Medical Insurance Cost prediction

This exercise is about performing some of the steps described in the notebook for the California Housing Data on another dataset for Medical Insurance Cost prediction.

Get the Data

In [ ]:
```
import pandas as pd

medical = pd.read_csv("https://bit.ly/44evDuW")
```

Take a Quick Look at the Data Structure

In [ ]:
```
# display the first 5 rows of the dataset by calling the head() function on medical
medical.head()
```

Out[ ]:

	age	sex	bmi	children	smoker	region	charges
0	19	female	27.900	0	yes	southwest	16884.92400
1	18	male	33.770	1	no	southeast	1725.55230
2	28	male	33.000	3	no	southeast	4449.46200
3	33	male	22.705	0	no	northwest	21984.47061
4	32	male	28.880	0	no	northwest	3866.85520

Each row represents one patient. There are 7 attributes.

The `info()` method is useful to get a quick description of the data, in particular the total number of rows, each attribute's type, and the number of non-null values:

In [ ]:
```
# get the number of rows, columns, and data types by using the info() method
medical.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1338 entries, 0 to 1337
Data columns (total 7 columns):
 #   Column    Non-Null Count  Dtype  
---  ------    --------------  -----  
 0   age       1338 non-null   int64  
 1   sex       1338 non-null   object 
 2   bmi       1338 non-null   float64
 3   children  1338 non-null   int64  
 4   smoker    1338 non-null   object 
 5   region    1338 non-null   object 
 6   charges   1338 non-null   float64
dtypes: float64(2), int64(2), object(3)
memory usage: 73.3+ KB
```

In [ ]:
```
# show the number of patients in each region by using the value_counts() method on
medical['region'].value_counts()
```

Out[ ]:
```
region
southeast    364
southwest    325
northwest    325
northeast    324
Name: count, dtype: int64
```

Let’s look at the other fields. The describe() method shows a summary of the numerical attributes.

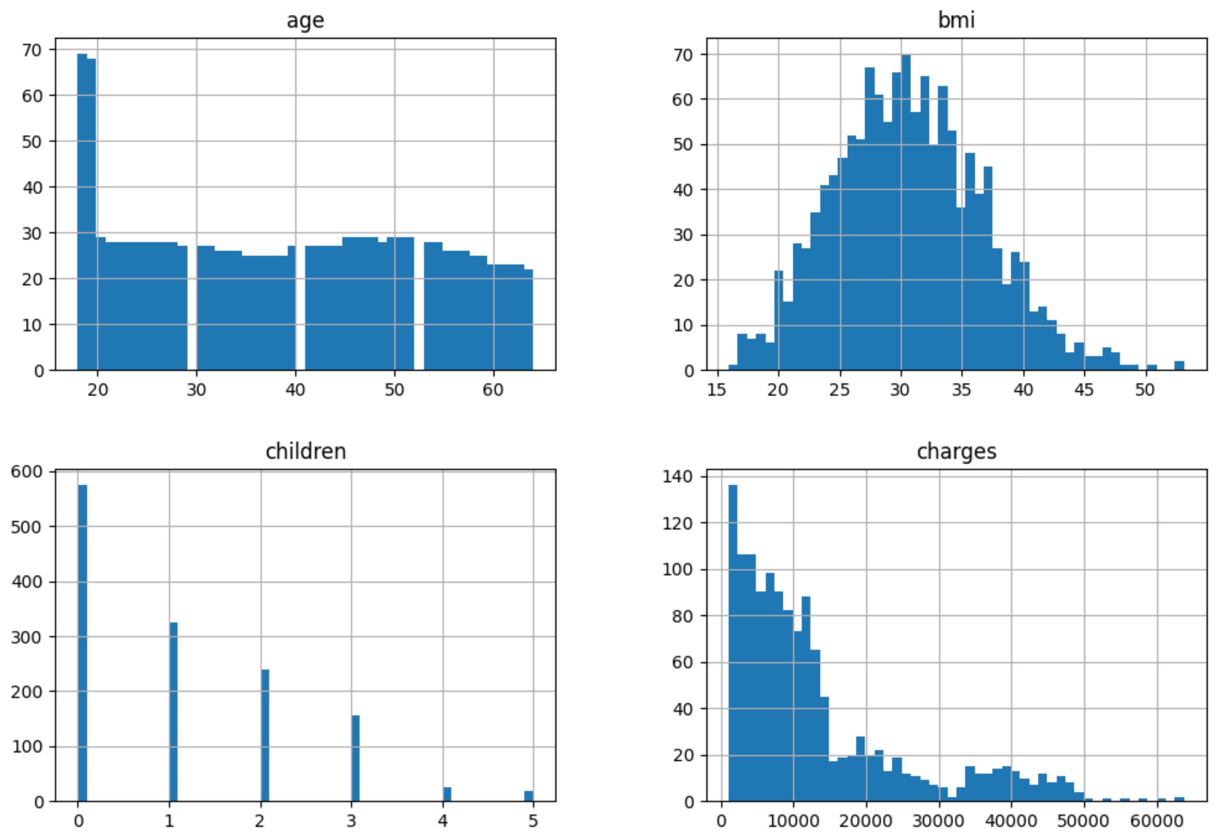
In [ ]:
```
# show descriptive statistics for the dataset by calling the describe() method on m
medical.describe()
```

Out[ ]:

	age	bmi	children	charges
count	1338.000000	1338.000000	1338.000000	1338.000000
mean	39.207025	30.663397	1.094918	13270.422265
std	14.049960	6.098187	1.205493	12110.011237
min	18.000000	15.960000	0.000000	1121.873900
25%	27.000000	26.296250	0.000000	4740.287150
50%	39.000000	30.400000	1.000000	9382.033000
75%	51.000000	34.693750	2.000000	16639.912515
max	64.000000	53.130000	5.000000	63770.428010

In [ ]:
```
# show histograms for the numerical columns by using the hist() method on medical
medical.hist(bins=50, figsize=(12,8))
```

Out[ ]:
```
array([[<Axes: title={'center': 'age'}>, <Axes: title={'center': 'bmi'}>],
       [<Axes: title={'center': 'children'}>,
        <Axes: title={'center': 'charges'}>]], dtype=object)
```



Briefly write here what you observe from these histograms.

No X and Y axis lables so I have no clue what these numbers represent.

Create a Test Set

In [ ]:

```
# use train_test_split() to split the data into training and test sets
from sklearn.model_selection import train_test_split

train_set, test_set = train_test_split(medical, test_size=0.2, random_state=42)
len(train_set), len(test_set)
```

Out[ ]:

```
(1070, 268)
```

Explore and Visualize the Data to Gain Insights

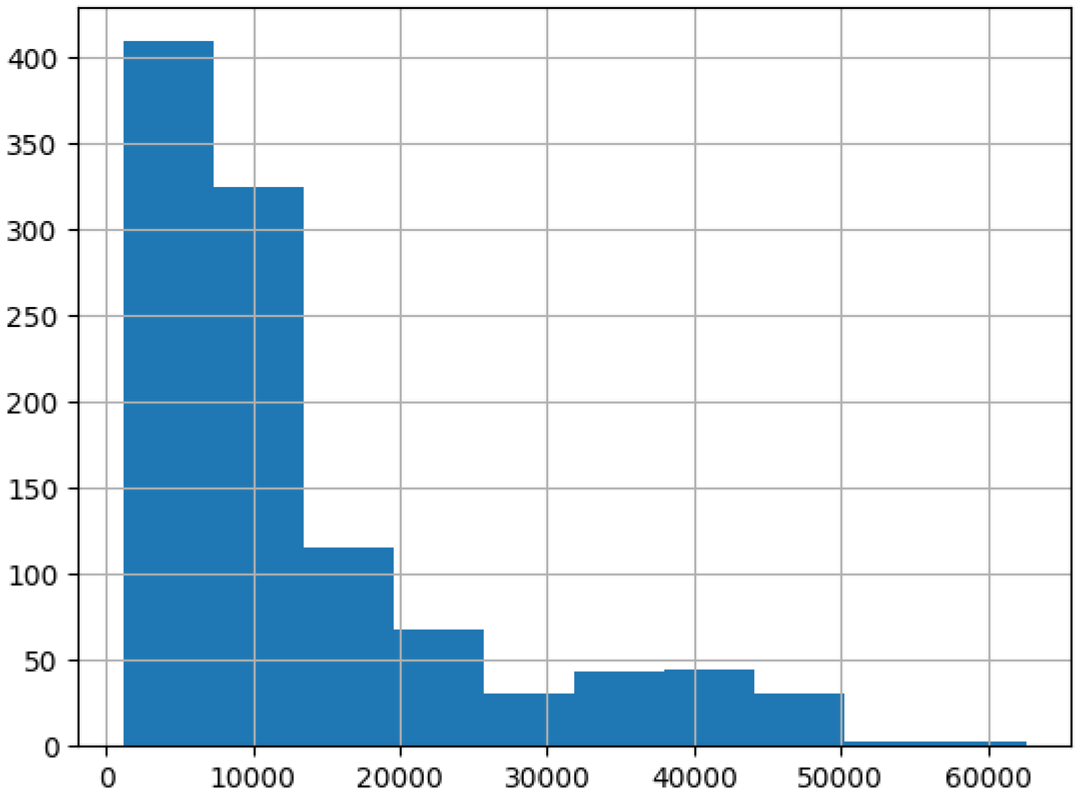
So far you have only taken a quick glance at the data to get a general understanding of the kind of data you are manipulating. Now the goal is to go into a little more depth.

First, make sure you have put the test set aside and you are only exploring the training set.

```
In [ ]: # make a copy of the train set and save it to a variable called medical
        medical = train_set.copy()
```

```
In [ ]: # build a histogram of the charges column
        medical['charges'].hist()
```

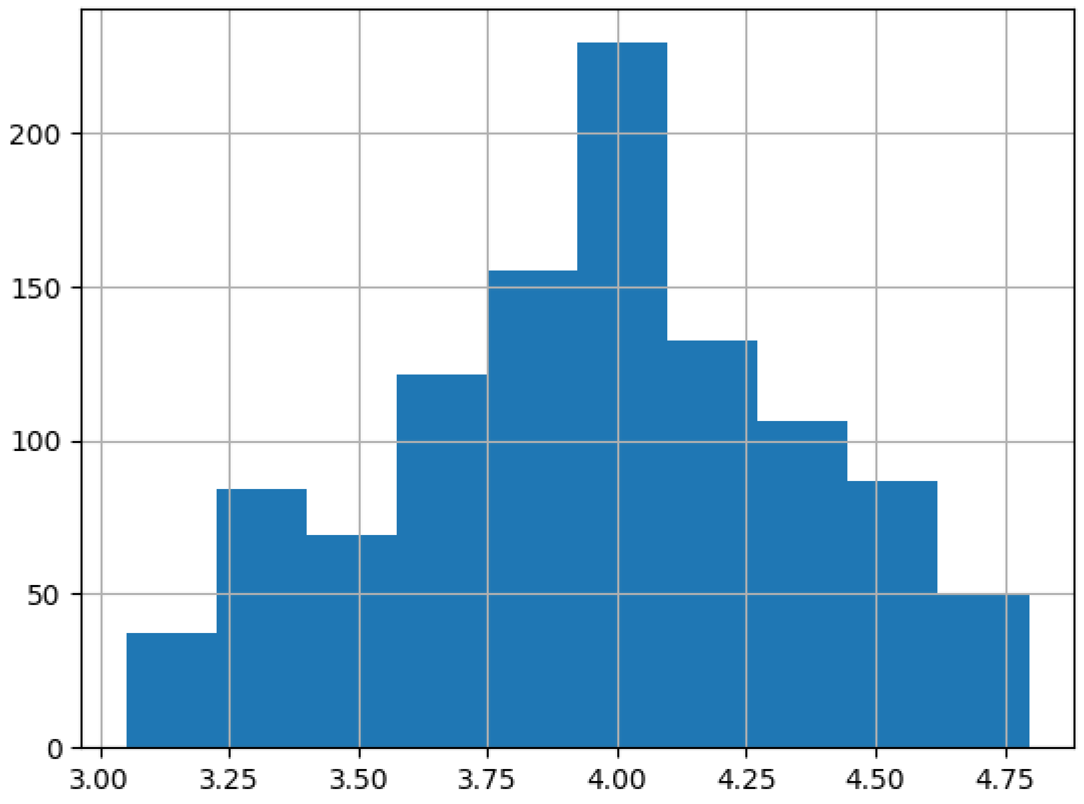
```
Out[ ]: <Axes: >
```



This distribution is right-skewed. To make it closer to normal we can apply natural log

```
In [ ]: # apply a log transformation to the charges column using the np.log10() function
        # build a histogram of the transformed column
        import numpy as np

        np.log10(medical['charges']).hist()
```

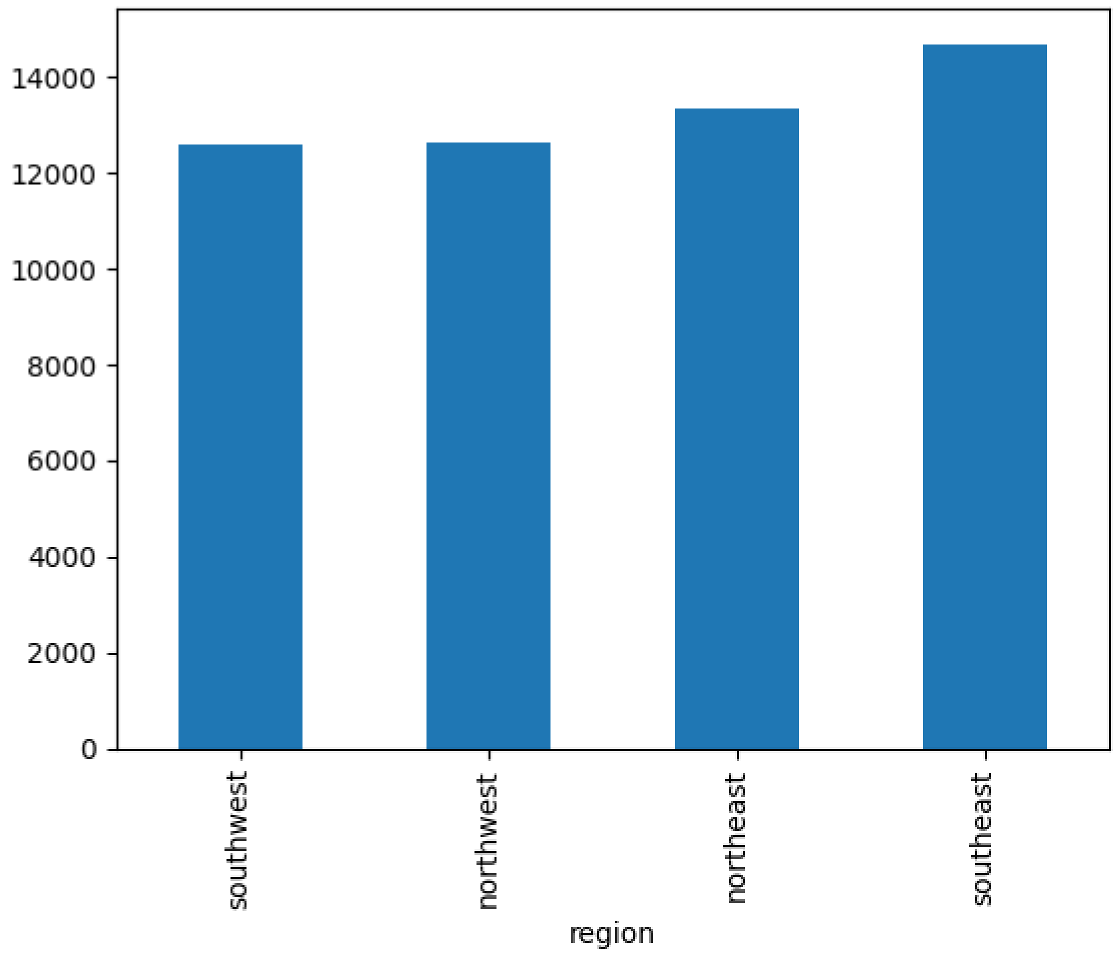
```
Out[ ]: <Axes: >
```



Now let's look at the mean charges by region

```
In [ ]: # compute the average insurance cost for each region
        # sort the charges_by_region Series from the lowest to highest cost
        # plot the sorted Series using the plot.bar() method
        charges_by_region = medical.groupby('region')['charges'].mean().sort_values()
        charges_by_region.plot.bar()
```

```
Out[ ]: <Axes: xlabel='region'>
```



Overall the highest medical charges are in the Southeast and the lowest are in the Southwest. Taking into account certain factors (sex, smoking, having children) let's see how it changes by region.

Now, create three grouped barcharts for average charges by region grouped by sex, smoking, and number of children.

How to create grouped barcharts?

Creating grouped bar charts with Seaborn is a bit more intuitive compared to Matplotlib. You can use the catplot function with kind='bar' to create grouped bar charts. Here is an example on the tips datasets that comes with Seaborn. The tips dataset contains information about the total bill and tip amount for different meals, along with additional information such as the sex of the individual paying for the meal, whether they are a smoker, the day and time of the meal, and the size of the party.

We will create a grouped bar chart showing the average total bill for each day, grouped by whether the meal took place at lunch or dinner.

```
import seaborn as sns
import matplotlib.pyplot as plt
```

```
# Load the 'tips' dataset
tips = sns.load_dataset("tips")

# Create a grouped bar chart
sns.catplot(data=tips, x="day", y="total_bill", hue="time",
kind="bar")

plt.show()
```

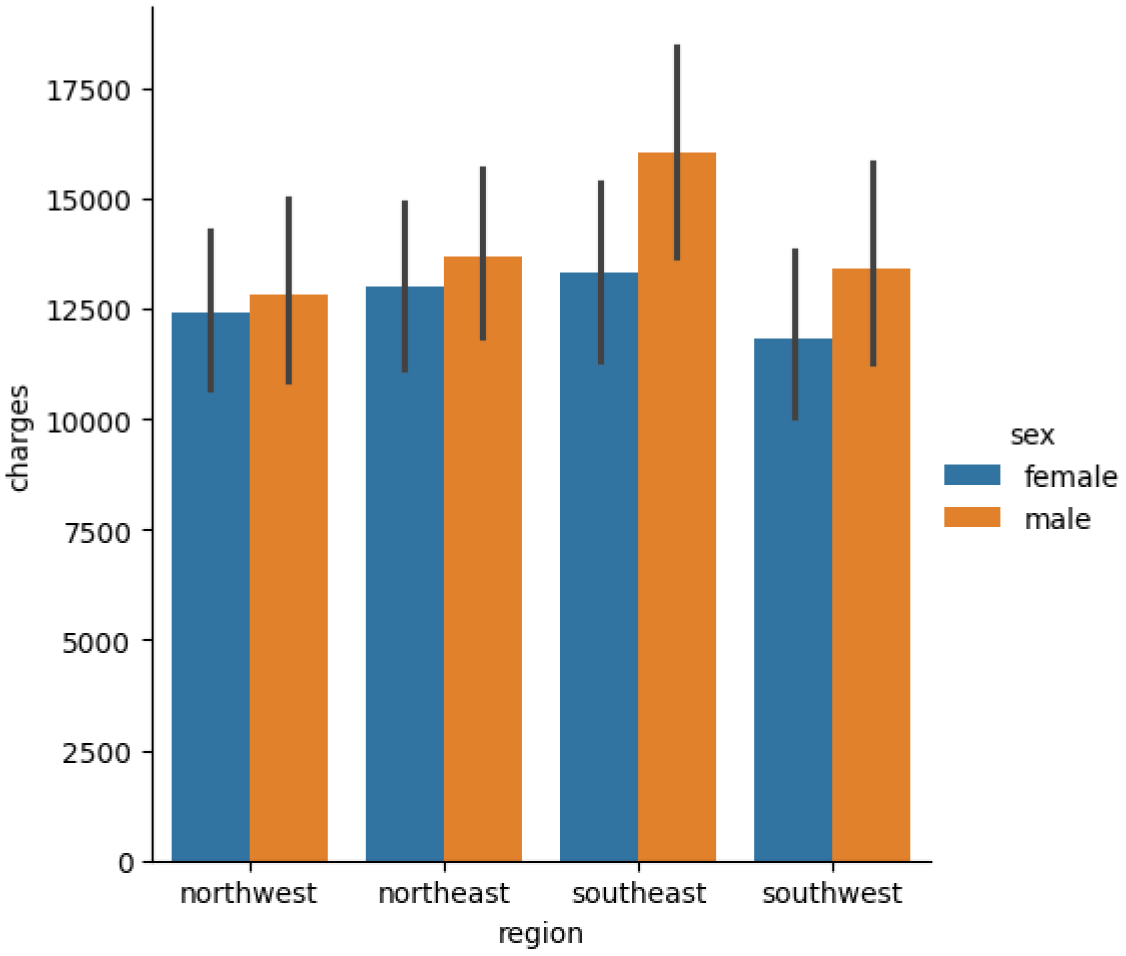
In this plot, the height of the bars represents the average total bill for meals on each day, with separate bars for lunch and dinner.

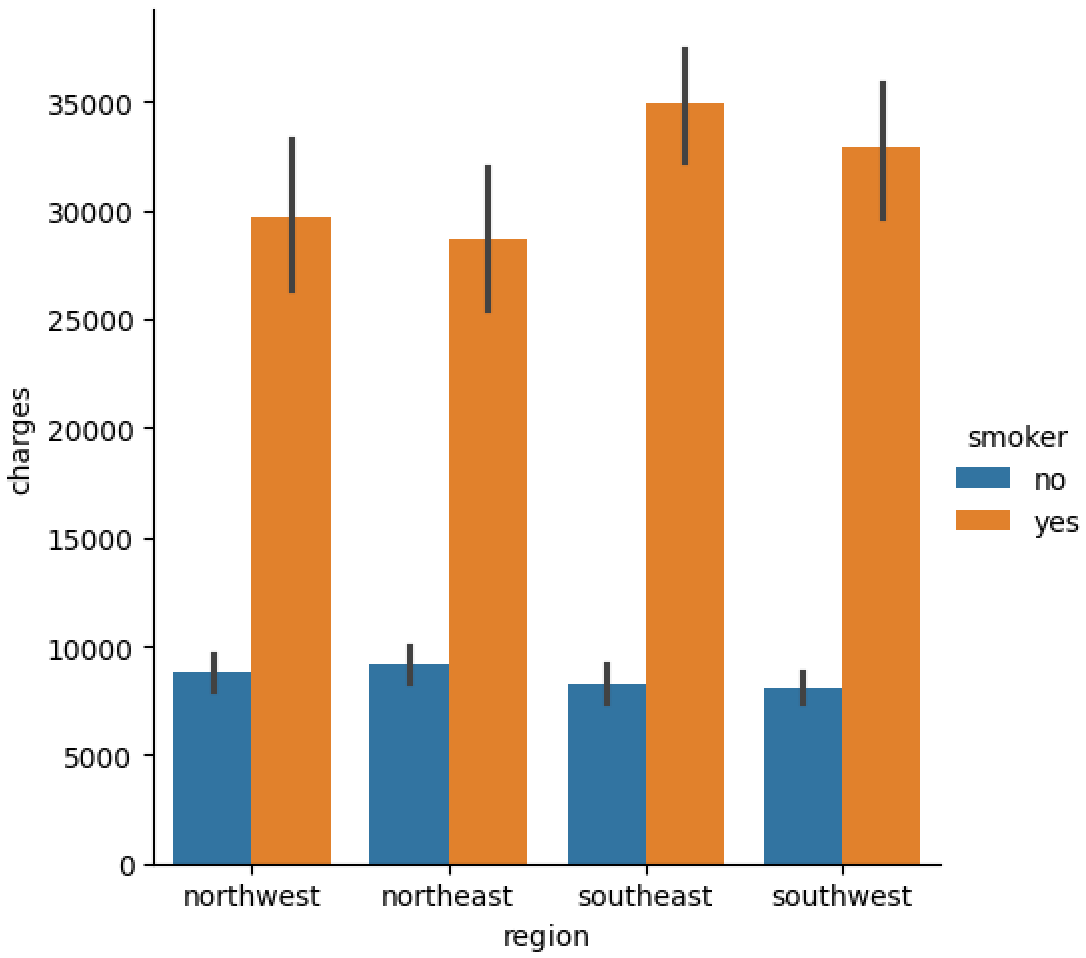
The `catplot` function is a flexible function that can create a variety of different plot types. By setting `kind='bar'`, we specify that we want a bar chart. The x and y arguments specify the data for the x and y axes, and the `hue` argument specifies a third variable that is used to group the data.

In the context of Seaborn and many other statistical visualization libraries, error bars commonly represent one standard deviation or standard error of the mean.

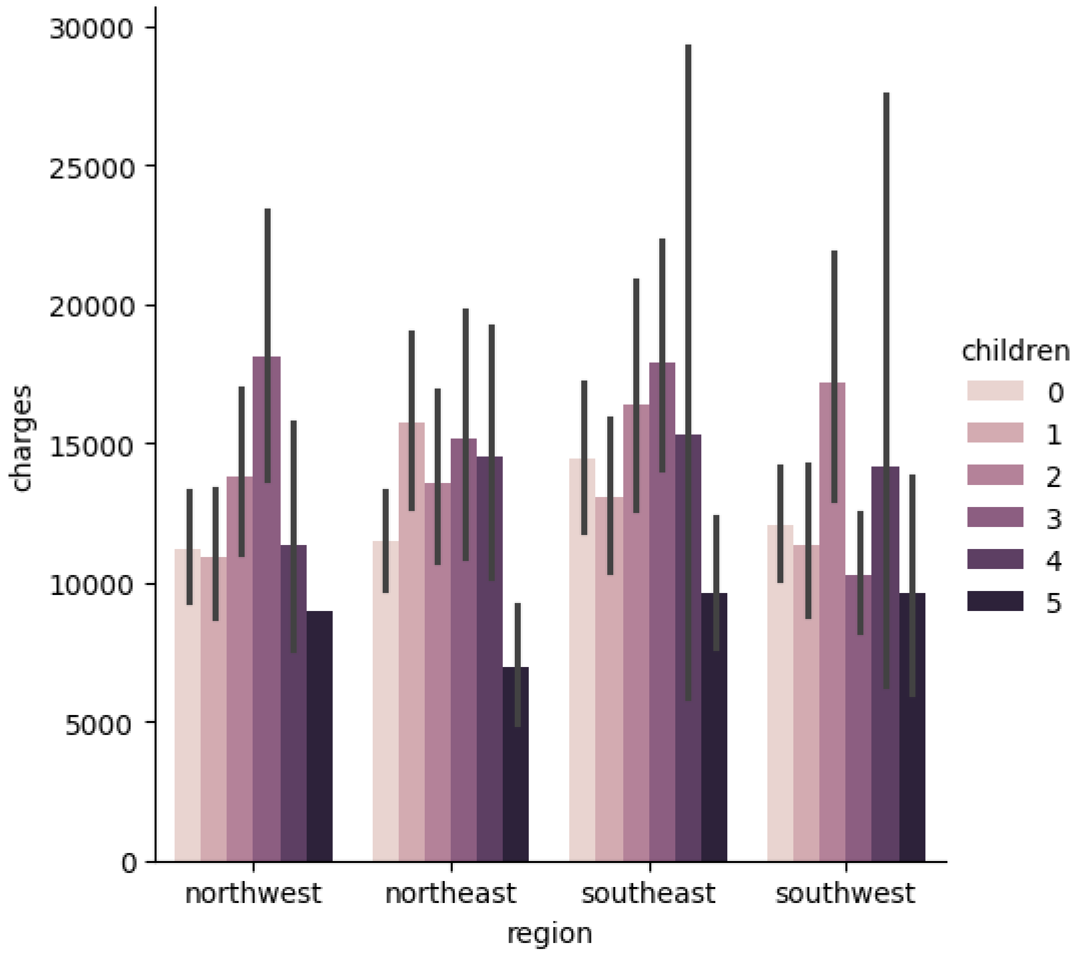
In [ ]:

```
# plot grouped bar charts of region and insurance costs hue by sex, smoker, and num
# use the catplot() function to create the bar charts
# set the kind parameter to "bar" and the data parameter to medical
import seaborn as sns
import matplotlib.pyplot as plt

#plot grouped bar charts of region and insurance costs hue by sex
sns.catplot(data=medical, x='region', y='charges', hue = 'sex', kind='bar')
sns.catplot(data=medical, x='region', y='charges', hue = 'smoker', kind='bar')
sns.catplot(data=medical, x='region', y='charges', hue = 'children', kind='bar')
plt.show()
```


charges
17500
15000
12500
10000
7500
5000
2500
0
northwest
northeast
southeast
southwest
region
sex
female
male



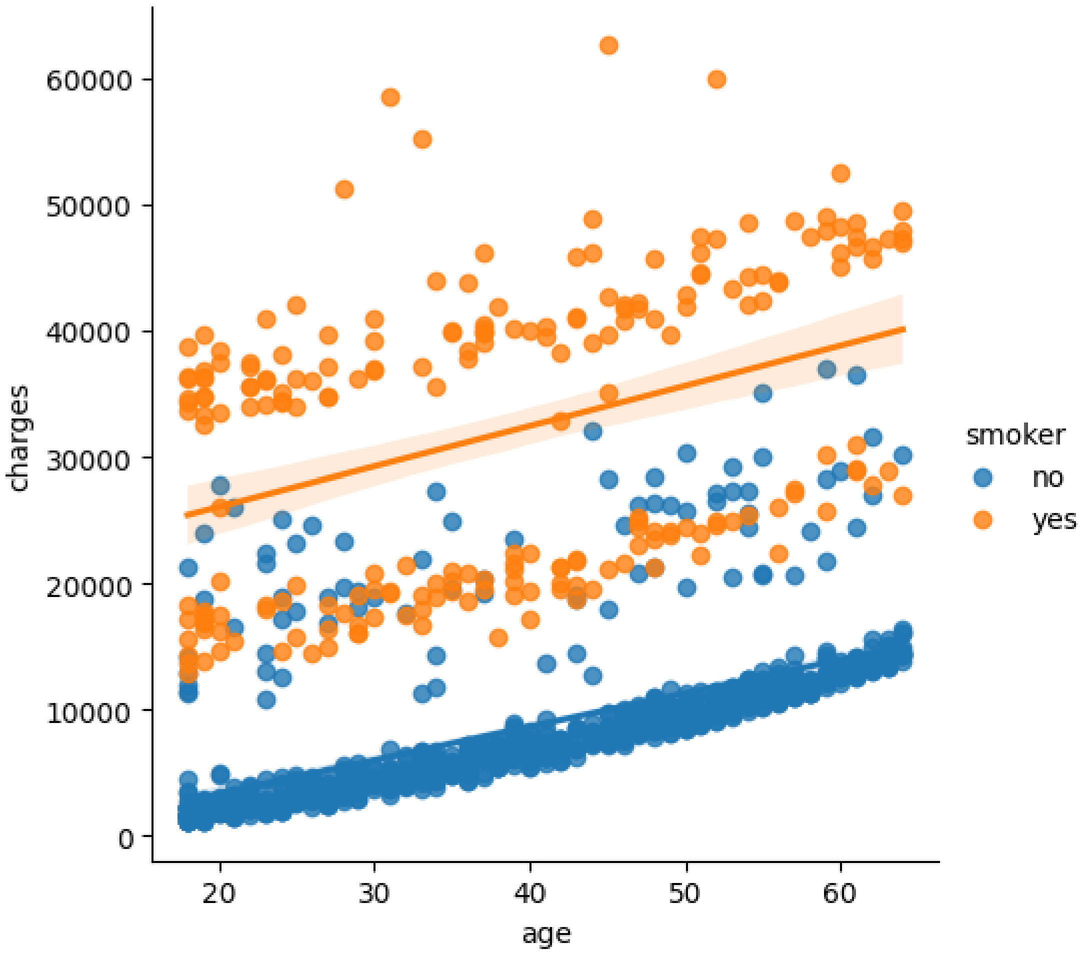
charges
35000
30000
25000
20000
15000
10000
5000
0
northwest
northeast
southeast
southwest
region
smoker
no
yes

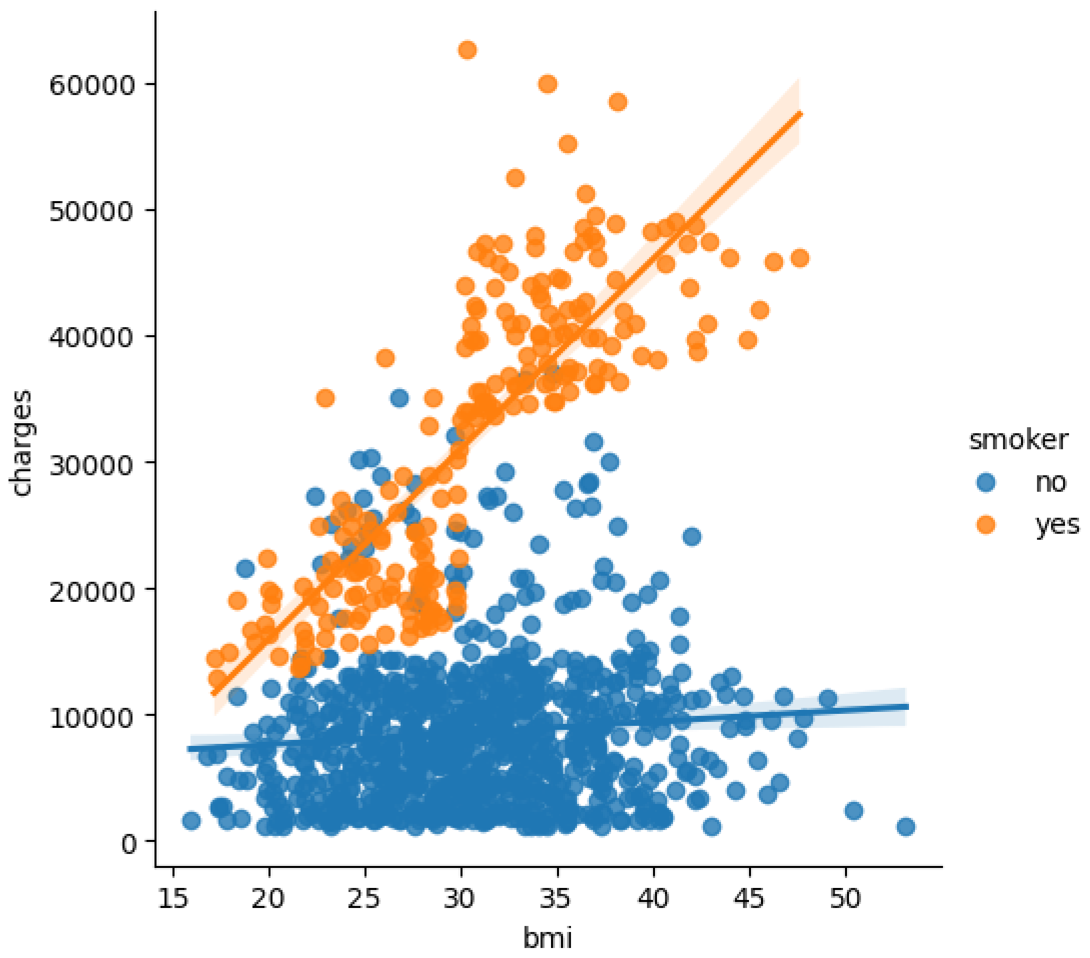


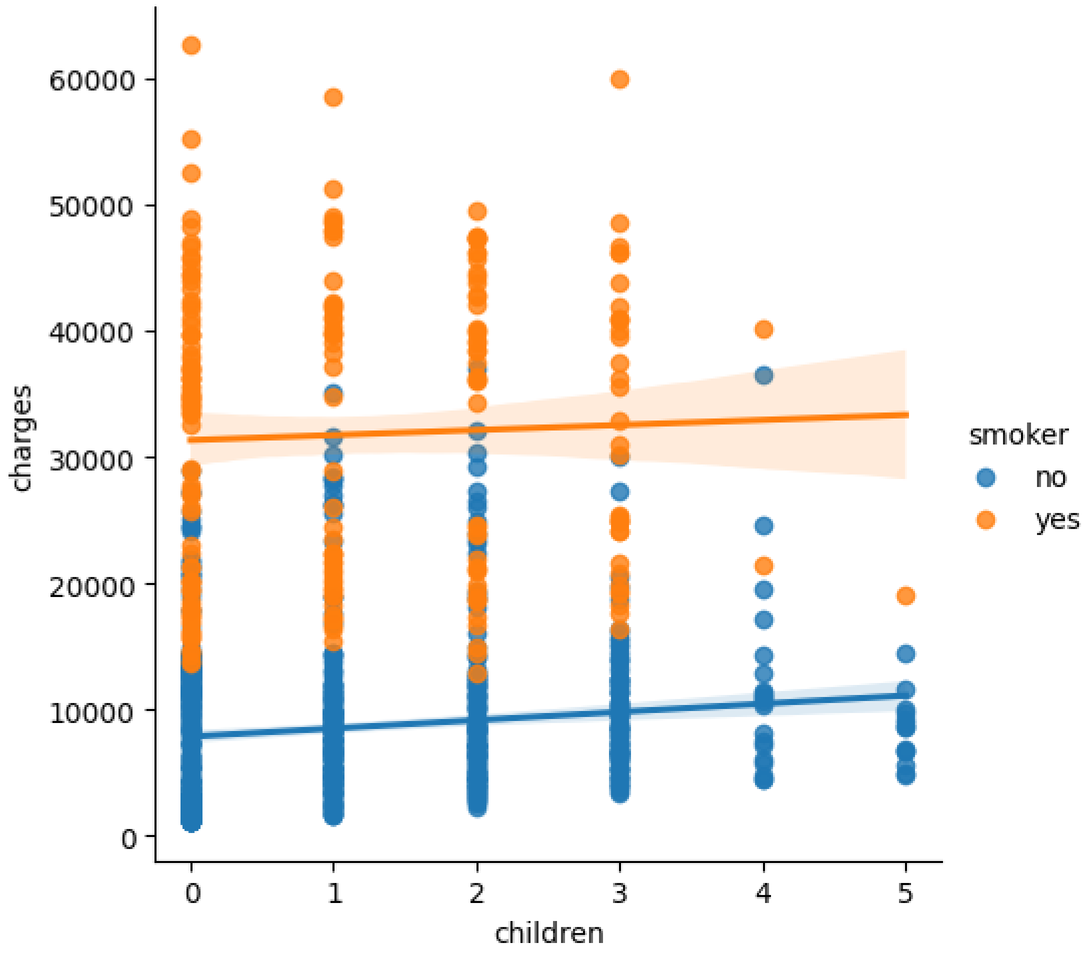
What do you observe? Briefly write what you observe from the charts.
Over all 4 regions males pay more than females, smokers pay more than non-smokers, and family with 2 and or 3 children pay more than family with no children and 4 or more children.

Now let's analyze the medical charges by age, bmi and children according to the smoking factor.

```
In [ ]: # using the lmplot() function of seaborn, build a scatter plot of age and insurance
        # build a second scatter plot of bmi and insurance costs, hue by smoker
        # build a third scatter plot of children and insurance costs, hue by smoker
        sns.lmplot(data=medical, x='age', y='charges', hue='smoker', scatter=True)
        sns.lmplot(data=medical, x='bmi', y='charges', hue='smoker', scatter=True)
        sns.lmplot(data=medical, x='children', y='charges', hue='smoker', scatter=True)
        plt.show()
```


charges
60000
50000
40000
30000
20000
10000
0
20
30
40
50
60
age
smoker
no
yes


charges
0
10000
20000
30000
40000
50000
60000
15
20
25
30
35
40
45
50
bmi
smoker
no
yes



Describe in a one-liner what you obeserve from the charts.

Look for Correlations

In [ ]:
```
# compute pairwise correlation of columns using the corr() method
medical_num = medical.select_dtypes(include=[np.number])
corr_matrix = medical_num.corr()
corr_matrix
```

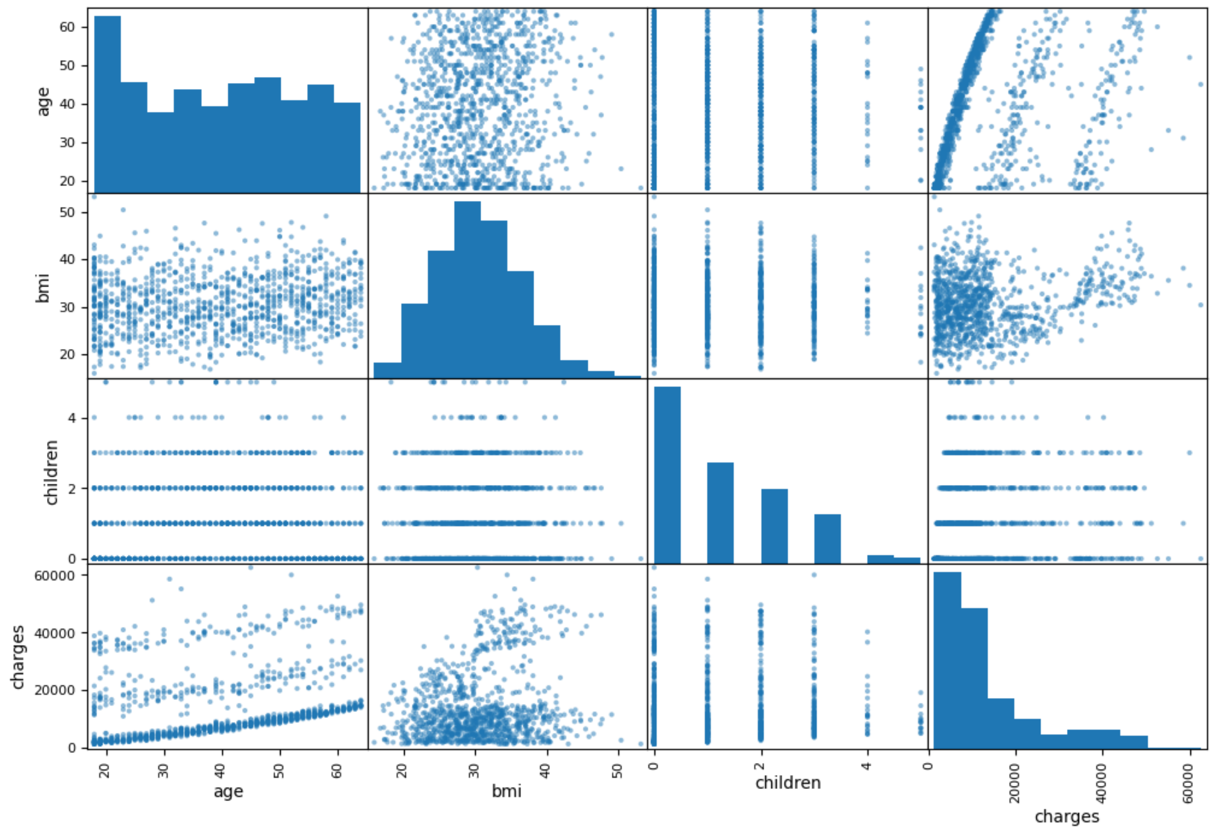
Out[ ]:

	age	bmi	children	charges
age	1.000000	0.118274	0.060999	0.281721
bmi	0.118274	1.000000	-0.005040	0.197316
children	0.060999	-0.005040	1.000000	0.071885
charges	0.281721	0.197316	0.071885	1.000000

The correlation coefficient ranges from –1 to 1. When it is close to 1, it means that there is a strong positive correlation. Finally, coefficients close to 0 mean that there is no linear correlation.

Another way to check for correlation between attributes is to use the Pandas `scatter_matrix()` function, which plots every numerical attribute against every other numerical attribute.

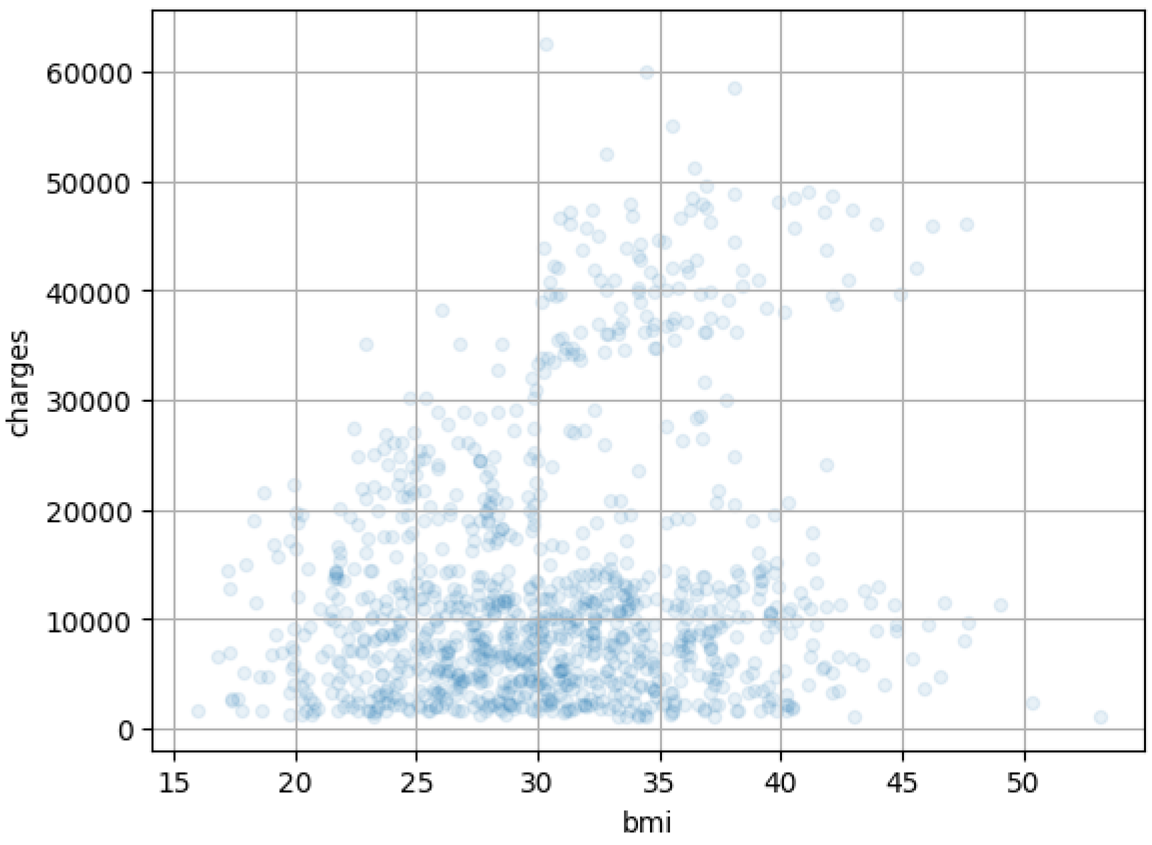
```
In [ ]: # plot correlation matrix using scatter_matrix() function from pandas.plotting
        from pandas.plotting import scatter_matrix

        attributes = ['age',
                      'bmi',
                      'children',
                      'charges']

        scatter_matrix(medical[attributes], figsize=(12, 8))
        plt.show()
```



The main diagonal would be full of straight lines if Pandas plotted each variable against itself, which would not be very useful. So instead, the Pandas displays a histogram of each attribute.

Looking at the correlation scatterplots, it seems like the most promising attribute to predict the charge value is bmi, so let's zoom in on their scatterplot.

```
In [ ]: # plot a scatter plot of bmi vs. insurance costs using the medical.plot() method, u
        medical.plot(kind="scatter",
                     x="bmi",
                     y="charges",
                alpha=0.1, grid=True)
plt.show()
```



The correlation is somewhat visible; you can clearly see the upward trend.

Prepare the data for ML

In [ ]:
```
# drop the charges column from the train_set and save the resulting dataset to a va
# create a copy of the train_set labels and save it to a variable called `medical_l
# replace None with the correct code

medical = train_set.drop("charges", axis=1)
medical_labels = train_set["charges"].copy()
```

Transformation Pipelines

As you can see, there are many data transformation steps that need to be executed in the right order. Fortunately, Scikit-Learn provides the Pipeline class to help with such sequences of transformations.

In [ ]:
```
# uncomment the following code to create a pipeline for preprocessing the data

from sklearn.compose import ColumnTransformer
from sklearn.impute import SimpleImputer
```

```python
from sklearn.preprocessing import StandardScaler
from sklearn.preprocessing import OneHotEncoder
from sklearn.pipeline import make_pipeline

num_attribs = ["age", "bmi", "children"]
cat_attribs = ["sex", "smoker", "region"]

num_pipeline = make_pipeline(
    SimpleImputer(strategy="median"),
    StandardScaler())

cat_pipeline = make_pipeline(
    SimpleImputer(strategy="most_frequent"),
    OneHotEncoder(handle_unknown="ignore"))

preprocessing = ColumnTransformer([
    ("num", num_pipeline, num_attribs),
    ("cat", cat_pipeline, cat_attribs)])

medical_prepared = preprocessing.fit_transform(medical)

print(medical_prepared.shape)
print(preprocessing.get_feature_names_out())
```

```
(1070, 11)
['num__age' 'num__bmi' 'num__children' 'cat__sex_female' 'cat__sex_male'
 'cat__smoker_no' 'cat__smoker_yes' 'cat__region_northeast'
 'cat__region_northwest' 'cat__region_southeast' 'cat__region_southwest']
```

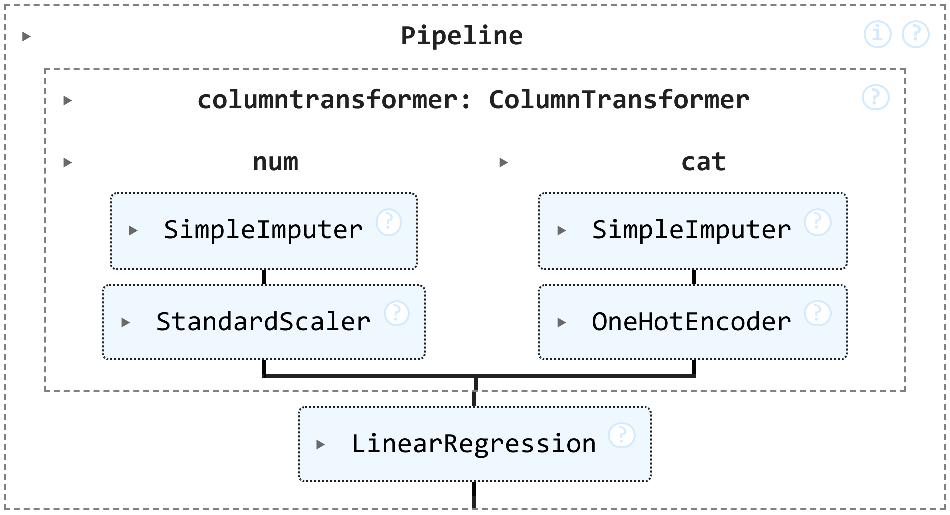
Select and Train a Model

At last! You framed the problem, you got the data and explored it, you sampled a training set and a test set, and you wrote a preprocessing pipeline to automatically clean up and prepare your data for machine learning algorithms. You are now ready to select and train a machine learning model.

Train and Evaluate on the Training Set

The good news is that thanks to all these previous steps, things are now going to be easy! You decide to train a very basic linear regression model to get started:

In [ ]:
```python
# create a pipeline for preprocessing the data and fitting a linear regression mode
from sklearn.linear_model import LinearRegression

lin_reg = make_pipeline(preprocessing, LinearRegression())
# lin_reg = ...

# housing_labels is the column we want to predict
# uncomment the following line to fit the model

lin_reg.fit(medical, medical_labels)
```

Out[ ]: 

Try out the model on the training set, look at the first five predictions and compare them to the labels:

In [ ]:
```
# uncomment the following line to make predictions

medical_predictions = lin_reg.predict(medical)
medical_predictions
```

Out[ ]:
```
array([ 7094.54007011,  8344.72998713,  9153.77419778, ...,
       11441.08519155, 37314.37460682, 11453.12102783])
```

In [ ]:
```
# uncomment the following lines to compute the RMSE

from sklearn.metrics import mean_squared_error

lin_rmse = mean_squared_error(medical_labels, medical_predictions, squared=False)
lin_rmse
```

```
/Library/Frameworks/Python.framework/Versions/3.12/lib/python3.12/site-packages/skle
arn/metrics/_regression.py:483: FutureWarning: 'squared' is deprecated in version 1.
4 and will be removed in 1.6. To calculate the root mean squared error, use the func
tion'root_mean_squared_error'.
  warnings.warn(
```

Out[ ]:
```
6105.545160099847
```

Now try `DecisionTreeRegressor`, as this is a fairly powerful model capable of finding complex nonlinear relationships in the data (decision trees are covered later in the course):

In [ ]:
```
# use DecisionTreeRegressor to train the model
# use the make_pipeline() function to create a pipeline for preprocessing and model
# use the preprocessing object you created earlier
# make predictions on the training set and compute the RMSE
from sklearn.tree import DecisionTreeRegressor

preprocess_pipeline = ColumnTransformer(
    [('num', num_pipeline, num_attribs),
     ('cat', cat_pipeline, cat_attribs)])
```

```
tree_reg = make_pipeline(preprocess_pipeline, DecisionTreeRegressor())
tree_reg.fit(medical, medical_labels)

medical_predictions = tree_reg.predict(medical)
tree_rmse = mean_squared_error(medical_labels, medical_predictions, squared=False)
tree_rmse
```

```
/Library/Frameworks/Python.framework/Versions/3.12/lib/python3.12/site-packages/skle
arn/metrics/_regression.py:483: FutureWarning: 'squared' is deprecated in version 1.
4 and will be removed in 1.6. To calculate the root mean squared error, use the func
tion'root_mean_squared_error'.
  warnings.warn(
```

```
Out[ ]: 494.20598375812835
```

Better Evaluation Using Cross-Validation

The following code randomly splits the training set into 10 nonoverlapping subsets called folds, then it trains and evaluates the decision tree model 10 times, picking a different fold for evaluation every time and using the other 9 folds for training. The result is an array containing the 10 evaluation scores:

```
In [ ]: # uncomment the following lines to train the model and make predictions

from sklearn.model_selection import cross_val_score

tree_rmses = -cross_val_score(tree_reg,
                              medical,medical_labels,
                              scoring="neg_root_mean_squared_error",
                              cv=10)
tree_rmses
```

```
Out[ ]: array([6091.81321495, 6424.79055347, 6485.97684875, 6681.58231864,
               6893.91412673, 6211.98074951, 7611.25689357, 6295.34712005,
               6909.02411453, 5540.17324982])
```

Warning. Scikit-Learn's cross-validation features expect a utility function (greater is better) rather than a cost function (lower is better), so the scoring function is actually the opposite of the RMSE. It's a negative value, so you need to switch the sign of the output to get the RMSE scores.

```
In [ ]: # uncomment the following line to compute the mean of the RMSEs

np.mean(tree_rmses)
```

```
Out[ ]: 6514.585919002371
```

Let's try one last model now: the RandomForestRegressor. As you will see later in the course, random forests work by training many decision trees on random subsets of the features, then averaging out their predictions.

```
In [ ]: # use RandomForestRegressor to train the model
        # use the make_pipeline() function to create a pipeline for preprocessing and model
        # use the preprocessing object you created earlier
        # make predictions on the training set and compute the RMSEs using cross-validation
        # compute the mean of the RMSEs

        from sklearn.ensemble import RandomForestRegressor

        tree_reg = make_pipeline(preprocess_pipeline, RandomForestRegressor())
        tree_reg.fit(medical, medical_labels)

        medical_predictions = tree_reg.predict(medical)
        tree_rmse = mean_squared_error(medical_labels, medical_predictions, squared=False)
        tree_rmse
```

```
/Library/Frameworks/Python.framework/Versions/3.12/lib/python3.12/site-packages/skle
arn/metrics/_regression.py:483: FutureWarning: 'squared' is deprecated in version 1.
4 and will be removed in 1.6. To calculate the root mean squared error, use the func
tion'root_mean_squared_error'.
  warnings.warn(
```

```
Out[ ]: 1905.2937932287698
```

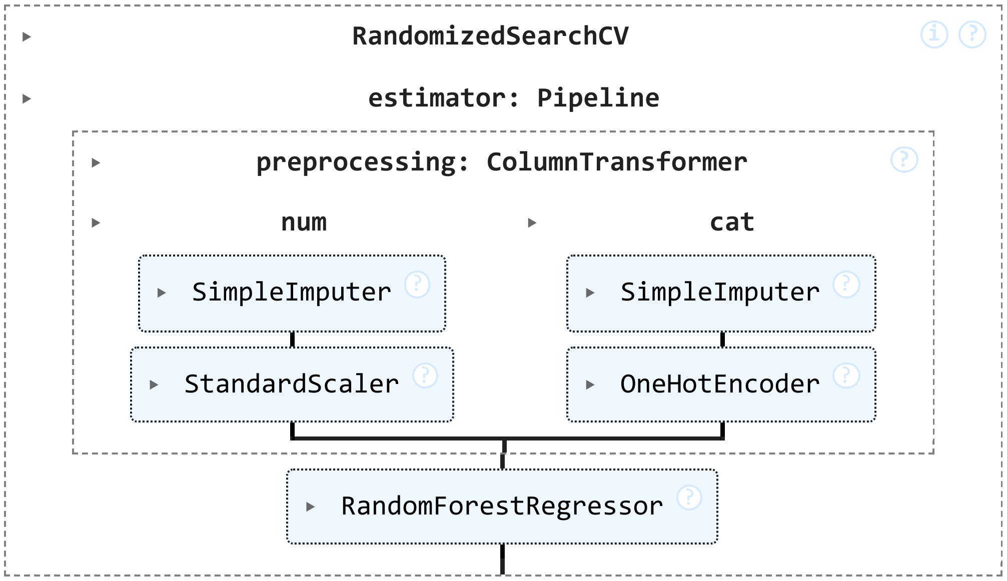
Fine-Tune Your Model

Let's assume that you now have a shortlist of promising models. You now need to fine-tune them.

Randomized Search for Good Hyperparameters

```
In [ ]: # uncomment the following lines to search for the best hyperparameters

        from sklearn.model_selection import RandomizedSearchCV
        from scipy.stats import randint
        from sklearn.pipeline import Pipeline

        full_pipeline = Pipeline([("preprocessing", preprocessing),
                                  ("random_forest", RandomForestRegressor(random_state=42))
                                  ])

        param_distribs = {'random_forest__max_features': randint(low=2,high=20)}

        rnd_search = RandomizedSearchCV(full_pipeline,
                                        param_distributions=param_distribs,
                                        n_iter=10,
                                        cv=3,
                                        scoring='neg_root_mean_squared_error',
                                        random_state=42)

        rnd_search.fit(medical, medical_labels)
```

Out[ ]:



In [ ]:
```
# uncomment the following lines to print the best search scores

rn_res = pd.DataFrame(rnd_search.cv_results_)
rn_res.sort_values(by="mean_test_score", ascending=False, inplace=True)
rn_res.head(5)["mean_test_score"]
```

Out[ ]:
```
7   -4810.698561
9   -4861.373750
0   -4912.976290
4   -4912.976290
3   -4976.129581
Name: mean_test_score, dtype: float64
```

In [ ]:
```
# uncomment the following lines to print the feature importances

final_model = rnd_search.best_estimator_ # includes preprocessing
feature_importances = final_model["random_forest"].feature_importances_
feature_importances
```

Out[ ]:
```
array([0.14032922, 0.18831699, 0.0230048 , 0.00493845, 0.00454404,
       0.28737838, 0.33010198, 0.00580561, 0.00521445, 0.00654471,
       0.00382136])
```

In [ ]:
```
# uncomment the following line to print the feature importances with the feature na

sorted(zip(feature_importances, final_model["preprocessing"].get_feature_names_out(
Out[ ]: [(0.3301019845385152, 'cat__smoker_yes'),
         (0.2873783836848969, 'cat__smoker_no'),
         (0.18831699212058217, 'num__bmi'),
         (0.1403292169242826, 'num__age'),
         (0.023004795671815754, 'num__children'),
         (0.006544713122635331, 'cat__region_southeast'),
         (0.005805609883995695, 'cat__region_northeast'),
         (0.0052144512790023795, 'cat__region_northwest'),
         (0.0049384524581677835, 'cat__sex_female'),
         (0.004544038586538502, 'cat__sex_male'),
         (0.0038213617295676603, 'cat__region_southwest')]
```

```
In [ ]: # now that you have a final model, evaluate it on the test set (find rmse)

        final_predictions = final_model.predict(test_set)
        final_mse = mean_squared_error(test_set["charges"], final_predictions)
        final_rmse = np.sqrt(final_mse)
        final_rmse
```

```
Out[ ]: 4541.672878563329
```