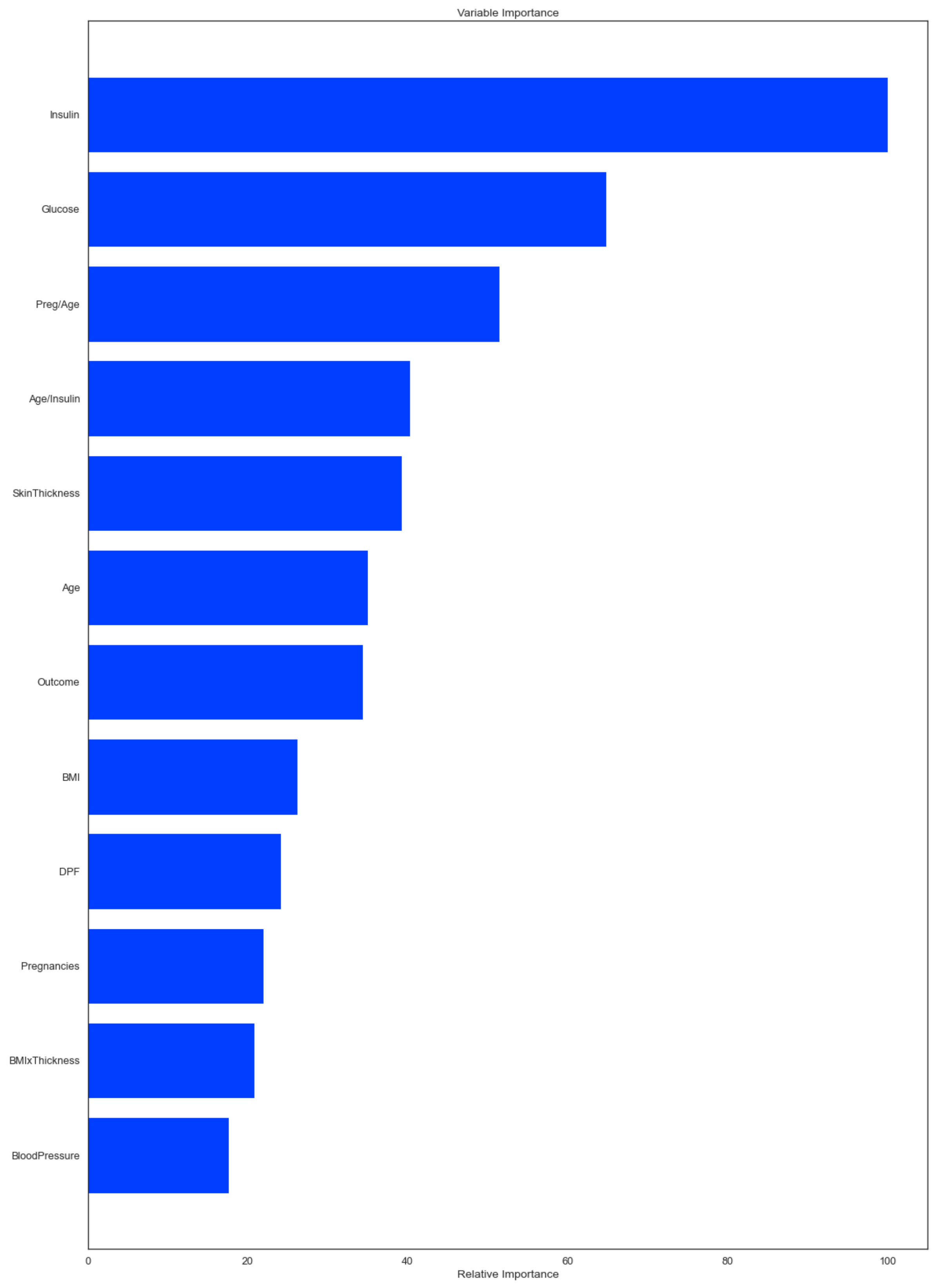
Extra Trees can be used to estimate the importance of features.

In [38]:

```
from sklearn.model_selection import train_test_split

df_clean_name = df.columns
X_c = df.drop('Outcome', axis=1)  # Use iloc to select columns by index
Y_c = df['Outcome']

X_train_c, X_test_c, y_train_c, y_test_c = train_test_split(X_c, Y_c,
                                                            test_size=0.25,
                                                            random_state=0,
                                                            stratify=df['Outcome'])
```

In [39]:

```
from sklearn.ensemble import ExtraTreesClassifier
clf = ExtraTreesClassifier(n_estimators=250,
                              random_state=7)

clf.fit(X_train_c, y_train_c)

# Plot feature importance
feature_importance = clf.feature_importances_
# make importances relative to max importance
feature_importance = 100.0 * (feature_importance / feature_importance.max())
sorted_idx = np.argsort(feature_importance)
pos = np.arange(sorted_idx.shape[0]) + .5
plt.subplot(2, 2, 2)
plt.barh(pos, feature_importance[sorted_idx], align='center')
plt.yticks(pos, df.columns[sorted_idx])#boston.feature_names[sorted_idx])
plt.xlabel('Relative Importance')
plt.title('Variable Importance')
plt.show()
```



Best K Features can also be used to select the best features.

In [40]:

```
from sklearn.datasets import load_diabetes
from sklearn.feature_selection import SelectKBest, chi2
from sklearn.model_selection import train_test_split
import pandas as pd

X = df.drop('Outcome', axis=1)
y = df['Outcome']

# Split the data into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.25, random_st

# Use SelectKBest with chi2 for feature selection
k_features = 7  # Specify the number of features to select
X_train_selected = SelectKBest(chi2, k=k_features).fit_transform(X_train, y_train)
X_test_selected = SelectKBest(chi2, k=k_features).fit_transform(X_test, y_test)

print(f"Original shape of X_train: {X_train.shape}")
print(f"Shape of X_train after feature selection: {X_train_selected.shape}")
print(f"Original shape of X_test: {X_test.shape}")
print(f"Shape of X_test after feature selection: {X_test_selected.shape}")
```

```
Original shape of X_train: (576, 12)
Shape of X_train after feature selection: (576, 7)
Original shape of X_test: (192, 12)
Shape of X_test after feature selection: (192, 7)
```

In [41]:

```
selector = SelectKBest(chi2, k=k_features).fit(X_train, y_train)

selected_features_indices = selector.get_support(indices=True)


selected_features_names = X.columns[selected_features_indices]

print(f"Selected features: {selected_features_names}")
```

```
Selected features: Index(['Pregnancies', 'Glucose', 'SkinThickness',
'Insulin', 'Age',
       'BMIxThickness', 'BMIxAge'],
      dtype='object')
```

Regularized Logistic Regression can also be used to select the best features

In [42]:

```
from sklearn.linear_model import LogisticRegression
from sklearn.feature_selection import SelectFromModel
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler

X = df.drop('Outcome', axis=1)
y = df['Outcome']

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.25, random_st

# Standardizing the features before choosing the best ones
scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test)

logreg = LogisticRegression(penalty='l1', solver='liblinear', random_state=0)

logreg.fit(X_train_scaled, y_train)

model = SelectFromModel(logreg, prefit=True)


X_train_selected = model.transform(X_train_scaled)
X_test_selected = model.transform(X_test_scaled)

selected_features = X.columns[model.get_support()]
print("Selected Features:", selected_features)
```

```
Selected Features: Index(['Glucose', 'BloodPressure', 'SkinThicknes
s', 'BMI', 'DPF', 'Age',
       'Preg/Age', 'Age/Insulin', 'BMIxAge'],
      dtype='object')
```

Extra Trees, K Best Features, and Regularized Logistics Regression produced slightly different results, we will choose the common features between them

In [43]:

```
df_feature_imp=df[['Pregnancies','Glucose','SkinThickness','Insulin','Age','BMIxThi
```

It seems that the features Pregnancies, Glucose, Insulin, SkinThickness, Age, BMIxThickness, and BMIxAge had the highest relative importance and therefore were selected to our final clean dataset

Normalizing the data

In [66]:

```
earn.preprocessing import StandardScaler
earn.preprocessing import MinMaxScaler
earn.pipeline import Pipeline
earn.linear_model import LogisticRegression
earn.tree import DecisionTreeClassifier
earn.neighbors import KNeighborsClassifier
earn.discriminant_analysis import LinearDiscriminantAnalysis
earn.naive_bayes import GaussianNB
earn.svm import SVC
earn.ensemble import AdaBoostClassifier
earn.ensemble import GradientBoostingClassifier
earn.ensemble import RandomForestClassifier
das import set_option
earn.preprocessing import StandardScaler
earn.model_selection import train_test_split
earn.model_selection import KFold
earn.model_selection import StratifiedKFold
earn.model_selection import cross_val_score
earn.model_selection import GridSearchCV
earn.metrics import classification_report
earn.metrics import confusion_matrix
earn.metrics import accuracy_score
lotly.offline as py
lotly.graph_objs as go
lotly.tools as tls
arnings
.filterwarnings('ignore')


caledModel(nameOfScaler):

ameOfScaler == 'standard':
scaler = StandardScaler()
 nameOfScaler =='minmax':
scaler = MinMaxScaler()

lines = []
lines.append((nameOfScaler+'LR'   , Pipeline([('Scaler', scaler),('LR'   , LogisticRe
lines.append((nameOfScaler+'LDA'  , Pipeline([('Scaler', scaler),('LDA'  , LinearDisc
lines.append((nameOfScaler+'KNN'  , Pipeline([('Scaler', scaler),('KNN'  , KNeighbors
lines.append((nameOfScaler+'CART', Pipeline([('Scaler', scaler),('CART', DecisionTr
lines.append((nameOfScaler+'NB'   , Pipeline([('Scaler', scaler),('NB'   , GaussianNB
lines.append((nameOfScaler+'SVM'  , Pipeline([('Scaler', scaler),('SVM'  , SVC())])))
lines.append((nameOfScaler+'AB'   , Pipeline([('Scaler', scaler),('AB'   , AdaBoostCl
lines.append((nameOfScaler+'GBM'  , Pipeline([('Scaler', scaler),('GMB'  , GradientBo
lines.append((nameOfScaler+'RF'   , Pipeline([('Scaler', scaler),('RF'   , RandomFore
lines.append((nameOfScaler+'ET'   , Pipeline([('Scaler', scaler),('ET'   , ExtraTrees


rn pipelines
```

In [67]:

```
def BasedLine2(X_train, y_train,models):
    # Test options and evaluation metric
    num_folds = 10
    scoring = 'accuracy'

    results = []
    names = []
    for name, model in models:
        kfold = StratifiedKFold(n_splits=num_folds)
        cv_results = cross_val_score(model, X_train, y_train, cv=kfold, scoring=sco
        results.append(cv_results)
        names.append(name)
        msg = "%s: %f (%f)" % (name, cv_results.mean(), cv_results.std())
        print(msg)

    return names, results
```

In [68]:

```
from sklearn.model_selection import train_test_split

df_clean_name = df_feature_imp.columns
X = df_feature_imp.drop('Outcome', axis=1)  # Use iloc to select columns by index
Y = df_feature_imp['Outcome']

X_train, X_test, y_train, y_test = train_test_split(X, Y,
                                                     test_size=0.25,
                                                     random_state=0,
                                                     stratify=df_feature_imp
```

In [69]:

```
class PlotBoxR(object):


    def __Trace(self,nameOfFeature,value):

        trace = go.Box(
            y=value,
            name = nameOfFeature,
            marker = dict(
                color = 'rgb(0, 128, 128)',
            )
        )
        return trace

    def PlotResult(self,names,results):

        data = []

        for i in range(len(names)):
            data.append(self.__Trace(names[i],results[i]))


        py.iplot(data)
```

In [70]:

```
def ScoreDataFrame(names,results):
    def floatingDecimals(f_val, dec=3):
        prc = "{:."+str(dec)+"f}"

        return float(prc.format(f_val))

    scores = []
    for r in results:
        scores.append(floatingDecimals(r.mean(),4))

    scoreDataFrame = pd.DataFrame({'Model':names, 'Score': scores})
    return scoreDataFrame
```

In [71]:

```
def ScoreDataFrame(names,results):
    def floatingDecimals(f_val, dec=3):
        prc = "{:."+str(dec)+"f}"

        return float(prc.format(f_val))

    scores = []
    for r in results:
        scores.append(floatingDecimals(r.mean(),4))

    scoreDataFrame = pd.DataFrame({'Model':names, 'Score': scores})
    return scoreDataFrame
```

In [72]:

```
basedLineScore = ScoreDataFrame(names,results)
basedLineScore
```

Out[72]:

	Model	Score
0	minmaxLR	0.7814
1	minmaxLDA	0.7866
2	minmaxKNN	0.7794
3	minmaxCART	0.8490
4	minmaxNB	0.7658
5	minmaxSVM	0.8249
6	minmaxAB	0.8716
7	minmaxGBM	0.8839
8	minmaxRF	0.8907
9	minmaxET	0.8769

In [73]:

```
models = GetScaledModel('minmax')
names,results = BasedLine2(X_train, y_train,models)
PlotBoxR().PlotResult(names,results)

scaledScoreStandard = ScoreDataFrame(names,results)
scaledScoreMinMax = ScoreDataFrame(names,results)
compareModels = pd.concat([basedLineScore,
                           scaledScoreStandard,
                          scaledScoreMinMax], axis=1)
compareModels
```

```
minmaxLR: 0.781397 (0.031097)
minmaxLDA: 0.786630 (0.030849)
minmaxKNN: 0.779431 (0.035329)
minmaxCART: 0.850817 (0.021389)
minmaxNB: 0.765759 (0.040377)
minmaxSVM: 0.824894 (0.038861)
minmaxAB: 0.871627 (0.032745)
minmaxGBM: 0.885602 (0.029546)
minmaxRF: 0.889020 (0.026566)
minmaxET: 0.869994 (0.030459)
```

Out[73]:

	Model	Score	Model	Score	Model	Score
0	minmaxLR	0.7814	minmaxLR	0.7814	minmaxLR	0.7814
1	minmaxLDA	0.7866	minmaxLDA	0.7866	minmaxLDA	0.7866
2	minmaxKNN	0.7794	minmaxKNN	0.7794	minmaxKNN	0.7794
3	minmaxCART	0.8490	minmaxCART	0.8508	minmaxCART	0.8508
4	minmaxNB	0.7658	minmaxNB	0.7658	minmaxNB	0.7658
5	minmaxSVM	0.8249	minmaxSVM	0.8249	minmaxSVM	0.8249
6	minmaxAB	0.8716	minmaxAB	0.8716	minmaxAB	0.8716
7	minmaxGBM	0.8839	minmaxGBM	0.8856	minmaxGBM	0.8856
8	minmaxRF	0.8907	minmaxRF	0.8890	minmaxRF	0.8890
9	minmaxET	0.8769	minmaxET	0.8700	minmaxET	0.8700

Scaled features

In [74]:

```
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test)
```

In [75]:

```
scaler = MinMaxScaler()
```

After dataset normalization, all classifiers proved a score above 0.7 which is relatively good.

In [76]:

```
X_train_scaled_df = pd.DataFrame(X_train_scaled, columns=X_train.columns)
X_test_scaled_df = pd.DataFrame(X_test_scaled, columns=X_test.columns)
```

In [77]:

```
X_train_scaled_df.reset_index(drop=True, inplace=True)
X_test_scaled_df.reset_index(drop=True, inplace=True)

y_train.reset_index(drop=True, inplace=True)
y_test.reset_index(drop=True, inplace=True)

#Putting the training and testing sets back together into one dataset to describe
combined_features_df = pd.concat([X_train_scaled_df, X_test_scaled_df], axis=0)
combined_target = pd.concat([y_train, y_test], axis=0)
final_df = pd.concat([combined_features_df, combined_target], axis=1)
```

In [78]:

```
final_df.describe()
```

Out[78]:

	Pregnancies	Glucose	SkinThickness	Insulin	Age	BMIxThickness	BMIx
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.00
mean	0.226180	0.501142	0.240107	0.153550	0.204015	0.233260	0.30
std	0.198210	0.196543	0.096639	0.107092	0.196004	0.125907	0.18
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.00
25%	0.058824	0.359677	0.195652	0.106370	0.050000	0.146290	0.15
50%	0.176471	0.470968	0.228261	0.106370	0.133333	0.218169	0.26
75%	0.352941	0.620968	0.271739	0.186899	0.333333	0.295569	0.42
max	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.00

In [79]:

```
final_df.shape
```

Out[79]:

```
(768, 8)
```

Our final dataset contains 8 features including the target feature "Outcome".

It does not have any missing values nor incorrect zero values.

Therefore we will continue our project with the final clean dataset after preprocessing and feature engineering.