DSC630 : Final Project (Brain-Stroke Prediction)

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Date : 03/04/2023

OVERVIEW:

Step1 - Importing model data.

Step2 - Dataset cleansing and adding dummy categorical variables.

Step3 - Modeling - As my target variable is a binary value (either stroke or not), I will be performing classification based model using KNN for finding the outcome.

Steps to be performed as part of Modeling:
1. Split the data into train/test (75/25) with stroke as the target variable. I will be dropping ID variable from dataset as the feature has no bearing.
2. Applying knn classification model to predict the outcome.
3. Scale the data using standard scalar, create a pipe with knn and then apply grid search using n_neighbors
4. Calculate the accuracy/precision/recall and f1 score along with a confusion matrix of result set.

The result is that there is >90% accuracy, but model could not detect true positives due to train dataset imbalance.

Step4 - Correct the imbalances in train using SMOTE to rebalance underbalanced class.

Step5 - Retrained the model using balanced dataset whics resulted in a little reduction in accuracy, but improved identification of True positives.

In [1]:
```
#Import libraries
%matplotlib inline
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
```

In [2]:
```
import warnings
warnings.filterwarnings("ignore")
warnings.simplefilter('ignore')
```

In [3]:
```
#Import source dataset
brain_stroke = pd.read_csv("healthcare-dataset-stroke-data.csv")
brain_stroke
```

Out[3]:

	id	gender	age	hypertension	heart_disease	ever_married	work_type	Residence_type	avg_g
0	9046	Male	67.0	0	1	Yes	Private	Urban	
1	51676	Female	61.0	0	0	Yes	Self-employed	Rural	
2	31112	Male	80.0	0	1	Yes	Private	Rural	
3	60182	Female	49.0	0	0	Yes	Private	Urban	
4	1665	Female	79.0	1	0	Yes	Self-employed	Rural	
...	...	...	...	...	...	...	...	...	
5105	18234	Female	80.0	1	0	Yes	Private	Urban	
5106	44873	Female	81.0	0	0	Yes	Self-employed	Urban	
5107	19723	Female	35.0	0	0	Yes	Self-employed	Rural	
5108	37544	Male	51.0	0	0	Yes	Private	Rural	
5109	44679	Female	44.0	0	0	Yes	Govt_job	Urban	

5110 rows × 12 columns

In [4]:

```
brain_stroke.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 5110 entries, 0 to 5109
Data columns (total 12 columns):
 #   Column             Non-Null Count  Dtype  
---  ------             --------------  -----  
 0   id                 5110 non-null   int64  
 1   gender             5110 non-null   object 
 2   age                5110 non-null   float64
 3   hypertension       5110 non-null   int64  
 4   heart_disease      5110 non-null   int64  
 5   ever_married       5110 non-null   object 
 6   work_type          5110 non-null   object 
 7   Residence_type     5110 non-null   object 
 8   avg_glucose_level  5110 non-null   float64
 9   bmi                4909 non-null   float64
 10  smoking_status     5110 non-null   object 
 11  stroke             5110 non-null   int64  
dtypes: float64(3), int64(4), object(5)
memory usage: 479.2+ KB
```

attributes information

The data contains 5110 observations with 12 attributes.

id: unique identifier.

gender: "Male", "Female" or "Other".
age: age of the patient.
hypertension: hypertension means high blood pressure. 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_job", "Never_worked", "Private" or "Self-employed".
Residence_type: "Rural" or "Urban".
avg_glucose_level: average glucose level in blood.
bmi: body mass index, As a measure of obesity.
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 [6]:
```
#Check for for Missing values
brain_stroke.isna().sum()
```

Out[6]:
```
id                   0
gender               0
age                  0
hypertension         0
heart_disease        0
ever_married         0
work_type            0
Residence_type       0
avg_glucose_level    0
bmi                201
smoking_status       0
stroke               0
dtype: int64
```

In [7]:
```
#Set missing values in bmi column to median value
brain_stroke['bmi'] = brain_stroke['bmi'].fillna(brain_stroke['bmi'].median())
brain_stroke.isna().sum()
```

Out[7]:
```
id                   0
gender               0
age                  0
hypertension         0
heart_disease        0
ever_married         0
work_type            0
Residence_type       0
avg_glucose_level    0
bmi                  0
smoking_status       0
stroke               0
dtype: int64
```

In [8]:
```
#Check basic info of all the data
brain_stroke.describe()
```

Out[8]:

	id	age	hypertension	heart_disease	avg_glucose_level	bmi	stro
count	5110.000000	5110.000000	5110.000000	5110.000000	5110.000000	5110.000000	5110.0000
mean	36517.829354	43.226614	0.097456	0.054012	106.147677	28.862035	0.0487
std	21161.721625	22.612647	0.296607	0.226063	45.283560	7.699562	0.2153
min	67.000000	0.080000	0.000000	0.000000	55.120000	10.300000	0.0000
25%	17741.250000	25.000000	0.000000	0.000000	77.245000	23.800000	0.0000
50%	36932.000000	45.000000	0.000000	0.000000	91.885000	28.100000	0.0000
75%	54682.000000	61.000000	0.000000	0.000000	114.090000	32.800000	0.0000
max	72940.000000	82.000000	1.000000	1.000000	271.740000	97.600000	1.0000

In [9]:
```
#Check info of the observaions which doesn't have stroke
brain_stroke[brain_stroke['stroke']==1].describe()
```

Out[9]:

	id	age	hypertension	heart_disease	avg_glucose_level	bmi	stroke
count	249.000000	249.000000	249.000000	249.000000	249.000000	249.000000	249.0
mean	37115.068273	67.728193	0.265060	0.188755	132.544739	30.090361	1.0
std	21993.344872	12.727419	0.442254	0.392102	61.921056	5.861877	0.0
min	210.000000	1.320000	0.000000	0.000000	56.110000	16.900000	1.0
25%	17013.000000	59.000000	0.000000	0.000000	79.790000	27.000000	1.0
50%	36706.000000	71.000000	0.000000	0.000000	105.220000	28.100000	1.0
75%	56669.000000	78.000000	1.000000	0.000000	196.710000	32.500000	1.0
max	72918.000000	82.000000	1.000000	1.000000	271.740000	56.600000	1.0

In [10]:
```
#Check info of the observaions which  have stroke
brain_stroke[brain_stroke['stroke']==0].describe()
```

Out[10]:

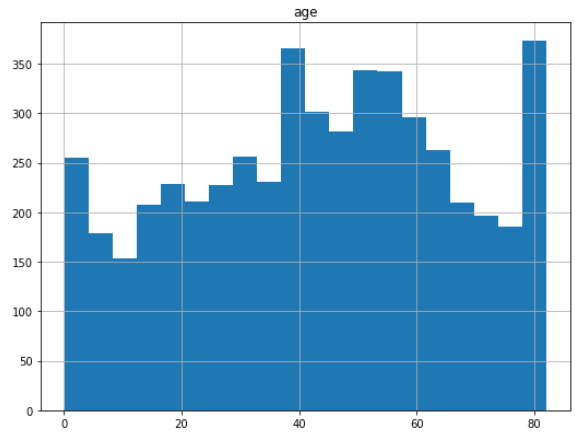
	id	age	hypertension	heart_disease	avg_glucose_level	bmi	stroke
count	4861.000000	4861.000000	4861.000000	4861.000000	4861.000000	4861.000000	4861.0
mean	36487.236371	41.971545	0.088871	0.047110	104.795513	28.799115	0.0
std	21120.133386	22.291940	0.284586	0.211895	43.846069	7.777269	0.0
min	67.000000	0.080000	0.000000	0.000000	55.120000	10.300000	0.0
25%	17762.000000	24.000000	0.000000	0.000000	77.120000	23.600000	0.0
50%	36958.000000	43.000000	0.000000	0.000000	91.470000	28.100000	0.0
75%	54497.000000	59.000000	0.000000	0.000000	112.830000	32.800000	0.0
max	72940.000000	82.000000	1.000000	1.000000	267.760000	97.600000	0.0

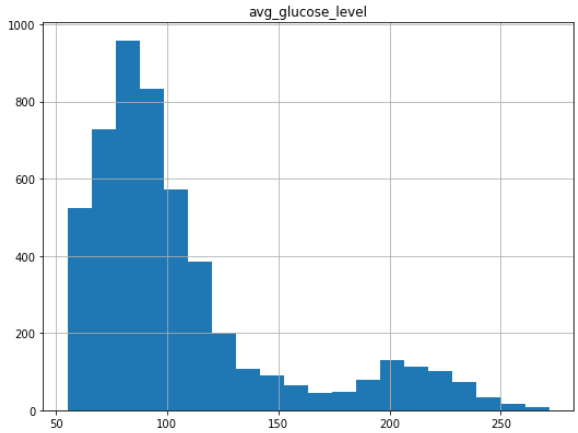
Observations:

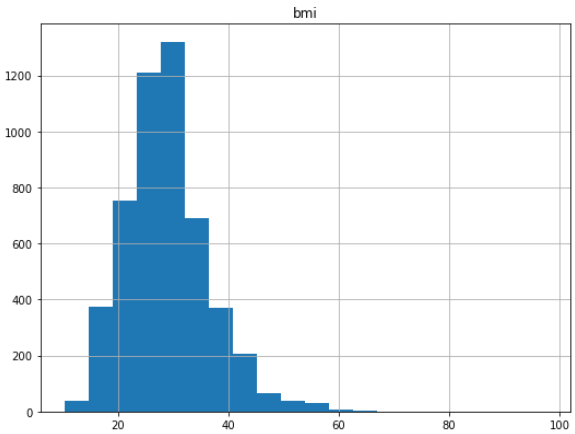
4.8% of the observation in this dataset had stroke.
There is a big difference between those who have stroke and those who don't have stroke. Among those who have a stroke - the average age and average glucose level is significantly higher and the number of people with heart disease and hypertension is significantly higher.

In [11]:
```
#numeric attributes histograms
atttibutes_hist = brain_stroke[["age", "avg_glucose_level", "bmi"]].hist(bins=20, figsi
atttibutes_hist
```

Out[11]:
```
array([[<AxesSubplot:title={'center':'age'}>,
        <AxesSubplot:title={'center':'avg_glucose_level'}>],
       [<AxesSubplot:title={'center':'bmi'}>, <AxesSubplot:>]],
      dtype=object)
```

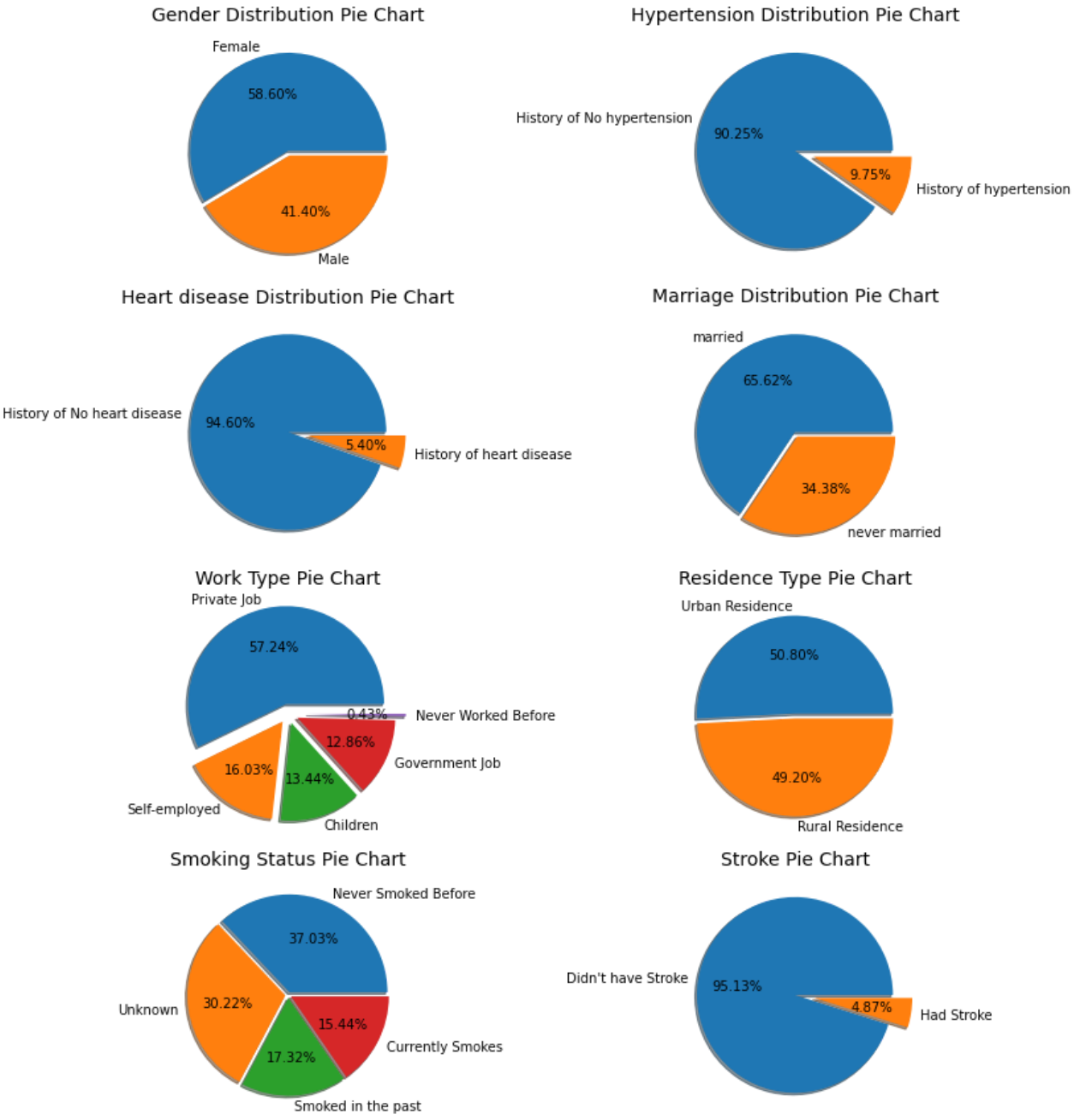






In [12]:
```
#categorical attributes histograms (as pie charts)
fig, ax = plt.subplots(4,2, figsize = (12,12))
((ax1, ax2), (ax3, ax4), (ax5, ax6), (ax7, ax8)) = ax

labels = brain_stroke['gender'].value_counts().index.tolist()[:2]
values = brain_stroke['gender'].value_counts().tolist()[:2]
ax1.pie(x=values, labels=labels, autopct="%1.2f%%", shadow=True, explode=[0, 0.05])
ax1.set_title("Gender Distribution Pie Chart", fontdict={'fontsize': 14})
```

```
labels = ["History of No hypertension", "History of hypertension"]
values = brain_stroke['hypertension'].value_counts().tolist()
ax2.pie(x=values, labels=labels, autopct="%1.2f%%", shadow=True, explode=[0, 0.2])
ax2.set_title("Hypertension Distribution Pie Chart", fontdict={'fontsize': 14})

labels = ["History of No heart disease", "History of heart disease"]
values = brain_stroke['heart_disease'].value_counts().tolist()
ax3.pie(x=values, labels=labels, autopct="%1.2f%%", shadow=True, explode=[0, 0.2])
ax3.set_title("Heart disease Distribution Pie Chart", fontdict={'fontsize': 14})

labels = ["married", "never married"]
values = brain_stroke['ever_married'].value_counts().tolist()
ax4.pie(x=values, labels=labels, autopct="%1.2f%%", shadow=True, explode=[0, 0.05])
ax4.set_title("Marriage Distribution Pie Chart", fontdict={'fontsize': 14})

labels = ["Private Job", "Self-employed", "Children", "Government Job", "Never Worked B
values = brain_stroke['work_type'].value_counts().tolist()
ax5.pie(x=values, labels=labels, autopct="%1.2f%%", shadow=True, explode=[0.1, 0.1, 0.1
ax5.set_title("Work Type Pie Chart", fontdict={'fontsize': 14})

labels = ["Urban Residence", "Rural Residence"]
values = brain_stroke['Residence_type'].value_counts().tolist()
ax6.pie(x=values, labels=labels, autopct="%1.2f%%", shadow=True, explode=[0, 0.05])
ax6.set_title("Residence Type Pie Chart", fontdict={'fontsize': 14})

labels = ["Never Smoked Before", "Unknown", "Smoked in the past", "Currently Smokes"]
values = brain_stroke['smoking_status'].value_counts().tolist()
ax7.pie(x=values, labels=labels, autopct="%1.2f%%", shadow=True, explode=[0.03, 0.03, 0
ax7.set_title("Smoking Status Pie Chart", fontdict={'fontsize': 14})

labels = ["Didn't have Stroke", "Had Stroke"]
values = brain_stroke['stroke'].value_counts().tolist()
ax8.pie(x=values, labels=labels, autopct="%1.2f%%", shadow=True, explode=[0, 0.2])
ax8.set_title("Stroke Pie Chart", fontdict={'fontsize': 14})

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



In [13]:
```
#validating type values and counts for gender attribute
print(brain_stroke['gender'].value_counts())
```

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

Observation: Above results show that there is an outlier - which will be removed.

In [16]:
```
#removing outlier
brain_stroke = brain_stroke[brain_stroke['gender'] != "Other"]
brain_stroke['gender'].value_counts()
```

Out[16]:
```
Female    2994
Male      2115
Name: gender, dtype: int64
```

In [17]:
```
#Creating list of columns that have categorical data
catCols = [col for col in brain_stroke.columns if brain_stroke[col].dtype=="O"]
catCols
```

Out[17]:
```
['gender', 'ever_married', 'work_type', 'Residence_type', 'smoking_status']
```

In [18]:
```
#creating dummy variables for all categorical columns
from sklearn.preprocessing import LabelEncoder # loading library
label_encoder = LabelEncoder() # setting encoder function
class MultiColumnLabelEncoder:
    def __init__(self,columns = None):
        self.columns = columns # array of column names to encode

    def fit(self,X,y=None):
        return self # not relevant here

    def transform(self,X):
        '''
        Transforms columns of X specified in self.columns using
        LabelEncoder(). If no columns specified, transforms all
        columns in X.
        '''
        output = X.copy()
        if self.columns is not None:
            for col in self.columns:
                output[col] = LabelEncoder().fit_transform(output[col])
        else:
            for colname,col in output.iteritems():
                output[colname] = LabelEncoder().fit_transform(col)
        return output
    def fit_transform(self,X,y=None):
        return self.fit(X,y).transform(X)
strokeCat = MultiColumnLabelEncoder(columns = catCols).fit_transform(brain_stroke)
```

In [19]:
```
#valdidating categorical value conversion
strokeCat.head
```

Out[19]:
```
<bound method NDFrame.head of          id  gender   age  hypertension  heart_disease  ev
er_married  \
0      9046       1  67.0             0              1              1
1     51676       0  61.0             0              0              1
2     31112       1  80.0             0              1              1
3     60182       0  49.0             0              0              1
4      1665       0  79.0             1              0              1
...     ...     ...   ...           ...            ...            ...
5105  18234       0  80.0             1              0              1
5106  44873       0  81.0             0              0              1
5107  19723       0  35.0             0              0              1
5108  37544       1  51.0             0              0              1
5109  44679       0  44.0             0              0              1

      work_type  Residence_type  avg_glucose_level   bmi  smoking_status  \
```

```
0              2                1              228.69  36.6              1
1              3                0              202.21  28.1              2
2              2                0              105.92  32.5              2
3              2                1              171.23  34.4              3
4              3                0              174.12  24.0              2
...          ...              ...                 ...   ...            ...
5105           2                1               83.75  28.1              2
5106           3                1              125.20  40.0              2
5107           3                0               82.99  30.6              2
5108           2                0              166.29  25.6              1
5109           0                1               85.28  26.2              0

      stroke
0          1
1          1
2          1
3          1
4          1
...      ...
5105       0
5106       0
5107       0
5108       0
5109       0

[5109 rows x 12 columns]>
```

In [20]:

```
#Correlation Matrix
strokeCat.corr()
```

Out[20]:

	id	gender	age	hypertension	heart_disease	ever_married	work_type
id	1.000000	0.001929	0.003677	0.003610	-0.001253	0.013944	-0.015730
gender	0.001929	1.000000	-0.027752	0.021223	0.085685	-0.030171	0.056576
age	0.003677	-0.027752	1.000000	0.276367	0.263777	0.679084	-0.361686
hypertension	0.003610	0.021223	0.276367	1.000000	0.108292	0.164187	-0.051772
heart_disease	-0.001253	0.085685	0.263777	0.108292	1.000000	0.114601	-0.028031
ever_married	0.013944	-0.030171	0.679084	0.164187	0.114601	1.000000	-0.352831
work_type	-0.015730	0.056576	-0.361686	-0.051772	-0.028031	-0.352831	1.000000
Residence_type	-0.001219	-0.006105	0.014031	-0.007980	0.003045	0.005988	-0.007348
avg_glucose_level	0.000943	0.054722	0.238323	0.174540	0.161907	0.155329	-0.050492
bmi	0.005708	-0.026452	0.324211	0.158252	0.036879	0.334770	-0.299218
smoking_status	0.014139	-0.062423	0.265165	0.111018	0.048445	0.259604	-0.305942
stroke	0.006430	0.009081	0.245239	0.127891	0.134905	0.108299	-0.032323

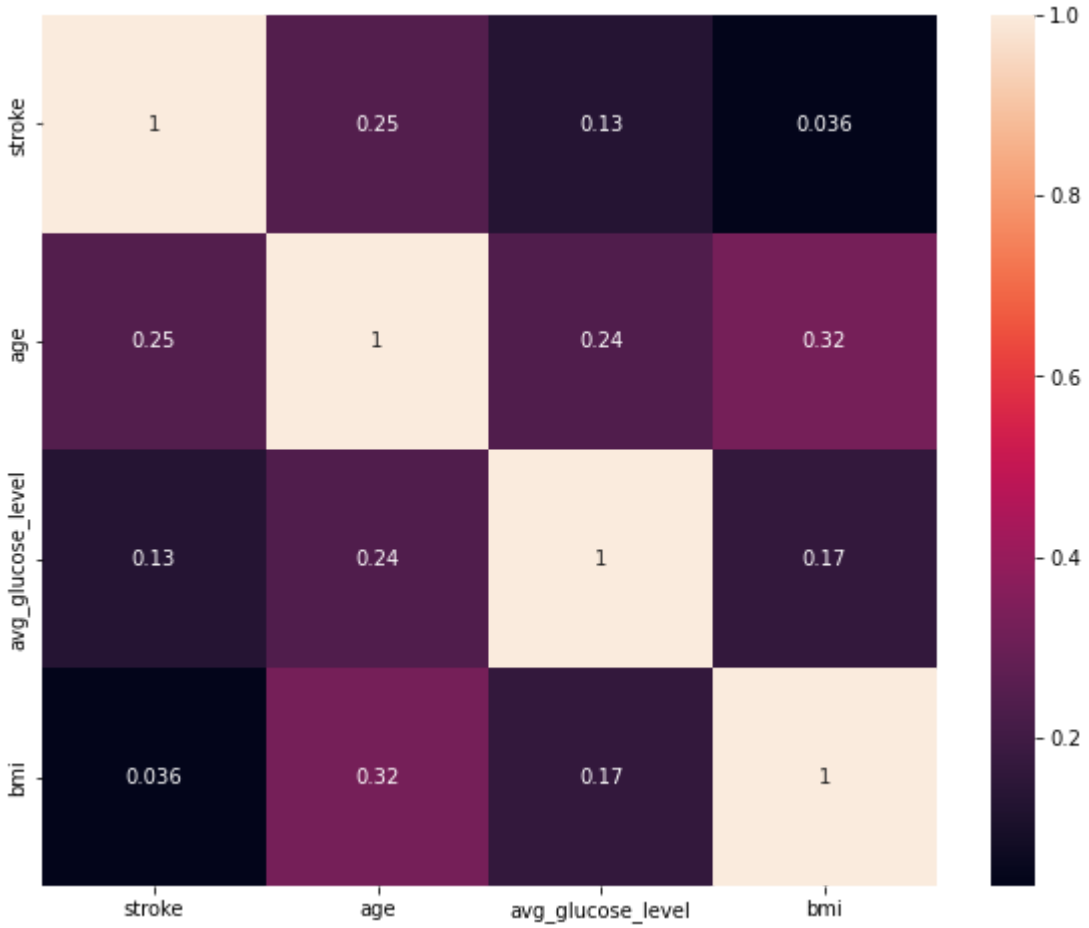
In [21]:

```
#Correlation against stroke outcome
corr_matrix = strokeCat.corr()
corr_matrix["stroke"].sort_values(ascending = False)
```

Out[21]:
```
stroke               1.000000
age                  0.245239
heart_disease        0.134905
avg_glucose_level    0.131991
hypertension         0.127891
ever_married         0.108299
bmi                  0.036075
smoking_status       0.028108
Residence_type       0.015415
gender               0.009081
id                   0.006430
work_type           -0.032323
Name: stroke, dtype: float64
```

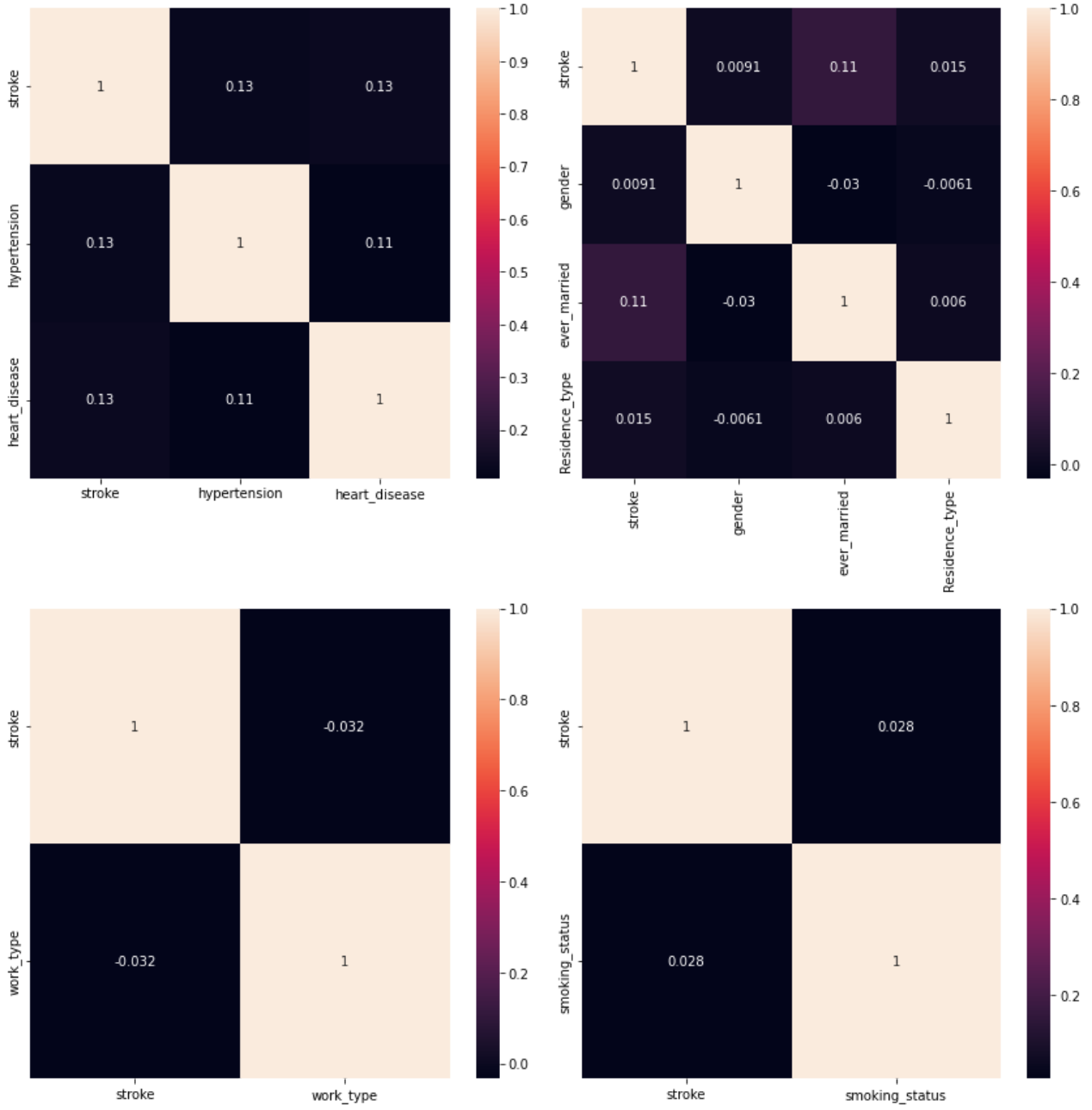
In [22]:
```
#plotting Correlation heat map against numeric attributes : 'stroke', 'age', 'avg_gluco
fig, ax = plt.subplots(figsize=(10,8))
sns.heatmap(strokeCat[['stroke', 'age', 'avg_glucose_level', 'bmi']].corr(),annot=True)
```

Out[22]:
```
<AxesSubplot:>
```



In [23]:
```
#Correlation heat map against categorical attributes
# 1. ['stroke', 'hypertension', 'heart_disease']
# 2. ['stroke', 'gender', 'ever_married', 'Residence_type']
# 3. ['stroke', 'work_type']
# 4. ['stroke', 'smoking_status']
fig, ax = plt.subplots(2,2, figsize = (12,12))
((ax1, ax2), (ax3, ax4)) = ax
```

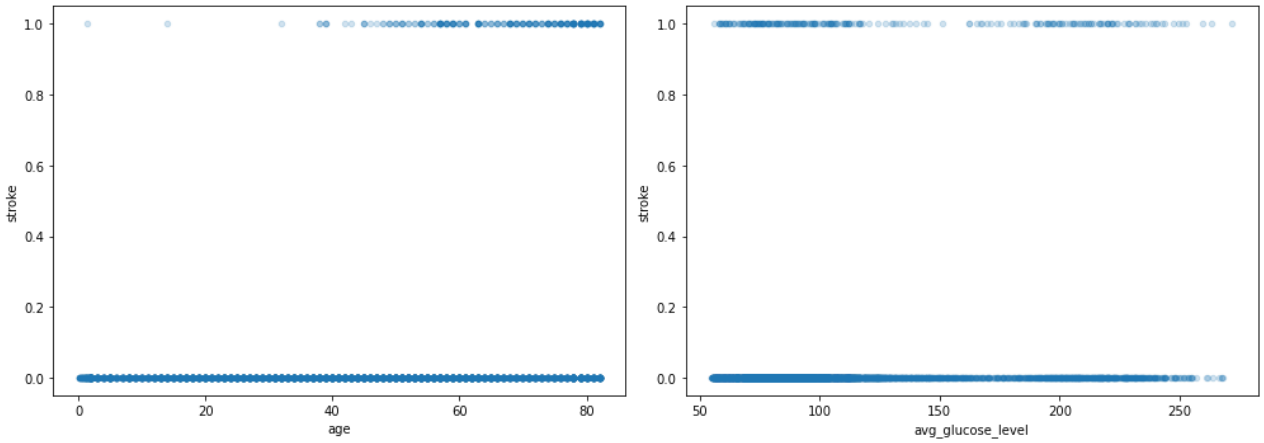
```
# the "no_" attributes is the opposite to the "yes_" attributes so the correlation to s
sns.heatmap(strokeCat[['stroke', 'hypertension', 'heart_disease']].corr(),annot=True, a
sns.heatmap(strokeCat[['stroke', 'gender', 'ever_married', 'Residence_type']].corr(),an
sns.heatmap(strokeCat[['stroke', 'work_type']].corr(),annot=True, ax=ax3)
sns.heatmap(strokeCat[['stroke', 'smoking_status']].corr(),annot=True, ax=ax4)

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



In [24]:

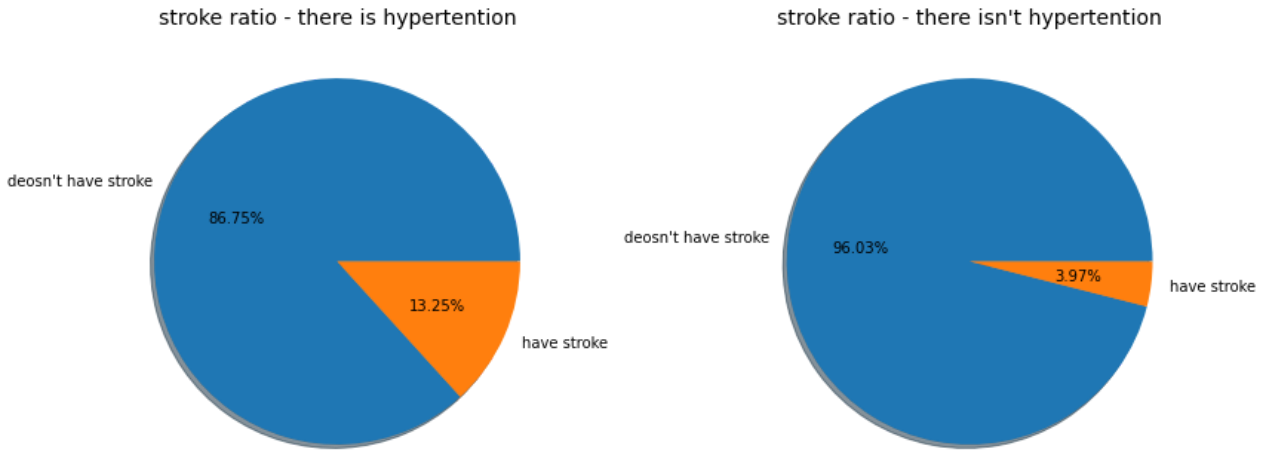
```
#Stroke plot against age and avg glucose level
strokeClean = strokeCat

fig, ax = plt.subplots(1,2, figsize = (14,5), )
((ax1, ax2)) = ax

strokeClean.plot(ax=ax1, kind='scatter', x='age', y='stroke', alpha = 0.2)
strokeClean.plot(ax=ax2, kind='scatter', x='avg_glucose_level', y='stroke', alpha = 0.2
```

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



In [25]:

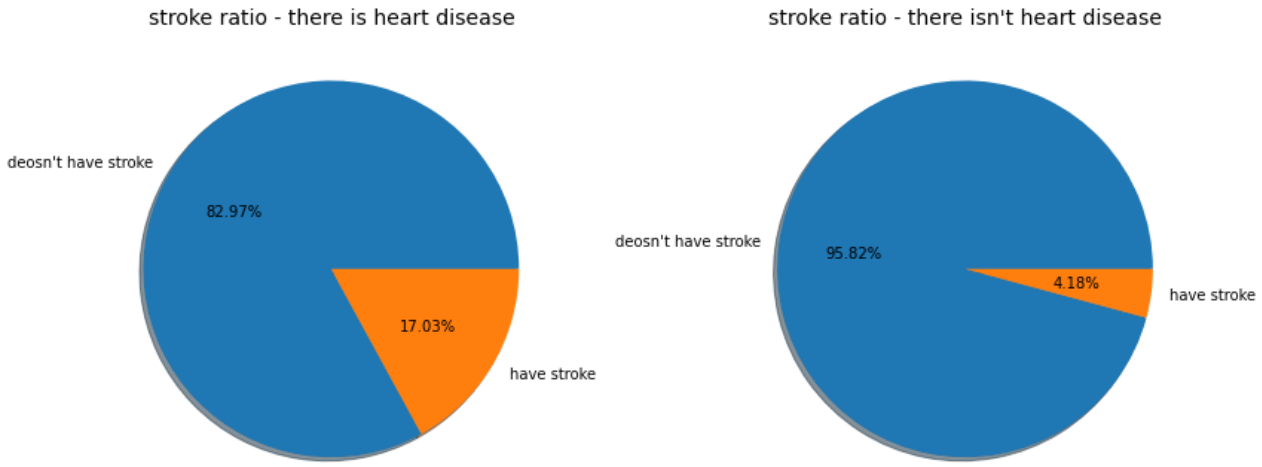
```
#Stroke correlation with hyptertention
fig, ax = plt.subplots(1,2, figsize = (12,12))
((ax1, ax2)) = ax

labels = ["deosn't have stroke", "have stroke"]
values = strokeClean[strokeClean['hypertension']==1]['stroke'].value_counts().tolist()
ax1.pie(x=values, labels=labels, autopct="%1.2f%%", shadow=True)
ax1.set_title("stroke ratio - there is hypertention", fontdict={'fontsize': 14})

labels = ["deosn't have stroke", "have stroke"]
values = strokeClean[strokeClean['hypertension']==0]['stroke'].value_counts().tolist()
ax2.pie(x=values, labels=labels, autopct="%1.2f%%", shadow=True)
ax2.set_title("stroke ratio - there isn't hypertention", fontdict={'fontsize': 14})

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



In [26]:

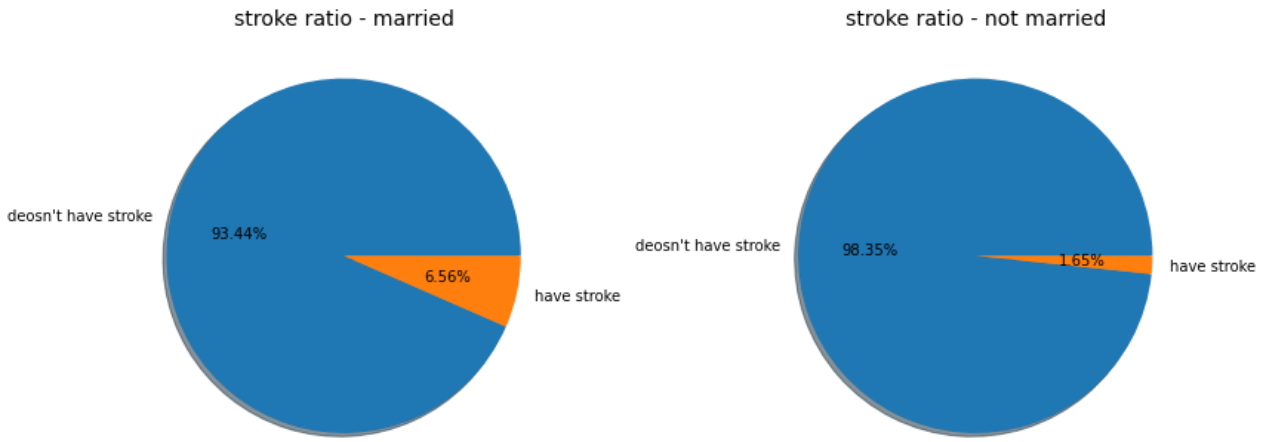
```
#Stroke Correlation with Heart disease
fig, ax = plt.subplots(1,2, figsize = (12,12))
((ax1, ax2)) = ax

labels = ["deosn't have stroke", "have stroke"]
values = strokeClean[strokeClean['heart_disease']==1]['stroke'].value_counts().tolist()
ax1.pie(x=values, labels=labels, autopct="%1.2f%%", shadow=True)
ax1.set_title("stroke ratio - there is heart disease", fontdict={'fontsize': 14})
```

```
labels = ["deosn't have stroke", "have stroke"]
values = strokeClean[strokeClean['heart_disease']==0]['stroke'].value_counts().tolist()
ax2.pie(x=values, labels=labels, autopct="%1.2f%%", shadow=True)
ax2.set_title("stroke ratio - there isn't heart disease", fontdict={'fontsize': 14})

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



In [27]:

```
#Stroke Correlation with Marriage
fig, ax = plt.subplots(1,2, figsize = (12,12))
((ax1, ax2)) = ax

labels = ["deosn't have stroke", "have stroke"]
values = strokeClean[strokeClean['ever_married']==1]['stroke'].value_counts().tolist()
ax1.pie(x=values, labels=labels, autopct="%1.2f%%", shadow=True)
ax1.set_title("stroke ratio - married", fontdict={'fontsize': 14})

labels = ["deosn't have stroke", "have stroke"]
values = strokeClean[strokeClean['ever_married']==0]['stroke'].value_counts().tolist()
ax2.pie(x=values, labels=labels, autopct="%1.2f%%", shadow=True)
ax2.set_title("stroke ratio - not married", fontdict={'fontsize': 14})

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

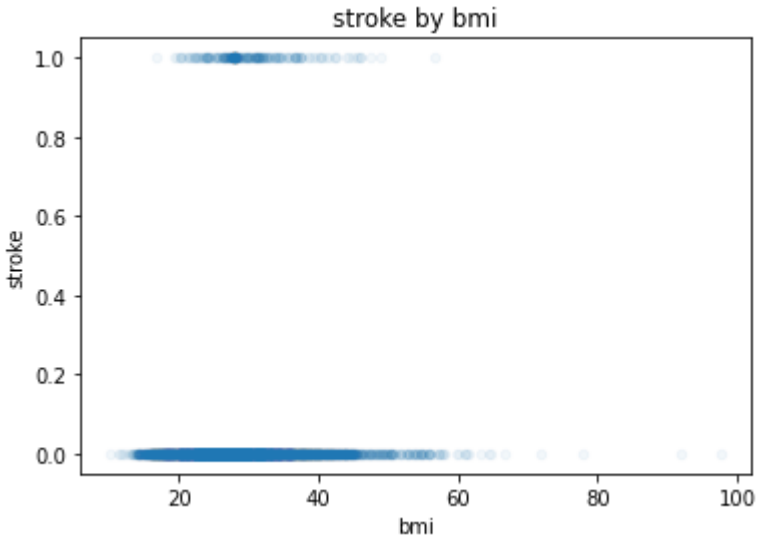


In [28]:
```
#BMI Correalation
corr_matrix = strokeClean.corr()
bmi_corr = corr_matrix["bmi"].sort_values(ascending = False).drop('bmi')
print(bmi_corr[bmi_corr>0.15])
print(bmi_corr[bmi_corr<-0.15])
```

```
ever_married         0.334770
age                  0.324211
smoking_status       0.218928
avg_glucose_level    0.167033
hypertension         0.158252
Name: bmi, dtype: float64
work_type   -0.299218
Name: bmi, dtype: float64
```

In [29]:
```
#BMI vs Stroke scatter plot
strokeClean.plot.scatter( x='bmi', y='stroke', alpha = 0.05, title="stroke by bmi")
```

Out[29]:
```
<AxesSubplot:title={'center':'stroke by bmi'}, xlabel='bmi', ylabel='stroke'>
```

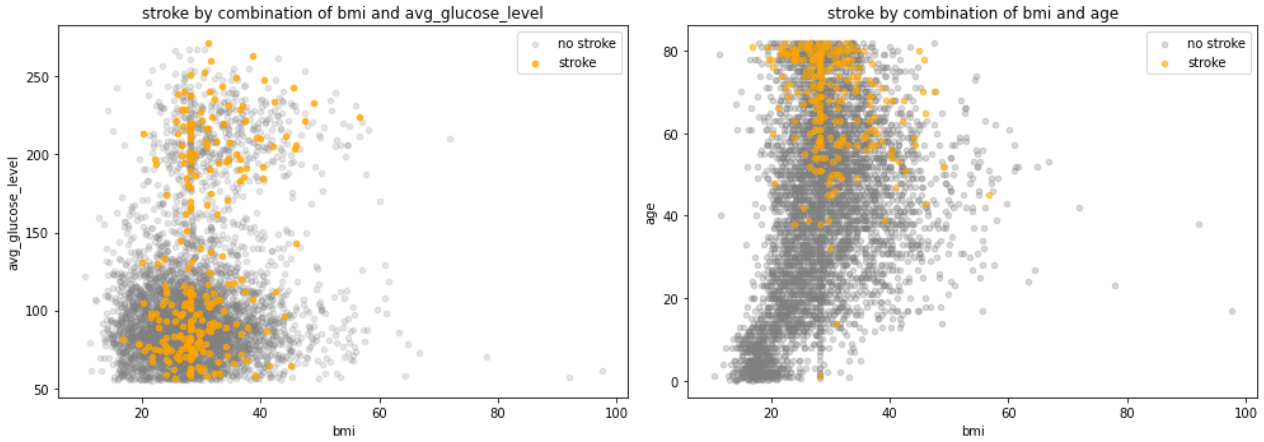


In [30]:
```
# check that the pattern above really exist and not because of the plot density:

values_30plusminusBMI = strokeClean[(strokeClean['bmi']>27) & (strokeClean['bmi']<33)][
values_stroke = strokeClean['stroke'].value_counts().tolist()

print("-+30bmi without stroke cases : all without stroke cases (ratio) = " + str(values
print("-+30bmi : all observations (ratio) = " + str(sum(values_30plusminusBMI)/sum(valu
print("-+30bmi with stroke cases : all stroke cases (ratio) = " + str(values_30plusminu
print("as we can see, among 1/2 of the stroke cases the bmi is around 30. In contrast t
```

```
-+30bmi without stroke cases : all without stroke cases (ratio) = 0.3228395061728395
-+30bmi : all observations (ratio) = 0.33235466823253085
-+30bmi with stroke cases : all stroke cases (ratio) = 0.5180722891566265
as we can see, among 1/2 of the stroke cases the bmi is around 30. In contrast to cases
where there is no stroke where the ratio is significantly lower, only 1/3.
```

In [31]:
```
#Scatter plot of bmi vs avg_glucose_level and bmi vs age
fig, ax = plt.subplots(1,2, figsize = (14,5))
((ax1, ax2)) = ax
```

```
#stroke by combination of bmi and avg_glucose_level
strokeClean[strokeClean['stroke'] ==0].plot.scatter(ax=ax1, x='bmi', y='avg_glucose_lev
strokeClean[strokeClean['stroke'] ==1].plot.scatter(ax=ax1, x='bmi', y='avg_glucose_lev
ax1.legend()
ax1.set_title('stroke by combination of bmi and avg_glucose_level')
#stroke by combination of bmi and age
strokeClean[strokeClean['stroke'] ==0].plot.scatter(ax=ax2, x='bmi', y='age', alpha = 0
strokeClean[strokeClean['stroke'] ==1].plot.scatter(ax=ax2, x='bmi', y='age', alpha = 0
ax2.legend()
ax2.set_title('stroke by combination of bmi and age')

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



Preparing Dataset for Modeling

I am going to Split my data set into train and test data sets(75/25) and apply knn modelling with standard Scalar and hyper parameters for grid search

In [32]:

```
strokeClean.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 5109 entries, 0 to 5109
Data columns (total 12 columns):
 #   Column             Non-Null Count  Dtype  
---  ------             --------------  -----  
 0   id                 5109 non-null   int64  
 1   gender             5109 non-null   int32  
 2   age                5109 non-null   float64
 3   hypertension       5109 non-null   int64  
 4   heart_disease      5109 non-null   int64  
 5   ever_married       5109 non-null   int32  
 6   work_type          5109 non-null   int32  
 7   Residence_type     5109 non-null   int32  
 8   avg_glucose_level  5109 non-null   float64
 9   bmi                5109 non-null   float64
 10  smoking_status     5109 non-null   int32  
 11  stroke             5109 non-null   int64  
dtypes: float64(3), int32(5), int64(4)
memory usage: 419.1 KB
```

In [33]:
```
#import necessary libraries
from sklearn.model_selection import train_test_split
```

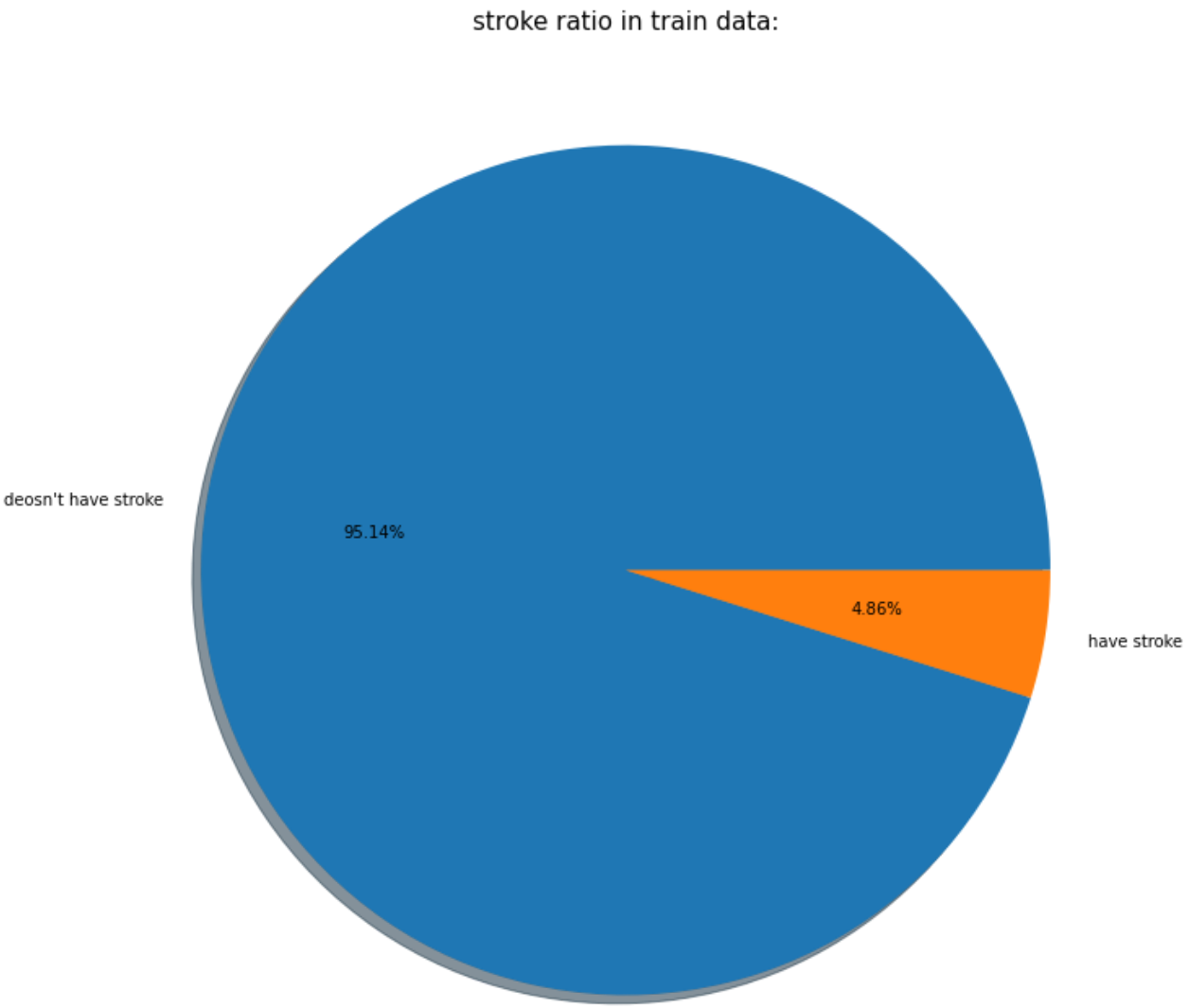
In [34]:
```
#stroke Target value is taken as a numpy array
y = strokeClean["stroke"].values
#All the features are separated from our target value or label and stored in x
X = strokeClean.drop(["stroke","id"],axis=1)
```

In [35]:
```
#Split data into training and testing sets - 75/25 Train and test size
X_train, X_test, y_train, y_test = train_test_split(X,y ,random_state=142, train_size=0
```

In [36]:
```
#printing Size and shape of the target and features for test and train
print(X_train.shape)
print(y_train.size)
print(X_test.shape)
print(y_test.size)
```

```
(3831, 10)
3831
(1278, 10)
1278
```

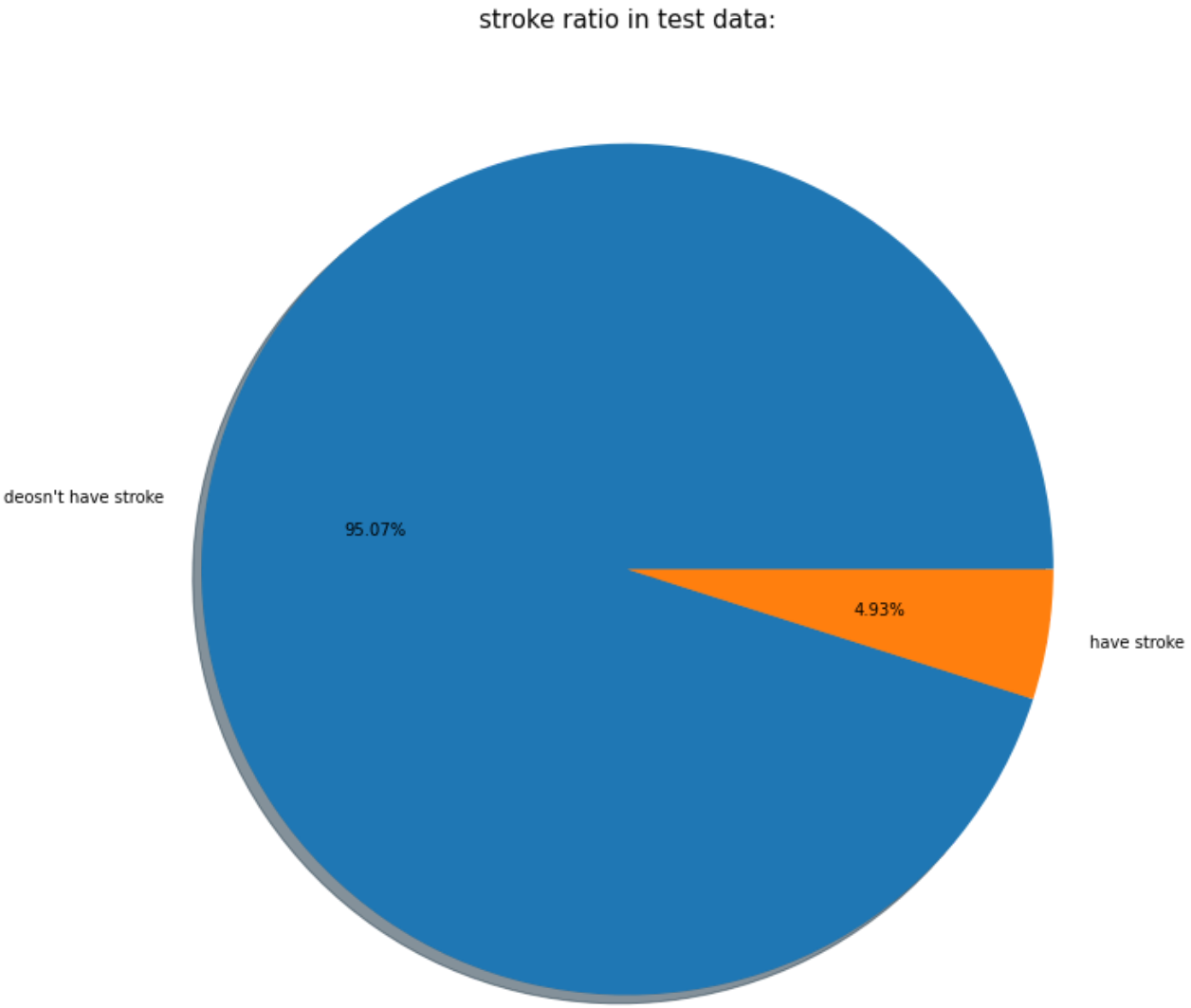
In [37]:
```
train_df = pd.DataFrame(y_train,columns=['Stroke'])

fig, ax = plt.subplots(1,1, figsize = (12,12))
labels = ["deosn't have stroke", "have stroke"]
values_train = train_df.value_counts().tolist()

ax.pie(x=values_train, labels=labels, autopct="%1.2f%%", shadow=True)
ax.set_title("stroke ratio in train data:", fontdict={'fontsize': 15})
plt.show()
print("Values for No and Yes Stroke: " +str(values_train))
```




```
Values for No and Yes Stroke: [3645, 186]
```

In [38]:

```
test_df = pd.DataFrame(y_test,columns=['Stroke'])

fig, ax = plt.subplots(1,1, figsize = (12,12))
labels = ["deosn't have stroke", "have stroke"]
values_test = test_df.value_counts().tolist()

ax.pie(x=values_test, labels=labels, autopct="%1.2f%%", shadow=True)
ax.set_title("stroke ratio in test data:", fontdict={'fontsize': 15})
plt.show()
print("Values for No and Yes Stroke: " +str(values_test))
```




```
Values for No and Yes Stroke: [1215, 63]
```

Knn Modelling With Original Train and Test data

In [39]:
```
# Load libraries
from sklearn.neighbors import KNeighborsClassifier
from sklearn import datasets
from sklearn.preprocessing import StandardScaler
from sklearn.pipeline import Pipeline, FeatureUnion
from sklearn.model_selection import GridSearchCV
from sklearn.preprocessing import StandardScaler, PolynomialFeatures, OneHotEncoder,Sta
```

In [40]:
```
#MinMax Scalacr
scaler = StandardScaler()
# Create a KNN classifier
knn = KNeighborsClassifier(n_neighbors=5, n_jobs=-1)
# Create a pipeline
pipe = Pipeline([("scaler", scaler),("knn", knn)])
```

In [41]:
```
#Scaling Test and Train Data feature set using MinMax Scaler
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test)
```

In [42]:
```
# Create space of candidate values
search_space = [{"knn__n_neighbors": [1, 2, 3, 4, 5, 6, 7, 8, 9, 10]}]
```

In [43]:
```
# Create grid search with fitting the train data
grid = GridSearchCV(pipe, search_space, cv=5, verbose=0).fit(X_train_scaled, y_train)
```

In [44]:
```
# Best neighborhood size (k)
print("Best K value: %.0f"  % (grid.best_estimator_.get_params()["knn__n_neighbors"]))
```

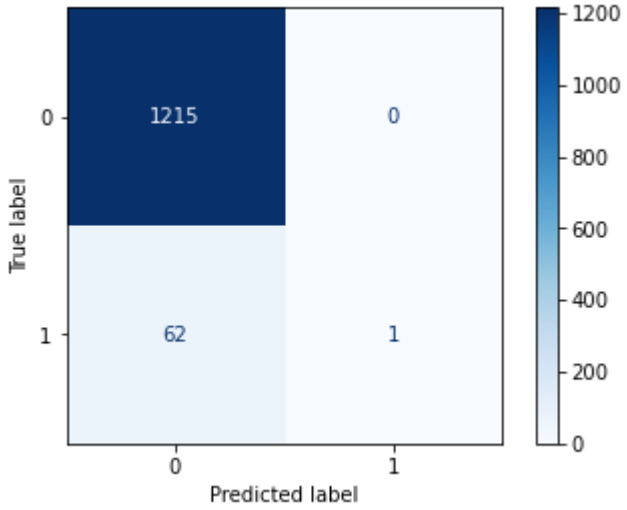
```
Best K value: 8
```

In [45]:
```
#Grid Search prediction on test set
grid_pred = grid.predict(X_test_scaled)
```

In [46]:
```
#Checking Accuracy Score
import math
from sklearn.metrics import accuracy_score
from sklearn.metrics import precision_score
from sklearn.metrics import recall_score
from sklearn.metrics import f1_score
from sklearn.metrics import confusion_matrix
from sklearn.metrics import ConfusionMatrixDisplay
```

In [47]:
```
#Calculating metrics
accuracy=accuracy_score(y_test, grid_pred)
precision = precision_score(y_test, grid_pred, average='weighted')
recall=recall_score(y_test, grid_pred, average='weighted')
f1 = f1_score(y_test, grid_pred, average='weighted')
print("Accuracy: %.4f"  % (accuracy))
print("precision: %.4f"  % (precision))
print("recall: %.4f"  % (recall))
print("f1 Score: %.4f"  % (f1))
print("Confusion Matrix for Prediction:")
cm=confusion_matrix(y_test, grid_pred)
disp = ConfusionMatrixDisplay(confusion_matrix=cm)

disp.plot(cmap=plt.cm.Blues)
plt.show()
```

```
Accuracy: 0.9515
precision: 0.9538
recall: 0.9515
f1 Score: 0.9286
Confusion Matrix for Prediction:
```



Observations

My target variable for the modelling is a classification which is essentially to predict based on the feature values, if the patient is going to have a stroke event or not.
Part of my modelling, I have imputed missing values and cleaned a outlier within gender variable. Then, I have created a knn model with standard Scalar and hyper parameter search using 10 n_neighbors.

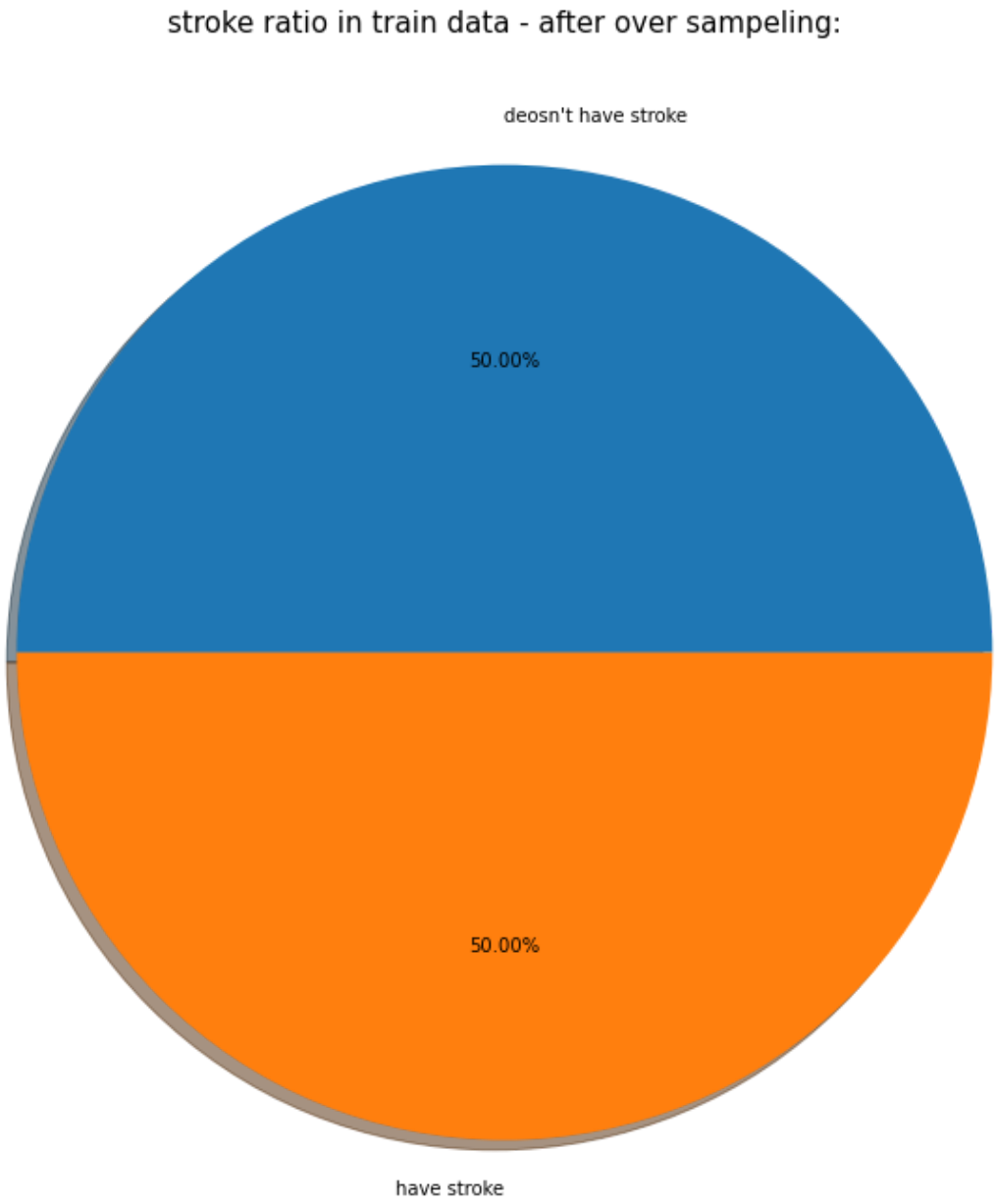
I see that knn model has resulted in very high accuracy/precision/recall and f1 scores - all of which are > 90%

This high accuracy could be a result of imbalanced dataset (95% negative outcomes, and 5% positive outcomes of stroke).

As a pathforward I am going to use SMOTE to oversample my unbalanced postive outcome

In [66]:
```
# Loading Library : imblearn
from imblearn.over_sampling import SMOTE
```

In [58]:
```
#Over Sampling data using SMOTE
from imblearn.over_sampling import SMOTE

oversample = SMOTE()
XUp, yUp = oversample.fit_resample(X_train_scaled, y_train)
upsampled_df = pd.DataFrame(yUp,columns=['Stroke'])

fig, ax = plt.subplots(1,1, figsize = (12,12))
labels = ["deosn't have stroke", "have stroke"]
values_upsample = upsampled_df.value_counts().tolist()

ax.pie(x=values_upsample, labels=labels, autopct="%1.2f%%", shadow=True)
ax.set_title("stroke ratio in train data - after over sampeling:", fontdict={'fontsize'
plt.show()
print("there are now equal number of cases with stroke and without: " +str(values_upsam
```




```
there are now equal number of cases with stroke and without: [3645, 3645]
```

Performing few Models to see individual accuracies

In [59]:
```
from sklearn.linear_model import LogisticRegression
from sklearn.neighbors import KNeighborsClassifier
from sklearn.naive_bayes import GaussianNB
from sklearn.naive_bayes import BernoulliNB
from sklearn.svm import SVC
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
```

In [60]:
```
from sklearn.metrics import accuracy_score, confusion_matrix, roc_auc_score, ConfusionM
from sklearn.model_selection import cross_val_score
```

In [61]:
```
# calculating accuracies from other modles :
# 'Logistic Regreesion', 'SVM', 'KNeighbors','GaussianNB','Decision Tree', 'Random Fore
```

```
models = []
models.append(['Logistic Regreesion', LogisticRegression(random_state=0)])
models.append(['SVM', SVC(random_state=0)])
models.append(['KNeighbors', KNeighborsClassifier()])
models.append(['GaussianNB', GaussianNB()])
models.append(['BernoulliNB', BernoulliNB()])
models.append(['Decision Tree', DecisionTreeClassifier(random_state=0)])
models.append(['Random Forest', RandomForestClassifier(random_state=0)])
x_train_res=XUp
y_train_res=yUp
x_test=X_test_scaled


lst_1= []

for m in range(len(models)):
    lst_2= []
    model = models[m][1]
    model.fit(x_train_res, y_train_res)
    y_pred = model.predict(x_test)
    cm = confusion_matrix(y_test, y_pred)  #Confusion Matrix
    accuracies = cross_val_score(estimator = model, X = x_train_res, y = y_train_res, c
    roc = roc_auc_score(y_test, y_pred)  #ROC AUC Score
    precision = precision_score(y_test, y_pred,average='weighted')  #Precision Score
    recall = recall_score(y_test, y_pred,average='weighted')  #Recall Score
    f1 = f1_score(y_test, y_pred,average='weighted')  #F1 Score
    print(models[m][0],':')
    print(cm)
    print('Accuracy Score: ',accuracy_score(y_test, y_pred))
    print('')
    print("K-Fold Validation Mean Accuracy: {:.2f} %".format(accuracies.mean()*100))
    print('')
    print("Standard Deviation: {:.2f} %".format(accuracies.std()*100))
    print('')
    print('ROC AUC Score: {:.2f}'.format(roc))
    print('')
    print('Precision: {:.2f}'.format(precision))
    print('')
    print('Recall: {:.2f}'.format(recall))
    print('')
    print('F1: {:.2f}'.format(f1))
    print('-----------------------------------')
    print('')
    lst_2.append(models[m][0])
    lst_2.append((accuracy_score(y_test, y_pred))*100)
    lst_2.append(accuracies.mean()*100)
    lst_2.append(accuracies.std()*100)
    lst_2.append(roc)
    lst_2.append(precision)
    lst_2.append(recall)
    lst_2.append(f1)
    lst_1.append(lst_2)
```

```
Logistic Regreesion :
[[899 316]
 [ 15  48]]
Accuracy Score:  0.741001564945227

K-Fold Validation Mean Accuracy: 78.18 %
```

```
Standard Deviation: 1.74 %

ROC AUC Score: 0.75

Precision: 0.94

Recall: 0.74

F1: 0.81
-----------------------------------

SVM :
[[943 272]
 [ 26  37]]
Accuracy Score:  0.7668231611893583

K-Fold Validation Mean Accuracy: 84.29 %

Standard Deviation: 1.41 %

ROC AUC Score: 0.68

Precision: 0.93

Recall: 0.77

F1: 0.83
-----------------------------------

KNeighbors :
[[1027  188]
 [  44   19]]
Accuracy Score:  0.8184663536776213

K-Fold Validation Mean Accuracy: 90.99 %

Standard Deviation: 1.02 %

ROC AUC Score: 0.57

Precision: 0.92

Recall: 0.82

F1: 0.86
-----------------------------------

GaussianNB :
[[873 342]
 [ 16  47]]
Accuracy Score:  0.7198748043818466

K-Fold Validation Mean Accuracy: 77.06 %

Standard Deviation: 1.39 %

ROC AUC Score: 0.73

Precision: 0.94
```

```
Recall: 0.72

F1: 0.80
-----------------------------------

BernoulliNB :
[[684 531]
 [  9  54]]
Accuracy Score:  0.5774647887323944

K-Fold Validation Mean Accuracy: 72.07 %

Standard Deviation: 1.04 %

ROC AUC Score: 0.71

Precision: 0.94

Recall: 0.58

F1: 0.69
-----------------------------------

Decision Tree :
[[1124   91]
 [  46   17]]
Accuracy Score:  0.8928012519561815

K-Fold Validation Mean Accuracy: 91.60 %

Standard Deviation: 3.27 %

ROC AUC Score: 0.60

Precision: 0.92

Recall: 0.89

F1: 0.91
-----------------------------------

Random Forest :
[[1177   38]
 [  56    7]]
Accuracy Score:  0.9264475743348983

K-Fold Validation Mean Accuracy: 96.49 %

Standard Deviation: 2.51 %

ROC AUC Score: 0.54

Precision: 0.92

Recall: 0.93

F1: 0.92
-----------------------------------
```

Rerunning same KNN Grid Searh Pipe with Train data augmented to balance classes using SMOTE

In [62]:
```
# Create grid search with fitting the train data
gridUp = GridSearchCV(pipe, search_space, cv=5, verbose=0).fit(XUp, yUp)
```

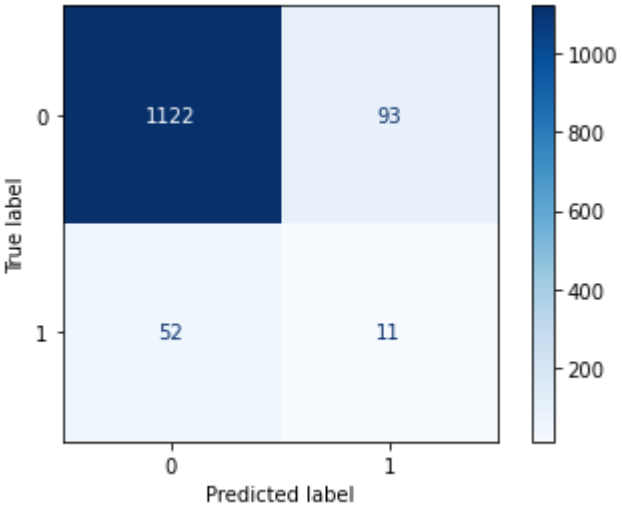
In [63]:
```
# Best neighborhood size (k)
print("Best K value: %.0f"  % (gridUp.best_estimator_.get_params()["knn__n_neighbors"])
```

```
Best K value: 1
```

In [64]:
```
#Grid Search prediction on test set
grid_predUp = gridUp.predict(X_test_scaled)
```

In [65]:
```
#Calculating metrics
accuracy=accuracy_score(y_test, grid_predUp)
precision = precision_score(y_test, grid_predUp, average='weighted')
recall=recall_score(y_test, grid_predUp, average='weighted')
f1 = f1_score(y_test, grid_predUp, average='weighted')
print("Accuracy: %.4f"  % (accuracy))
print("precision: %.4f"  % (precision))
print("recall: %.4f"  % (recall))
print("f1 Score: %.4f"  % (f1))
print("Confusion Matrix for Prediction:")
cm1=confusion_matrix(y_test, grid_predUp)
disp1 = ConfusionMatrixDisplay(confusion_matrix=cm1)

disp1.plot(cmap=plt.cm.Blues)
plt.show()
```

```
Accuracy: 0.8865
precision: 0.9138
recall: 0.8865
f1 Score: 0.8995
Confusion Matrix for Prediction:
```



Observation

1. Initial model(KNN) evaluation shows that it's not really identifying any positive outcome is it has 95% negative outcomes and 5% positive outcomes.

2. So the I planned to use SMOTE to balance my training set to include more values for positive outcome.
3. Several of the individual models like Logistics regression to Random Forest classifier had lesser precision(lesser by few percentage points) than original KNN Model which makes the case of KNN model application to be strong for this stroke prediction.
4. Retaining of the dataset with KNN using SMOTE should most likely yield better accuracy than other models and positive outcomes of stroke and therefore feel this is a better model. But have successfully classified the outcomes that are postive.

Finally :

I see that knn model has resulted in very high accuracy/precision/recall and f1 scores - all of which are in high 80s
This is a slight drop in the metrics from previous iteration, however this is a better model as the data properly identifies all target classes.