Acknowledgment to the poster of this data set. Username 'fedesoriano' from Kaggle.com

Here is a comprehensive list of the columns in this dataset and their corresponding meanings. The following list is directly copy/pasted from the original user's post.

- ***id:*** **unique identifier**
- ***gender:*** **"Male", "Female" or "Other"**
- ***age:*** **age of the patient**
- ***hypertension:*** **0 if the patient doesn't have hypertension, 1 if the patient has hypertension**
- ***heart_disease:*** **0 if the patient doesn't have any heart diseases, 1 if the patient has a heart disease**
- ***ever_married:*** **"No" or "Yes"**
- ***work_type:*** **"children", "Govt_jov", "Never_worked", "Private" or "Self-employed"**
- ***Residence_type:*** **"Rural" or "Urban"**
- ***avg_glucose_level:*** **average glucose level in blood**
- ***bmi:*** **body mass index**
- ***smoking_status:*** **"formerly smoked", "never smoked", "smokes" or "Unknown"**
- ***stroke:*** **1 if the patient had a stroke or 0 if not**

Note: **"Unknown" in smoking_status means that the information is unavailable for this patient**

In [1]:

```
import pandas as pd
import seaborn as sns
import numpy as np
import category_encoders as ce
from sklearn.preprocessing import StandardScaler, MinMaxScaler, RobustScaler
from sklearn.model_selection import train_test_split
from sklearn.metrics import r2_score, mean_squared_error, f1_score, plot_confusion_matrix
, accuracy_score, precision_score, recall_score
```

In [2]:

```
df = pd.read_csv('PredictStrokes/healthcare-dataset-stroke-data.csv')
df
```

Out[2]:

	id	gender	age	hypertension	heart_disease	ever_married	work_type	Residence_type	avg_glucose_level	bmi	sr
0	9046	Male	67.0	0	1	Yes	Private	Urban	228.69	36.6	
1	51676	Female	61.0	0	0	Yes	Self-employed	Rural	202.21	NaN	
2	31112	Male	80.0	0	1	Yes	Private	Rural	105.92	32.5	
3	60182	Female	49.0	0	0	Yes	Private	Urban	171.23	34.4	
4	1665	Female	79.0	1	0	Yes	Self-employed	Rural	174.12	24.0	
...	...	...	...	...	...	...	...	...	...	...	
5105	18234	Female	80.0	1	0	Yes	Private	Urban	83.75	NaN	
5106	44873	Female	81.0	0	0	Yes	Self-employed	Urban	125.20	40.0	
5107	19723	Female	35.0	0	0	Yes	Self-employed	Rural	82.99	30.6	
5108	37544	Male	51.0	0	0	Yes	Private	Rural	166.29	25.6	
5109	44679	Female	44.0	0	0	Yes	Govt_job	Urban	85.28	26.2	

5110 rows × 12 columns

In [3]:

```
#This is just to rename the columns because I don't like underscores
df = df.rename(columns = {'heart_disease': 'heartDisease'})
df = df.rename(columns = {'ever_married': 'everMarried'})
df = df.rename(columns = {'work_type': 'workType'})
df = df.rename(columns = {'Residence_type': 'residenceType'})
df = df.rename(columns = {'avg_glucose_level': 'avgGlucoseLevel'})
df = df.rename(columns = {'smoking_status': 'smokingStatus'})
```

In [4]:

```
len(df['id'])
```

Out[4]:

```
5110
```

First look at the data

First thing I noticed is that this data set seem pretty small. 5,110 records. I don't have much room to remove data so I'll need to avoid that as much as possible.

Let's check for anything that might cause problems in our data.

In [5]:

```
df.isna().sum()
```

Out[5]:

```
id                   0
gender               0
age                  0
hypertension         0
heartDisease         0
everMarried          0
workType             0
residenceType        0
avgGlucoseLevel      0
bmi                201
smokingStatus        0
stroke               0
dtype: int64
```

In [6]:

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 5110 entries, 0 to 5109
Data columns (total 12 columns):
id                 5110 non-null int64
gender             5110 non-null object
age                5110 non-null float64
hypertension       5110 non-null int64
heartDisease       5110 non-null int64
everMarried        5110 non-null object
workType           5110 non-null object
residenceType      5110 non-null object
avgGlucoseLevel    5110 non-null float64
bmi                4909 non-null float64
smokingStatus      5110 non-null object
stroke             5110 non-null int64
dtypes: float64(3), int64(4), object(5)
memory usage: 479.2+ KB
```

In [7]:

```
df['gender'].value_counts()
```

Out[7]:

```
Female    2994
Male      2115
Other        1
Name: gender, dtype: int64
```

In [8]:

```
df['everMarried'].value_counts()
```

Out[8]:

```
Yes    3353
No     1757
Name: everMarried, dtype: int64
```

In [9]:

```
df['workType'].value_counts()
```

Out[9]:

```
Private          2925
Self-employed     819
children          687
Govt_job          657
Never_worked       22
Name: workType, dtype: int64
```

In [10]:

```
df['residenceType'].value_counts()
```

Out[10]:

```
Urban    2596
Rural    2514
Name: residenceType, dtype: int64
```

In [11]:

```
df['smokingStatus'].value_counts()
```

Out[11]:

```
never smoked       1892
Unknown            1544
formerly smoked     885
smokes              789
Name: smokingStatus, dtype: int64
```

In [12]:

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 5110 entries, 0 to 5109
Data columns (total 12 columns):
id                   5110 non-null int64
gender               5110 non-null object
age                  5110 non-null float64
hypertension         5110 non-null int64
heartDisease         5110 non-null int64
everMarried          5110 non-null object
workType             5110 non-null object
residenceType        5110 non-null object
avgGlucoseLevel      5110 non-null float64
bmi                  4909 non-null float64
smokingStatus        5110 non-null object
smokingStatus      5110 non-null object
stroke             5110 non-null int64
dtypes: float64(3), int64(4), object(5)
memory usage: 479.2+ KB
```

Here are some places where I see some problems.

- **BMI has 201 records with missing info.**
- **gender, hypertension, heartDisease, everMarried, residenceType, and stroke look like their a bianary classification. Simply a 'yes' or 'no' answer. No reason we can't make it a '1' or a '0'**
- **workType and smokingStatus seems to be broken up into categories. I see no reason why we couldn't use a category encoder.**
- **'id' may cause noise in our data so let's remove that column to avoid it.**

Cleaning the data

Let's go through each one and start to solve the problems that come up, starting with dealing with the NaN values in BMI. Our records only have about 5,000 records to start with so removing 201 records is a lot of data being removed. The safest thing to do without swkeing the data is to take an average of everything in this column and fill in the NaN's with the average.

In [13]:

```
df = df.fillna(df.mean())
df.isna().sum()
```

Out[13]:

```
id                 0
gender             0
age                0
hypertension       0
heartDisease       0
everMarried        0
workType           0
residenceType      0
avgGlucoseLevel    0
bmi                0
smokingStatus      0
stroke             0
dtype: int64
```

Sweet. Simple and clean, like my favorite song. Next, let's deal with the columns that could be a binary answer. Since hyptertension, heartDisease, and stroke are already binary 1's and 0's we can leave them alone. Let's deal with gender and everMarried

In [14]:

```
df
```

Out[14]:

	id	gender	age	hypertension	heartDisease	everMarried	workType	residenceType	avgGlucoseLevel	bmi	s
0	9046	Male	67.0	0	1	Yes	Private	Urban	228.69	36.600000	
1	51676	Female	61.0	0	0	Yes	Self-employed	Rural	202.21	28.893237	
2	31112	Male	80.0	0	1	Yes	Private	Rural	105.92	32.500000	
3	60182	Female	49.0	0	0	Yes	Private	Urban	171.23	34.400000	
4	1665	Female	79.0	1	0	Yes	Self-employed	Rural	174.12	24.000000	
...	...	...	...	...	...	...	...	...	...	...	
5105	18234	Female	80.0	1	0	Yes	Private	Urban	83.75	28.893237	

	id	gender	age	hypertension	heartDisease	everMarried	workType	residenceType	avgGlucoseLevel	bmi	s
5106	44873	Female	81.0	0	0	Yes	Self-employed	Urban	125.20	40.000000	
5107	19723	Female	35.0	0	0	Yes	Self-employed	Rural	82.99	30.600000	
5108	37544	Male	51.0	0	0	Yes	Private	Rural	166.29	25.600000	
5109	44679	Female	44.0	0	0	Yes	Govt_job	Urban	85.28	26.200000	

5110 rows × 12 columns

In [15]:

```
#These are the lists vlaues we want replaced
genderList = ['Male', 'Female']
marriedList = ['No', 'Yes']
residenceList = ['Urban', 'Rural']
```

In [16]:

```
#This function takes in a list of old values to find,
# and the specific column name we wish to apply this function to.
#What it returns is the modified df with the column was spcified,
#turned into a binary classification.

def makeBinary(oldList, columnName):
    binaryList = [0, 1]
    newVals = dict(zip(oldList, binaryList))
    return df[columnName].replace(newVals, inplace = True)

makeBinary(genderList, 'gender')
```

In [17]:

```
df['gender'].value_counts()
```

Out[17]:

```
1         2994
0         2115
Other        1
Name: gender, dtype: int64
```

Shoots, almost. We missed one. Fortunately, removing one row isn't that big a deal, let's just drop them.

In [18]:

```
df.drop(df[df['gender'] == 'Other'].index, inplace = True)
```

In [19]:

```
df['gender'].value_counts()
```

Out[19]:

```
1    2994
0    2115
Name: gender, dtype: int64
```

Success! Next is married. Second verse, same as the first. We'll apply the makeBinary function to the everMarried column the same way, with the marriedList we set aside earlier.

In [20]:

```
makeBinary(marriedList, 'everMarried')
```

In [21]:

```
df
```

Out[21]:

	id	gender	age	hypertension	heartDisease	everMarried	workType	residenceType	avgGlucoseLevel	bmi	s
0	9046	0	67.0	0	1	1	Private	Urban	228.69	36.600000	
1	51676	1	61.0	0	0	1	Self-employed	Rural	202.21	28.893237	
2	31112	0	80.0	0	1	1	Private	Rural	105.92	32.500000	
3	60182	1	49.0	0	0	1	Private	Urban	171.23	34.400000	
4	1665	1	79.0	1	0	1	Self-employed	Rural	174.12	24.000000	
...	...	...	...	...	...	...	...	...	...	...	
5105	18234	1	80.0	1	0	1	Private	Urban	83.75	28.893237	
5106	44873	1	81.0	0	0	1	Self-employed	Urban	125.20	40.000000	
5107	19723	1	35.0	0	0	1	Self-employed	Rural	82.99	30.600000	
5108	37544	0	51.0	0	0	1	Private	Rural	166.29	25.600000	
5109	44679	1	44.0	0	0	1	Govt_job	Urban	85.28	26.200000	

5109 rows × 12 columns

In [22]:

```
df['everMarried'].value_counts()
```

Out[22]:

```
1    3353
0    1756
Name: everMarried, dtype: int64
```

In [23]:

```
makeBinary(residenceList, 'residenceType')
```

In [24]:

```
df['residenceType'].value_counts()
```

Out[24]:

```
0    2596
1    2513
Name: residenceType, dtype: int64
```

Success again! Lastly, let's drop 'id' and let's move on to starting our model!

In [25]:

```
df = df.drop(['id'], axis = 1)
```

Step 1: Testing different model types

In this section we'll test and fit a number of different models onto our data to see which one's make the most sense and give us the best predictions in our results. We're not just looking at how good our scores are but how accurate our models are from the start.

Note: When we start to look at our model, 0's will represent a "No" meaning "This patient has *not* had a stroke before."

1's will represent "Yes" meaning "This patient *has* had a stroke before.

In [26]:

```
df
```

Out[26]:

	gender	age	hypertension	heartDisease	everMarried	workType	residenceType	avgGlucoseLevel	bmi	smoking
0	0	67.0	0	1	1	Private	0	228.69	36.600000	fo sr
1	1	61.0	0	0	1	Self-employed	1	202.21	28.893237	never sr
2	0	80.0	0	1	1	Private	1	105.92	32.500000	never sr
3	1	49.0	0	0	1	Private	0	171.23	34.400000	sr
4	1	79.0	1	0	1	Self-employed	1	174.12	24.000000	never sr
...	...	...	...	...	...	...	...	...	...	
5105	1	80.0	1	0	1	Private	0	83.75	28.893237	never sr
5106	1	81.0	0	0	1	Self-employed	0	125.20	40.000000	never sr
5107	1	35.0	0	0	1	Self-employed	1	82.99	30.600000	never sr
5108	0	51.0	0	0	1	Private	1	166.29	25.600000	fo sr
5109	1	44.0	0	0	1	Govt_job	0	85.28	26.200000	Unl

5109 rows × 11 columns

In [27]:

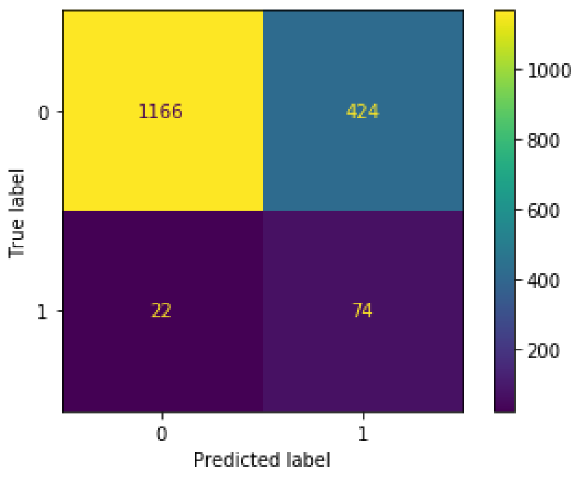
```
#Data Prep

#Scales my data
scaler = StandardScaler()
#Ecoder to categorize onto cols 'workType' and 'smokingStatus'
encoder = ce.CountEncoder(cols = ['workType', 'smokingStatus'])

xCols = [c for c in df.columns.to_list() if c not in ['stroke']]

x = df[xCols]
y = df['stroke']

xTrain, xTest, yTrain, yTest = train_test_split(
    x, y, test_size=0.33, random_state=42)

xTrainEncoded = encoder.fit_transform(xTrain)
xTestEncoded = encoder.transform(xTest)

xTrainScaled = scaler.fit_transform(xTrainEncoded)
xTestScaled = scaler.transform(xTestEncoded)
```

In [28]:

```
from sklearn.linear_model import LogisticRegression

logReg = LogisticRegression(random_state = 123, class_weight = 'balanced')
logReg.fit(xTrainScaled, yTrain)
```

```
yPredTrain = logReg.predict(xTrainScaled)
yPredTest = logReg.predict(xTestScaled)

plot_confusion_matrix(logReg, xTestScaled, yTest)

print(f"Accuracy Train Score: {accuracy_score(yTrain, yPredTrain)}")
print(f"Accuracy Test Score: {accuracy_score(yTest, yPredTest)}")
print('-----')
print(f"F1-Train Score: {f1_score(yTrain, yPredTrain)}")
print(f"F1-Test Score: {f1_score(yTest, yPredTest)}")
print('-----')
print(f"Precision Train Score: {precision_score(yTrain, yPredTrain)}")
print(f"Precision Test Score: {precision_score(yTest, yPredTest)}")
print('-----')
print(f"Recall Train Score: {recall_score(yTrain, yPredTrain, average='weighted')}")
print(f"Recall Test Score: {recall_score(yTest, yPredTest, average='weighted')}")
print('-----')
print('0 is "Not at risk of a stroke"')
print('1 is "At risk of a stroke"')
```

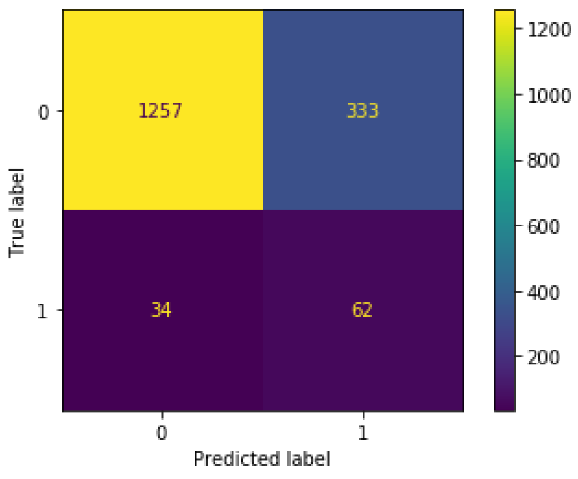
```
Accuracy Train Score: 0.7449605609114811
Accuracy Test Score: 0.7354685646500593
-----
F1-Train Score: 0.22399999999999998
F1-Test Score: 0.24915824915824913
-----
Precision Train Score: 0.12962962962962962
Precision Test Score: 0.14859437751004015
-----
Recall Train Score: 0.7449605609114811
Recall Test Score: 0.7354685646500593
-----
0 is "Not at risk of a stroke"
1 is "At risk of a stroke"
```



In [29]:

```
from sklearn.svm import SVC

clf = SVC(random_state=0, class_weight = 'balanced')
clf.fit(xTrainScaled, yTrain)

yPredTrain = clf.predict(xTrainScaled)
yPredTest = clf.predict(xTestScaled)

plot_confusion_matrix(clf, xTestScaled, yTest)

print(f"Accuracy Train Score: {accuracy_score(yTrain, yPredTrain)}")
print(f"Accuracy Test Score: {accuracy_score(yTest, yPredTest)}")
print('-----')
print(f"F1-Train Score: {f1_score(yTrain, yPredTrain)}")
print(f"F1-Test Score: {f1_score(yTest, yPredTest)}")
print('-----')
print(f"Precision Train Score: {precision_score(yTrain, yPredTrain)}")
print(f"Precision Test Score: {precision_score(yTest, yPredTest)}")
print('-----')
print(f"Recall Train Score: {recall_score(yTrain, yPredTrain, average='weighted')}")
print(f"Recall Test Score: {recall_score(yTest, yPredTest, average='weighted')}")
print('-----')
print('0 is "Not at risk of a stroke"')
print('1 is "At risk of a stroke"')
```

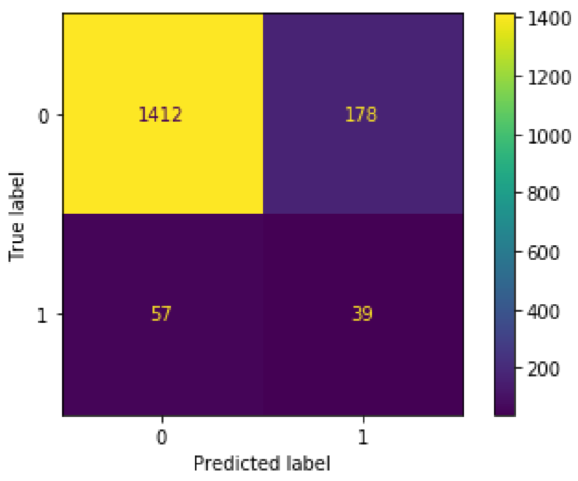
```
Accuracy Train Score: 0.8051416885772714
Accuracy Test Score: 0.7823250296559905
-----
F1-Train Score: 0.2866310160427808
F1-Test Score: 0.2525458248472505
-----
Precision Train Score: 0.17135549872122763
Precision Test Score: 0.1569620253164557
-----
Recall Train Score: 0.8051416885772714
Recall Test Score: 0.7823250296559905
-----
0 is "Not at risk of a stroke"
1 is "At risk of a stroke"
```



In [30]:

```
from sklearn.naive_bayes import GaussianNB

gauNB = GaussianNB()
gauNB.fit(xTrainScaled, yTrain)

yPredTrain = gauNB.predict(xTrainScaled)
yPredTest = gauNB.predict(xTestScaled)

plot_confusion_matrix(gauNB, xTestScaled, yTest)

print(f"Accuracy Train Score: {accuracy_score(yTrain, yPredTrain)}")
print(f"Accuracy Test Score: {accuracy_score(yTest, yPredTest)}")
print('-----')
print(f"F1-Train Score: {f1_score(yTrain, yPredTrain)}")
print(f"F1-Test Score: {f1_score(yTest, yPredTest)}")
print('-----')
print(f"Average Precision Train Score: {precision_score(yTrain, yPredTrain)}")
print(f"Average Precision Test Score: {precision_score(yTest, yPredTest)}")
print('-----')
print(f"Recall Train Score: {recall_score(yTrain, yPredTrain, average='weighted')}")
print(f"Recall Test Score: {recall_score(yTest, yPredTest, average='weighted')}")
print('-----')
print('0 is "Not at risk of a stroke"')
print('1 is "At risk of a stroke"')
```

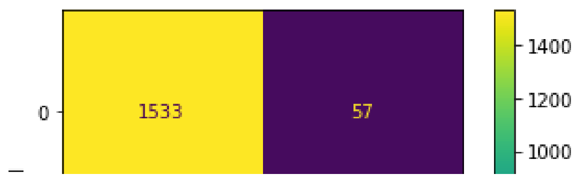
```
Accuracy Train Score: 0.8740870581361379
Accuracy Test Score: 0.8606168446026097
-----
F1-Train Score: 0.21493624772313297
F1-Test Score: 0.24920127795527158
-----
Average Precision Train Score: 0.14898989898989898
Average Precision Test Score: 0.17972350230414746
-----
Recall Train Score: 0.8740870581361379
Recall Test Score: 0.8606168446026097
-----
0 is "Not at risk of a stroke"
1 is "At risk of a stroke"
```

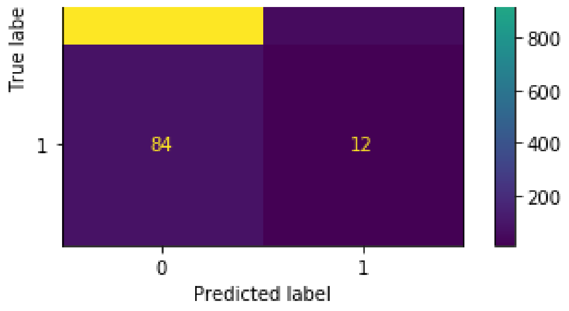


In [31]:

```python
from sklearn.tree import DecisionTreeClassifier
decTree = DecisionTreeClassifier(class_weight='balanced')

decTree.fit(xTrainScaled, yTrain)

yPredTrain = decTree.predict(xTrainScaled)
yPredTest = decTree.predict(xTestScaled)

plot_confusion_matrix(decTree, xTestScaled, yTest)

print(f"Accuracy Train Score: {accuracy_score(yTrain, yPredTrain)}")
print(f"Accuracy Test Score: {accuracy_score(yTest, yPredTest)}")
print('-----')
print(f"F1-Train Score: {f1_score(yTrain, yPredTrain)}")
print(f"F1-Test Score: {f1_score(yTest, yPredTest)}")
print('-----')
print(f"Average Precision Train Score: {precision_score(yTrain, yPredTrain)}")
print(f"Average Precision Test Score: {precision_score(yTest, yPredTest)}")
print('-----')
print(f"Recall Train Score: {recall_score(yTrain, yPredTrain, average='weighted')}")
print(f"Recall Test Score: {recall_score(yTest, yPredTest, average='weighted')}")
print('-----')
print('0 is "Not at risk of a stroke"')
print('1 is "At risk of a stroke"')
```

```
Accuracy Train Score: 1.0
Accuracy Test Score: 0.9163701067615658
-----
F1-Train Score: 1.0
F1-Test Score: 0.14545454545454545
-----
Average Precision Train Score: 1.0
Average Precision Test Score: 0.17391304347826086
-----
Recall Train Score: 1.0
Recall Test Score: 0.9163701067615658
-----
0 is "Not at risk of a stroke"
1 is "At risk of a stroke"
```



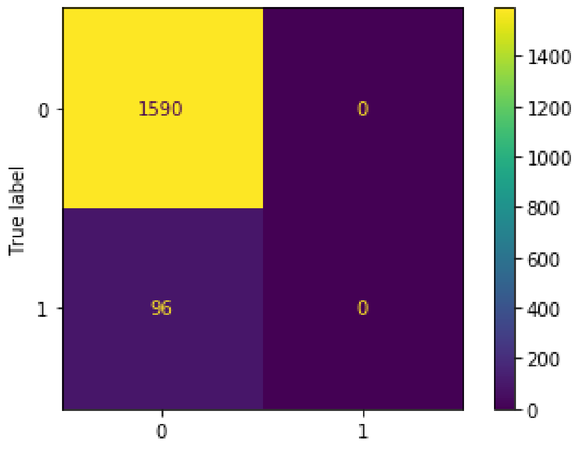


In [32]:

```
from sklearn.ensemble import RandomForestClassifier
rngForest = RandomForestClassifier(class_weight='balanced')

rngForest.fit(xTrainScaled, yTrain)

yPredTrain = rngForest.predict(xTrainScaled)
yPredTest = rngForest.predict(xTestScaled)

plot_confusion_matrix(rngForest, xTestScaled, yTest)

print(f"Accuracy Train Score: {accuracy_score(yTrain, yPredTrain)}")
print(f"Accuracy Test Score: {accuracy_score(yTest, yPredTest)}")
print('-----')
print(f"F1-Train Score: {f1_score(yTrain, yPredTrain)}")
print(f"F1-Test Score: {f1_score(yTest, yPredTest)}")
print('-----')
print(f"Average Precision Train Score: {precision_score(yTrain, yPredTrain)}")
print(f"Average Precision Test Score: {precision_score(yTest, yPredTest)}")
print('-----')
print(f"Recall Train Score: {recall_score(yTrain, yPredTrain, average='weighted')}")
print(f"Recall Test Score: {recall_score(yTest, yPredTest, average='weighted')}")
print('-----')
print('0 is "Not at risk of a stroke"')
print('1 is "At risk of a stroke"')
```

```
Accuracy Train Score: 1.0
Accuracy Test Score: 0.9430604982206405
-----
F1-Train Score: 1.0
F1-Test Score: 0.0
-----
Average Precision Train Score: 1.0
Average Precision Test Score: 0.0
-----
Recall Train Score: 1.0
Recall Test Score: 0.9430604982206405
-----
0 is "Not at risk of a stroke"
1 is "At risk of a stroke"
```

```
C:\Users\Sweet Deals\anaconda3\envs\learn-env\lib\site-packages\sklearn\metrics\_classifi
cation.py:1221: UndefinedMetricWarning: Precision is ill-defined and being set to 0.0 due
to no predicted samples. Use `zero_division` parameter to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
```



Predicted label

In [33]:

```
df['stroke'].value_counts()
```

Out[33]:

```
0    4860
1     249
Name: stroke, dtype: int64
```

In [34]:

```
#XGBClassifier doesn't have a function to automatically balance imbalanced
#datasets so we need to find out what number to give as the weight.
#scale_pos_weight = total_negative_examples (not stroke) / total_positive_examples (strok
e)
4860/249
```

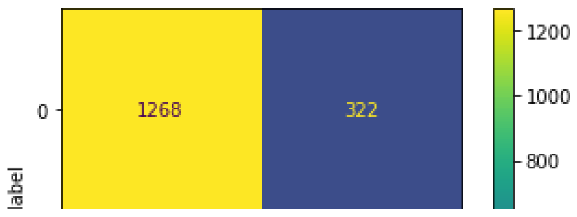
Out[34]:

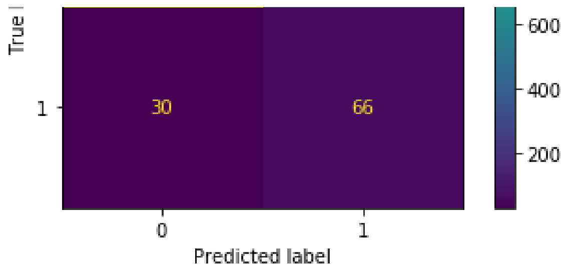
```
19.518072289156628
```

In [35]:

```
import xgboost as xgb
xgbClass = xgb.XGBClassifier(scale_pos_weight = 19.518072289156628)

xgbClass.fit(xTrainScaled, yTrain)

yPredTrain = xgbClass.predict(xTrainScaled)
yPredTest = xgbClass.predict(xTestScaled)

plot_confusion_matrix(xgbClass, xTestScaled, yTest)

print(f"Accuracy Train Score: {accuracy_score(yTrain, yPredTrain)}")
print(f"Accuracy Test Score: {accuracy_score(yTest, yPredTest)}")
print('-----')
print(f"F1-Train Score: {f1_score(yTrain, yPredTrain)}")
print(f"F1-Test Score: {f1_score(yTest, yPredTest)}")
print('-----')
print(f"Average Precision Train Score: {precision_score(yTrain, yPredTrain)}")
print(f"Average Precision Test Score: {precision_score(yTest, yPredTest)}")
print('-----')
print(f"Recall Train Score: {recall_score(yTrain, yPredTrain, average='weighted')}")
print(f"Recall Test Score: {recall_score(yTest, yPredTest, average='weighted')}")
print('-----')
print('0 is "Not at risk of a stroke"')
print('1 is "At risk of a stroke"')
```

```
Accuracy Train Score: 0.8191644756061934
Accuracy Test Score: 0.7912218268090154
-----
F1-Train Score: 0.3234972677595629
F1-Test Score: 0.2727272727272727
-----
Average Precision Train Score: 0.1942257217847769
Average Precision Test Score: 0.17010309278350516
-----
Recall Train Score: 0.8191644756061934
Recall Test Score: 0.7912218268090154
-----
0 is "Not at risk of a stroke"
1 is "At risk of a stroke"
```





Moving forward after experimenting with a few different model types, I've chosen RandomForestClassifier. Using a decision tree model as apposed to a regression model fits with this data better as most of the data in this set seems to be mostly binary, with a few acceptions. As for Specifically RandomForestClassifier as apposed to say XGBClassification, while XGBC did seem to have a better score result due to learning the data better, RandomForestClassifier's documentaiton was more descriptive and lended itself better to be run multitudes of times to inch closer to a more accurate model.

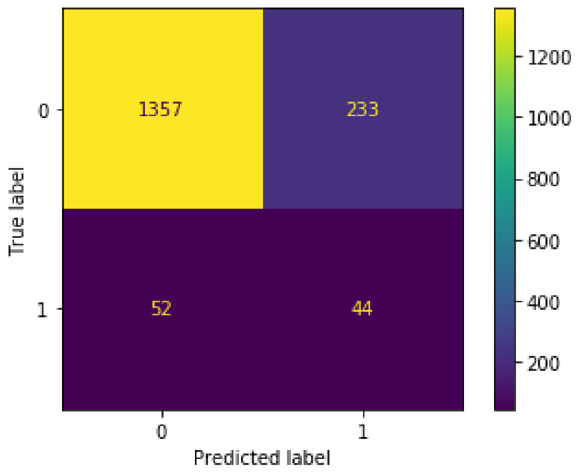
Model 1: Commitment to RandomForestClassifier

Time for feature engineering with RandomForestClassifier! Let's make a second model for this and name it something different for, just for the sake of oganization.

In [36]:

```
rngForest2 = RandomForestClassifier(class_weight='balanced',
                                    max_depth=None,
                                    n_estimators=100,
                                    min_samples_split=20,
                                    min_samples_leaf=20,
                                    min_weight_fraction_leaf=0.497,
                                    random_state = 123,
                                    max_features = 'auto',
                                    max_leaf_nodes = 100,
                                    min_impurity_decrease = 0,
                                    n_jobs = 1000
                                    )

rngForest2.fit(xTrainScaled, yTrain)

yPredTrain = rngForest2.predict(xTrainScaled)
yPredTest = rngForest2.predict(xTestScaled)

plot_confusion_matrix(rngForest2, xTestScaled, yTest)
# The bellow text field is only for grabbing images, doesn't need to be run every time
# plt.savefig('images/Models/Model1.png')

print(f"Accuracy Train Score: {accuracy_score(yTrain, yPredTrain)}")
print(f"Accuracy Test Score: {accuracy_score(yTest, yPredTest)}")
print('-----')
print(f"F1-Train Score: {f1_score(yTrain, yPredTrain)}")
print(f"F1-Test Score: {f1_score(yTest, yPredTest)}")
print('-----')
print(f"Average Precision Train Score: {precision_score(yTrain, yPredTrain)}")
print(f"Average Precision Test Score: {precision_score(yTest, yPredTest)}")
print('-----')
print(f"Recall Train Score: {recall_score(yTrain, yPredTrain, average='weighted')}")
print(f"Recall Test Score: {recall_score(yTest, yPredTest, average='weighted')}")
```

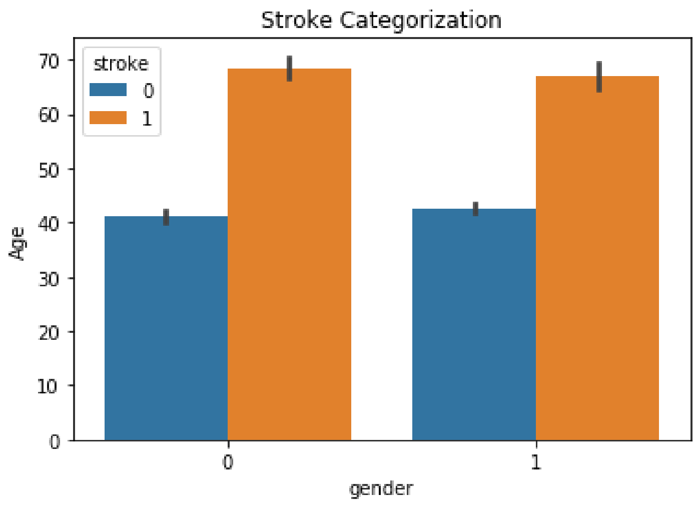
```
Accuracy Train Score: 0.8445807770961146
Accuracy Test Score: 0.8309608540925267
-----
F1-Train Score: 0.2222222222222224
F1-Test Score: 0.23592493297587133
-----
Average Precision Train Score: 0.1431261770244821
Average Precision Test Score: 0.1588447653429603
-----
Recall Train Score: 0.8445807770961146
Recall Test Score: 0.8309608540925267
Recall Test Score: [illegible]
```

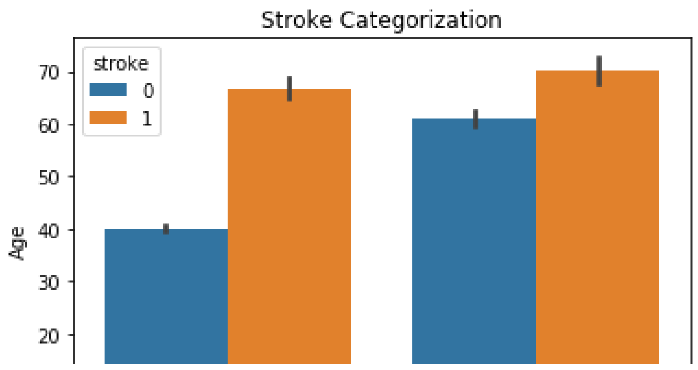


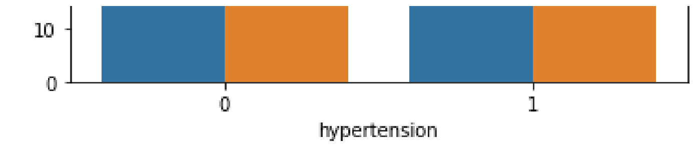
So, as we've seen already our test model is dramatically too over fit and doesn't learn the data well. The above model is the result of maticulously itterating through each parameter in RandomForestClassifier and inching towards a more properly fit model.

In [37]:

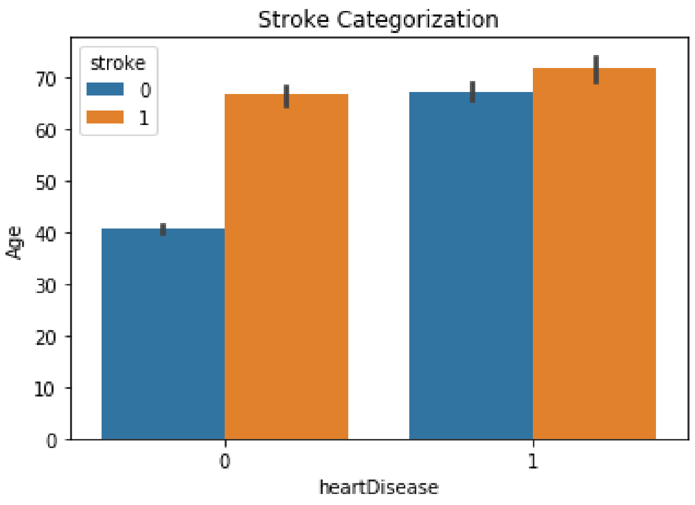
```python
import matplotlib.pyplot as plt

disCols = [c for c in df.columns.to_list() if c not in ['stroke', 'age', 'avgGlucoseLeve
l', 'bmi']]


for x in disCols:
    sns.barplot(x = df[x], y = df['age'], hue = df['stroke'])
    plt.title(f'Age Vs. {x} categorized by Stroke')
    plt.xlabel(x)
    plt.ylabel('Age')
    plt.title('Stroke Categorization')
    # The bellow text field is only for grabbing images, doesn't need to be run every tim
e
    # plt.savefig(f'images/ageImages/Age Vs. {x} categorized by Stroke.png')
    plt.show()
    plt.clf()
```



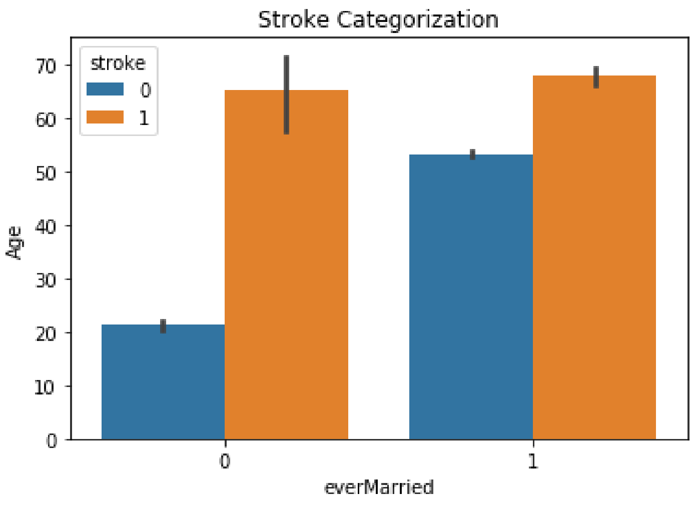




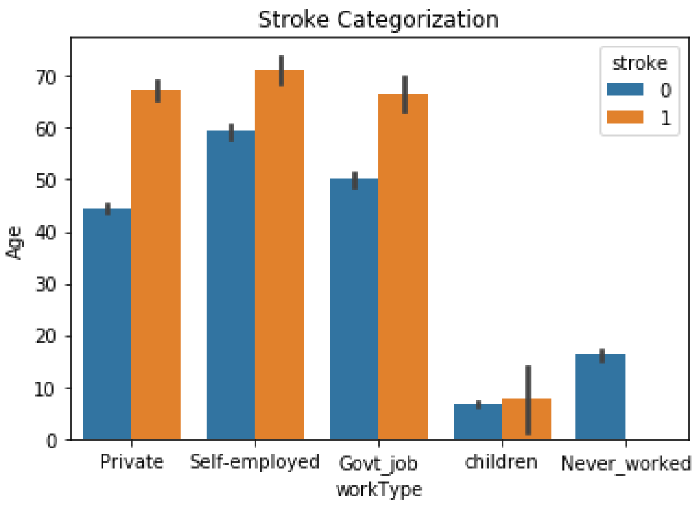
10
0
0
1
hypertension



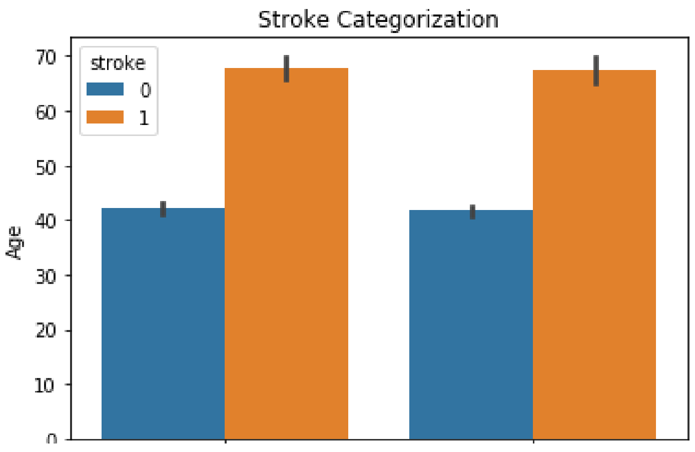
Stroke Categorization
stroke
0
1
Age
0
10
20
30
40
50
60
70
0
1
heartDisease



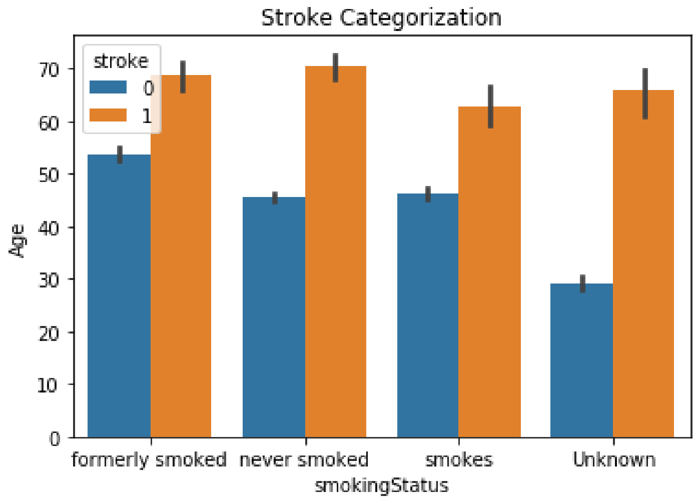
Stroke Categorization
stroke
0
1
Age
0
10
20
30
40
50
60
70
0
1
everMarried



Stroke Categorization
stroke
0
1
Age
0
10
20
30
40
50
60
70
Private
Self-employed
Govt_job
children
Never_worked
workType



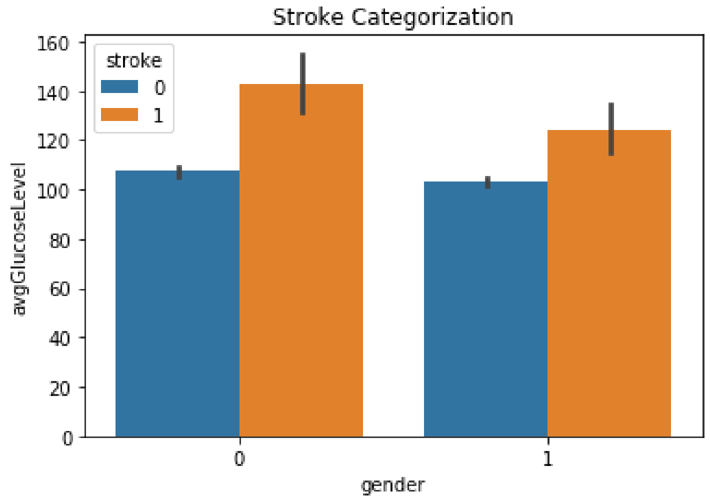
Stroke Categorization
stroke
0
1
Age
0
10
20
30
40
50
60
70

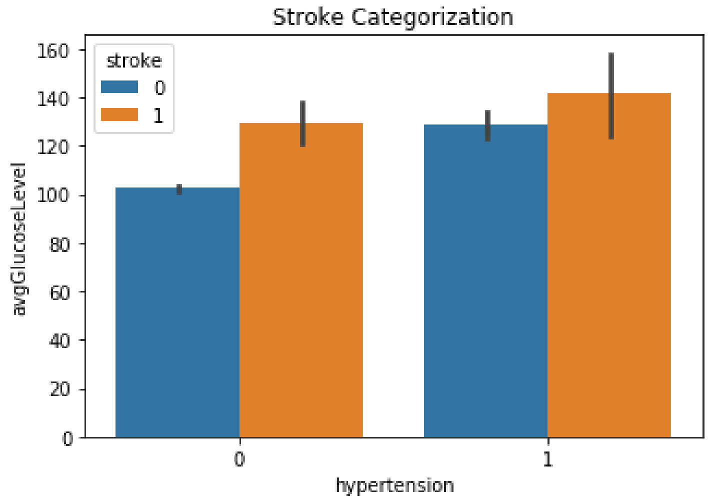


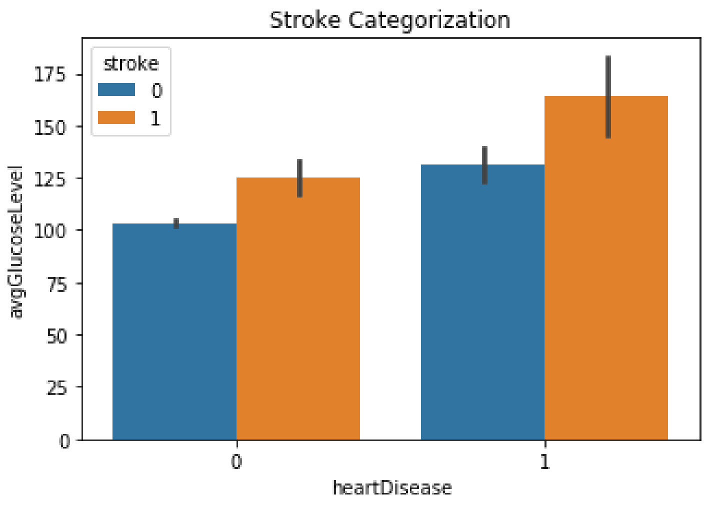
```
<Figure size 432x288 with 0 Axes>
```

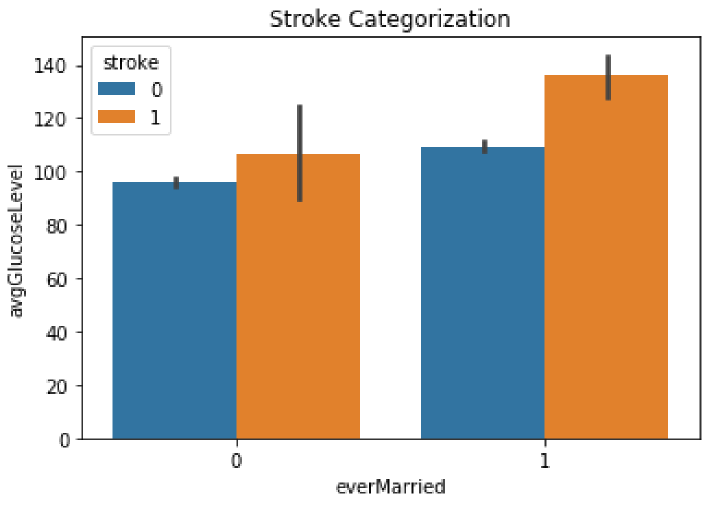
In [38]:

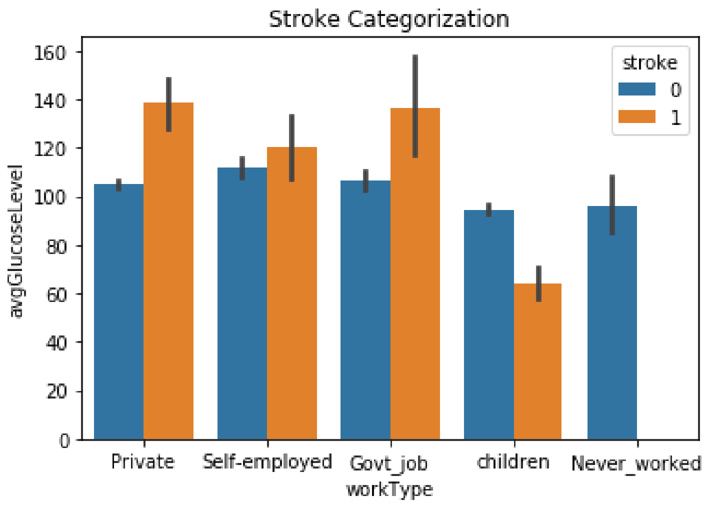
```
for x in disCols:
    sns.barplot(x = df[x], y = df['avgGlucoseLevel'], hue = df['stroke'])
    plt.title(f'avgGlucoseLevel Vs. {x} categorized by Stroke')
    plt.xlabel(x)
    plt.ylabel('avgGlucoseLevel')
    plt.title('Stroke Categorization')
    # The bellow text field is only for grabbing images, doesn't need to be run every tim
e
    # plt.savefig(f'images/avgGlucoseLevelImages/avgGlucoseLevel Vs. {x} categorized by S
troke.png')
    plt.show()
    plt.clf()
```

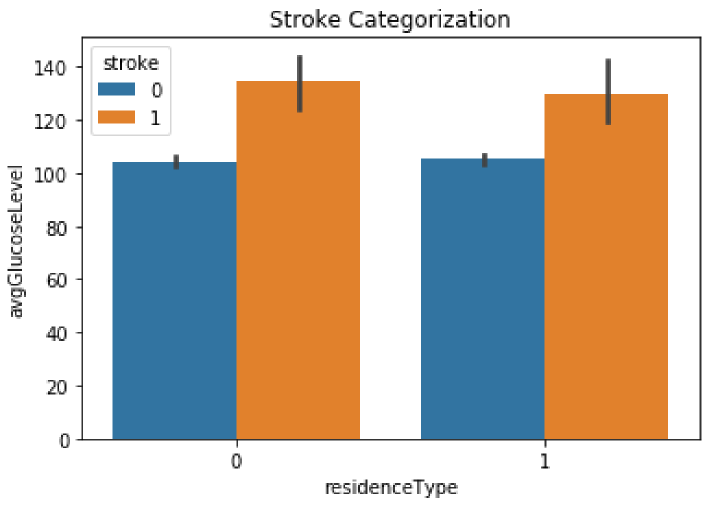




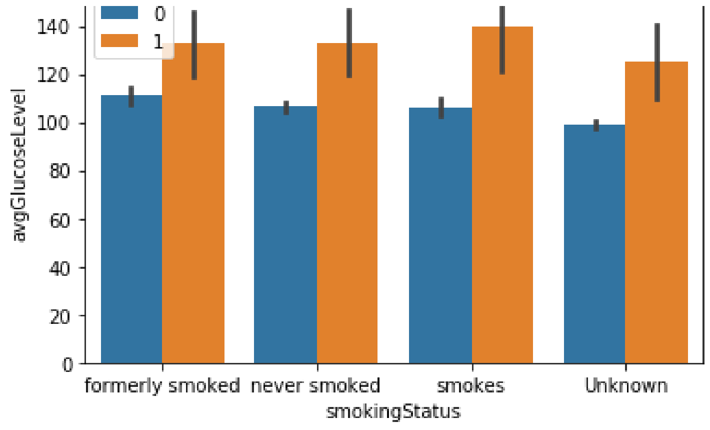

Stroke Categorization
stroke
0
1
avgGlucoseLevel
175
150
125
100
75
50
25
0
0
1
heartDisease


Stroke Categorization
stroke
0
1
avgGlucoseLevel
140
120
100
80
60
40
20
0
0
1
everMarried


Stroke Categorization
stroke
0
1
avgGlucoseLevel
160
140
120
100
80
60
40
20
0
Private
Self-employed
Govt_job
children
Never_worked
workType


Stroke Categorization
stroke
0
1
avgGlucoseLevel
140
120
100
80
60
40
20
0
0
1
residenceType

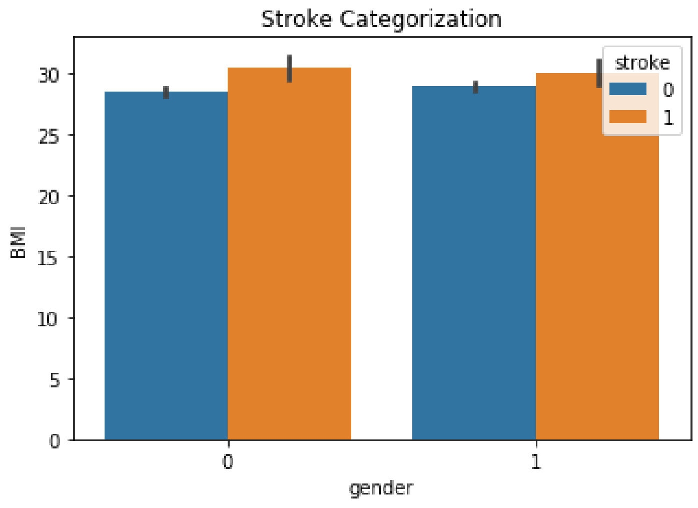
Stroke Categorization
160
stroke

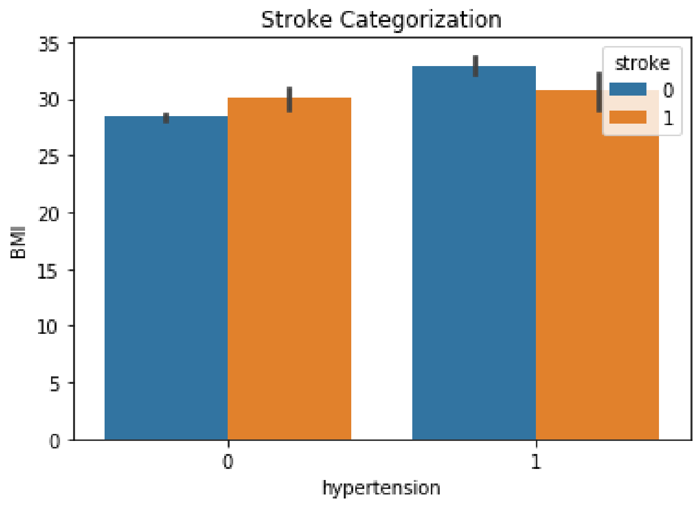


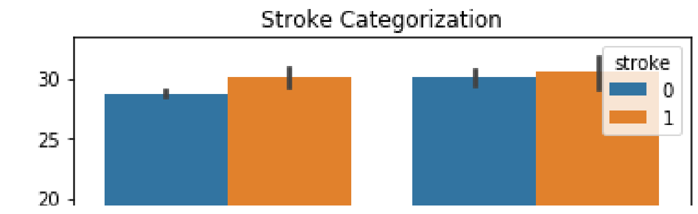
```
<Figure size 432x288 with 0 Axes>
```

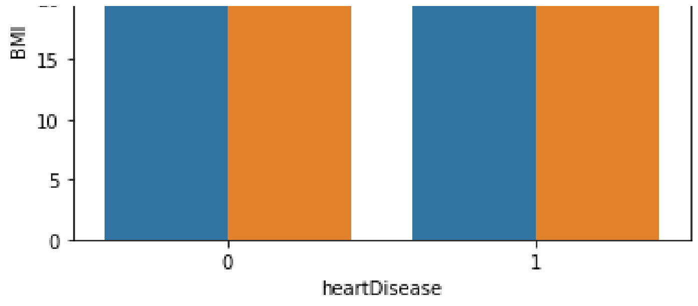
In [39]:

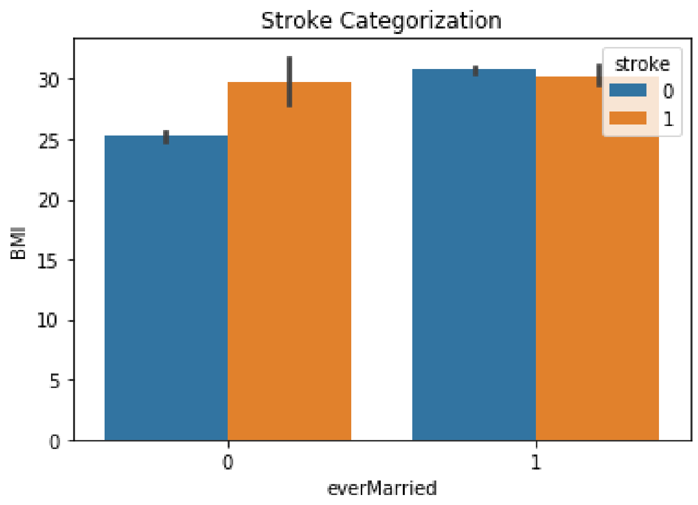
```
for x in disCols:
    sns.barplot(x = df[x], y = df['bmi'], hue = df['stroke'])
    plt.title(f'BMI Vs. {x} categorized by Stroke')
    plt.xlabel(x)
    plt.ylabel('BMI')
    plt.title('Stroke Categorization')
    # The bellow text field is only for grabbing images, doesn't need to be run every tim
e
    # plt.savefig(f'images/bmiImages/BMI Vs. {x} categorized by Stroke.png')
    plt.show()
    plt.clf()
```

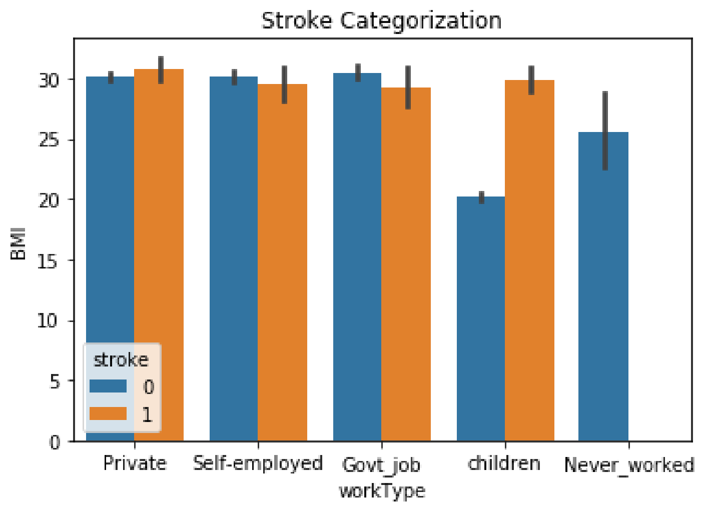


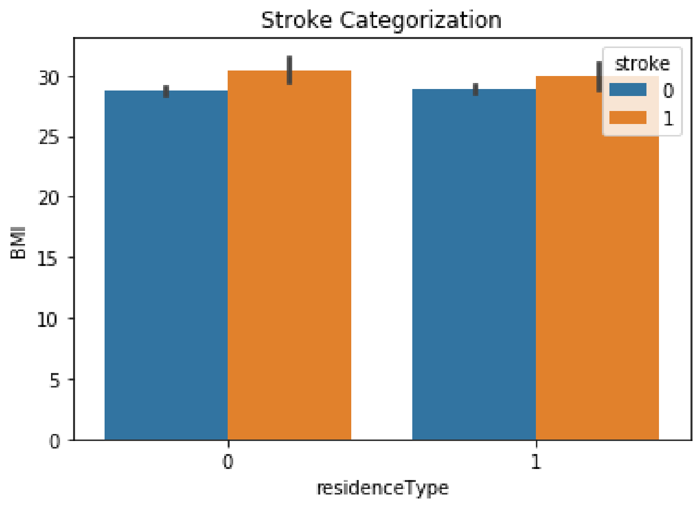


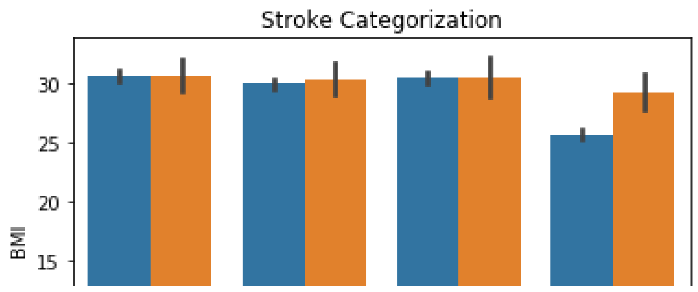


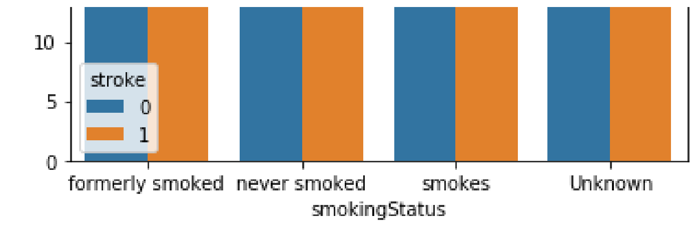

BMI
heartDisease


Stroke Categorization
BMI
everMarried
stroke
0
1


Stroke Categorization
BMI
Private
Self-employed
Govt_job
children
Never_worked
workType
stroke
0
1


Stroke Categorization
BMI
residenceType
stroke
0
1


Stroke Categorization
BMI



```
<Figure size 432x288 with 0 Axes>
```

In [40]:

```python
# Returns a list of most important features
y = 0
while y < 10:
    imp = rngForest2.feature_importances_
    var = [x for x in xCols]
    print(var[y], imp[y])
    y+=1
```

```
gender 0.0
age 0.24242424242424243
hypertension 0.0
heartDisease 0.0
everMarried 0.0
workType 0.0
residenceType 0.0
avgGlucoseLevel 0.7272727272727273
bmi 0.030303030303030304
smokingStatus 0.0
```

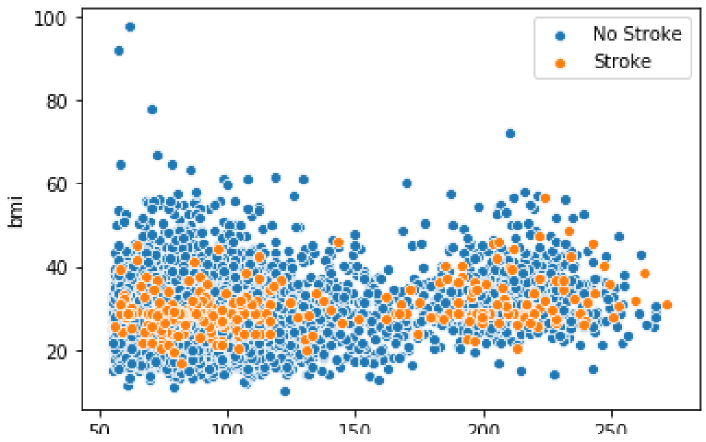
avgGlucoseLevel looks like it has the biggest impact on health so lets take a closer look ath that.

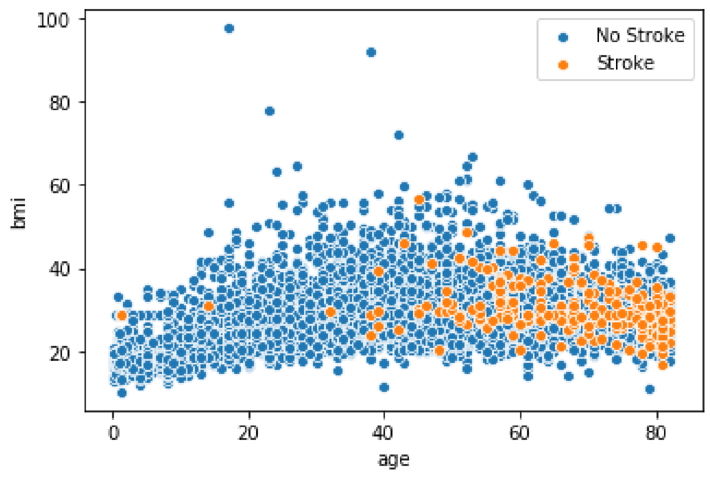
In [41]:

```python
strokeDF = df[(df['stroke'] == 1)]
strokeDF
notStrokeDF = df[(df['stroke'] == 0)]
```

In [45]:

```python
sns.scatterplot(x = df.avgGlucoseLevel[df.stroke == 0], y = df.bmi[df.stroke==0])
sns.scatterplot(x = df.avgGlucoseLevel[df.stroke == 1], y = df.bmi[df.stroke==1])
plt.legend(['No Stroke', 'Stroke'])
# The bellow text field is only for grabbing images, doesn't need to be run every time
plt.savefig(f'images/futureWorkExamples/bmi_vs_avgGlucoseLevel.png')
plt.show()
plt.clf()

sns.scatterplot(x = df.age[df.stroke == 0], y = df.bmi[df.stroke==0])
sns.scatterplot(x = df.age[df.stroke == 1], y = df.bmi[df.stroke==1])
plt.legend(['No Stroke', 'Stroke'])
# The bellow text field is only for grabbing images, doesn't need to be run every time
plt.savefig(f'images/futureWorkExamples/bmi_vs_age.png')
plt.show()
plt.clf()
```





```
<Figure size 432x288 with 0 Axes>
```

In [43]:

```
age = 30
strokeAge = strokeDF[(strokeDF['age'] < age)]
strokesAgeFilters = strokeAge.age.value_counts().sum()
strokesAgeAll = strokeDF.age.value_counts().sum()
print(f'strokesAgeFilters: {strokesAgeFilters}')
print(f'strokesAgeAll: {strokesAgeAll}')
print(f'% of number of strokes above the age of {age}: {(((strokesAgeFilters/strokesAgeAl
l)*100)-100)*-1}%')
```

```
strokesAgeFilters: 2
strokesAgeAll: 249
% of number of strokes above the age of 30: 99.19678714859438%
```

In [44]:

```
df.describe()
```

Out[44]:

	age	hypertension	heartDisease	everMarried	residenceType	avgGlucoseLevel	bmi	stroke
count	5109.000000	5109.000000	5109.000000	5109.000000	5109.000000	5109.000000	5109.000000	5109.000000
mean	43.229986	0.097475	0.054022	0.656293	0.491877	106.140399	28.894508	0.048738
std	22.613575	0.296633	0.226084	0.474991	0.499983	45.285004	7.698235	0.215340
min	0.080000	0.000000	0.000000	0.000000	0.000000	55.120000	10.300000	0.000000
25%	25.000000	0.000000	0.000000	0.000000	0.000000	77.240000	23.800000	0.000000
50%	45.000000	0.000000	0.000000	1.000000	0.000000	91.880000	28.400000	0.000000
75%	61.000000	0.000000	0.000000	1.000000	1.000000	114.090000	32.800000	0.000000
max	82.000000	1.000000	1.000000	1.000000	1.000000	271.740000	97.600000	1.000000

After playing around with the features for a while, I've settled on this for the moment. This seems to be the sweet spot in the overall accuracy of my model. Though it wasn't the highest percentile score I was able to acheive, it has the msot minimal false negative predicitons. In the case of predicting someone health and the amount of medical attention, it's better to over predicit if someone needs help than to underpredict it.

This model will essentially:

- **Predict 84.4% if a patient will or will not be at risk of a stroke correctly.**
- **Only a minimal Aprox. 3.1% of patients predicted to be 'not at risk' will be misdiagnosed**
- **Model has been made to air on the side of caution and over predict risk as opposed to underpredict.**

[illegible]

The use case I see this model being most useful for is for family phasicians and general practitioners having a way knowing if the patients they receive are at risk of a stroke being onset later in life. This model can be used for a new patient or garnering a list of current patients inorder to service them better. Calls can be made on behalf of the practitioners to inform patients that they may be at risk and a check up/consultation may be in benefitial.

It should also be noted that while this model can be made to be more accurate be reducing the ranges that the model can predict on (such as only including date on patients over the age of 30) this is ultimately unwise due to the nature of medicine and the targeted use case for this model being general practitioners. Being that General practitioners see all body types from all walks of life, cherry picking patient information would be self desrtuctive.