Import libraries

In [1]:
```python
import pandas as pd # data manipulation
import numpy as np # linear algebra
import matplotlib.pyplot as plt # plots
import seaborn as sns # plots
import warnings # Ignore warning messages
```

In [2]:
```python
warnings.filterwarnings("ignore")
```

Load Data

In [3]:
```python
df=pd.read_csv("insurance.csv")
```

Using the histogram and the box plot. We confirm the presence of outliers. So we have to give it special processing.

Technically we can give outliers the same treatment as missing values.

- **Delete** those values.
- **Replace** them with a **statistical measure**.
- Use a **model**. So that it generates values closer to the real ones.

Feature engineering

In [4]:
```python
class lower_upper_limits():

    def __init__(self,dataset,feature,limit):

        self.dataset=dataset
        self.mean=dataset[feature].mean()
        self.std=dataset[feature].std()

        self.limit=limit


    def upper_limit(self):

        return self.mean+self.limit*self.std


    def lower_limit(self):

        return self.mean-self.limit*self.std
```

In [5]:
```python
df.groupby("sex").describe()["bmi"]
```

Out[5]:

sex	count	mean	std	min	25%	50%	75%	max
female	662.0	30.377749	6.046023	16.815	26.125	30.1075	34.31375	48.07
male	676.0	30.943129	6.140435	15.960	26.410	30.6875	34.99250	53.13

Selected from the best interval

In [14]:
```python
def selected_interval_upper(dataframe,feature,limits):


    for limit in limits:

        upper_limit=lower_upper_limits(dataframe,feature,limit).upper_limit()


        print(limit,upper_limit)

def selected_interval_lower(dataframe,feature,limits):


    for limit in limits:

        upper_limit=lower_upper_limits(df,"bmi",limit).lower_limit()

        print(limit,upper_limit)
```

Upper limit

In [8]:
```python
upper_intervals=np.arange(2,4,step=0.2)
upper_intervals=upper_intervals.round(2)
```

In [10]:
```python
selected_interval_upper(df,"bmi",upper_intervals)
```

```
2.0 42.85977068434457
2.2 44.07940806668037
2.4 45.29904544901618
2.6 46.51868283135198
2.8 47.738320213687786
3.0 48.95795759602359
3.2 50.177594978359394
3.4 51.3972323606952
3.6 52.616869743031
3.8 53.8365071253668
```

With an interval of 3 it gives a good value. To be able to replace outliers.

Replaces values greater than the upper range

In [11]:
```python
df["bmi"]=np.where(df["bmi"]>48.95,48.95,df["bmi"])
```

Lower limit

Replaces values less than the lower range

In [12]:
```python
lower_intervals=np.arange(2,4,step=0.2)
lower_intervals=upper_intervals.round(2)
```

In [15]:
```python
selected_interval_lower(df,"bmi",lower_intervals)
```

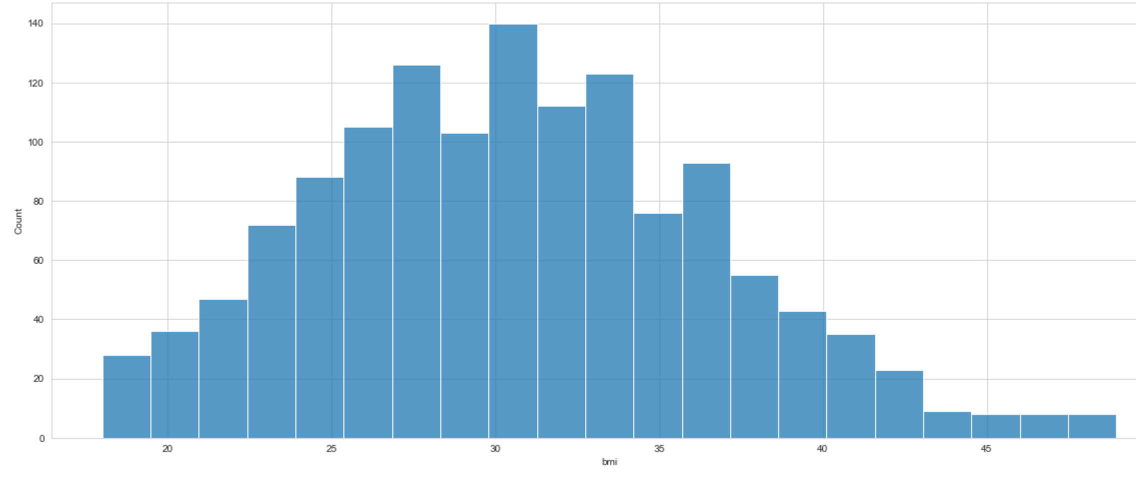
```
2.0 18.506082727141177
2.2 17.291050117941992
2.4 16.076017508742808
2.6 14.860984899543622
2.8 13.64595229034444
3.0 12.430919681145252
3.2 11.215887071946067
3.4 10.000854462746883
3.6 8.785821853547699
3.8 7.570789244348514
```

The appropriate interval value is 2. Since considered with the minimum BMI values regardless of sex is 18.

In [16]:
```python
df["bmi"]=np.where(df["bmi"]<18,18,df["bmi"])
```

In [17]:
```python
sns.set_style(style="whitegrid")
```

In [18]:
```python
plt.subplots(1,1,figsize=(20,8))
sns.histplot(data=df,x="bmi")
plt.show()
```



In [19]:
```python
smoker_no_split=df.query("smoker=='no'")
smoker_yes_split=df.query("smoker=='yes'")
```

We still see outliers. Therefore, I will decide to divide the dataset based on the age of the user. For better cleaning.

Smoker no split

Upper limit

In [20]:
```python
lower_upper_limits(smoker_no_split,"charges",2).upper_limit()
```

Out[20]:
```
20421.831936246064
```

Using an interval of 2 gives good results. In addition, for this case, the values that are out of the normal, we are going to transform them by null values and later we are going to replace said value, using a linear model. Since there are variables that are highly correlated.

Transform the outliers to null

In [21]:
```python
smoker_no_split["charges"]=smoker_no_split["charges"].apply(lambda x: np.nan if x > 20000 else x)
```

Calculate the percentage of null values

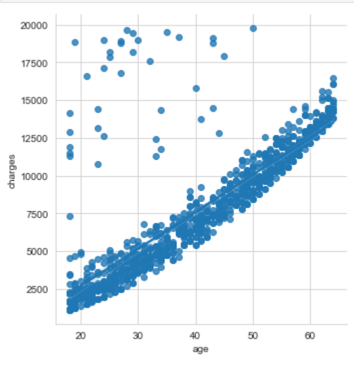
In [22]:
```python
((smoker_no_split.isnull().sum() / len(df))*100).sort_values(ascending = False)
```

Out[22]:
```
charges     4.559043
age         0.000000
sex         0.000000
bmi         0.000000
children    0.000000
smoker      0.000000
region      0.000000
dtype: float64
```

In [25]:
```python
def scatter_plot(dataframe,x,y):


    sns.lmplot(data=dataframe,x=x,y=y)
    plt.show()
```

In [26]:
```python
scatter_plot(smoker_no_split,"age","charges")
```



Divide according to age.

In [27]:
```python
young_adults_split=smoker_no_split.query("age<30")
adults_split=smoker_no_split.query("age>=30 and age<50")
old_adults_split=smoker_no_split.query("age>=50")
```

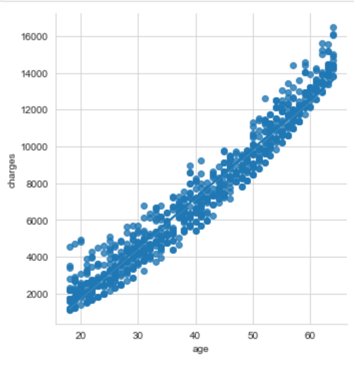
In [28]:
```python
def outlires_to_nan(dataframe,upper_limit):

    return dataframe["charges"].apply(lambda x: np.nan if x>upper_limit else x)
```

In [29]:
```python
young_adults_split["charges"]=outlires_to_nan(young_adults_split,7000)
adults_split["charges"]=outlires_to_nan(adults_split,10000)
old_adults_split["charges"]=outlires_to_nan(old_adults_split,18000)
```

In [30]:
```python
smoker_no_split=pd.concat([young_adults_split,
                           adults_split,
                           old_adults_split])
```

In [31]:
```python
scatter_plot(smoker_no_split,"age","charges")
```



Now the data set is devoid of outliers. But to avoid data loss, we are going to create a model to be able to substitute null values. To have a better closeness than to replace them with a statistical measure.

Replace null values

I will obtain by creating a linear regression model. To replace those values. Since the variables of age and insurance charge. It has a linear trend for non-smokers.

In [32]:
```python
smoker_no_clear=smoker_no_split.dropna() # Eliminate nan values
smoker_no_nan=smoker_no_split[smoker_no_split["charges"].isnull()] # Select nan values
```

In [33]:
```python
X=smoker_no_clear.drop(["charges","smoker"],axis="columns")
y=smoker_no_clear.charges
```

Split data in train and test

In [34]:
```python
from sklearn.model_selection import train_test_split,cross_val_score
```

In [35]:
```python
X_train,X_test,Y_train,Y_test=train_test_split(X,y,test_size=0.33,random_state=0)

X_train.shape,X_test.shape
```

Out[35]:
```
((636, 5), (314, 5))
```

In [36]:
```python
from sklearn.pipeline import Pipeline
from sklearn.compose import make_column_transformer #  Variables transform
```

In [37]:
```python
from sklearn.preprocessing import OneHotEncoder,MinMaxScaler
```

In [38]:
```python
tf_col=make_column_transformer((MinMaxScaler(),["age","bmi","children"]),
                               (OneHotEncoder(drop="if_binary"),["sex","region"]))
```

Linear Model

In [39]:
```python
from sklearn.linear_model import LinearRegression
```

In [40]:
```python
lm=Pipeline([("preprocessor",tf_col),("linear_model",LinearRegression())])

lm.fit(X_train,Y_train)
```

Out[40]:
```
Pipeline(steps=[('preprocessor',
                 ColumnTransformer(transformers=[('minmaxscaler',
                                                  MinMaxScaler(),
                                                  ['age', 'bmi', 'children']),
                                                 ('onehotencoder',
                                                  OneHotEncoder(drop='if_binary'),
                                                  ['sex', 'region'])])),
                ('linear_model', LinearRegression())])
```

In [41]:
```python
lm.score(X_train,Y_train)
```

Out[41]:
```
0.9792977979690041
```

In [42]:
```python
lm.score(X_test,Y_test)
```

Out[42]:
```
0.9818515223070252
```

Cross validation

In [43]:
```python
cross_val_score(lm,X_test,Y_test,cv=5).mean()
```

Out[43]:
```
0.9806776769021471
```

The generalization value was quite high. By which the linear model can describe 97% of the observations. We can use it to substitute missing values to avoid excessive data loss.

Substitution of null values

In [44]:
```python
new_data=smoker_no_nan.drop(["charges"],axis="columns")
smoker_no_nan["charges"]=lm.predict(new_data)
```

In [45]:
```python
smoker_no_nan.head()
```

Out[45]:

	age	sex	bmi	children	smoker	region	charges
102	18	female	30.115	0	no	northeast	1516.455194
143	29	male	29.735	2	no	northwest	4585.151560
219	24	female	23.210	0	no	southeast	2404.761100
291	29	male	29.640	1	no	northeast	4411.947852
305	29	male	33.345	2	no	northwest	4610.707459

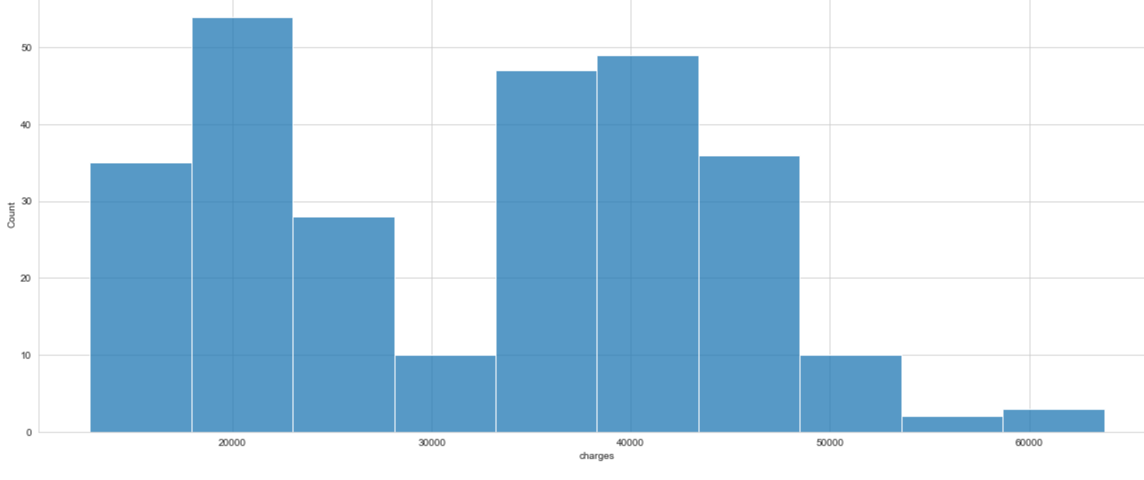
In [46]:
```python
smoker_no_nan.isnull().sum()
```

Out[46]:
```
age         0
sex         0
bmi         0
children    0
smoker      0
region      0
charges     0
dtype: int64
```

In [47]:
```python
smoker_no_clear=pd.concat([smoker_no_clear,
                           smoker_no_nan])
```

Smoker yes splitt

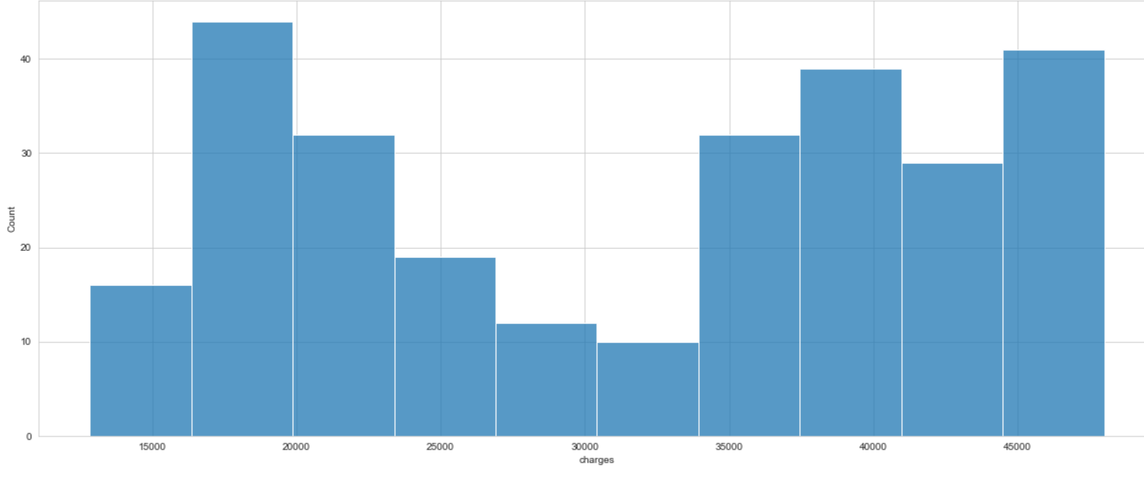
In [48]:
```python
plt.figure(figsize=(20,8))
sns.histplot(data=smoker_yes_split,x="charges")
plt.show()
```



We replace the outliers

In [52]:
```python
smoker_yes_split["charges"]=smoker_yes_split["charges"].apply(lambda x: 48000 if x > 48000 else x)
```

In [53]:
```python
plt.figure(figsize=(20,8))
sns.histplot(data=smoker_yes_split,x="charges")
plt.show()
```



In [55]:
```python
smoker_yes_clear=smoker_yes_split
```

In [56]:
```python
df_clear=pd.concat([smoker_no_clear,smoker_yes_clear])
```

We save the dataset with the clean data

In [57]:
```python
df_clear.to_csv("insurence_clear.csv")
```