medical_costs_post

July 1, 2023

1 Get the Data

[52]:
```
import numpy as np
import pandas as pd
import seaborn as sns
from scipy.stats import randint
import matplotlib.pyplot as plt
from sklearn.pipeline import Pipeline
from sklearn.impute import SimpleImputer
from sklearn.pipeline import make_pipeline
from sklearn.compose import ColumnTransformer
from sklearn.tree import DecisionTreeRegressor
from sklearn.metrics import mean_squared_error
from sklearn.preprocessing import MinMaxScaler
from sklearn.preprocessing import OneHotEncoder
from sklearn.preprocessing import StandardScaler
from sklearn.linear_model import LinearRegression
from sklearn.ensemble import RandomForestRegressor
from sklearn.model_selection import cross_val_score
from sklearn.model_selection import train_test_split
from sklearn.model_selection import RandomizedSearchCV

medical = pd.read_csv("insurance.csv")
```

2 Take a Quick Look at the Data Structure

[53]:
```
medical.head()
```

[53]:

	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

[54]:
```
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
```

[55]:
```
medical.region.value_counts()
```

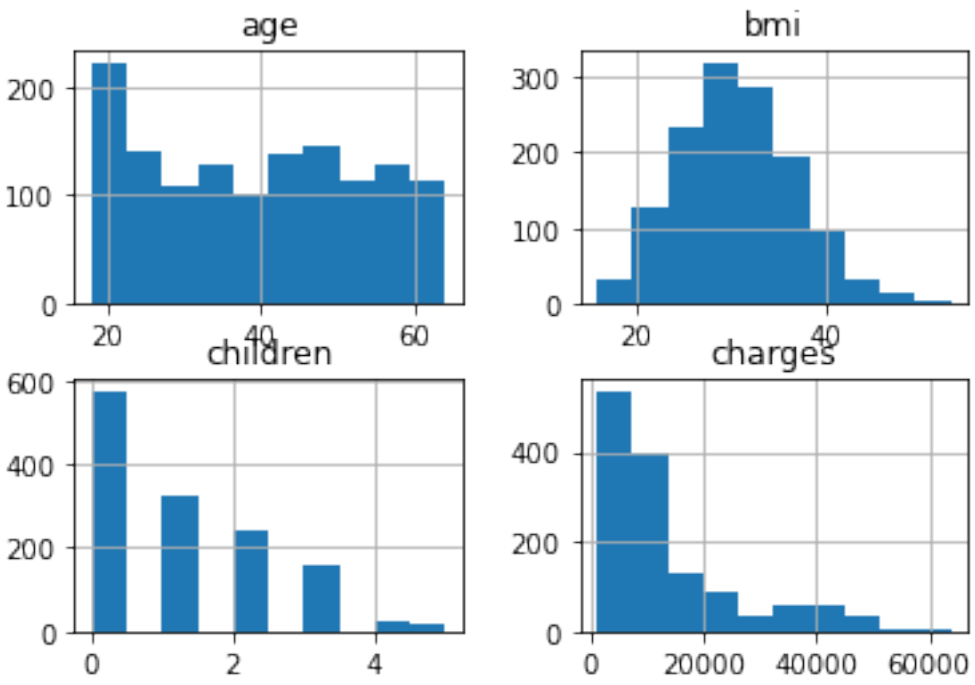
[55]:
```
southeast    364
southwest    325
northwest    325
northeast    324
Name: region, dtype: int64
```

[56]:
```
medical.describe()
```

[56]:

	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

[57]:
```
medical.hist()
plt.show()
```



[58]:
```
# age, children and charges are positively skewed
# bmi is normal
```

2.1 Create a Test Set

[59]:
```
RS = 13
```

[60]:
```
X = medical.drop(["charges"], axis = 1)
y = medical[["charges"]]
```

[61]:
```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.3,␣
↪random_state = RS)
```

3 Explore and Visualize the Data to Gain Insights

[62]:
```
X_train
```

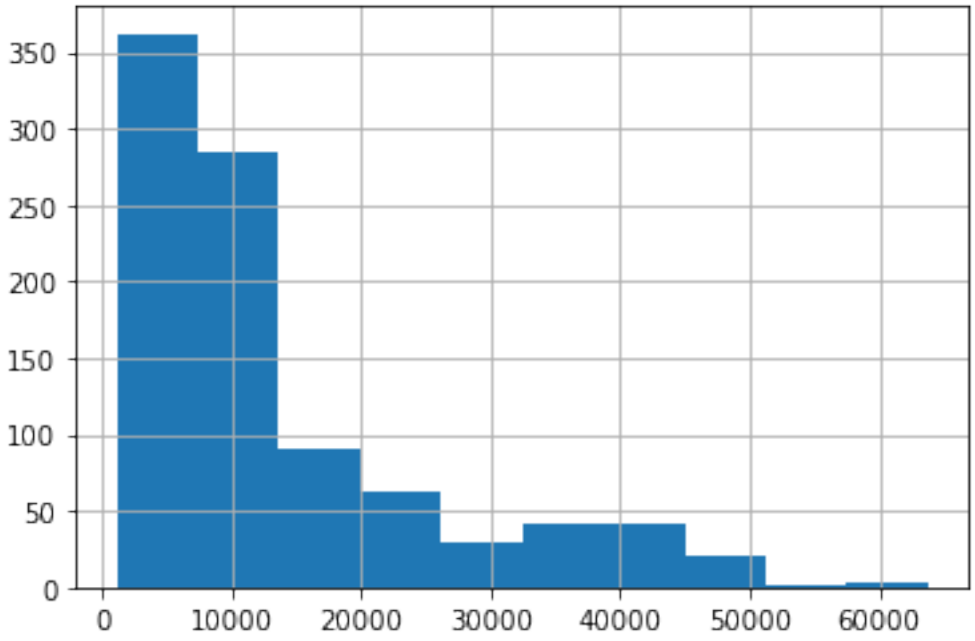
[62]:

	age	sex	bmi	children	smoker	region
448	40	female	29.600	0	no	southwest
443	59	female	36.520	1	no	southeast
581	19	male	30.590	0	no	northwest
913	44	female	27.500	1	no	southwest
708	31	female	30.495	3	no	northeast

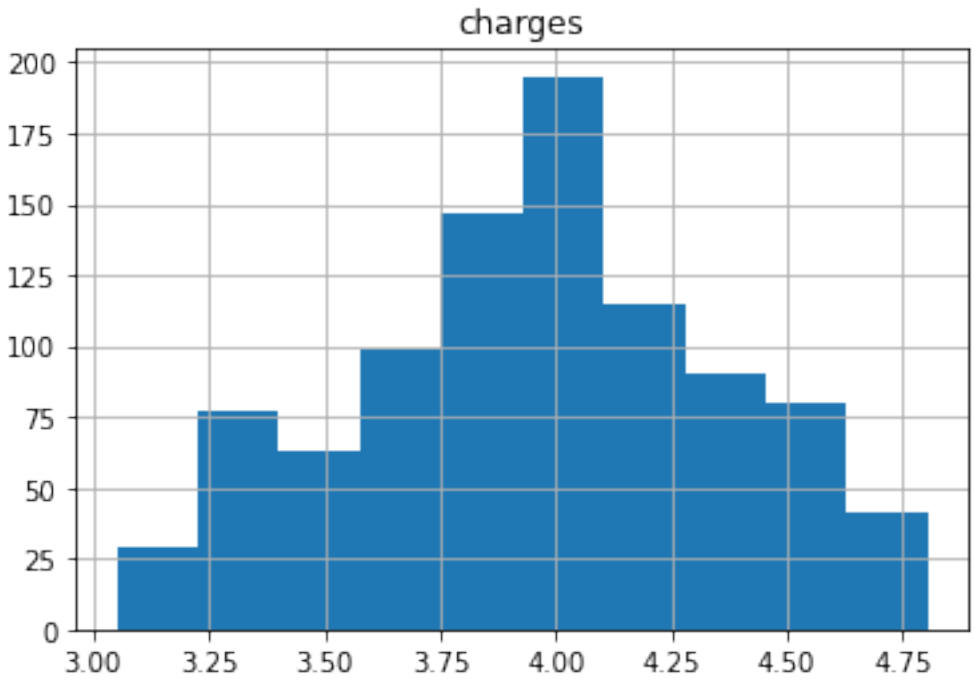
```
..    …      …      …         …     …         …
866   18     male   37.290          0     no   southeast
742   53     male   34.105          0    yes   northeast
74    44     male   27.400          2     no   southwest
176   38     male   27.835          2     no   northwest
338   50     male   32.300          1    yes   northeast

[936 rows x 6 columns]
```

[63]:
```
train = X_train.copy()
train["charges"] = y_train.copy()
```

[64]:
```
train["charges"].hist()
plt.show()
```



[65]:
```
pd.DataFrame(np.log10(train.charges)).hist()
plt.show()
```

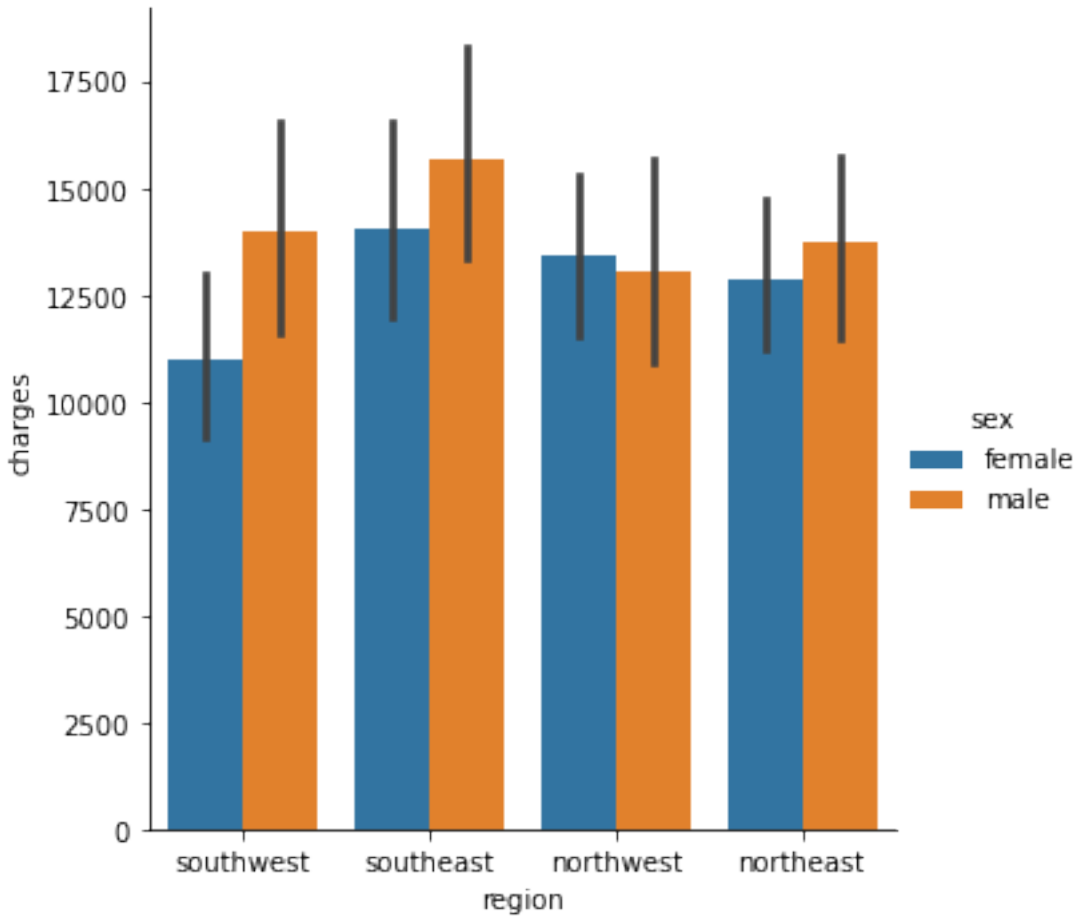


Now let's look at the mean charges by region

[66]:
```
train[["region","charges"]].groupby(["region"]).mean()
```

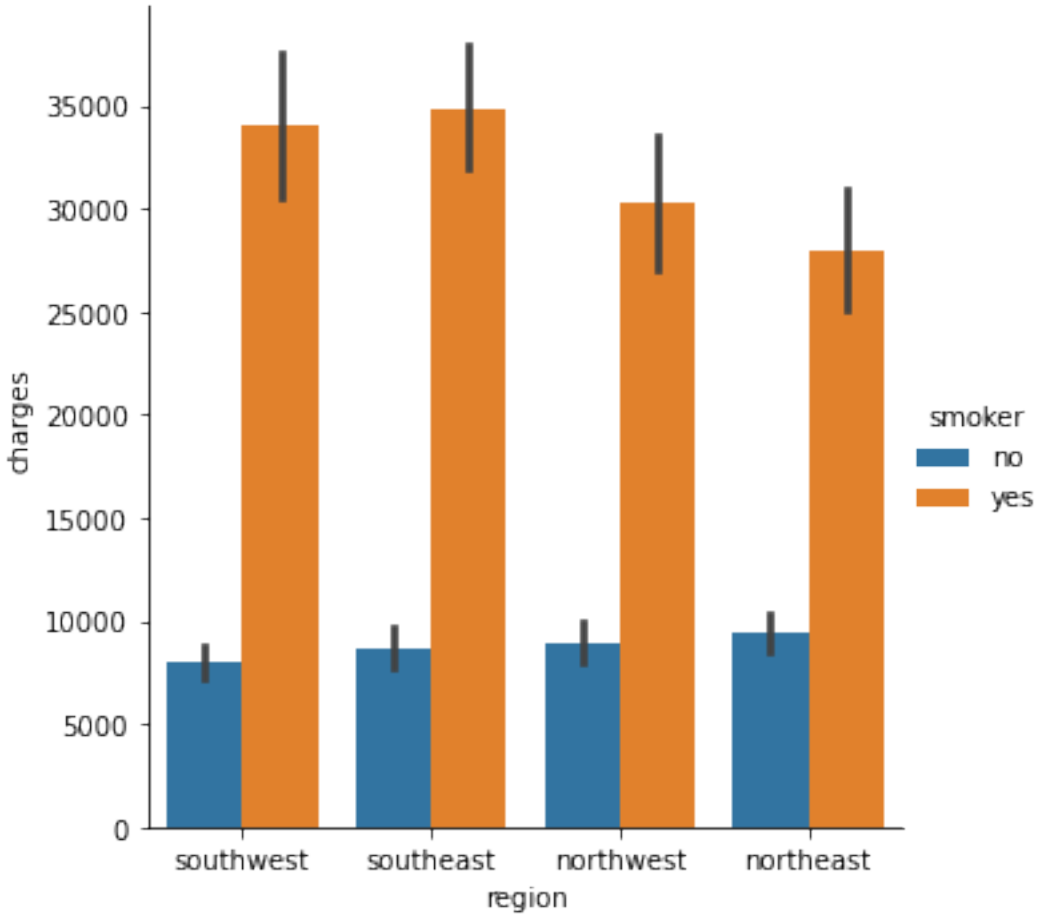
[66]:
```
                charges
region
northeast  13265.552265
northwest  13225.413686
southeast  14871.818962
southwest  12466.903493
```

[67]:
```
sns.catplot(data = train, x = "region", y = "charges", hue = "sex", kind =␣
 ↪"bar")
plt.show()
```



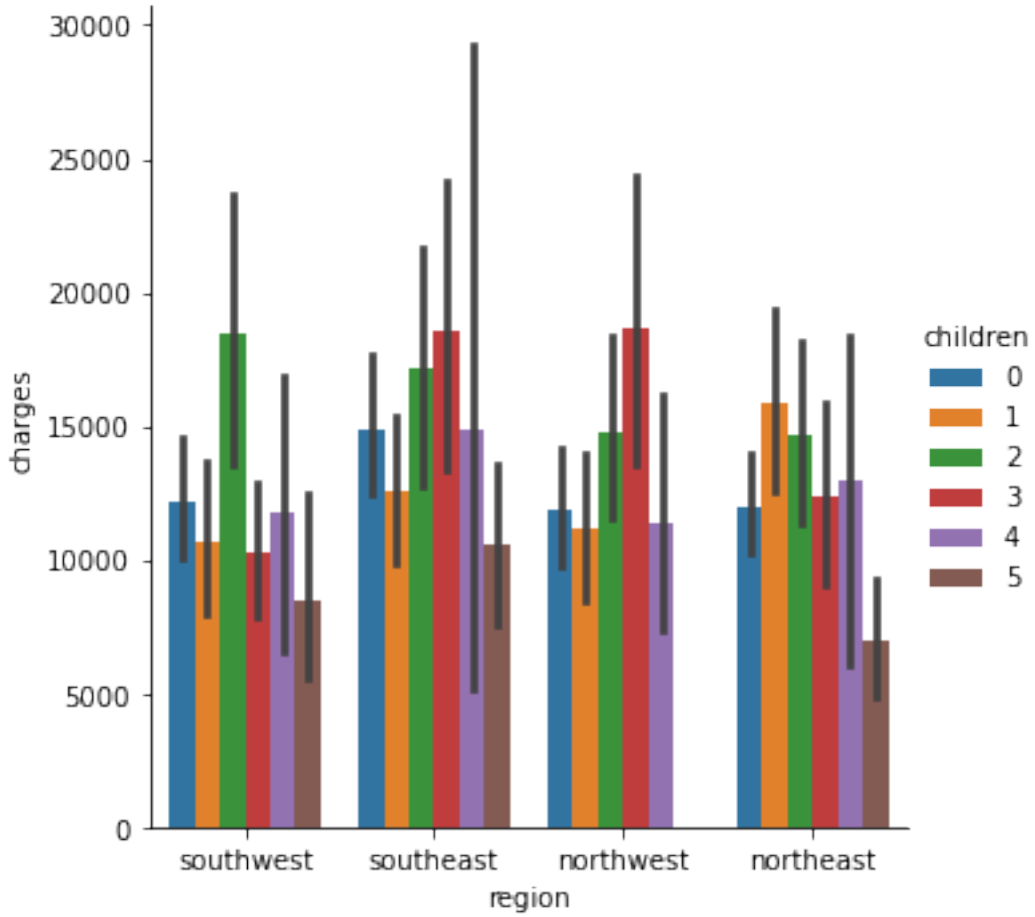
[68]:
```
# males charges are more than females (in 3/4 cases)
# southwest has the lowest charges for females
# northwest has the lowest charges for males
# southeast has the highest charges for both
```

[69]:
```
sns.catplot(data = train, x = "region", y = "charges", hue = "smoker", kind =␣
↪"bar")
plt.show()
```



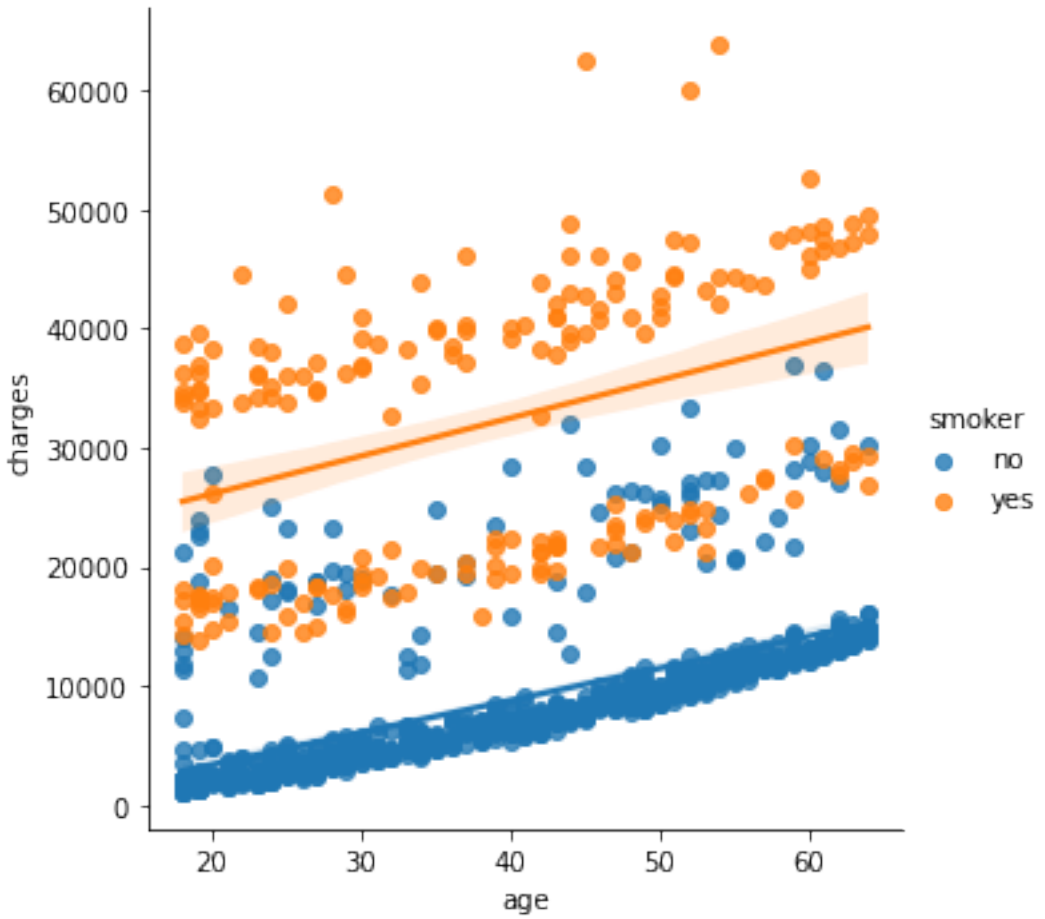
[70]:
```
# smokers has 3 times more charges than non-smokers
# north east has the highest charges for non-smokers, but the lowest charges␣
↪for smokers
```

[71]:
```
sns.catplot(data = train, x = "region", y = "charges", hue = "children", kind =␣
↪"bar")
plt.show()
```



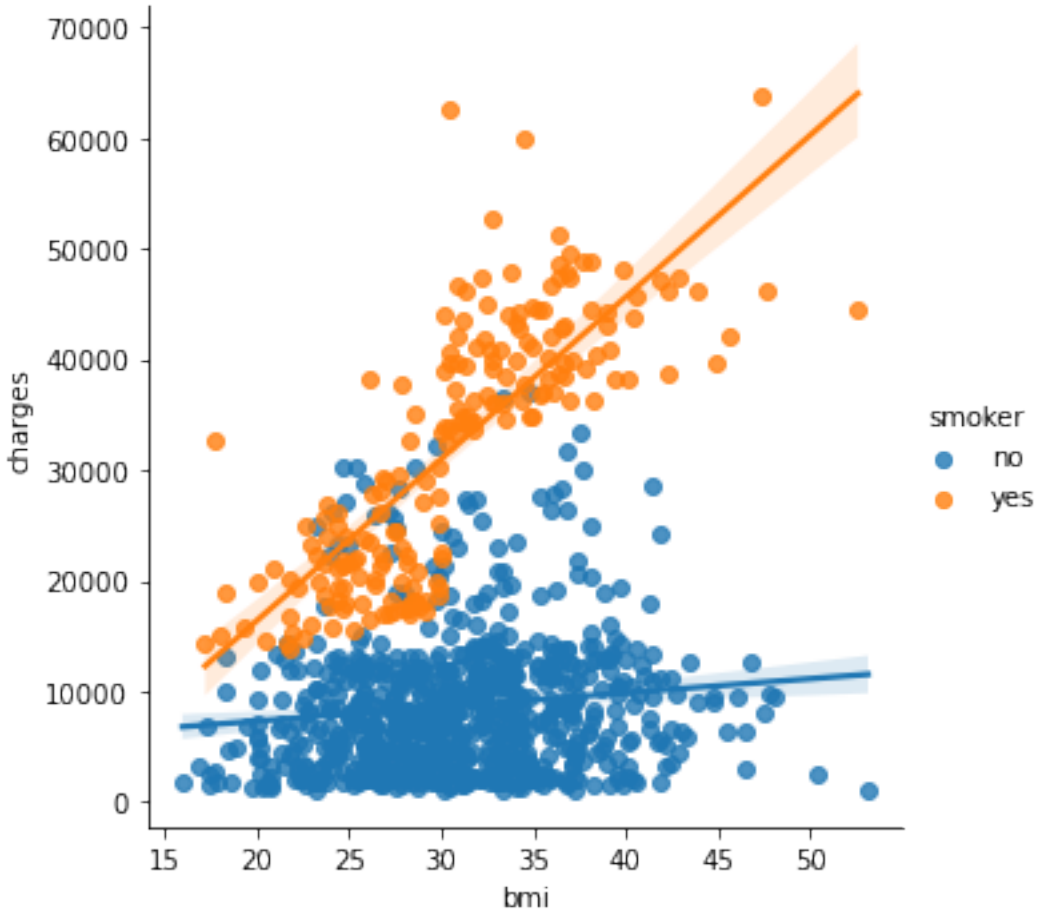
[72]:
```
# in southwest family with 2 children has the highest charge and with 5␣
 ↪childern hast the lowest charge
# in southeast family with 3 children has the highest charge and with 5␣
 ↪children hast the lowest charge
# in northwest family with 3 children hast the highest charge and with 1 child␣
 ↪has the lowest charge
# in northeast family with 1 child has the highest charge and with 5 children␣
 ↪has the lowest charge
```

[73]:
```
sns.lmplot(data = train,x = "age", y = "charges", hue = "smoker",)
plt.show()
```



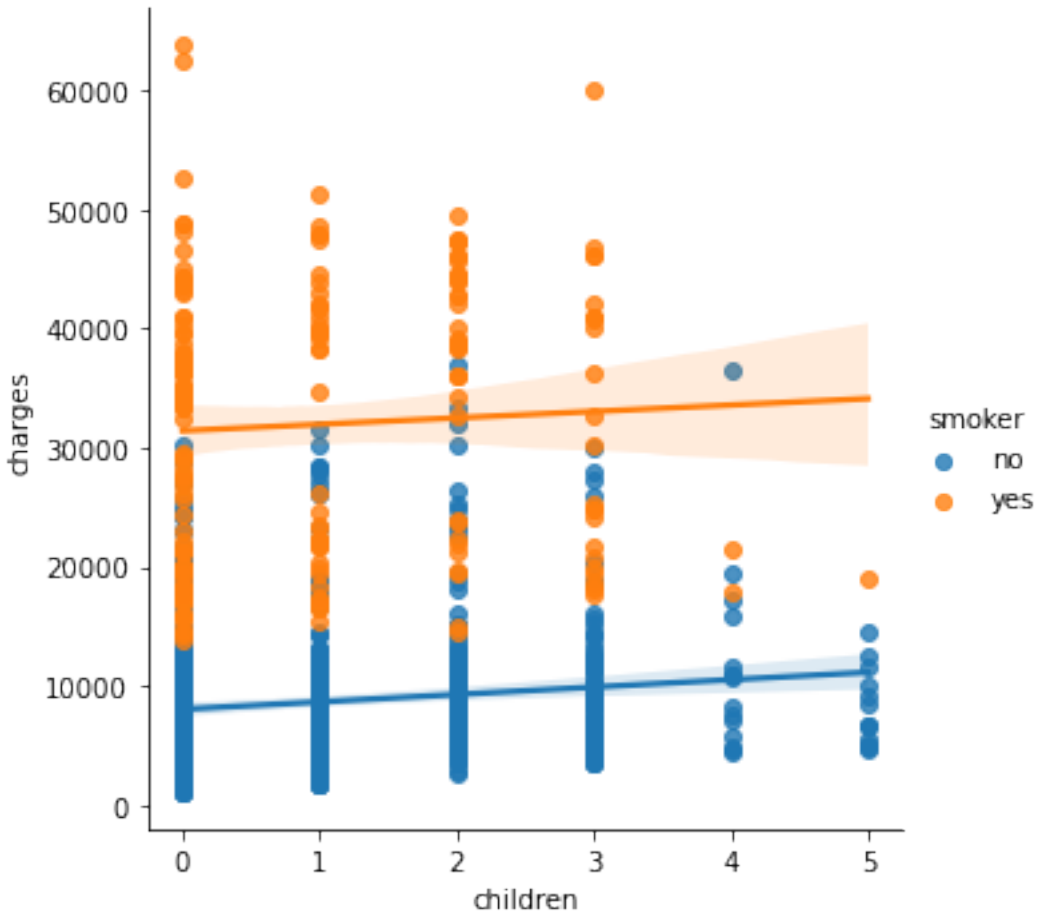
[74]:
```
# age and smoking both positively effect on charges
```

[75]:
```
sns.lmplot(data = train,x = "bmi", y = "charges", hue = "smoker",)
plt.show()
```



[76]:
```
# smoking highly effect on charges
# bmi effect on charges, but needs more clear plot for analyze
```

[77]:
```
sns.lmplot(data = train,x = "children", y = "charges", hue = "smoker",)
plt.show()
```



[78]:
```
# outliers of charges are mostly smokers and have less than 4 children
```

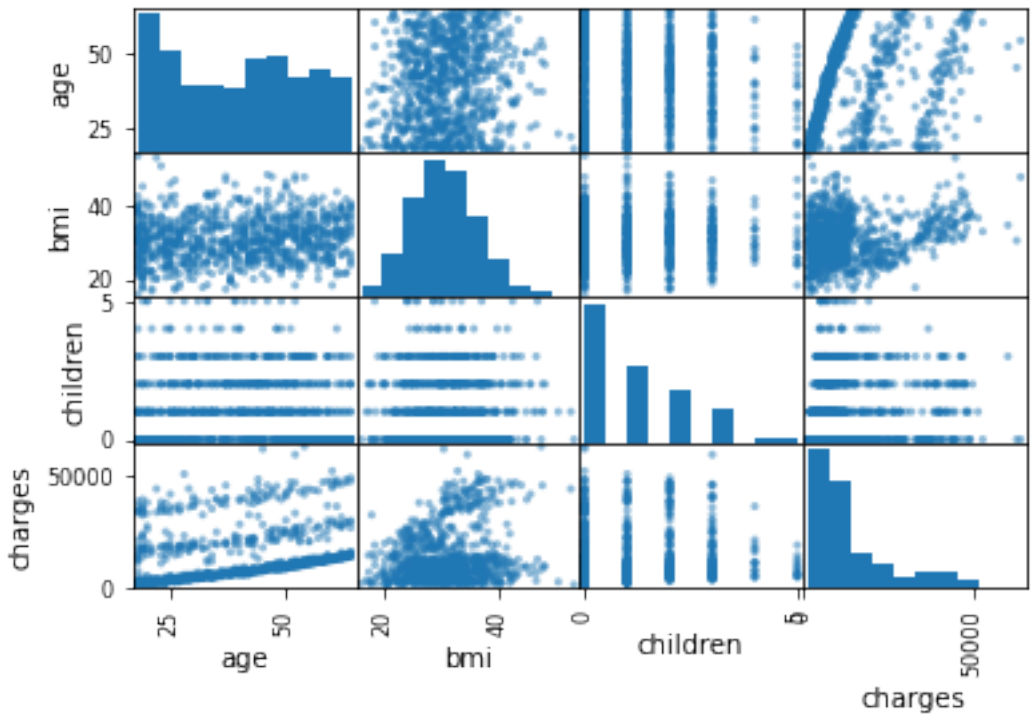
3.0.1 Look for Correlations

[79]:
```
train.corr()
```

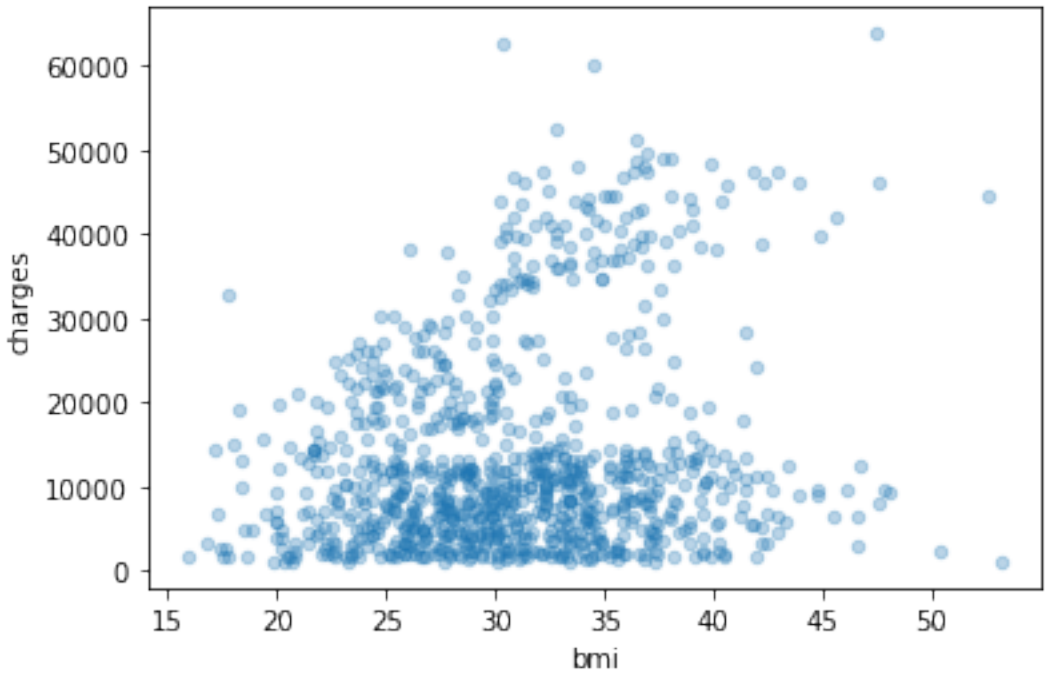
[79]:

	age	bmi	children	charges
age	1.000000	0.130788	0.025381	0.295932
bmi	0.130788	1.000000	0.023346	0.198454
children	0.025381	0.023346	1.000000	0.051307
charges	0.295932	0.198454	0.051307	1.000000

[80]:
```
pd.plotting.scatter_matrix(train)
plt.show()
```



[81]:
```
train.plot(kind = 'scatter', x = "bmi", y = 'charges', alpha = 0.3)
plt.show()
```



4 Transformation Pipelines

[82]:
```
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", drop = 'first'))

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

X_train_perpared = preprocessing.fit_transform(X_train)

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

```
(936, 8)
['num__age' 'num__bmi' 'num__children' 'cat__sex_male' 'cat__smoker_yes'
 'cat__region_northwest' 'cat__region_southeast' 'cat__region_southwest']
```

5 Select and Train a Model

5.1 Train and Evaluate on the Training Set

[83]:
```
lin_reg = Pipeline([
    ("preprocessing", preprocessing),
    ("linear_regression",LinearRegression())
])

lin_reg.fit(X_train, y_train)
```

[83]:
```
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(drop='first',
 handle_unknown='ignore'))]),
                                                   ['sex', 'smoker',
                                                    'region'])])),
                ('linear_regression', LinearRegression())])
```

[84]:
```
y_predictions_lin = lin_reg.predict(X_test)
y_predictions_lin[:5]
```

[84]:
```
array([[ 3578.74351013],
       [10216.27622265],
       [ 7398.59872957],
       [ 6238.60129349],
       [ 2562.75811151]])
```

[85]:
```
lin_rmse = mean_squared_error(y_test, y_predictions_lin, squared=False)
lin_rmse
```

[85]:
```
5834.133007290974
```

[86]:
```
dt_reg = Pipeline([
    ("preprocessing", preprocessing),
    ("decision_tree",DecisionTreeRegressor(random_state=RS))
])

dt_reg.fit(X_train, y_train)
```

[86]:
```
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(drop='first',
 handle_unknown='ignore'))]),
                                                  ['sex', 'smoker',
                                                   'region'])])),
                ('decision_tree', DecisionTreeRegressor(random_state=13))])
```

[87]:
```
y_predictions_dt = dt_reg.predict(X_test)
y_predictions_dt[:5]
```

[87]:
```
array([ 2055.3249 , 12224.35085,  4320.41085,  5227.98875,  2457.21115])
```

[88]:
```
dt_rmse = mean_squared_error(y_test, y_predictions_dt, squared=False)
dt_rmse
```

[88]:
```
6122.432350426551
```

6 Better Evaluation Using Cross-Validation

[89]:
```
tree_pipeline = Pipeline([
    ("preprocessing",preprocessing),
    ("tree", DecisionTreeRegressor(random_state = RS))
])

tree_rmses = cross_val_score(tree_pipeline,
                             X_train, y_train,
                             scoring="neg_root_mean_squared_error",
                             cv=10)
tree_rmses
```

[89]:
```
array([-6265.29485138, -7377.28208902, -7085.38856846, -7997.65675418,
       -7567.24221623, -6805.94150941, -7849.43824253, -7307.06282526,
       -6137.19432622, -6172.97182115])
```

[90]:
```
np.mean(tree_rmses * -1)
```

[90]:
```
7056.547320386965
```

[91]:
```
np.median(tree_rmses * -1)
```

[91]:
```
7196.225696860822
```

[92]:
```
rfr_reg = Pipeline([
    ("preprocessing",preprocessing),
    ("random_forest",RandomForestRegressor(random_state=RS))
])
rfr_reg.fit(X_train, y_train)
```

```
/home/amyrmahdy/.local/lib/python3.10/site-packages/sklearn/pipeline.py:382:
DataConversionWarning: A column-vector y was passed when a 1d array was
expected. Please change the shape of y to (n_samples,), for example using
ravel().
  self._final_estimator.fit(Xt, y, **fit_params_last_step)
```

[92]:
```
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(drop='first',
 handle_unknown='ignore'))]),
                                                 ['sex', 'smoker',
                                                  'region'])])),
                ('random_forest', RandomForestRegressor(random_state=13))])
```

[93]:
```
y_predictions_rfr = rfr_reg.predict(X_test)
y_predictions_rfr[:5]
```

[93]:
```
array([ 2401.83384026, 12397.9298855 ,  6870.0941465 ,  5123.836125  ,
        2875.93995009])
```

[94]:
```
rfr_rmse = mean_squared_error(y_test, y_predictions_rfr, squared=False)
rfr_rmse
```

[94]:
```
4251.558189926003
```

7 Fine-Tune Your Model

7.1 Randomized Search for Good Hyperparameters

[95]:
```
full_pipeline = Pipeline([("preprocessing", preprocessing),
                          ("random_forest",␣
 ↪RandomForestRegressor(random_state=RS))
                          ])

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=RS)
rnd_search.fit(X_train, y_train.values.ravel())
```

[95]:
```
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(drop='first',
                               handle_unknown='ignore'))]),
['sex',
'smoker',
'region'])])),
                                                ('random_forest',
RandomForestRegressor(random_state=13))]),
                   param_distributions={'random_forest__max_features':
<scipy.stats._distn_infrastructure.rv_frozen object at 0x7fd329ed8850>},
                   random_state=13, scoring='neg_root_mean_squared_error')
```

[96]:
```
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"]
```

[96]:
```
4   -5039.948650
7   -5039.948650
6   -5093.283311
9   -5152.495411
0   -5213.865327
Name: mean_test_score, dtype: float64
```

[97]:
```
final_model = rnd_search.best_estimator_ # includes preprocessing
feature_importances = final_model["random_forest"].feature_importances_
feature_importances
```

[97]:
```
array([0.14900893, 0.17895356, 0.02726622, 0.00850256, 0.61334952,
       0.00765398, 0.0084463 , 0.00681894])
```

[98]:
```
sorted(zip(feature_importances, final_model["preprocessing"].
 ↪get_feature_names_out()),reverse=True)
```

[98]:
```
[(0.6133495188155264, 'cat__smoker_yes'),
 (0.17895356150843594, 'num__bmi'),
 (0.14900892609866512, 'num__age'),
 (0.02726621957381335, 'num__children'),
 (0.008502558710902405, 'cat__sex_male'),
 (0.008446295284785842, 'cat__region_southeast'),
 (0.00765397739374062, 'cat__region_northwest'),
 (0.006818942614130391, 'cat__region_southwest')]
```

[99]:
```
final_rfr_reg = Pipeline([
    ("preprocessing", preprocessing),
    ("final_random_forest", RandomForestRegressor(random_state=RS, max_features␣
 ↪= 4))
])

final_rfr_reg.fit(X_train, y_train.values.ravel())
```

[99]:
```
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(drop='first',
 handle_unknown='ignore'))]),
                                                 ['sex', 'smoker',
                                                  'region'])])),
                ('final_random_forest',
                 RandomForestRegressor(max_features=4, random_state=13))])
```

[100]:
```
y_predictions_final_rfr = final_rfr_reg.predict(X_test)
y_predictions_final_rfr[:5]
```

[100]:
```
array([ 3251.5963769, 12139.4326819,  5544.7433706,  5053.354543 ,
        2925.5519552])
```

[101]:
```
final_rfr_rmse = mean_squared_error(y_test, y_predictions_final_rfr,␣
 ↪squared=False)
final_rfr_rmse
```

[101]:
```
4158.257085533594
```