medical-costs-post-2

February 4, 2024

1 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.

2 Get the Data

```
[3]: import pandas as pd

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

3 Take a Quick Look at the Data Structure

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

```
[4]:    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:

```
[5]: # 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
```

[6]:

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

[6]:

```
southeast    364
southwest    325
northwest    325
northeast    324
Name: region, dtype: int64
```

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

[7]:

```
# show descriptive statistics for the dataset by calling the describe() method on medical
medical.describe()
```

[7]:

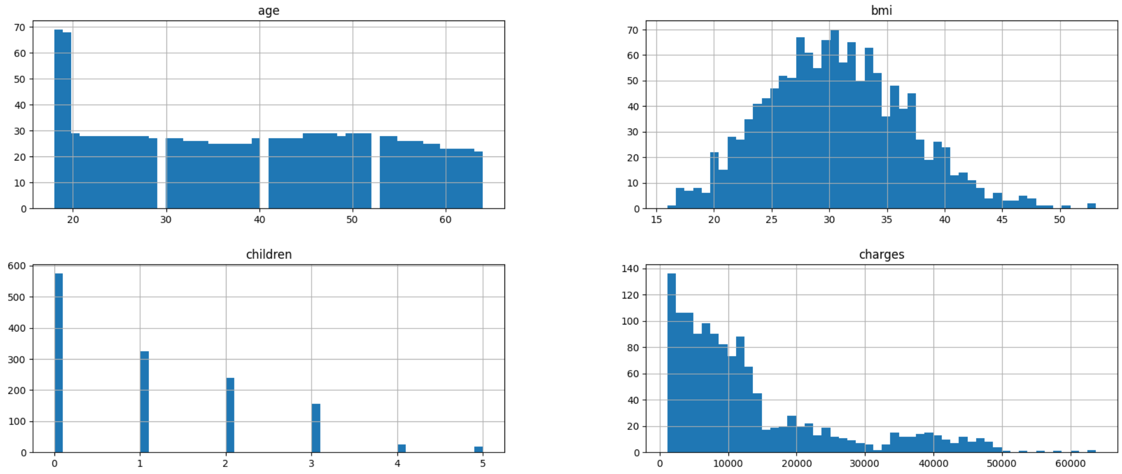
```
               age          bmi     children       charges
count  1338.000000  1338.000000  1338.000000   1338.000000
mean     39.207025    30.663397     1.094918  13270.422265
std      14.049960     6.098187     1.205493  12110.011237
min      18.000000    15.960000     0.000000   1121.873900
25%      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
```

[8]:

```
# show histograms for the numerical columns by using the hist() method on medical
medical.hist(bins=50, figsize=(20,8))
```

[8]:

```
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.

The age histogram shows that the mode in the population is around 18-19. The rest of the sample has an even number of people of all ages between 20 and 64. In the bmi histogram we see a near normal Gauss distribution on bmi, with a bit of a right skew. This suggests that more people on are the extreme high bmi end than are on the extreme low bmi end, relative to the mean of the sample. The sample mean and mode seem to be roughly 30bmi. The mode number of children is 0 and with each increase in number of children the sample data has less people with that number of children. In other words, the sample numbers decrease as children numbers increase. The charges histogram show the mode on the far left where the chargest are teh lowest around 1000, and the number of people in the population tend to decrease as the charges increase. There looks to be a long right skew tail showing that, while not popular, there are some people in the population on the extreme right side of the charges histogram.

3.1 Create a Test Set

```
[ ]: # use train_test_split() to split the data into training and test sets
```

```
[9]: 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)
```

```
[9]: (1070, 268)
```

4 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.

[12]:

```
# make a copy of the train set and save it to a variable called medical
```

[10]:

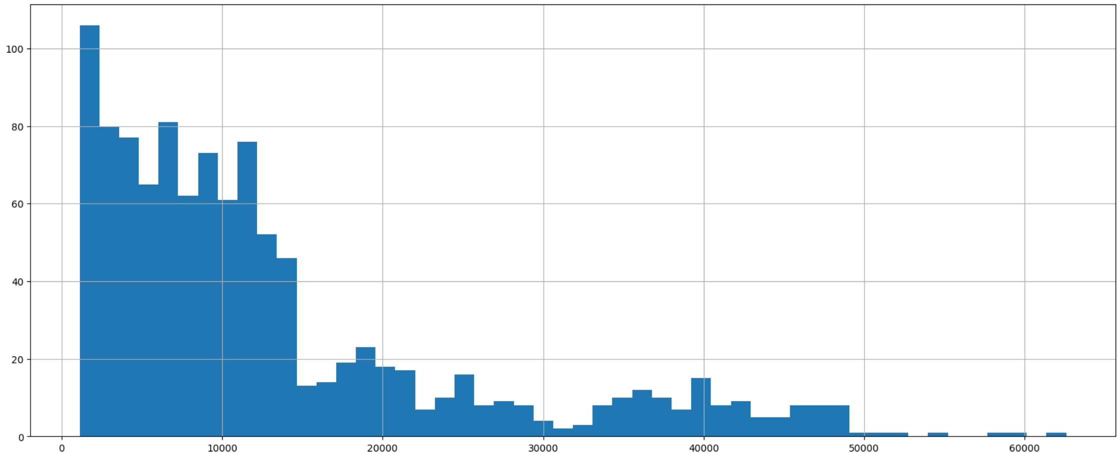
```
medical = train_set.copy()
```

[11]:

```
# build a histogram of the charges column
medical['charges'].hist(bins=50, figsize=(20,8))
```

[11]:

```
<Axes: >
```



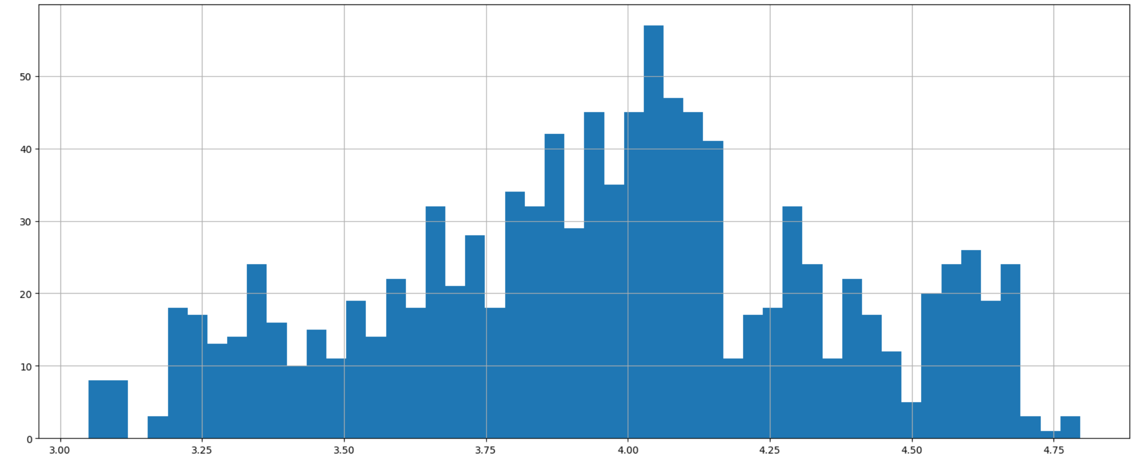
This distribution is right-skewed. To make it closer to normal we can apply natural log

[12]:

```
# apply a log transformation to the charges column using the np.log10() function
# build a histogram of the transformed column
from sklearn.preprocessing import FunctionTransformer
import numpy as np
log_transformer = FunctionTransformer(np.log10, inverse_func=lambda x: 10**x)
log_charges = log_transformer.fit_transform(medical['charges'])
log_charges.hist(bins=50, figsize=(20,8))
```

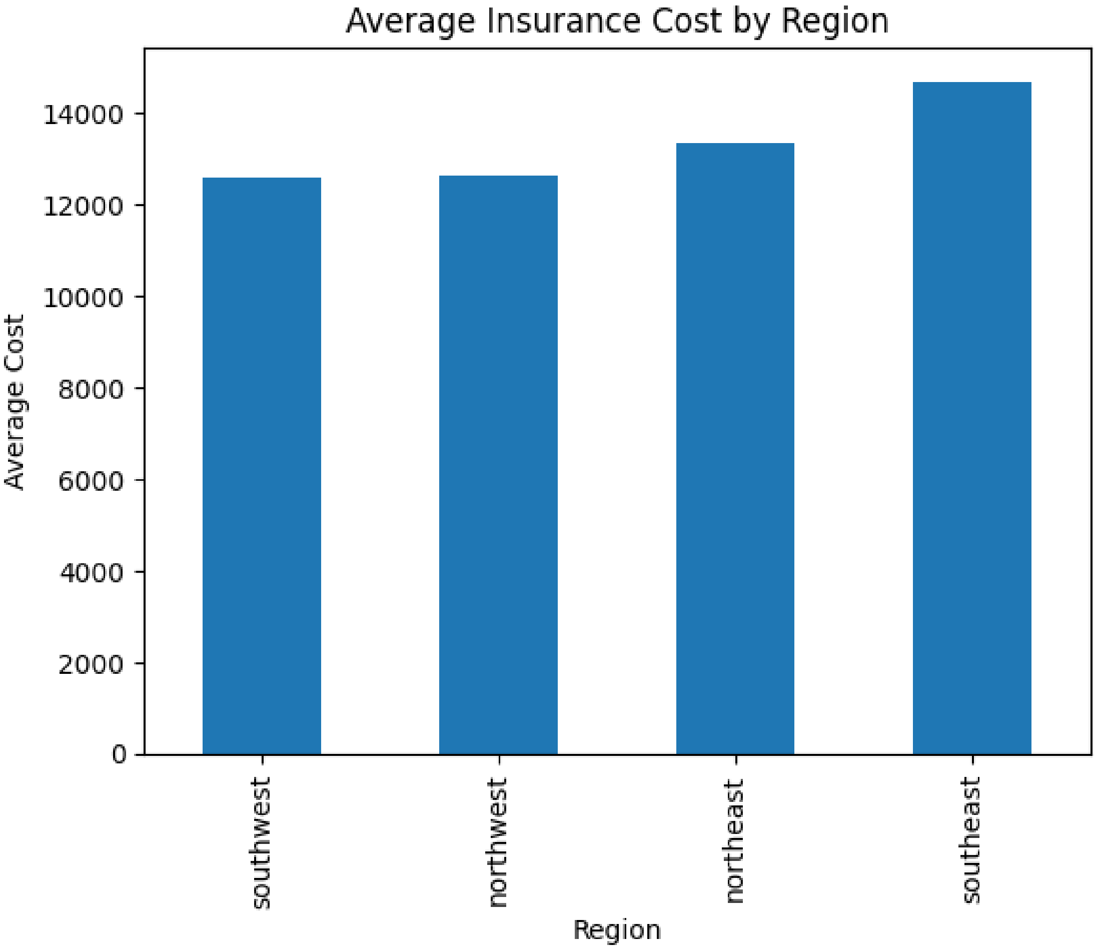
[12]:

```
<Axes: >
```



Now let’s look at the mean charges by region

[13]:
```python
# 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
import matplotlib.pyplot as plt
average_costs = medical.groupby('region')['charges'].mean()
sorted_average_costs = average_costs.sort_values()
sorted_average_costs.plot.bar()
plt.title('Average Insurance Cost by Region')
plt.xlabel('Region')
plt.ylabel('Average Cost')
plt.show()
```



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.

4.0.1 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.

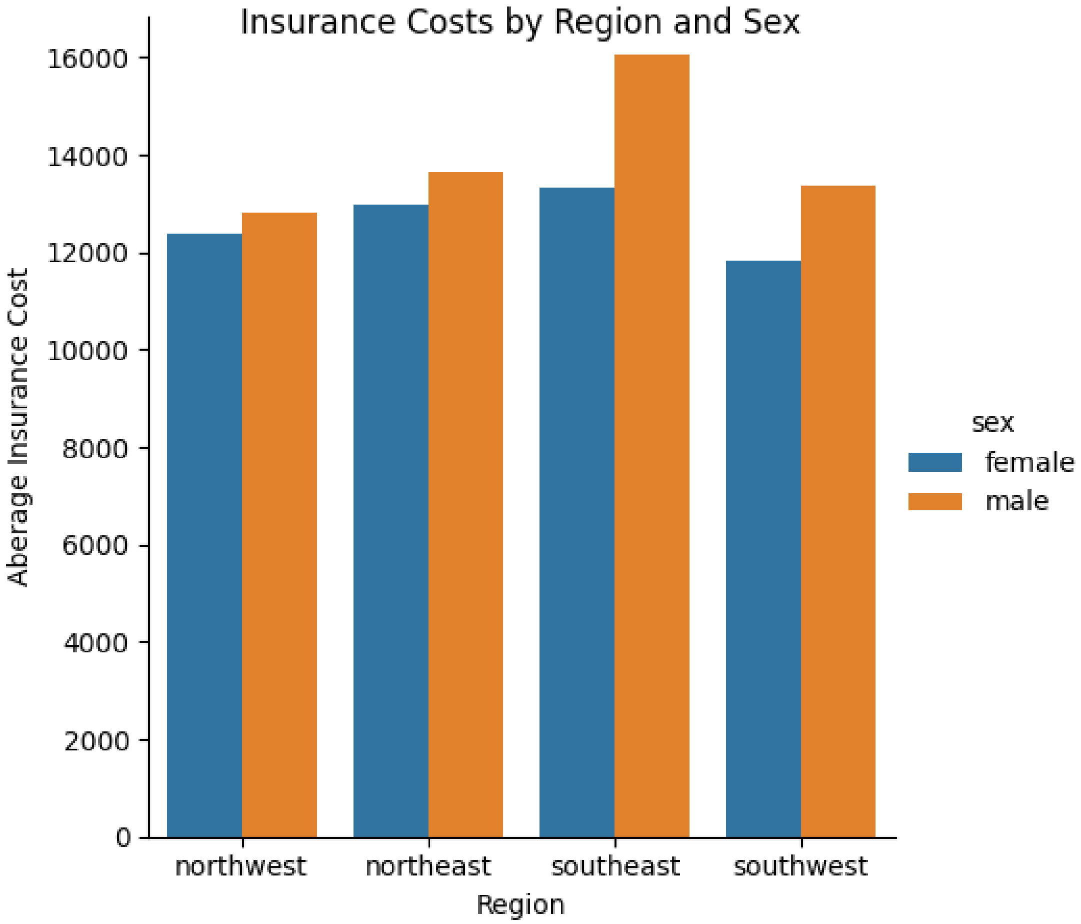
In the context of Seaborn and many other statistical visualization libraries, error bars commonly represent one standard deviation or standard error of the mean.

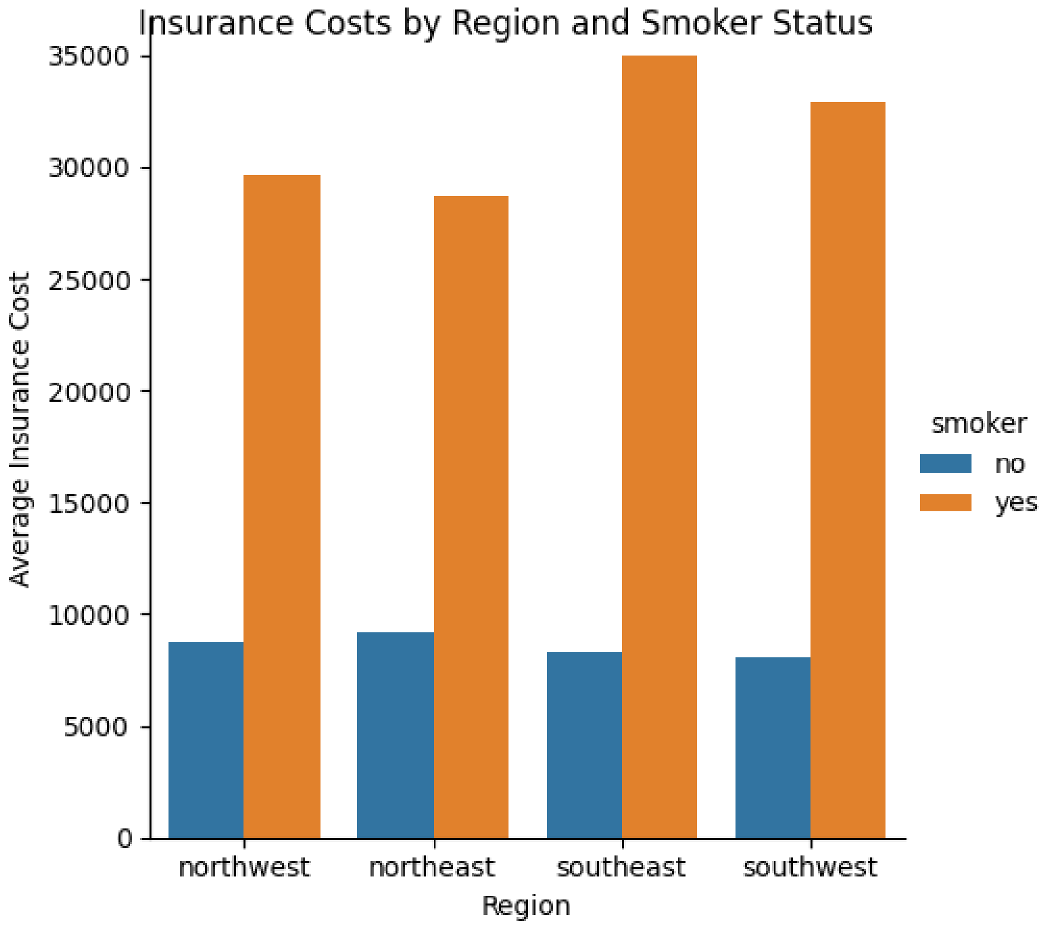
[14]:

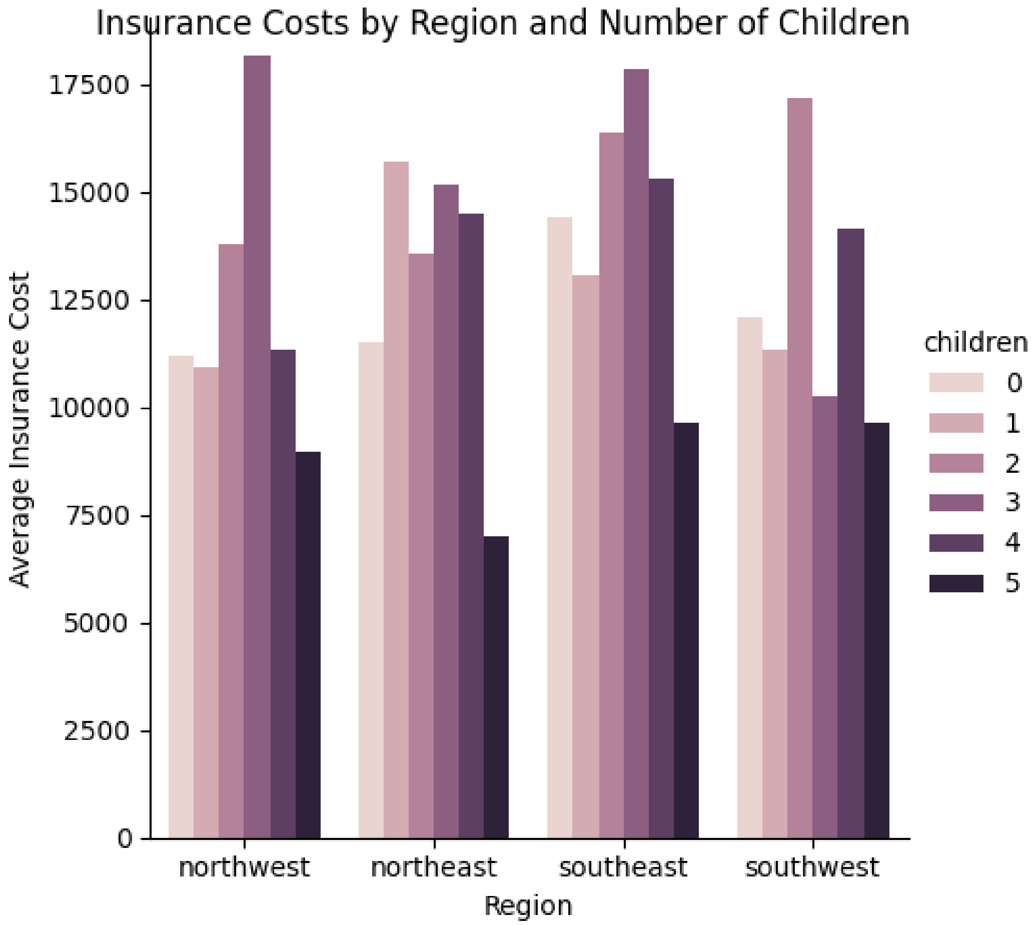
```python
# plot grouped bar charts of region and insurance costs hue by sex, smoker, and␣
 ↪number of children (three separate charts)
# use the catplot() function to create the bar charts
# set the kind parameter to "bar" and the data parameter to medical
import seaborn as sns
g1 = sns.catplot(x='region', y='charges', hue='sex', data=medical, kind='bar',␣
 ↪ci=None)
g1.fig.suptitle('Insurance Costs by Region and Sex')
g1.set_axis_labels('Region', 'Aberage Insurance Cost')

g2 = sns.catplot(x='region', y='charges', hue='smoker', data=medical,␣
 ↪kind='bar', ci=None)
g2.fig.suptitle('Insurance Costs by Region and Smoker Status')
g2.set_axis_labels('Region', 'Average Insurance Cost')

g3 = sns.catplot(x='region', y='charges', hue='children', data=medical,␣
 ↪kind='bar', ci=None)
g3.fig.suptitle('Insurance Costs by Region and Number of Children')
g3.set_axis_labels('Region', 'Average Insurance Cost')

plt.show()
```

```
<ipython-input-14-55ebd211587a>:5: FutureWarning:

The `ci` parameter is deprecated. Use `errorbar=None` for the same effect.

  g1 = sns.catplot(x='region', y='charges', hue='sex', data=medical, kind='bar',
ci=None)
```

```
<ipython-input-14-55ebd211587a>:9: FutureWarning:

The `ci` parameter is deprecated. Use `errorbar=None` for the same effect.

  g2 = sns.catplot(x='region', y='charges', hue='smoker', data=medical,
kind='bar', ci=None)
<ipython-input-14-55ebd211587a>:13: FutureWarning:

The `ci` parameter is deprecated. Use `errorbar=None` for the same effect.

  g3 = sns.catplot(x='region', y='charges', hue='children', data=medical,
kind='bar', ci=None)
```




Insurance Costs by Region and Smoker Status
Average Insurance Cost
0
5000
10000
15000
20000
25000
30000
35000
northwest
northeast
southeast
southwest
Region
smoker
no
yes



What do you observe? Briefly write what you observe from the charts.

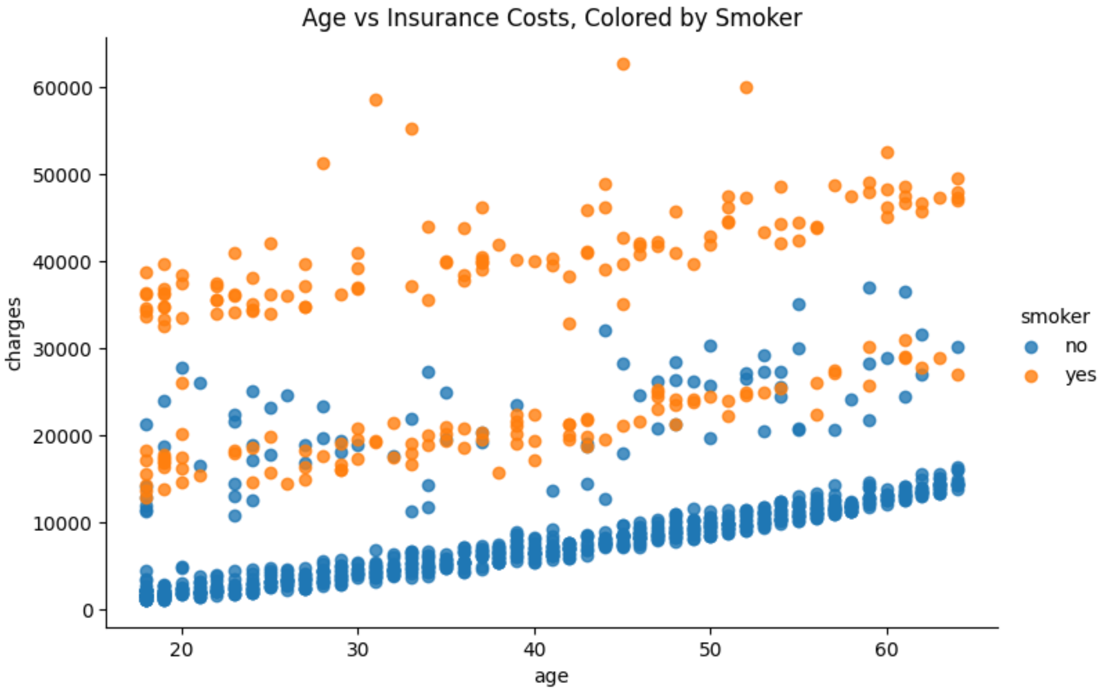
Now let's analyze the medical charges by age, bmi and children according to the smoking factor.

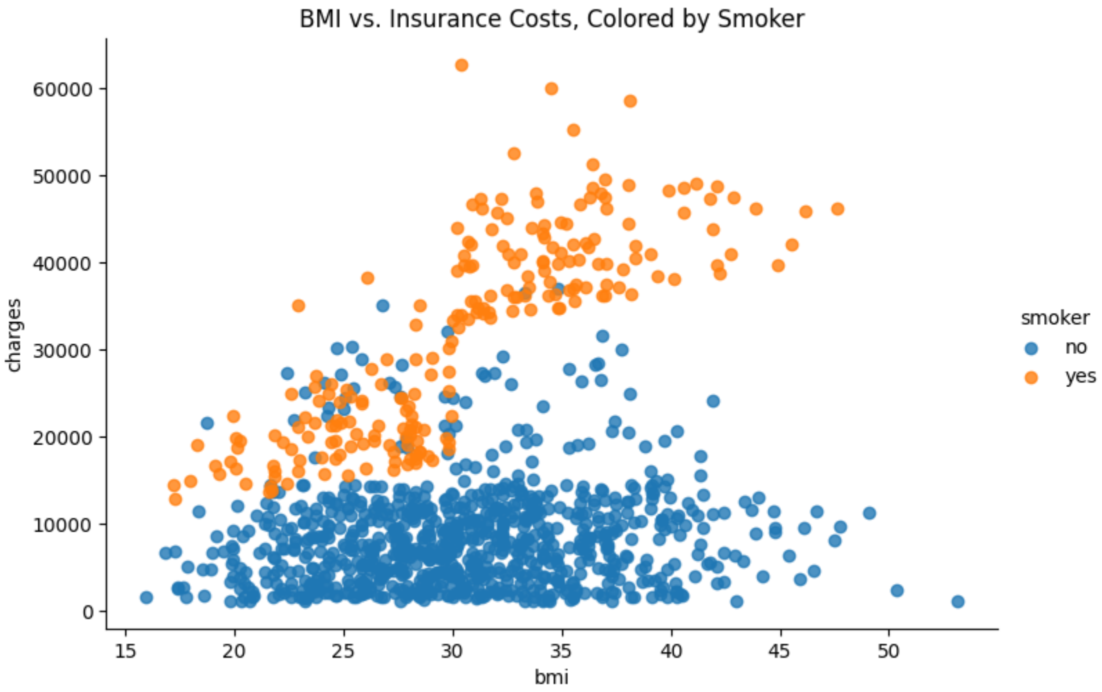
I observe that insurance costs are a lot more expensive in all 4 regions for smokers. I also observe that insurance costs are slightly more expensive in all 4 regions for males. I notice that in all 4 regions, the insurance is cheapest for those with 5 children. It looks like on average it may be most expensive for 3 and 4 children.

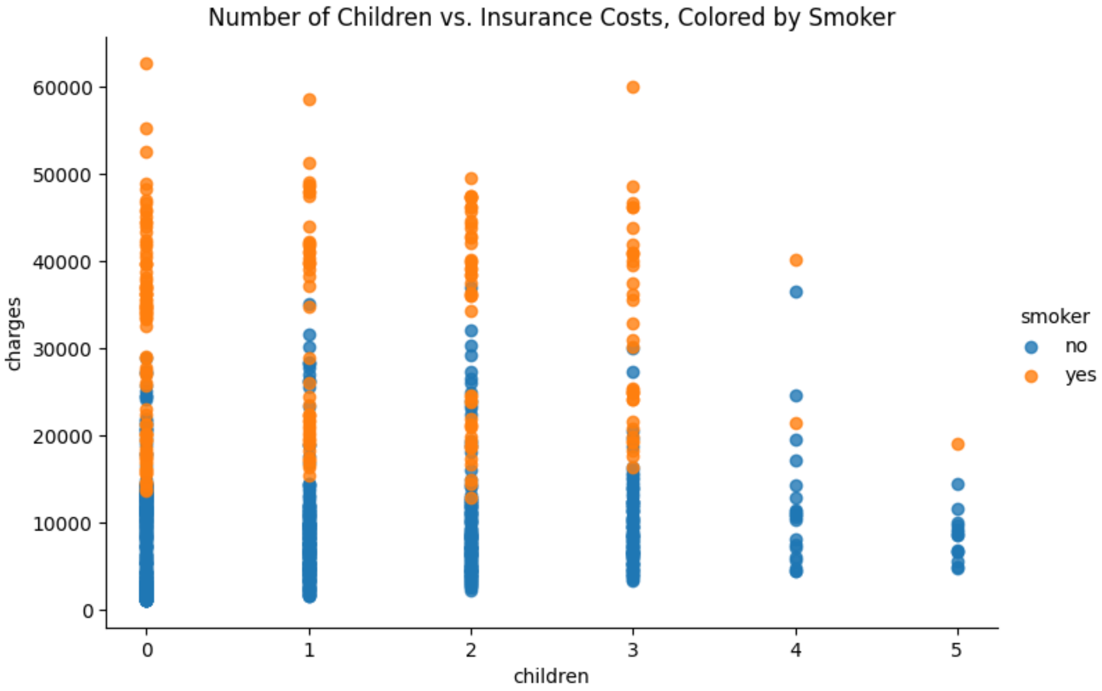
[15]:
```
# using the lmplot() function of seaborn, build a scatter plot of age and␣
 ↪insurance costs, hue by smoker
# build a second scatter plot of bmi and insurance costs, hue by smoker
# build a third scatter plot of children and insurance costs, hue by smoker
sns.lmplot(x='age', y='charges', data=medical, hue='smoker', aspect=1.5,␣
 ↪fit_reg=False)
plt.title('Age vs Insurance Costs, Colored by Smoker')

sns.lmplot(x='bmi', y='charges', data=medical, hue='smoker', aspect=1.5,␣
 ↪fit_reg=False)
```

```
plt.title('BMI vs. Insurance Costs, Colored by Smoker')

sns.lmplot(x='children', y='charges', data=medical, hue='smoker', aspect=1.5,␣
 ↪fit_reg=False)
plt.title('Number of Children vs. Insurance Costs, Colored by Smoker')
```

```
[15]: Text(0.5, 1.0, 'Number of Children vs. Insurance Costs, Colored by Smoker')
```







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

The insurance charges are higher for smokers than non-smokers in all 3 charts.

4.0.2 Look for Correlations

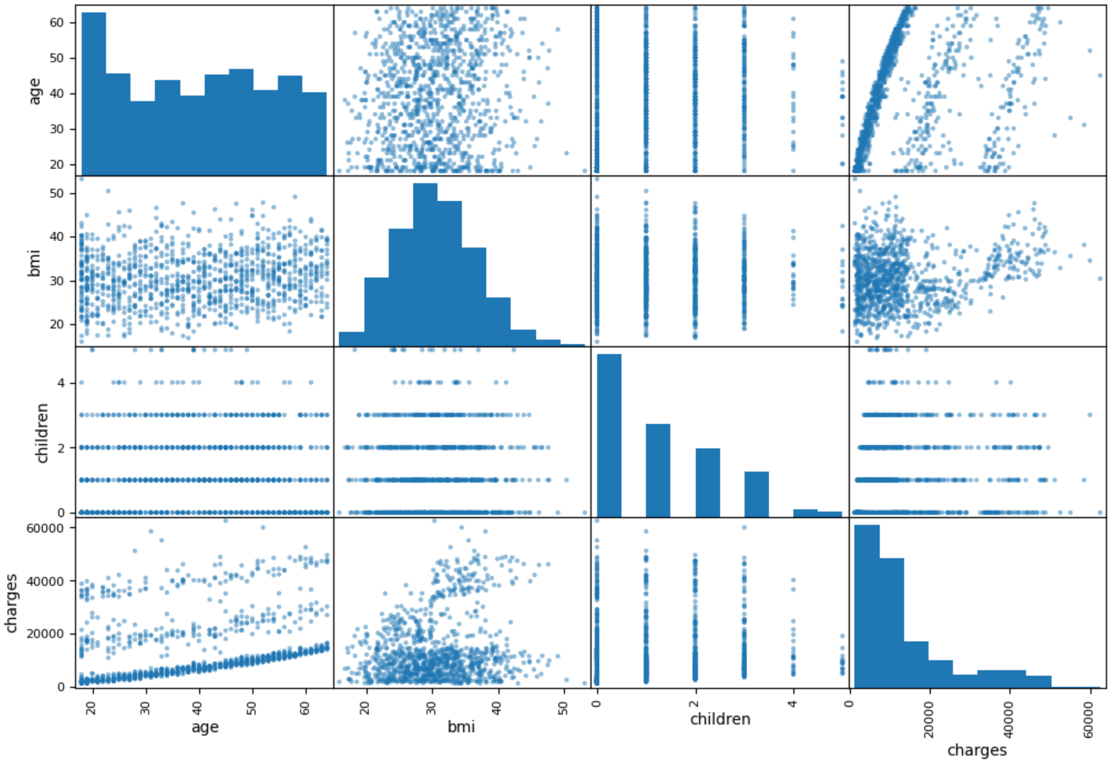
[22]:
```
# compute pairwise correlation of columns using the corr() method
medical_num = medical.select_dtypes(include=[np.number])
medical_num.corr()
```

[22]:
```
               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.

[25]:
```
# plot correlation matrix using scatter_matrix() function from pandas.plotting
pd.plotting.scatter_matrix(medical, 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.

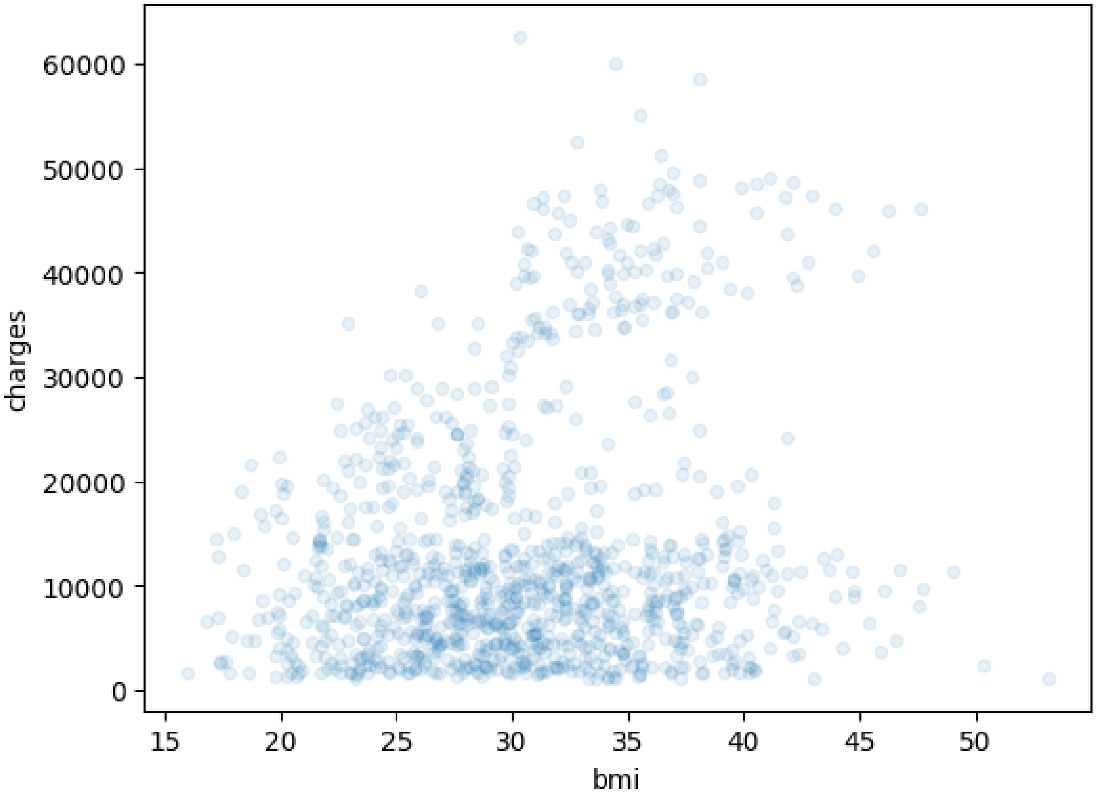
Looking at the correlation scatterplots, it seems like the most promising attribute to predict the charge value is bmi, so let's zoom in on their scatterplot.

[26]:

```
# plot a scatter plot of bmi vs. insurance costs using the medical.plot()␣
  ↪method, use the alpha parameter to set the opacity of the points to 0.1
medical.plot(kind='scatter', x='bmi', y='charges', alpha=0.1)
```

[26]:

```
<Axes: xlabel='bmi', ylabel='charges'>
```



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

5 Prepare the data for ML

[29]:

```
# drop the charges column from the train_set and save the resulting dataset to␣
  ↪a variable called `medical`
# create a copy of the train_set labels and save it to a variable called␣
  ↪`medical_labels`
# replace None with the correct code
medical = train_set.drop('charges', axis=1)
medical_labels = train_set['charges'].copy()
```

6 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.

[27]:

```
# uncomment the following code to create a pipeline for preprocessing the data

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

7 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.

7.1 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:

[30]:
```
# create a pipeline for preprocessing the data and fitting a linear regression␣
 ↪model
from sklearn.linear_model import LinearRegression
lin_reg = make_pipeline(preprocessing, LinearRegression())

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

lin_reg.fit(medical, medical_labels)
```

[30]:
```
Pipeline(steps=[('columntransformer',
                 ColumnTransformer(transformers=[('num',
Pipeline(steps=[('simpleimputer',
SimpleImputer(strategy='median')),
('standardscaler',
StandardScaler())]),
                                                  ['age', 'bmi', 'children']),
                                                 ('cat',
Pipeline(steps=[('simpleimputer',
SimpleImputer(strategy='most_frequent')),
('onehotencoder',
OneHotEncoder(handle_unknown='ignore'))]),
                                                  ['sex', 'smoker',
                                                   'region'])])),
                ('linearregression', LinearRegression())])
```

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

[31]:
```
# uncomment the following line to make predictions

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

[31]:
```
array([ 7094.54007011,  8344.72998713,  9153.77419778, …,
       11441.08519155, 37314.37460682, 11453.12102783])
```

[32]:
```
# 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
```

[32]:
```
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):

[34]:
```
# use DecisionTreeRegressor to train the model
# use the make_pipeline() function to create a pipeline for preprocessing and␣
 ↪model training
# use the preprocessing object you created earlier
# make predictions on the training set and compute the RMSE
from sklearn.tree import DecisionTreeRegressor
tree_reg = make_pipeline(preprocessing, DecisionTreeRegressor())

tree_reg.fit(medical, medical_labels)

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

[34]:
```
494.20598375812835
```

8 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:

[35]:
```
# 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
```

[35]:
```
array([5810.76640315, 6568.7713215 , 6642.73107366, 7021.19298449,
       6708.18216903, 6286.46010956, 7340.57325296, 7090.95309032,
       6829.86603279, 5301.97064652])
```

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.

[36]:
```
# uncomment the following line to compute the mean of the RMSEs
```

```
np.mean(tree_rmses)
```

[36]:

```
6560.1467083983325
```

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.

[37]:

```
# use RandomForestRegressor to train the model
# use the make_pipeline() function to create a pipeline for preprocessing and␣
 ↪model training
# 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
forest_reg = make_pipeline(preprocessing, RandomForestRegressor())

forest_reg.fit(medical, medical_labels)

medical_predictions = forest_reg.predict(medical)
medical_predictions
forest_rmse = mean_squared_error(medical_labels, medical_predictions,␣
 ↪squared=False)
forest_rmse
```

[37]:

```
1877.8494013944746
```

9 Fine-Tune Your Model

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

9.1 Randomized Search for Good Hyperparameters

[38]:

```
# 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)
```

[38]:

```
RandomizedSearchCV(cv=3,
                   estimator=Pipeline(steps=[('preprocessing',
ColumnTransformer(transformers=[('num',
Pipeline(steps=[('simpleimputer',
                SimpleImputer(strategy='median')),
               ('standardscaler',
                StandardScaler())]),
['age',
'bmi',
'children']),
('cat',
Pipeline(steps=[('simpleimputer',
                SimpleImputer(strategy='most_frequent')),
               ('onehotencoder',
                OneHotEncoder(handle_unknown='ignore'))]),
['sex',
'smoker',
'region'])])),
                                             ('random_forest',
RandomForestRegressor(random_state=42))]),
                   param_distributions={'random_forest__max_features':
<scipy.stats._distn_infrastructure.rv_discrete_frozen object at
0x7cd2bce567a0>},
                   random_state=42, scoring='neg_root_mean_squared_error')
```

[39]:

```
# 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"]
```

[39]:

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

[40]:
```
# 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
```

[40]:
```
array([0.14032922, 0.18831699, 0.0230048 , 0.00493845, 0.00454404,
       0.28737838, 0.33010198, 0.00580561, 0.00521445, 0.00654471,
       0.00382136])
```

[41]:
```
# uncomment the following line to print the feature importances with the␣
 ↪feature names

sorted(zip(feature_importances, final_model["preprocessing"].
 ↪get_feature_names_out()),reverse=True)
```

[41]:
```
[(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')]
```

[42]:
```
# now that you have a final model, evaluate it on the test set (find rmse)
medical_predictions = rnd_search.predict(medical)
medical_predictions
rnd_rmse = mean_squared_error(medical_labels, medical_predictions,␣
 ↪squared=False)
rnd_rmse
```

[42]:
```
1857.6573579690826
```