In []:	<pre># problem statements # age - age of policyholder # sex - male(1)/female(0) # bmi - body mass index (kg/m2) # children - number of children/ dependents of policyholder # smoker - smoking state nonsmoke(0)/ smoker(1) # region - residental area northeast(0)/northwest(1)/southeast(2)/southwest(3) # charges - medical cost # insuranceclaim - yes(1)/no(0)</pre>
In [18]:	Load libraries
<pre>In [8]: Out[8]:</pre>	# loading data data= pd.read_csv('insurance.csv') age sex bmi children smoker region charges insuranceclaim 0 19 0 27.900 0 1 3 16884.92400 1 1 18 1 33.770 1 0 2 1725.55230 1 2 28 1 33.000 3 0 2 4449.46200 0 3 33 1 22.705 0 0 1 21984.47061 0
In []:	# here insurance is our - target variable # others are categorical features(such as sex, smoker , region) # EDA (Exploratory Data Analysis) - # shape - it shows the no of rows and columns in dataset data.shape # 1338 rows and 8 columns (1338, 8)
In [4]: Out[4]: In [5]:	<pre># size - product of no of rows and no of column data.size 10704 # Data types data.info() <class 'pandas.core.frame.dataframe'=""> RangeIndex: 1338 entries, 0 to 1337 Data columns (total 8 columns): # Column Non-Null Count Dtype</class></pre>
In [6]:	0 age 1338 non-null int64 1 sex 1338 non-null int64 2 bmi 1338 non-null int64 3 children 1338 non-null int64 4 smoker 1338 non-null int64 5 region 1338 non-null int64 6 charges 1338 non-null float64 7 insuranceclaim 1338 non-null int64 dtypes: float64(2), int64(6) memory usage: 83.8 KB # unique = it shows different data types present in the data data.dtypes.unique()
Out[6]: In [7]: Out[7]: In [8]: Out[8]:	<pre>array([dtype('int64'), dtype('float64')], dtype=object) # unique values for children sorted(data['children'].unique()) [0, 1, 2, 3, 4, 5] sorted(data['sex'].unique())</pre> <pre>sorted(data['sex'].unique())</pre>
Out[9]: In [10]:	<pre># column = it shows column data.columns Index(['age', 'sex', 'bmi', 'children', 'smoker', 'region', 'charges',</pre>
Out[10]: In [11]: Out[11]:	sex 0 bmi 0 children 0 smoker 0 region 0 charges 0 dataset data.describe() # describe - gives statistical measure of dataset data.describe()
	count 1338.000000 1338.000000 1338.000000 1338.000000 1338.000000 1338.000000 mean 39.207025 0.505232 30.663397 1.094918 0.204783 1.515695 13270.422265 0.585202 std 14.049960 0.500160 6.098187 1.205493 0.403694 1.104885 12110.011237 0.492871 min 18.000000 0.000000 15.960000 0.000000 0.000000 1121.873900 0.000000 25% 27.000000 0.000000 26.296250 0.000000 0.000000 1.000000 4740.287150 0.000000 50% 39.000000 1.000000 30.400000 0.000000 0.000000 2.000000 9382.033000 1.000000 75% 51.000000 1.000000 53.130000 5.000000 1.000000 3.000000 63770.428010 1.000000
In []:	<pre># above values for only numerical value not for categorical features # 25%, 50% , 75% are percentiles # distribution of age value - sns.set() plt.figure(figsize=(5,5)) sns.distplot(data['age']) plt.title('Distribution of age ') plt.show() C:\Users\Vaibhav\anaconda3\lib\site-packages\seaborn\distributions.py:2619: FutureWarning: `distplot` is a deprecated function and will be removed in a future version. Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `histplot` (an axes-level</pre>
	function for histograms). warnings.warn(msg, FutureWarning) Distribution of age 0.040 0.035 0.030
	0.025 0.020 0.015 0.010 0.005
In []:	# gender - male or female # count - it gives no of males and no of females plt.figure(figsize=(5,5)) sns.countplot(x='sex', data=data)
In [28]:	plt.title('sex distribution') plt.show() sex distribution 600 500
	400 300 200 100
Out[31]:	0 1 sex # here we can find count of male(1) and female(0) data['sex'].value_counts() 1 676 0 662 Name: sex, dtype: int64
In [36]:	# bmi (body mass index) = It gives person is over weight, under weight or normal weight plt.figure(figsize=(5,5)) sns.distplot(data['bmi']) plt.title('bmi Distribution') plt.show() C:\Users\Vaibhav\anaconda3\lib\site-packages\seaborn\distributions.py:2619: FutureWarning: `distplot` is a deprecated function and will be removed in a future version. Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `histplot` (an axes-level function for histograms). warnings.warn(msg, FutureWarning) bmi Distribution 0.07
	0.06 0.05 ≥ 0.04 0.03
	0.02 0.01 0.00 10 20 30 40 50 bmi
In []: In [39]:	<pre># here we get normal distribution curve = its normal range is = approxi 18 to 25 # below 18 = we can say person is under weight # above 25 = we can say person is over weight # more no of values between 25 to 40 hence we can say more no of people might be over weighted # children - plt.figure(figsize=(5,5)) sns.countplot(x='children', data=data) plt.title('children') plt.show()</pre> <pre>children</pre>
	600 500 400
	200 100 0 1 2 3 4 5 children
<pre>In [41]: Out[41]: In [49]:</pre>	<pre>data['children'].value_counts() 0 574 1 324 2 240 3 157 4 25 5 18 Name: children, dtype: int64 # smoker -</pre>
	plt.figure(figsize=(5,5)) sns.countplot(x='smoker', data=data) plt.title('smoker') plt.show() smoker
	## 600 400 200
<pre>In [50]: Out[50]:</pre>	# count of smoker [if yes(1)= smoker and no(0)= non-smoker] data['smoker'].value_counts() 0 1064 1 274 Name: complexe divisor int64
In [51]:	Name: smoker, dtype: int64 # region plt.figure(figsize=(5,5)) sns.countplot(x='region', data=data) plt.title('region') plt.show() region
	300 250 tung 200 150
In [52]:	# northeast(0), northwest(1), southeast(2), southwest(3) data['region'].value_counts()
Out[52]: In [15]:	<pre>2 364 3 325 1 325 0 324 Name: region, dtype: int64 # charges - sns.set() plt.figure(figsize=(5,5)) sns.distplot(data['charges']) plt.title('charges distribution ') plt.show()</pre>
	C:\Users\Vaibhav\anaconda3\lib\site-packages\seaborn\distributions.py:2619: FutureWarning: `distplot` is a deprecated function and will be removed in a future version. Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `histplot` (an axes-level function for histograms). warnings.warn(msg, FutureWarning) 1e-5
	Shi 4 3 2 1
In [4]:	0 20000 40000 60000 charges spliting features and target variable # here remove target variable (insuranceclaim) x = data.drop(columns='insuranceclaim', axis=1) # take axis = 1 to delete column
In [5]:	<pre>y = data('insuranceclaim') print(y)</pre>
In [29]:	1336
In [14]:	1333 50 1 30.970 3 0 1 10600.54830 1334 18 0 31.920 0 0 0 2205.98080 1335 18 0 36.850 0 0 0 2 1629.83350 1336 21 0 25.800 0 0 0 3 2007.94500 1337 61 0 29.070 0 1 1 29141.36030 [1338 rows x 7 columns] Spliting the data into Traing and Testing data x_train, x_test, y_train, y_test =train_test_split(x,y, test_size=0.2, random_state=2)
In [15]: In [12]: In [16]:	<pre>print(x.shape, x_train.shape, x_test.shape) (1338, 7) (1070, 7) (268, 7) Model training # classification by using Decision tree classifier = DecisionTreeClassifier() classifier.fit(x_train, y_train)</pre>
Out[16]: In []: In [17]:	DecisionTreeClassifier() Model Evaluation # prediction of Training data training_data_prediction=classifier.predict(x_train) # accuracy score
In []: In [23]:	<pre>acc=accuracy_score(y_train, training_data_prediction) print("training" ,acc) training 1.0 # prediction of Testing data testing_data_prediction=classifier.predict(x_test) # accuracy score acc=accuracy_score(y_test, testing_data_prediction) print("testing" ,acc)</pre>
In [30]: In [34]: In [33]:	<pre>testing 0.9589552238805971 # Building a predictive system input_data=(28,1,33.000,3,0,2,4449.4620) # changing input_data to numpy array input_data_as_numpy_array= np.asarray(input_data) # reshape the array input_data_reshaped = input_data_as_numpy_array.reshape(1,-1) prediction= classifier.predict(input_data_reshaped) if prediction=classifier.predict(input_data_reshaped)</pre>
In [35]: In [37]:	<pre>prediction= classifier.predict(input_data_reshaped) if prediction[0]==1: print("Insurance will be claimed") else: print("Insurance will not be claimed") Insurance will not be claimed C:\Users\Vaibhav\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but DecisionTreeClassifier was fitted with feature names warnings.warn(input_data=(18,1,33.770,1,0,2,1725.55230) input_data_as_numpy_array= np.asarray(input_data)</pre>
[3/]:	<pre># reshape the array input_data_reshaped = input_data_as_numpy_array.reshape(1,-1) prediction= classifier.predict(input_data_reshaped) if prediction[0]==1: print("Insurance will be claimed") else: print("Insurance will not be claimed") Insurance will be claimed C:\Users\Vaibhav\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but DecisionTreeClassifier was fitted with feature names</pre>
In []: In []:	conclusion # if my prediction value is equal to zero then insurance will be claimed and # if my prediction is equal to one then it will not be claimed