Predicting health insurance charges

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[1]:
```
import time
import math
import torch
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns

import warnings
warnings.filterwarnings('ignore')
```

1 The aim of this notebook is to do an exploratory data analysis of health insurance data, and then use a linear regression model to be able to predict health insurance charges.

- An exploratory data analysis
- Univariate linear regression from scratch
- Multivariate linear regression from scratch

1.1 The exploratory data analysis

[2]:
```
# Importing the dataset
df = pd.read_csv('./insurance.csv')
print(df.head())
print(df.info())
print(df.isnull().sum())
# Looking for how many unique values there are in the categorical features
print('Different regions - ', df['region'].unique())
print('Different numbers of children - ', df['children'].unique())
```

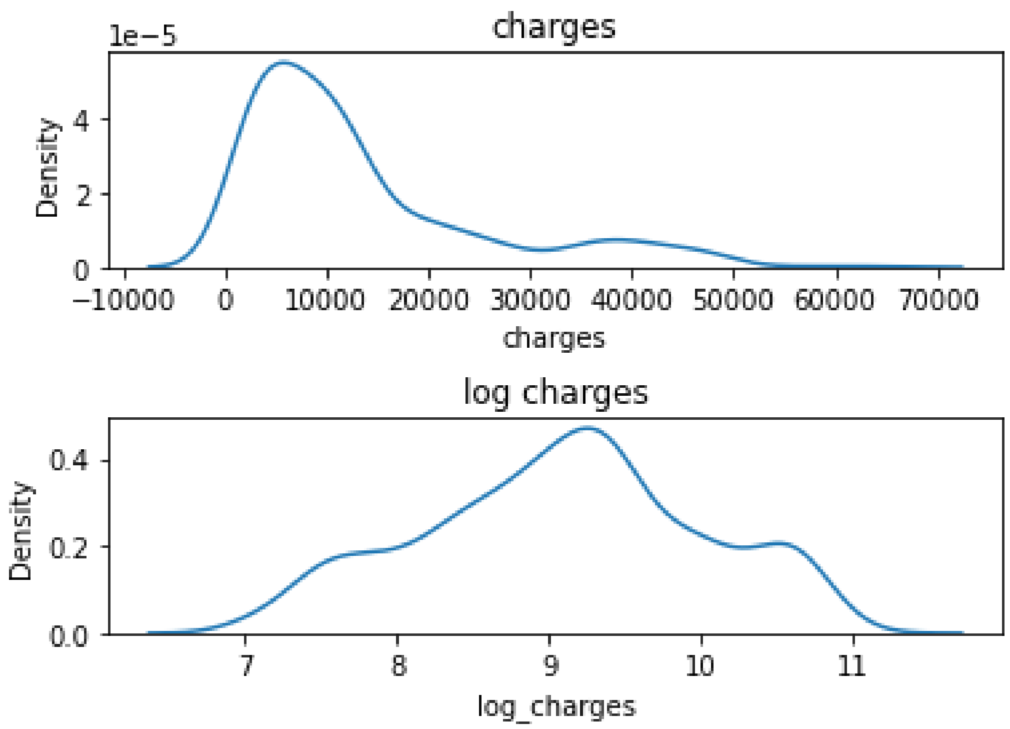
```
   age     sex     bmi  children smoker     region      charges
0   19  female  27.900         0    yes  southwest  16884.92400
1   18    male  33.770         1     no  southeast   1725.55230
2   28    male  33.000         3     no  southeast   4449.46200
3   33    male  22.705         0     no 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

```
<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
None
age         0
sex         0
bmi         0
children    0
smoker      0
region      0
charges     0
dtype: int64
Different regions -  ['southwest' 'southeast' 'northwest' 'northeast']
Different numbers of children -  [0 1 3 2 5 4]
```

The data given is quite a small data-set with only 1338 people. There are a set of features describing the age, sex, bmi and reigion for each instance, as well as information on the number of children and whether they are a smoker or not. There are four categories in the region: southeast, southwest, northeast and northwest. The data is completely clean with no typos or missing data.

This is all compared against the charges on the health insurance.

[3]:
```python
# Adding a log charges as well as charges to train a model to later
df['log_charges'] = np.log(df['charges'])

# PLotting the distribution of charges and log charges to check for normal␣
 ↪distribution
fig, ax = plt.subplots(nrows=2)
sns.distplot(df['charges'], ax=ax[0], hist=False).set_title('charges')
sns.distplot(df['log_charges'], ax=ax[1], hist=False).set_title('log charges')
plt.subplots_adjust(hspace=0.7)
plt.show()
```



The distribution of the charges shows a the data is positively skewed. When the log is taken, the data looks much better. The presence of peaks in the distribution suggests to me there are groups within the instances.

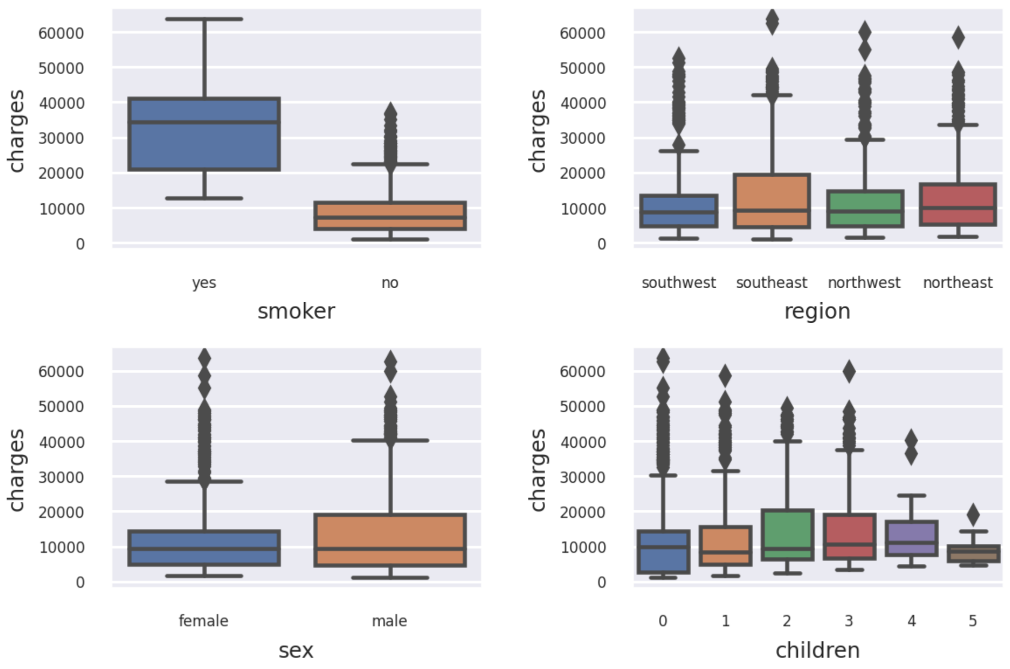
[4]:
```
print('bmi correlation - ', df['charges'].corr(df['bmi']))
print('age correlation - ', df['charges'].corr(df['age']))
```

```
bmi correlation -  0.19834096883362892
age correlation -  0.29900819333064765
```

There is a significant correlation between both bmi and age with charges. I am slightly surprised at how low the correlation is though, especially with bmi which I would have thought would have a significant effect on health. I will look into why this is later.

[5]:
```
# Adjusting the font size of the figures to match the overall figure size
sns.set(font_scale = 0.5)

# Plotting box and whiskers to show the distribution of charges according to␣
 ↪these features
fig = plt.figure(dpi=220)
plt.rcParams["axes.labelsize"] = 8
fig.subplots_adjust(hspace=0.4, wspace=0.4)
ax = fig.add_subplot(2, 2, 1)
sns.boxplot(data=df, x='smoker', y='charges', ax=ax)
```

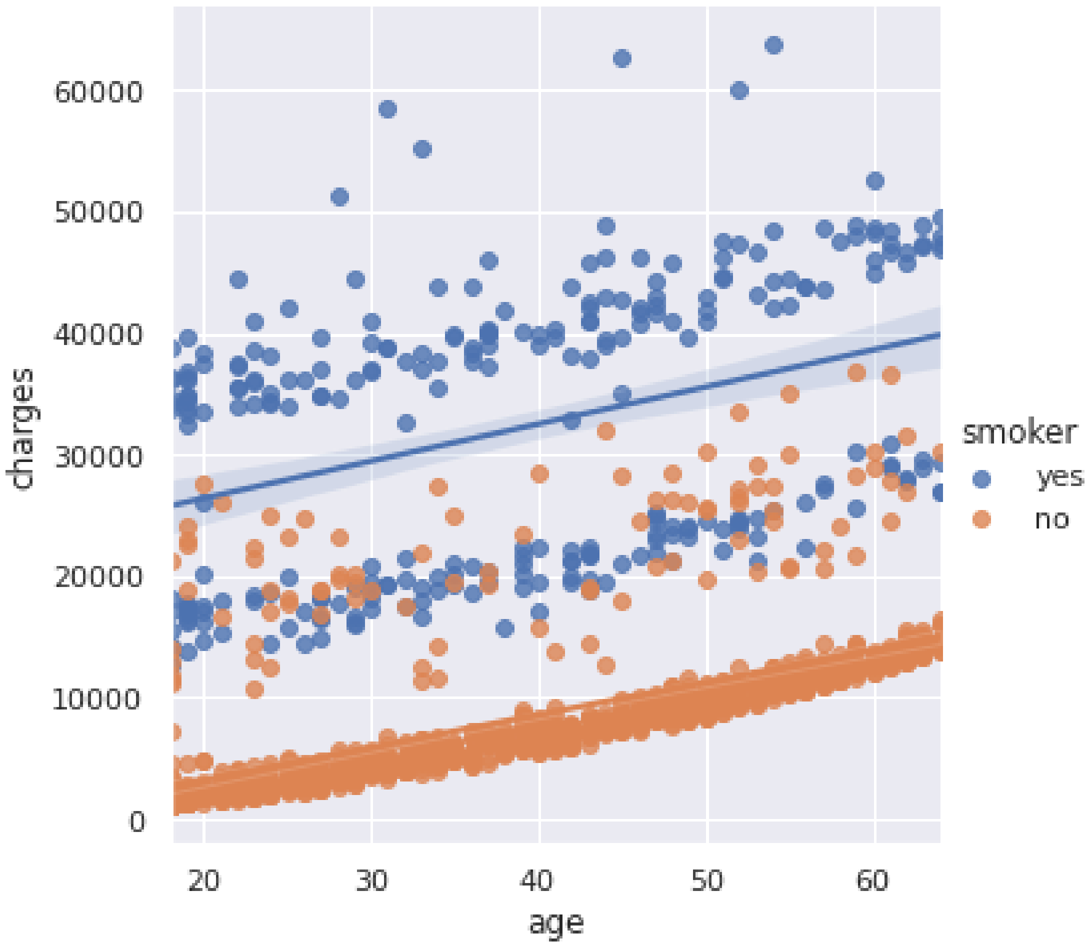
```
ax = fig.add_subplot(2, 2, 2)
sns.boxplot(data=df, x='region', y='charges', ax=ax)
ax = fig.add_subplot(2, 2, 3)
sns.boxplot(data=df, x='sex', y='charges', ax=ax)
ax = fig.add_subplot(2, 2, 4)
sns.boxplot(data=df, x='children', y='charges', ax=ax)
plt.show()
sns.set(font_scale = 1)

# How many are in each category of children
print(df['children'].value_counts())
```

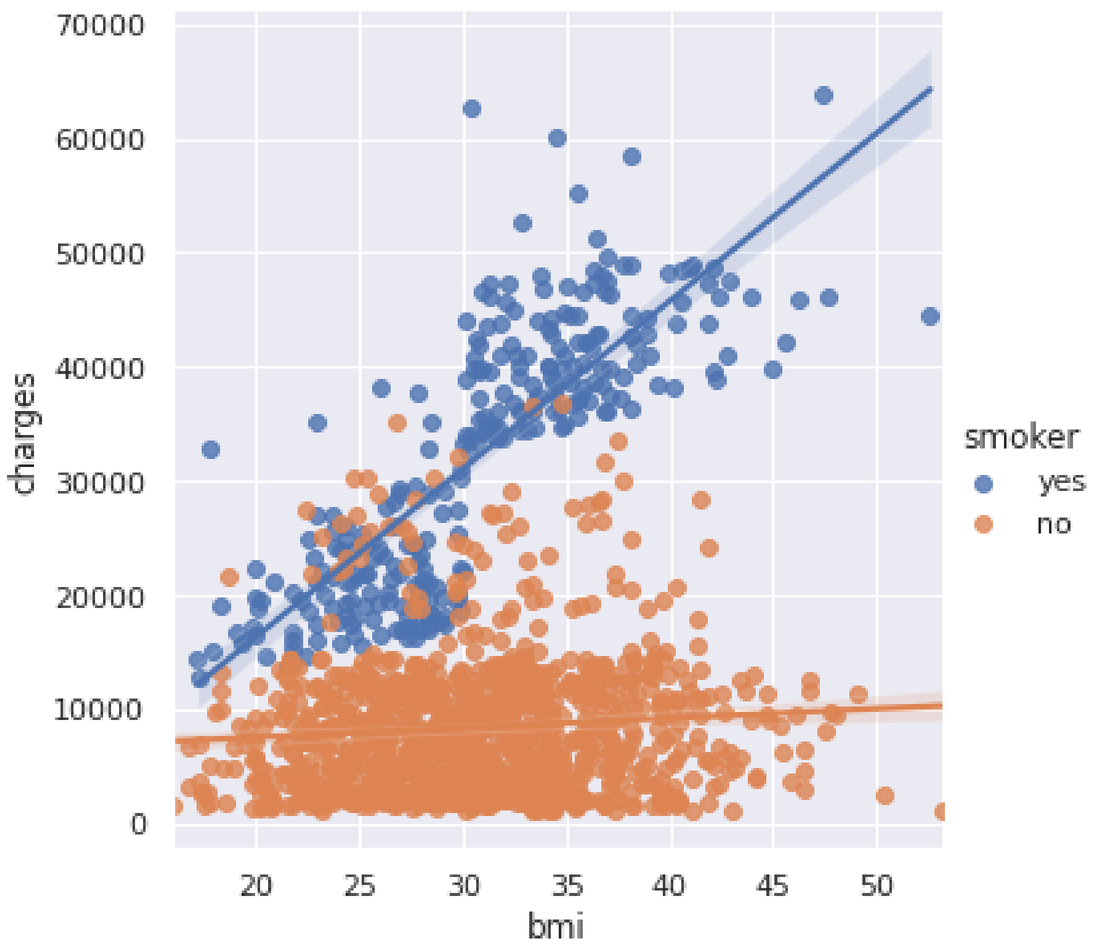


```
0    574
1    324
2    240
3    157
4     25
5     18
Name: children, dtype: int64
```

With the categorical data, it is clear the biggest correlation to charges is with smoking. There appears to be some correlation with sex and region but not large. The number of children seems to have some effect on the charges but I am not sure how significant it is. Firstly the number of instances with 4 or 5 children is very low so I would not trust that data. Secondly, the 0 children category does not seem to fit an overall trend. I would therefore split this category up for a linear regresssion analysis into its contituent categories, rather than leave it as an ordinal feature (0-5).

[6]:
```
# Scatter plots to show the correlation between features and charges
sns.lmplot(data=df, x='age', y='charges', hue='smoker')
plt.show()
sns.lmplot(data=df, x='bmi', y='charges', hue='smoker')
plt.show()
```



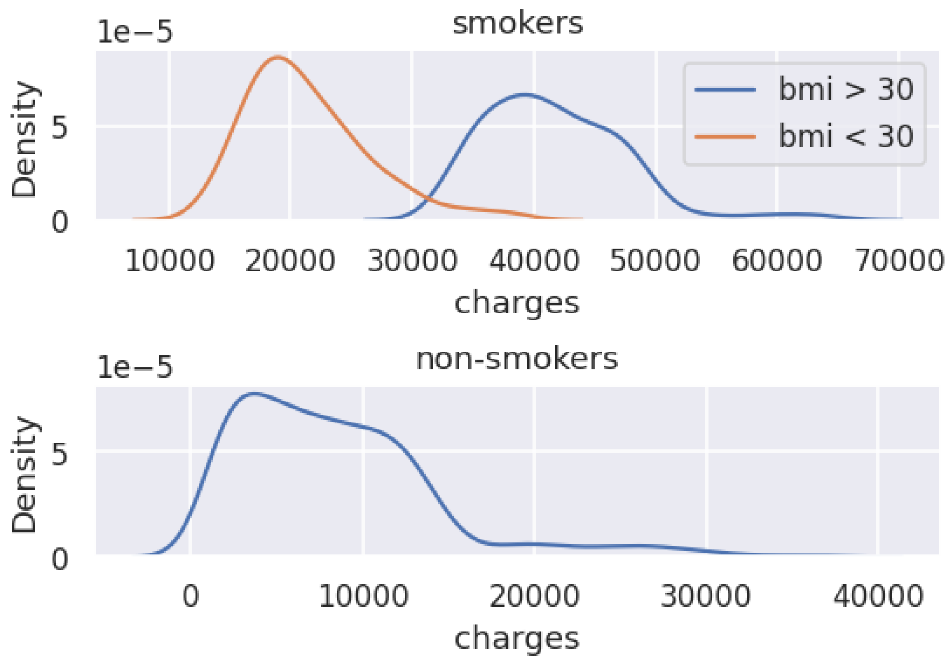


The scatter plot of age and charges shows there is an obvious distinction with how the smoking and non-smoking instances are treated. The smokers appear to be split again into another two groups while the non-smoking is probably all one group but with a set of outliers. These will probably be due to some other health concerns and is probably mirrored in in the smoking group; you can see the set of outliers at the top of the plot.

The scatter plot of bmi against charges shows this distinction between smokers and non-smokers again. Here though we see how the smoker group is subdivided: those with below and those with above a bmi of 30. There does not appear to be the same distinction for non-smokers. We cannot see from these plots what would cause the particularly high charges in some instances.

[7]:
```
fig, ax = plt.subplots(nrows=2, dpi=110)
fig.tight_layout(pad=3.0)
# Plotting for smokers with bmi over 30
sns.distplot(df[(df['smoker'] == 'yes') & (df['bmi'] > 30)]["charges"],␣
 ↪ax=ax[0], hist=False,
             label='bmi > 30').set_title('smokers')
# Plotting for smokers with bmi under 30
```

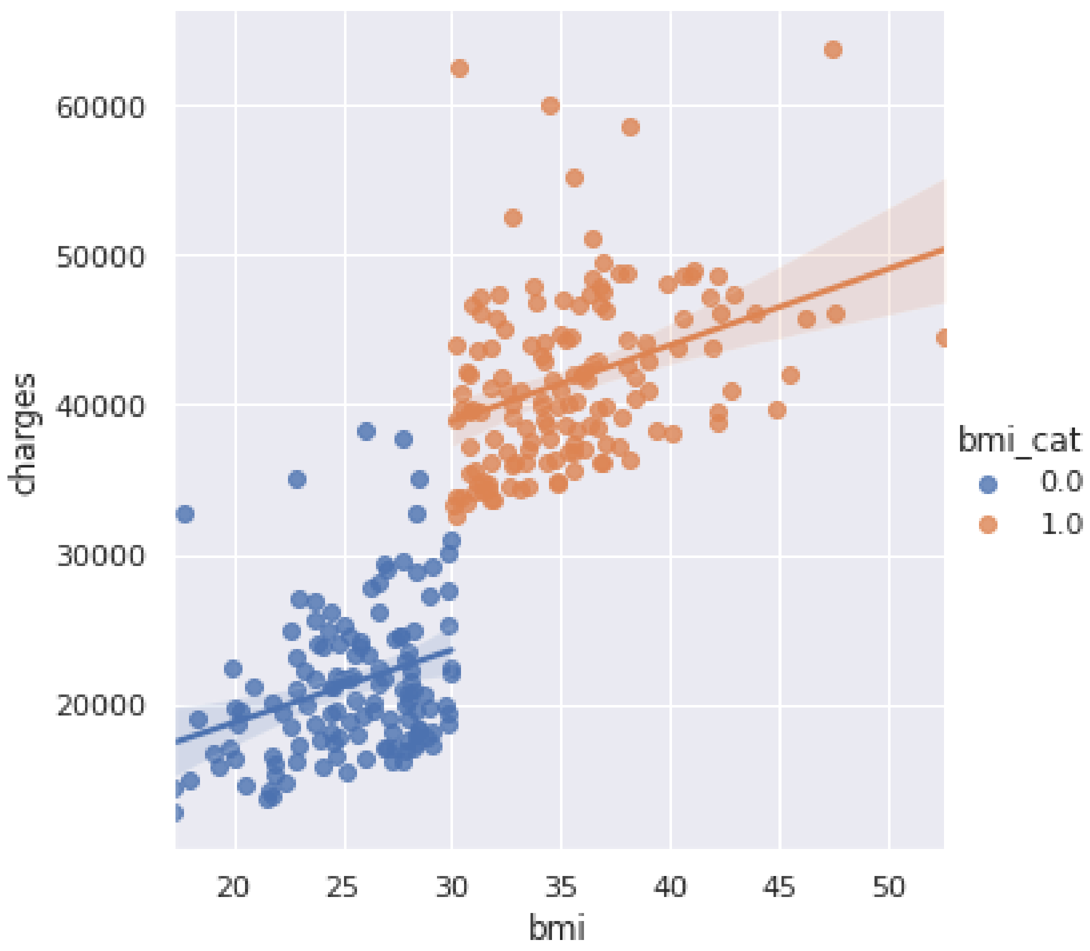
```
sns.distplot(df[(df['smoker'] == 'yes') & (df['bmi'] < 30)]["charges"],␣
↪ax=ax[0], hist=False, label='bmi < 30')
# Plotting for non smokers
sns.distplot(df[(df['smoker'] == 'no')]["charges"], ax=ax[1], hist=False).
↪set_title('non-smokers')
ax[0].legend()
plt.show()
```



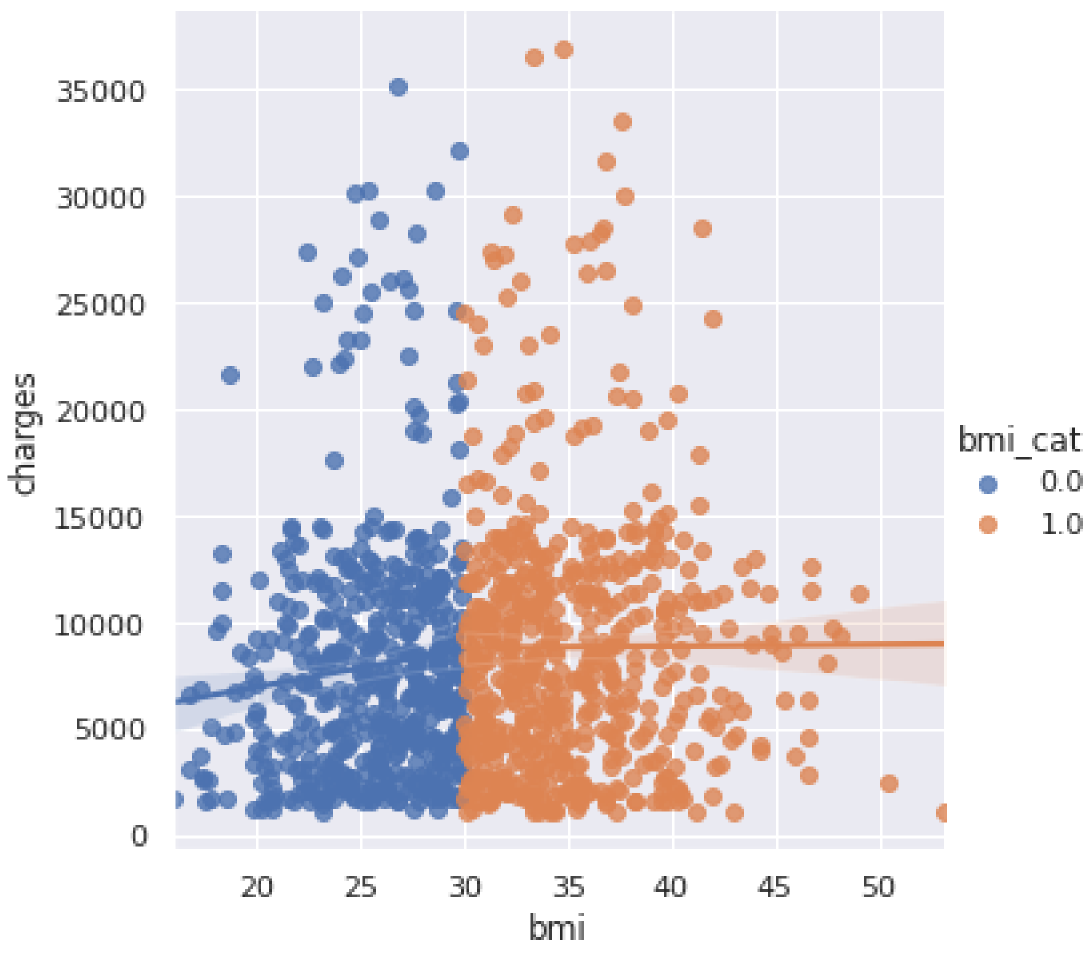
With this knowledge in mind we can now show the distribution of charges but split it into our three easily defined groups: non-smokers, smokers with bmi > 30 and smokers with bmi <30. As predicted there is a tail on some of the peak which we can see on the above scatter plots as (outlier) although it is very consistent so these will be for some medical reason. Interestingly, the same tail does not exist in the smokers with bmi < 30.

We will inesitigate whether one of the other features can account for these instances later.

[8]:
```
# Creates a new categorical feature for bmi (30 is the cuttoff point for obese)
df['bmi_cat'] = np.nan
df.loc[df['bmi'] <= 30, 'bmi_cat'] = 0
df.loc[df['bmi'] > 30, 'bmi_cat'] = 1

sns.lmplot(data=df[df['smoker'] == 'yes'], x='bmi', y='charges', hue='bmi_cat')
plt.show()
sns.lmplot(data=df[df['smoker'] == 'no'], x='bmi', y='charges', hue='bmi_cat')
plt.show()
```



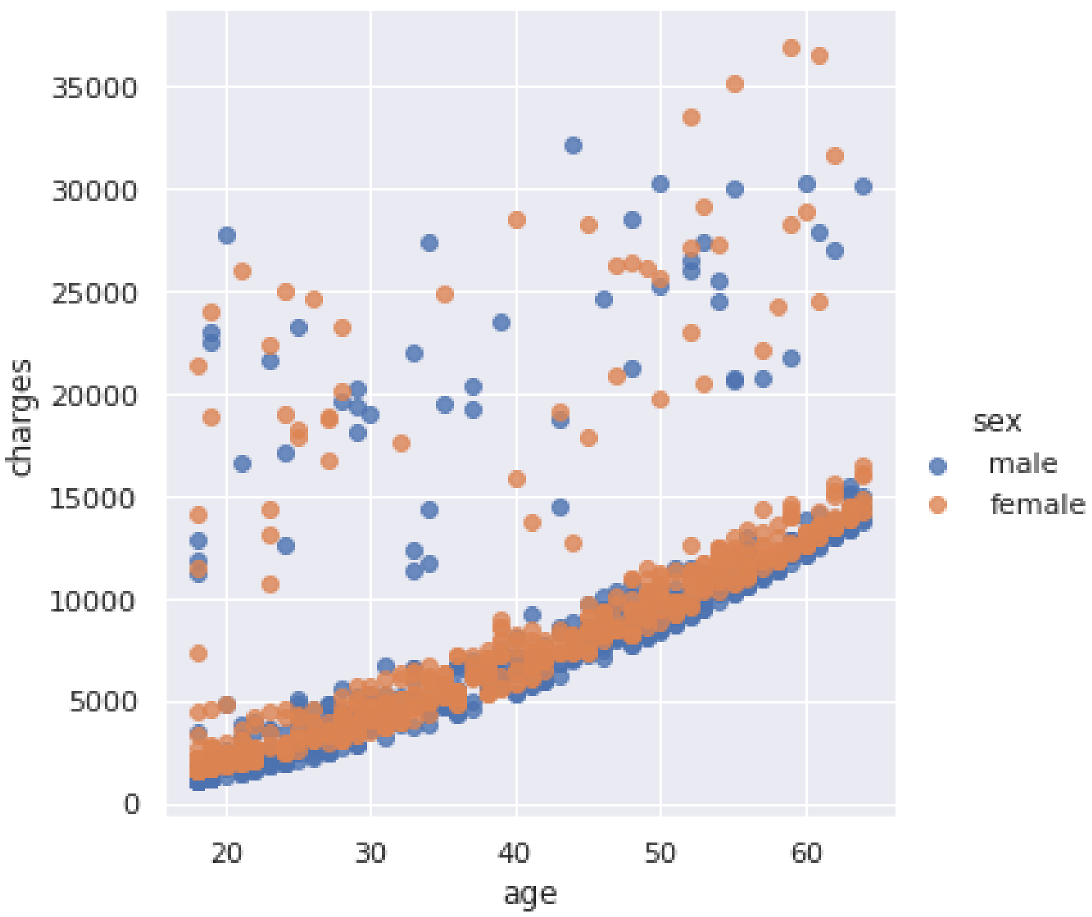
charges
60000
50000
40000
30000
20000
20
25
30
35
40
45
50
bmi
bmi_cat
0.0
1.0



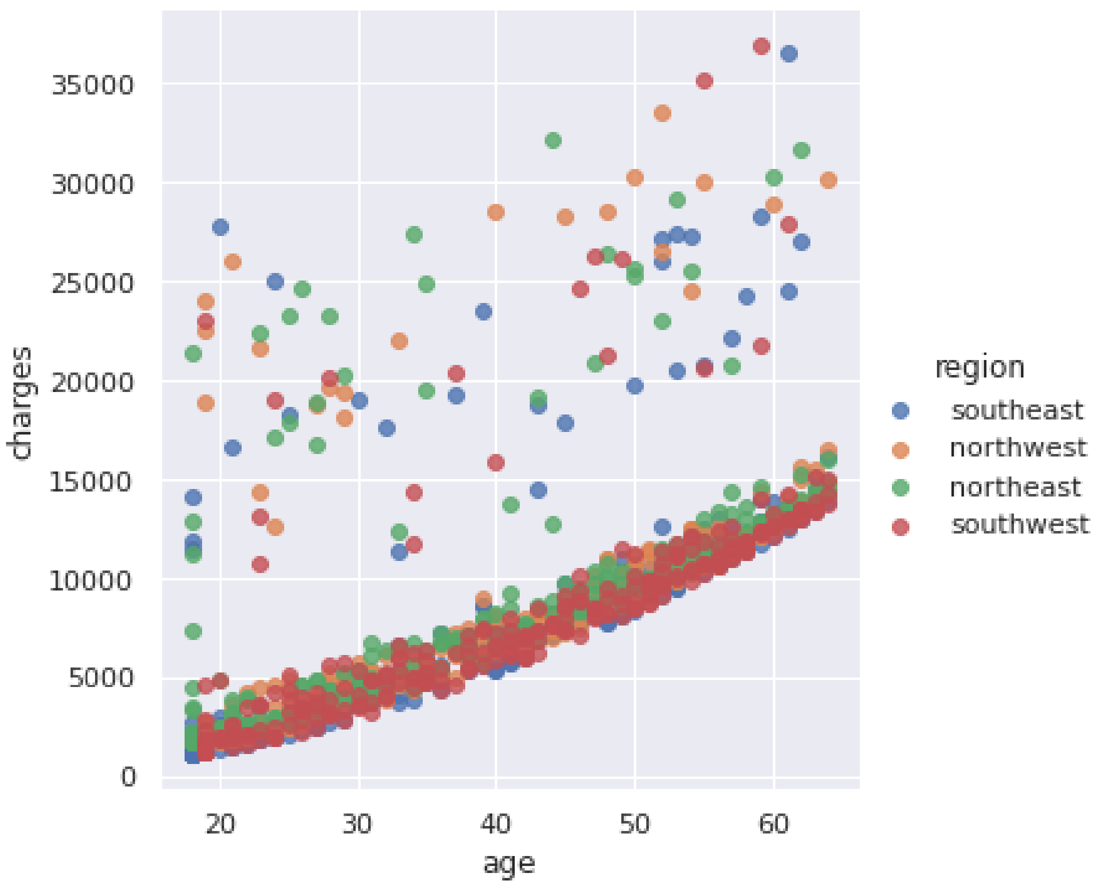
It seems important to split the smokers and non-smokers into different groups to fit a line trhough them. The comparison to the above lmplot with them combined shows a completely different gradient of the line of best fit. We can see that actually having a bmi of over 30 doesnt change the gradiant but the bias is significantly increased.

Finally, we confirm that there is no split of the non-smokers along the bmi = 30 line.

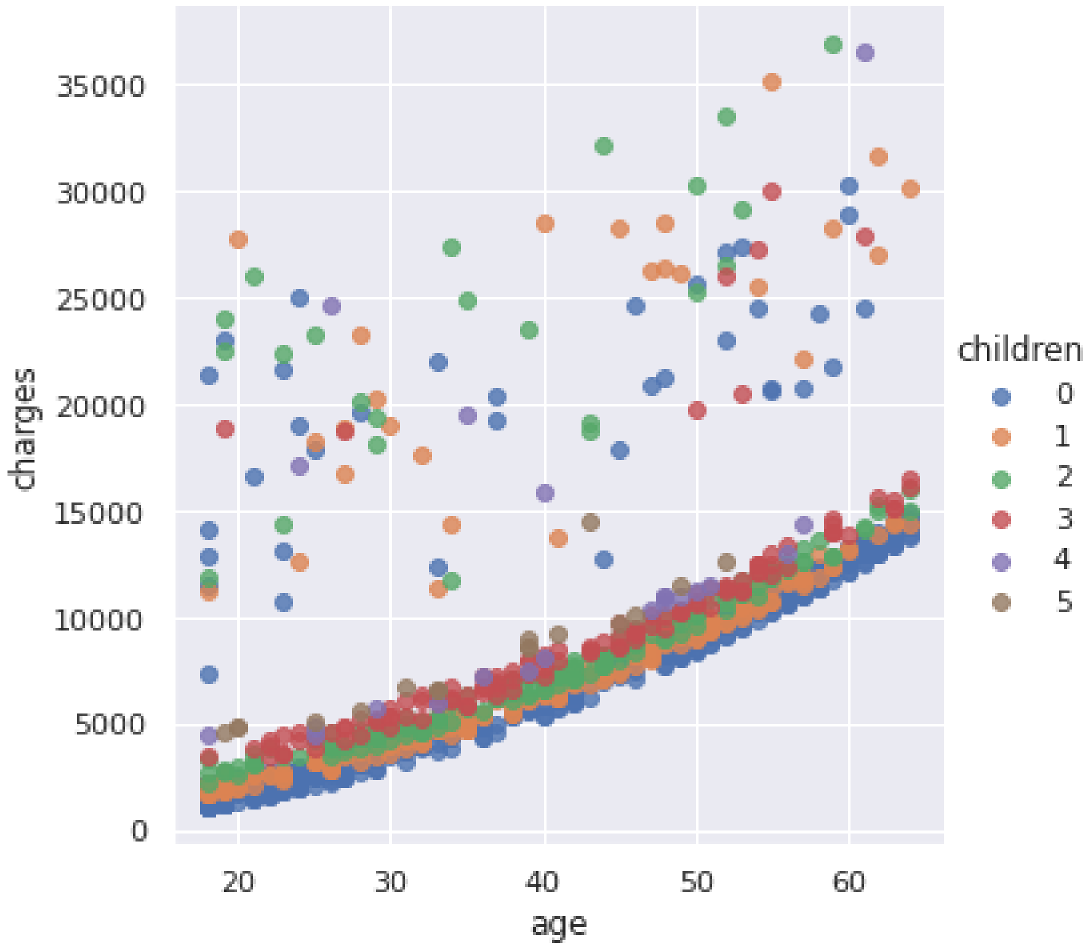
[9]:
```
sns.lmplot(data=df[df['smoker'] == 'no'], x='age', y='charges', hue='sex',␣
 ↪fit_reg=False)
plt.show()
sns.lmplot(data=df[df['smoker'] == 'no'], x='age', y='charges', hue='region',␣
 ↪fit_reg=False)
plt.show()
sns.lmplot(data=df[df['smoker'] == 'no'], x='age', y='charges', hue='children',␣
 ↪fit_reg=False)
plt.show()
```



35000
30000
25000
20000
15000
10000
5000
0
charges
20
30
40
50
60
age
sex
male
female



charges
35000
30000
25000
20000
15000
10000
5000
0
20
30
40
50
60
age
region
southeast
northwest
northeast
southwest



Here we are looking for a reason for the unusually high charges on some instances. We have taken the non-smokers but can find no correlation between any of our remaining features. This suggests a medical reason which is not in our data. We therefor will not be able to model this and it will certainly cause some error in our final model. However, the number of instances and the spread is far to consistent to assume these are outliers and remove them.

We can also see some exponential behaviour. This will need to be included when making a predictive model.

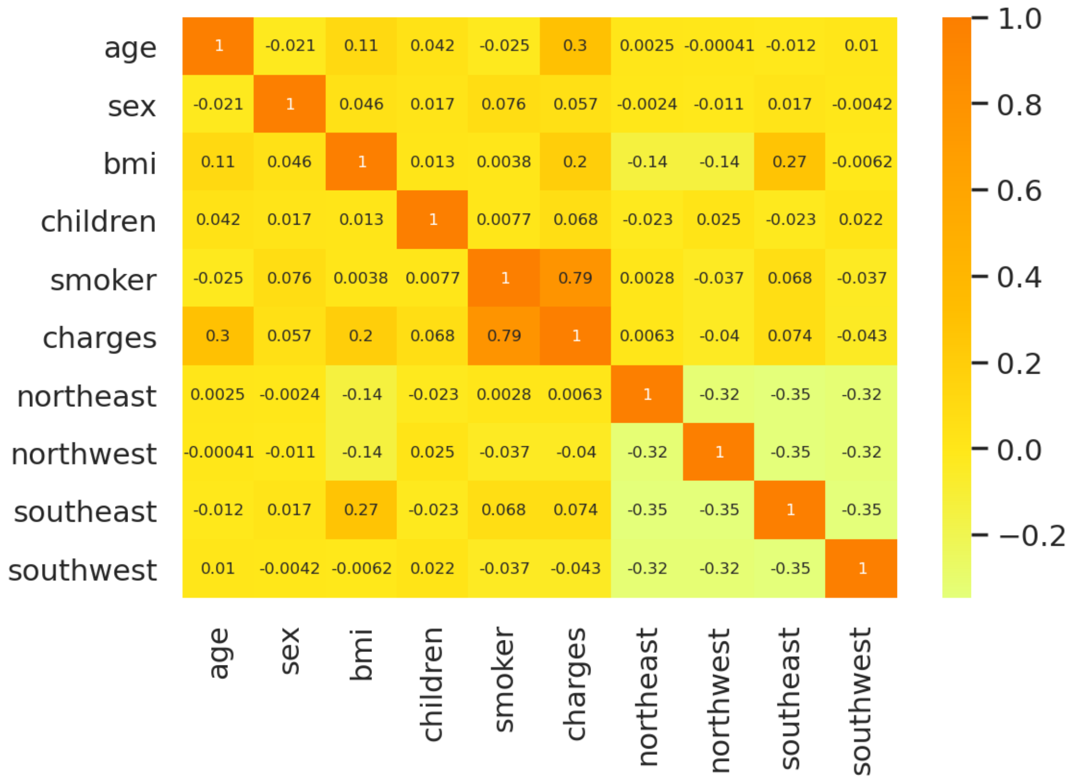
[10]:
```
# Showing the correlation for various subgroups within the data
print('bmi correlation (smokers) - ', df[df['smoker'] == 'yes']['charges'].
 ↪corr(df['bmi']), '\n')
print('bmi correlation (smokers & bmi > 30) - ',
      df[(df['smoker'] == 'yes') & (df['bmi'] > 30)]["charges"].corr(df['bmi']))
print('bmi correlation (smokers & bmi < 30) - ',
      df[(df['smoker'] == 'yes') & (df['bmi'] > 30)]['charges'].corr(df['bmi']),␣
 ↪'\n')
```

```
print('bmi correlation (non-smokers) - ', df[(df['smoker'] == 'no')]['charges'].
 ↪corr(df['bmi']))
print('age correlation (smokers) - ', df[df['smoker'] == 'yes']['charges'].
 ↪corr(df['age']))
print('age correlation (non-smokers) - ', df[(df['smoker'] == 'no')]['charges'].
 ↪corr(df['age']))
```

```
bmi correlation (smokers) -  0.8064806070155404

bmi correlation (smokers & bmi > 30) -  0.3650624941873683
bmi correlation (smokers & bmi < 30) -  0.3650624941873683

bmi correlation (non-smokers) -  0.08403654312833268
age correlation (smokers) -  0.3682244437307778
age correlation (non-smokers) -  0.6279467837664195
```

We can now see correlations for our groups. As indicated earlier, the correlation between bmi and charges for smokers is probably not so large but just has a shift upwards at bmi=30. Interestingly we see almost no correlation between charges and bmi for non-smokers.

[11]:
```
# Replacing yes/no with 1/0 to aid in modelling
df['smoker'].replace(('yes', 'no'), (1, 0), inplace=True)
df['sex'].replace(('male', 'female'), (1, 0), inplace=True)

# Converts categorical data with more than two categories into a set of new␣
 ↪features
# one for each different value in the old feature and only 1/0 as possible values
dummies = pd.get_dummies(df['region'])
df = pd.concat((df, dummies), axis = 1)
df = df.drop('region', axis = 1)

# Creating a Pearson correlation matrix to visualise correlations between␣
 ↪features
df_corr = df.drop(['log_charges', 'bmi_cat'], axis = 1)
corr = df_corr.corr()
fig, ax = plt.subplots(dpi=200)
sns.heatmap(corr, cmap = 'Wistia', annot= True, ax=ax, annot_kws={"size": 6})
plt.show()
```



There are no large correlations with charges other than bmi, age and obviously smoker. Here we are also looking for correlations between the features. We see a correlation between people living in the southeast and bmi which we should look out for when buliding the model.

[12]:
```
# A new df where we split up the number of children into new features to check␣
 ↪for correlations
df_children = df[['charges', 'children']]

dummies_children = pd.get_dummies(df_children['children'])
df_children = pd.concat((df_children, dummies_children), axis = 1)
df_children = df_children.drop('children', axis = 1)

print('0 children - ', df_children['charges'].corr(df_children[0]))
print('1 children - ', df_children['charges'].corr(df_children[1]))
print('2 children - ', df_children['charges'].corr(df_children[2]))
print('3 children - ', df_children['charges'].corr(df_children[3]))
print('4 children - ', df_children['charges'].corr(df_children[4]))
print('5 children - ', df_children['charges'].corr(df_children[5]))
```

```
0 children -  -0.06476047639409546
1 children -  -0.025180354353601806
2 children -  0.06963892513022256
```

```
3 children -  0.06279529451603874
4 children -  0.006613915717664698
5 children -  -0.04325837294882492
```

There are some slight correlations between the number of children and charges but no overall trend so we were right to split this feature up.

1.2 Univariate linear regression from scratch

Now I will demonstrate linear regression with just one variable from scratch. In this case we will choose a feature that we know has good correlation with charges. We will therefore choose age for non-smokers.

[13]:
```
def linear_func(X, th0, th1):
    return (X * th1) + th0

def cost_func(X, y, th0, th1):
    mm = len(X)
    return (1/2*mm) * np.sum((linear_func(X, th0, th1) - y)**2)

# The partial derivative of the cost function with respect to theta 0
def grad_descent_th0(X, y, alpha, th0, th1):
    mm = len(X)
    return (alpha / mm) * np.sum(linear_func(X, th0, th1) - y)

# The partial derivative of the cost function with respect to theta 1
def grad_descent_th1(X, y, alpha, th0, th1):
    mm = len(X)
    return (alpha / mm) * np.sum((linear_func(X, th0, th1) - y)*X)
```

- The linear func is just the function for a line.

$$y = \theta_1 X + \theta_0$$

- The cost function gives us an indication of the accuracy of our linear function. It compares the generated y values (from the given x values) with the given y values. A cost of 0 would indicate a very good fit to the data.
- grad_descent_th0 is the partial derivative of the cost function with respect to theta0 and timesed by alpha (the learning rate).
- grad_descent_th1 is the partial derivative of the cost function with respect to theta1 and timesed by alpha (the learning rate).

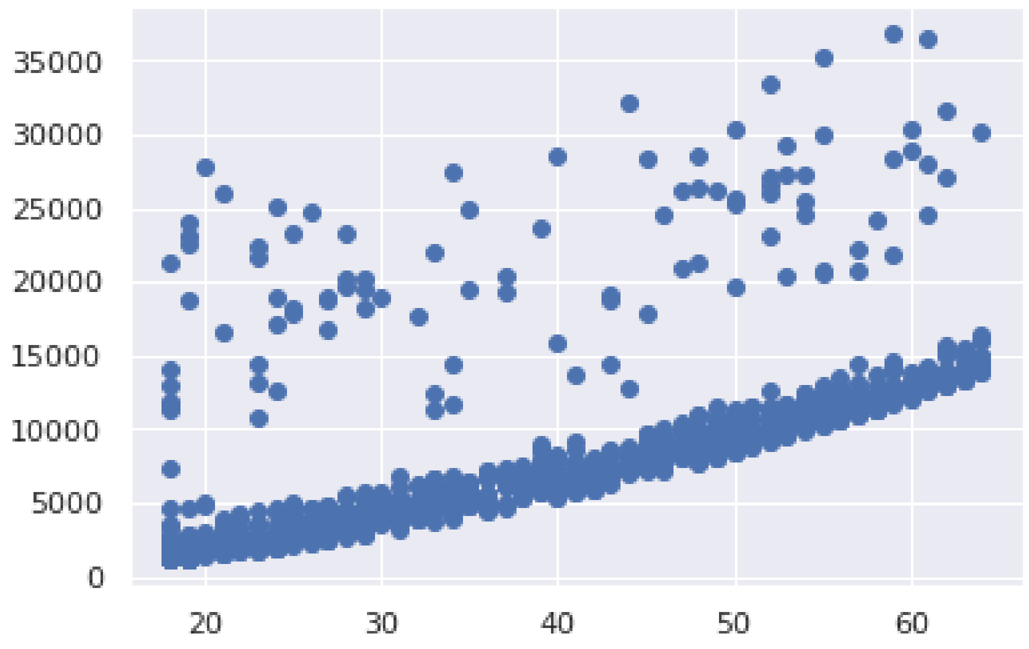
[14]:
```
X = df[df['smoker'] == 0]['age'].values
y = df[df['smoker'] == 0]['charges'].values
print(df.head())
print(X[:5])
print(y[:5])
```

```
   age  sex     bmi  children  smoker      charges  log_charges  bmi_cat  \
0   19    0  27.900         0       1  16884.92400     9.734176      0.0
```

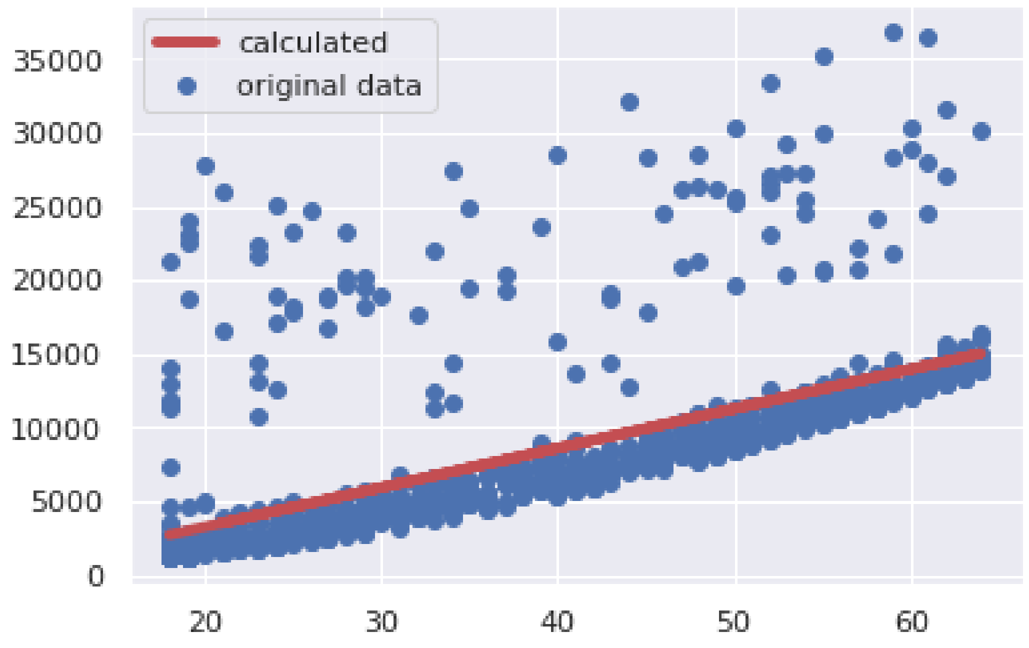
```
1   18    1  33.770         1       0   1725.55230     7.453302      1.0
2   28    1  33.000         3       0   4449.46200     8.400538      1.0
3   33    1  22.705         0       0  21984.47061     9.998092      0.0
4   32    1  28.880         0       0   3866.85520     8.260197      0.0

   northeast  northwest  southeast  southwest
0          0          0          0          1
1          0          0          1          0
2          0          0          1          0
3          0          1          0          0
4          0          1          0          0
[18 28 33 32 31]
[ 1725.5523   4449.462   21984.47061  3866.8552   3756.6216 ]
```

I have chosen a group of the data with a fairly good correlation and without obvious subgroups to enable a reasonably good fit to the data. With a univariate linear regression we can now find out the relationship between age and charges for non-smokers.

[15]:
```python
# Our chosen data set
plt.scatter(X, y)
plt.show()

# these are our inital guesses for the values of theta0 and theta1
# (they do not have to be good guesses)
th0 = -15
th1 = 16
# The optimization parameter controls how quickly we descend the gradient
alpha = 0.001
loops = 100000
print('initial cost - ', cost_func(X, y, th0, th1))

for ii in range(loops):
    # We must store the values in temporary holders so we can use
    # the same values for both gradiant descent parts
    temp_th0 = th0 - grad_descent_th0(X, y, alpha, th0, th1)
    temp_th1 = th1 - grad_descent_th1(X, y, alpha, th0, th1)
    th0 = temp_th0
    th1 = temp_th1

print('theta0 - ', th0)
print('theta1 - ', th1)
print('final cost - ', cost_func(X, y, th0, th1))

# Plotting the old data plus our predictions
plt.plot(X, linear_func(X, th0, th1), label='calculated', c='r', linewidth=4)
plt.scatter(X, y, label='original data', c='b')
plt.legend()
plt.show()
```



```
initial cost -  53993128354144.91
theta0 -  -2091.3953745523404
theta1 -  267.24834584340255
final cost -  12305294843659.188
```



We are only looking at health insurance charges for non-smokers aged 18 and over. Our base charge is -2091 and 267 is added for each year. This means that as a non-smoker, at 18 we would expect to pay 2719 and at age 80 we would expect to pay 19288. Obviously many other factors could alter this but looking only at age we can make these predictions.

Again we see the slight exponential dependence on age which we will take care of later in our model.

1.3 Multivariate linear regression from scratch

We now go back to our full data set to use all of these features to create a linear regression model.

[16]:
```
def linear_func_mv(x, weights):
    return  x @ weights.t()

def cost_func_mv(X, y, weights):
    mm = len(X)
    return (1/2*mm) * torch.sum((linear_func_mv(X, weights) - y)**2)
```

The linear_func_mv is our new model for a multivariate linear regression. In this case the matrix of input features are multiplied by the transpose of the weights vector. This now includes the bias as a sort of dummy feature which always equals 1. In this way the bias can be optimised with the weights. The cost function is the same but now takes the weight vector as an argument in the calculated y-value.

We use torch for its ability to treat our parameters, inputs and targets as tensors. Using torch we can compute gradients of the loss function for each partial derivative on the fly.

[17]:
```
def mv_linear_regression_alg(inputs, targets, loops, alpha):

    # require_grad = True in order to backwards compute derivatives of the␣
 ↪weights
    # number of weight coefficients equal to the number of features
    w = torch.randn(1, inputs.shape[1], requires_grad=True)

    print('initial cost - ', cost_func_mv(inputs, targets, w))
    print('Improving parameters...')

    cost_tracker = []

    t_mv1 = time.time()
    for i in range(loops):
        # Calculate the cost each time to analyse the current paramters
        cost = cost_func_mv(inputs, targets, w)
        # Adds the cost to a list to we ca see it change over time
        cost_tracker.append(cost_func_mv(inputs, targets, w).detach().numpy())
        # Calculating the partial derivatives
        cost.backward()
        # stop autograd from tracking history on Tensor
        with torch.no_grad():
            w -= w.grad * alpha
            # Resetting calculated derivatives to 0
            w.grad.zero_()
    t_mv2 = time.time()

    print(f'...time taken is {t_mv2 - t_mv1} s to complete {loops} loops')
    print('final cost - ', cost_func_mv(inputs, targets, w))

    return w, cost_tracker
```

This function uses PyTorch to automatically compute gradients of each parameter. The cost tracker is a way for us to show how the cost is changing over iterations. If it is not descending we can reduce alpha. If it does not descend to a minimum, we can increase alpha or increase number of loops.

[18]:
```
df = pd.read_csv('./insurance.csv')

instances_tot = df.shape[0]

# Splitting our dataset into a test and train to test our model and avoid over␣
 ↪parameterisation
df_train = df[:int((instances_tot * 4)/5)]
df_test = df[int((instances_tot * 4)/5):]

# Inputting the features we want for our model
df_edit = pd.DataFrame()
bias = [1] * int((instances_tot * 4)/5)
df_edit['bias'] = bias
df_edit['smoker'] = df_train['smoker']
df_edit['bmi'] = df_train['bmi']
df_edit['age'] = df_train['age']
df_edit['age^2'] = df_train['age'] ** 2
df_edit['log_charges'] = np.log(df_train['charges'])

df_edit['bmi_cat'] = np.nan
df_edit.loc[df_edit['bmi'] <= 30, 'bmi_cat'] = 0
df_edit.loc[df_edit['bmi'] > 30, 'bmi_cat'] = 1

df_edit['smoker'].replace(('yes', 'no'), (1, 0), inplace=True)
df_edit['age'] = df_edit['age'] / (df_edit['age'].max() - df_edit['age'].min())
df_edit['age^2'] = df_edit['age^2'] / (df_edit['age^2'].max() - df_edit['age^2'].
 ↪min())
df_edit['bmi'] = df_edit['bmi'] / (df_edit['bmi'].max() - df_edit['bmi'].min())

# splitting the features and the target ot create our inputs
df_inputs = df_edit.drop('log_charges', axis=1)
```

```
df_targets = pd.DataFrame()
df_targets['targets'] = df_edit['log_charges']

print(df_inputs.head())
print(df_targets.head())
```

```
   bias  smoker       bmi       age     age^2  bmi_cat
0     1       1  0.761879  0.413043  0.095705      0.0
1     1       0  0.922174  0.391304  0.085896      1.0
2     1       0  0.901147  0.608696  0.207847      1.0
3     1       0  0.620016  0.717391  0.288706      0.0
4     1       0  0.788640  0.695652  0.271474      0.0
    targets
0  9.734176
1  7.453302
2  8.400538
3  9.998092
4  8.260197
```

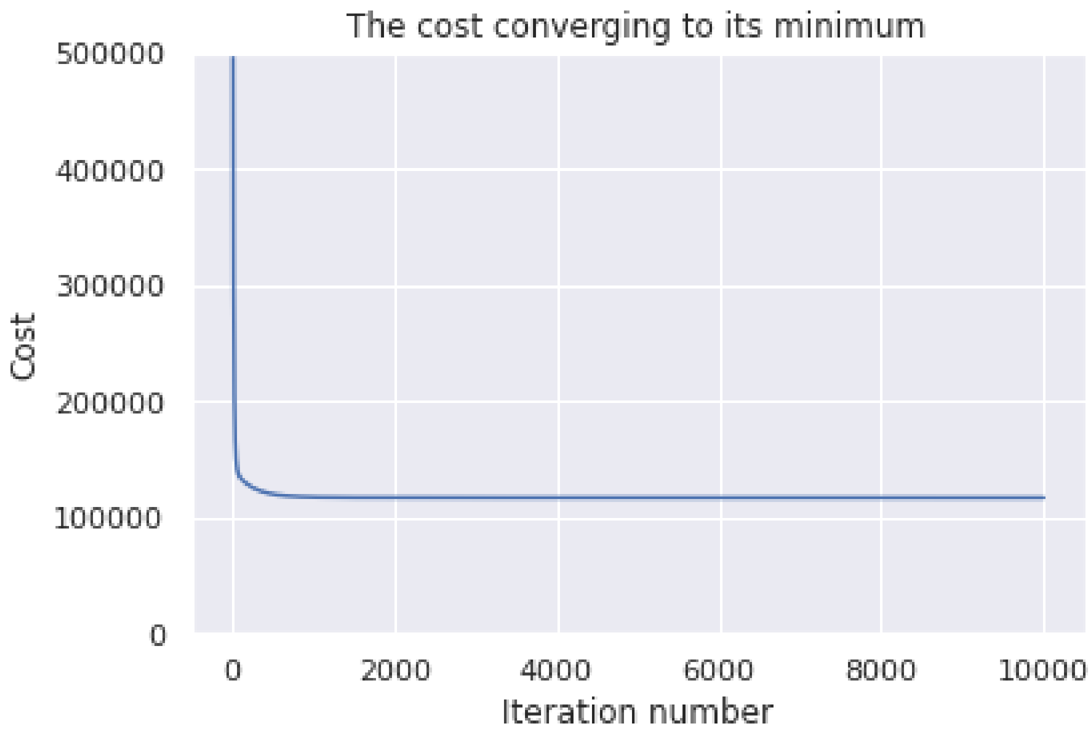
Here we set up the health insurance data ready for linear regression.

- The first 'feature' is the bias. Any features which are only 0 or 1 act as a sort of bias only applied to the instances with a 1. The bias will then be whatever weight corresponds to that features. Our 'bias' feature is 1 for every instance and so it acts like a lypical bias.
- The second feature is 'smoker' which is either 0 or 1. This assumes there is a bias which is added for being a smoker.
- 'bmi' and 'age' are both continuous features. These have been scaled to be be at a similar range to the categorical features) by dividing by the range.
- age^2 is included as a feature as there appears to be some exponential component to the age component to cost. This can be treated as just another linear feature and is again scaled down to the a similar range.
- The final feature is bmi_cat which is whether the bmi is over 30 or not. We saw earlier that, at least for smokers, these two groups seem to be treated differently.
- 'sex', 'region' and number of children have all been omitted as there is very little correlation to charges and in some cases there is a correlation with our chosen features.

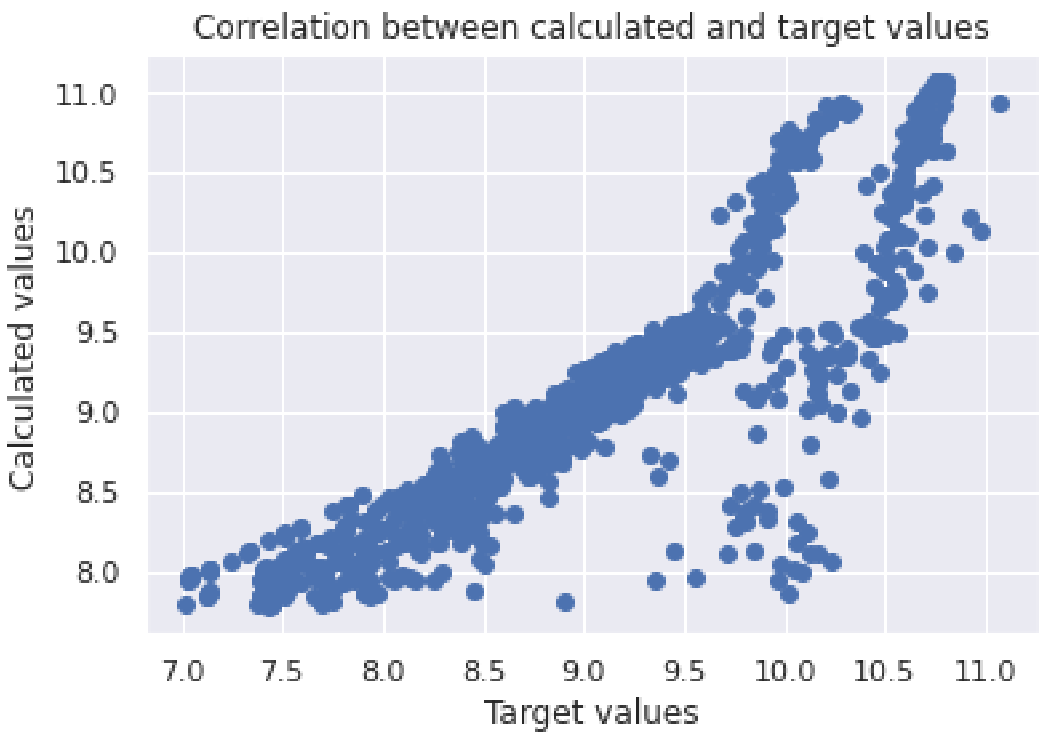
The target has been changed to $\log_e charges$ to give it a more normal distribution.

[19]:
```
# Our inputs must be torch tensors
inputs = torch.tensor(df_inputs.values).float()
targets = torch.tensor(df_targets.values).float()
loops = 10000
alpha = 3e-7
# Calculating our parameters
w, costs = mv_linear_regression_alg(inputs, targets, loops, alpha)

print('\nRESULTS\n')
plt.plot(costs)
plt.title('The cost converging to its minimum')
plt.xlabel('Iteration number')
plt.ylabel('Cost')
plt.ylim(0, 5e5)
plt.show()
print(df_inputs.columns.tolist())
print(w)
# Calculating our values for the target from our calculated parameters
df_targets['results'] = linear_func_mv(inputs, w).detach().numpy()
print(df_targets.head())
print(df_targets['targets'].corr(df_targets['results']))

plt.scatter(df_targets['targets'].values, df_targets['results'].values)
plt.title('Correlation between calculated and target values')
plt.xlabel('Target values')
plt.ylabel('Calculated values')
plt.show()
```

```
initial cost -  tensor(81324480., grad_fn=<MulBackward0>)
Improving parameters...
...time taken is 1.7112805843353271 s to complete 10000 loops
final cost -  tensor(116898.9688, grad_fn=<MulBackward0>)

RESULTS
```



```
['bias', 'smoker', 'bmi', 'age', 'age^2', 'bmi_cat']
tensor([[ 6.5443,  1.5221,  0.1308,  3.3665, -1.7628,  0.1180]],
       requires_grad=True)
    targets   results
0  9.734176  9.387901
1  7.453302  7.948876
2  8.400538  8.462996
3  9.998092  8.531569
4  8.260197  8.510812
0.8718650440685164
```

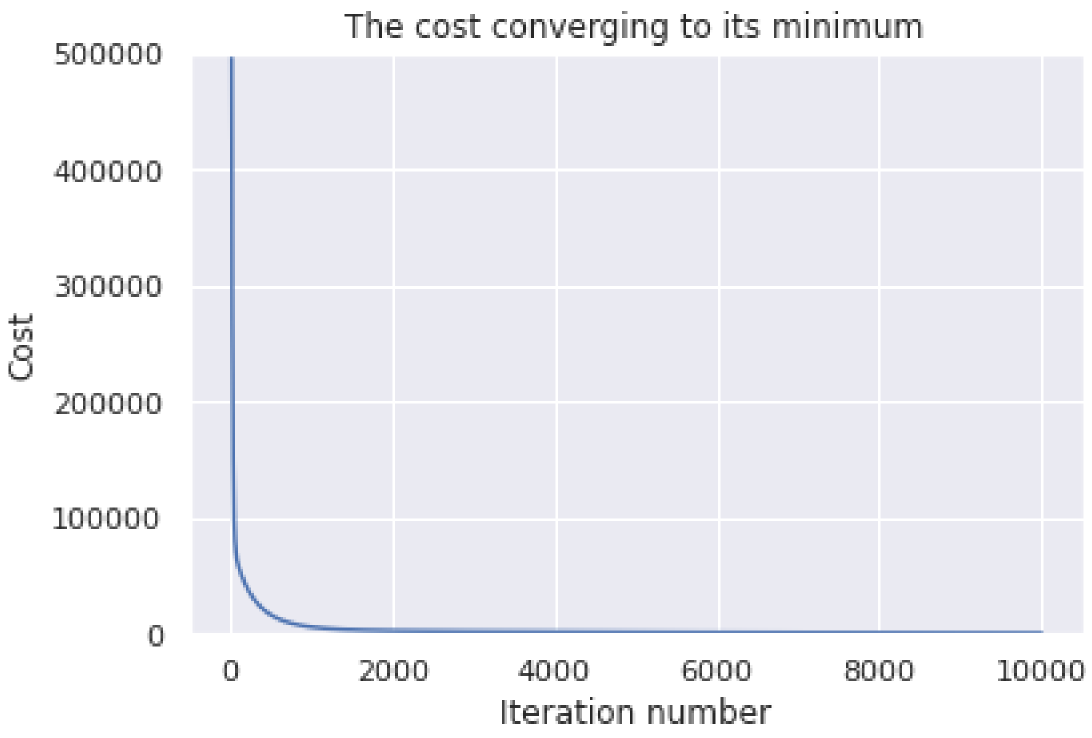


This fit seemds very good with a Pearson correlation factor of 0.87. The cost function runs down to its minimum consistently showing the gradient descent has worked properly. Our calculated values match the target values reasonably well but there seems to be a couple of trends not quite captured by our model as the error seems systematic. There is also a second group of instances which don't seem to be captured anywhere near as well.

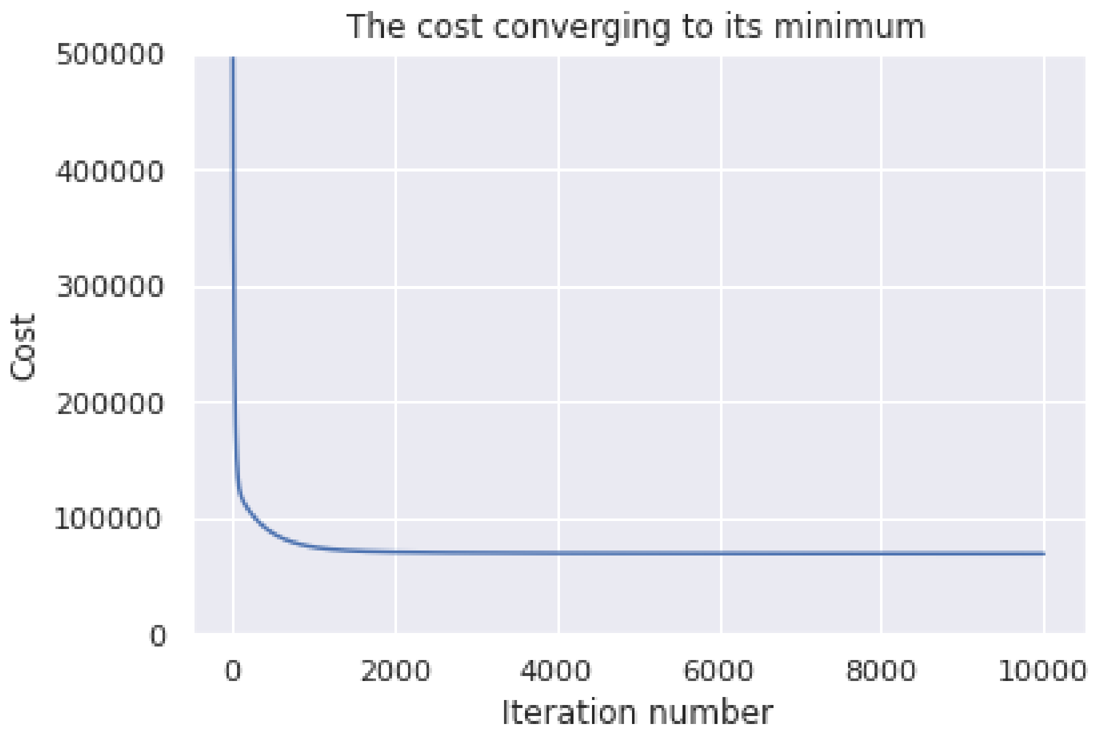
My theory here is that the smokers and non smokers are treated very differently by the insurance company and there is more than a simple bias between them. For instance, we know that for smokers there is a increase in charge at bmi over 30 but this is not the case for non-smokers. I will therefore split smokers and non smokers, treat them differently and combine them at the end.

[20]:
```
# Creating our smokers group and forming inputs and targets
df_smokers_i = df_edit[df_edit['smoker'] == 1]
df_smokers_t = pd.DataFrame()
df_smokers_t['targets'] = df_smokers_i['log_charges']
df_smokers_i = df_smokers_i.drop(['log_charges', 'smoker'], axis=1)

print('\nSmokers gradient descent\n')
inputs_s = torch.tensor(df_smokers_i.values).float()
targets_s = torch.tensor(df_smokers_t.values).float()
loops = 10000
alpha = 3e-7
w_s, costs_s = mv_linear_regression_alg(inputs_s, targets_s, loops, alpha)

plt.plot(costs_s)
plt.title('The cost converging to its minimum')
plt.xlabel('Iteration number')
plt.ylabel('Cost')
plt.ylim(0, 5e5)
plt.show()

# Creating our non smokers group and forming inputs and targets
df_nonsmokers_i = df_edit[df_edit['smoker'] == 0]
df_nonsmokers_t = pd.DataFrame()
df_nonsmokers_t['targets'] = df_nonsmokers_i['log_charges']
df_nonsmokers_i = df_nonsmokers_i.drop(['log_charges', 'smoker'], axis=1)

print('\nNon-smokers gradient descent\n')
inputs_ns = torch.tensor(df_nonsmokers_i.values).float()
targets_ns = torch.tensor(df_nonsmokers_t.values).float()
loops = 10000
alpha = 3e-7
w_ns, costs_ns = mv_linear_regression_alg(inputs_ns, targets_ns, loops, alpha)

plt.plot(costs_ns)
plt.title('The cost converging to its minimum')
plt.xlabel('Iteration number')
plt.ylabel('Cost')
plt.ylim(0, 5e5)
plt.show()
```

```
Smokers gradient descent

initial cost -  tensor(3364059.7500, grad_fn=<MulBackward0>)
Improving parameters...
...time taken is 1.6598751544952393 s to complete 10000 loops
final cost -  tensor(872.2900, grad_fn=<MulBackward0>)
```



```
Non-smokers gradient descent

initial cost -  tensor(53681412., grad_fn=<MulBackward0>)
Improving parameters...
...time taken is 1.7044296264648438 s to complete 10000 loops
final cost -  tensor(69005.4609, grad_fn=<MulBackward0>)
```



Both smokers and non-smokers converge nicely with a gradient descent which always decreases. The final cost for smokers is very low showing we have a very good model for this category. For non-smokers it is not quite so low but is still much lower than the final cost when both categories are treated the same.

[21]:
```
print('\nSMOKER RESULTS\n')
# looking at the names of the features with the calculated parameters for them
print(df_smokers_i.columns.tolist())
print(w_s)
df_smokers_t['results'] = linear_func_mv(inputs_s, w_s).detach().numpy()

print('\nNON SMOKER RESULTS\n')
print(df_nonsmokers_i.columns.tolist())
print(w_ns)
df_nonsmokers_t['results'] = linear_func_mv(inputs_ns, w_ns).detach().numpy()
```

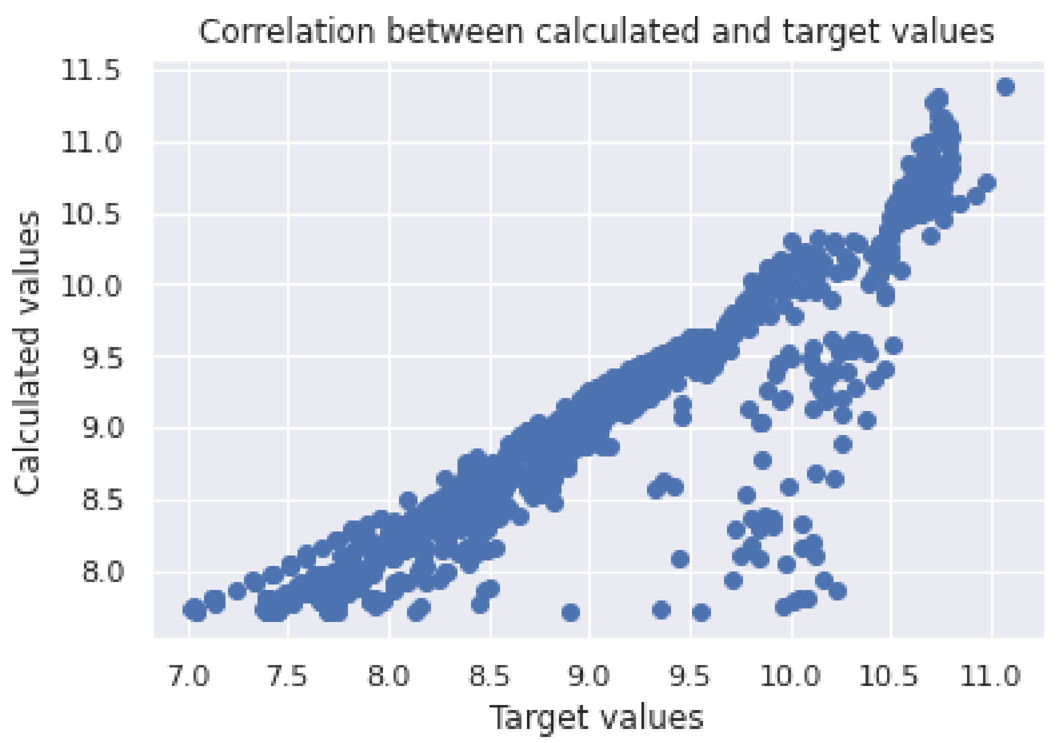
```
SMOKER RESULTS

['bias', 'bmi', 'age', 'age^2', 'bmi_cat']
tensor([[ 7.5425,  1.9461,  2.1695, -1.7450,  0.1330]], requires_grad=True)

NON SMOKER RESULTS
```

```
['bias', 'bmi', 'age', 'age^2', 'bmi_cat']
tensor([[ 6.4664, -0.1217,  3.8574, -1.9582,  0.0418]], requires_grad=True)
```

We can see the results of treating these two groups separately. The smoker bias is now shown in the different overall bias for each. The correlation with bmi is completely different with non-smokers having almost no correlatin with bmi. There also appears to be a different correlation with age across the two groups with there being more exponential character in the smokers. This makes sense as smoking related health issues are much more likely to appear in older age. We also see a small bmi>30 bias in the smoker category as we expected.

[22]:
```python
# Combining our final results for smokers and non smokers
df_final_i = pd.concat([df_nonsmokers_i, df_smokers_i])
df_final_i = df_final_i.sort_index()
df_final_t = pd.concat([df_nonsmokers_t, df_smokers_t])
df_final_t = df_final_t.sort_index()
print(df_final_t.head())
print(df_final_t['targets'].corr(df_final_t['results']))

plt.scatter(df_final_t['targets'].values, df_final_t['results'].values)
plt.title('Correlation between calculated and target values')
plt.xlabel('Target values')
plt.ylabel('Calculated values')
plt.show()
```

```
    targets   results
0  9.734176  9.754260
1  7.453302  7.737223
2  8.400538  8.339545
3  9.998092  8.592908
4  8.260197  8.522279
0.9021889308658362
```



We now see the results of our new model. The line is much more accurately up the middle with some obvious subgroups at the higher charge range. However these have now been treated appropriately as they are falling on the diagonal line. There are still some values which have a much lower calculated value than the target. Based on the cost functions these are probably from the non-smokers primarily and are likely the outliers that we saw before. I could not find anything in the data given to explain these higher charges and so its not surprising that the model does not accurately predict them.

[23]:
```
# Separating the inputs and the target data in our test group
df_targets_test = pd.DataFrame()
df_targets_test['targets'] = df_test['charges']

df_inputs_test = df_test.drop('charges', axis=1)

print(df_inputs_test.head())
print(df_targets_test.head())
```

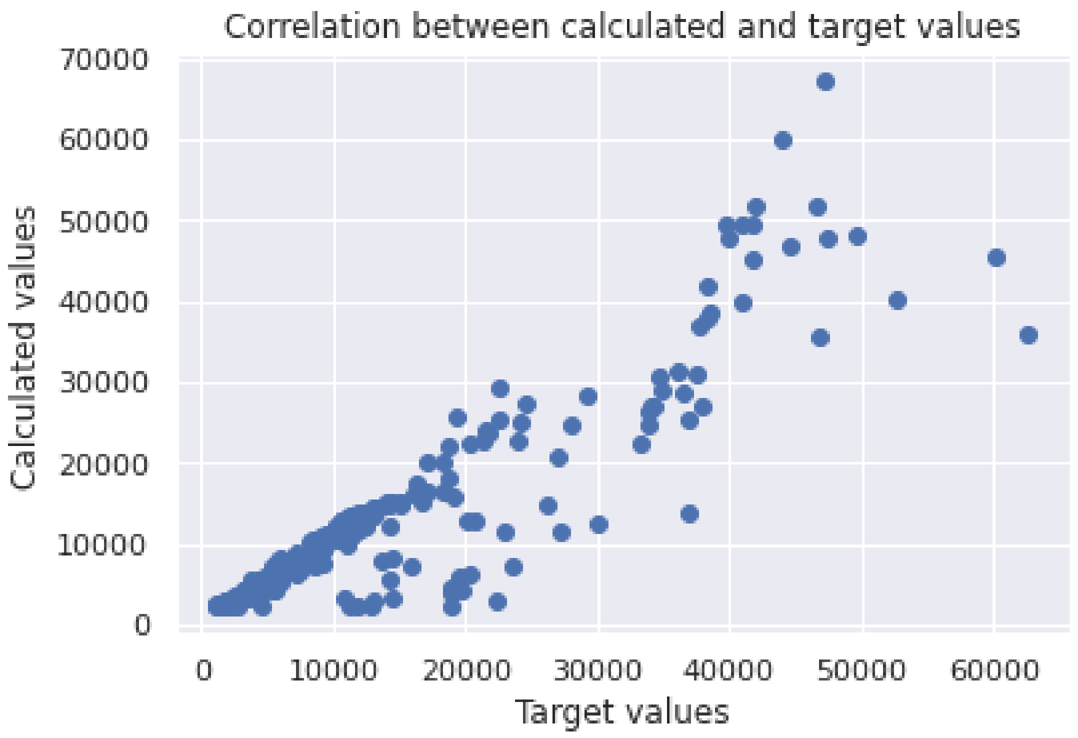
```
      age     sex     bmi  children smoker     region
1070   37    male  37.070         1    yes  southeast
1071   63    male  31.445         0     no  northeast
1072   21    male  31.255         0     no  northwest
1073   54  female  28.880         2     no  northeast
1074   60  female  18.335         0     no  northeast
          targets
```

```
1070   39871.70430
1071   13974.45555
1072    1909.52745
1073   12096.65120
1074   13204.28565
```

We will now look at our test dataframe to give an indication on how we would use our model to predict charges. The data would be given in this form so we will create a function which gives us the appropriate charges from this.

[24]:
```
def predict_changes(dfin, dfout):

    # The old indexing creates problems when operating across different␣
↪dataframes
    dfin = dfin.reset_index(drop=True)
    dfout = dfout.reset_index(drop=True)

    # We dont want the smoker feature in our inputs but we still need to to␣
↪treat our two groups separately
    dfout['smoker'] = dfin['smoker']

    # Creating our inputs in the same way as we did to train the model
    dfin_edit = pd.DataFrame()
    dfin_edit['bias'] = [1] * dfin.shape[0]

    dfin_edit['bmi'] = dfin['bmi']
    dfin_edit['age'] = dfin['age']
    dfin_edit['age^2'] = dfin['age'] ** 2
    dfin_edit['bmi_cat'] = np.nan
    dfin_edit.loc[dfin_edit['bmi'] <= 30, 'bmi_cat'] = 0
    dfin_edit.loc[dfin_edit['bmi'] > 30, 'bmi_cat'] = 1

    dfin_edit['age'] = dfin_edit['age'] / (dfin_edit['age'].max() -␣
↪dfin_edit['age'].min())
    dfin_edit['age^2'] = dfin_edit['age^2'] / (dfin_edit['age^2'].max() -␣
↪dfin_edit['age^2'].min())
    dfin_edit['bmi'] = dfin_edit['bmi'] / (dfin_edit['bmi'].max() -␣
↪dfin_edit['bmi'].min())

    # Go through each row, check if they are smoker, and apply the correct␣
↪parameters accordingly
    dfout['results_log'] = np.nan
    for index, row in dfin_edit.iterrows():
        if dfout.loc[index, 'smoker'] == 'yes':
            xx = torch.tensor(row.values).float()
            dfout.loc[index, 'results_log'] = (xx @ w_s.t()).detach().numpy()[0]
        if dfout.loc[index, 'smoker'] == 'no':
            xx = torch.tensor(row.values).float()
            dfout.loc[index, 'results_log'] = (xx @ w_ns.t()).detach().numpy()[0]

    # Our model predicts log(charges). We want to see what the actual charges are
    dfout['results'] = math.e ** dfout['results_log']

    print(dfout['targets'].corr(dfout['results']))
    plt.scatter(dfout['targets'].values, dfout['results'].values)
    plt.title('Correlation between calculated and target values')
    plt.xlabel('Target values')
    plt.ylabel('Calculated values')
    plt.show()

    # returns the predicted charges as a list (not part of a dataframe)
    return dfout['results'].values


df_test['predicted_charges'] = predict_changes(df_inputs_test, df_targets_test)

print(df_test.head())
```

```
0.9062148212670792
```



```
      age     sex     bmi  children smoker     region      charges  \
1070   37    male  37.070         1    yes  southeast  39871.70430
1071   63    male  31.445         0     no  northeast  13974.45555
1072   21    male  31.255         0     no  northwest   1909.52745
1073   54  female  28.880         2     no  northeast  12096.65120
1074   60  female  18.335         0     no  northeast  13204.28565

      predicted_charges
1070       47747.938747
1071       15143.723208
1072        2794.862787
1073       11897.672277
1074       14292.246378
```

A similar process is done here as when our data was first prepared for liner regression. We change the input data to the same form as used in our model so that the weights correspond to the appropriate features.

Our predicted values match the target values very well showing we have created a good model for predicting health insurance charges. We can make the prediction that a 37 year old man with a bmi of 37, living in the southeast, with 1 child and who smokes, will have to pay around 48000.