In [79]:
```
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
import scipy.stats as stats
import statsmodels.api as sm
from statsmodels.stats.proportion import proportions_ztest
import pylab
import warnings
warnings.simplefilter(action='ignore', category=FutureWarning)
```

Math 189 HW1 smoking vs. pregancy

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This project researches the difference between the babie' weights of smoker mother and those of non-smoker mother

Reading Data & Cleaning Data

In [80]:
```
temp = open('babies23-17em2pa-1r6aufk.txt').read().splitlines()
templist = []
for i in temp:
    templist += [i.split(' ')]
data_2_raw = []
for i in templist:
    lst = []
    for j in i:
        if j != '':
            lst += [j]
    data_2_raw += [lst]
    lst = []
```

In [81]:
```
data_2 = pd.DataFrame(data_2_raw[1:], columns = data_2_raw[0])
```

In [82]:
```
data_2 = data_2.applymap(lambda x: pd.to_numeric(x))
data_2.columns = ['id', 'pluralty', 'outcome', 'date', 'gestation', 'sex',
       'race', 'age', 'ed', 'ht', 'wt2', 'drace', 'dage', 'ded', 'dht', 'dw
       'marital', 'inc', 'smoke', 'time', 'number']
```

Comparison Set 1

Non-smoker Mothers vs. Mothers who smoke at pregancy

(below will be denoted as Non-Smokers & Smokers for simplicity)

In [51]:
```
non_smoking = data_2.loc[(data_2['smoke'] == 0) |(data_2['smoke'] == 3) | (
smoking = data_2.loc[(data_2['smoke'] > 0) & (data_2['smoke'] < 2)]
baby_weights = pd.DataFrame(
        {
            "Babies' Birth Weights born to Non-smoking in pregancy (in ounc
            "Babies' Birth Weights born to pregant smoking mothers (in ounc
        }
)
baby_weights
```

Out[51]:

	Babies' Birth Weights born to Non-smoking in pregancy (in ounce)	Babies' Birth Weights born to pregant smoking mothers (in ounce)
count	742.000000	484.000000
mean	123.047170	114.109504
std	17.398689	18.098946
min	55.000000	58.000000
25%	113.000000	102.000000
50%	123.000000	115.000000
75%	134.000000	126.000000
max	176.000000	163.000000

In [52]:
```
smoking['wt1'].skew()
```

Out[52]: -0.033699506713282625

In [53]:
```
non_smoking['wt1'].skew()
```

Out[53]: -0.18736306526595664

In [54]:
```
stats.kurtosis(smoking['wt1'], fisher = False)
```

Out[54]: 2.988032478793404

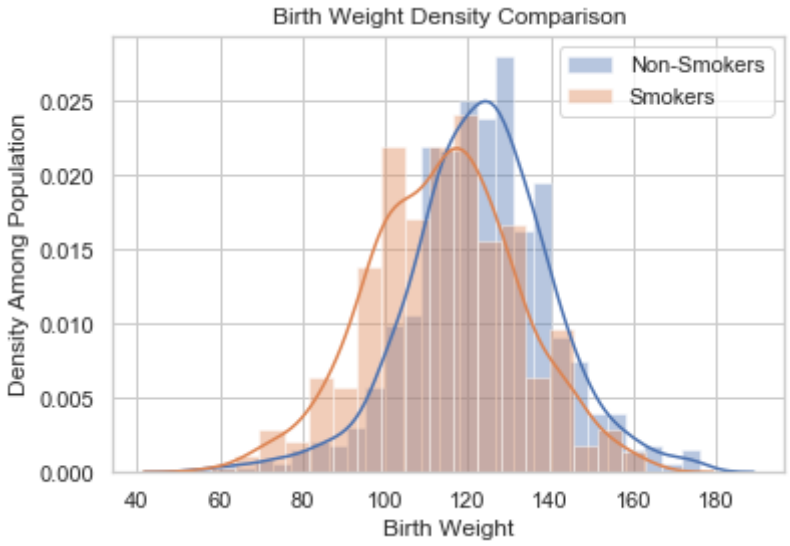
In [55]:
```
stats.kurtosis(non_smoking['wt1'], fisher = False)
```

Out[55]: 4.037060312433822

Graphical Comparison

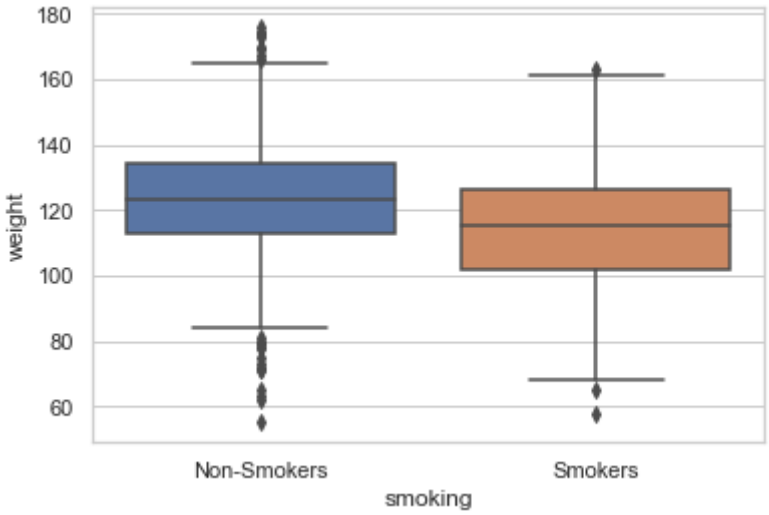
In [56]:
```
sns.distplot(non_smoking['wt1'], label="Non-Smokers")
sns.distplot(smoking['wt1'], label="Smokers")
plt.legend()
plt.title('Birth Weight Density Comparison')
plt.xlabel('Birth Weight')
plt.ylabel('Density Among Population')
```

Out[56]:
```
Text(0, 0.5, 'Density Among Population')
```

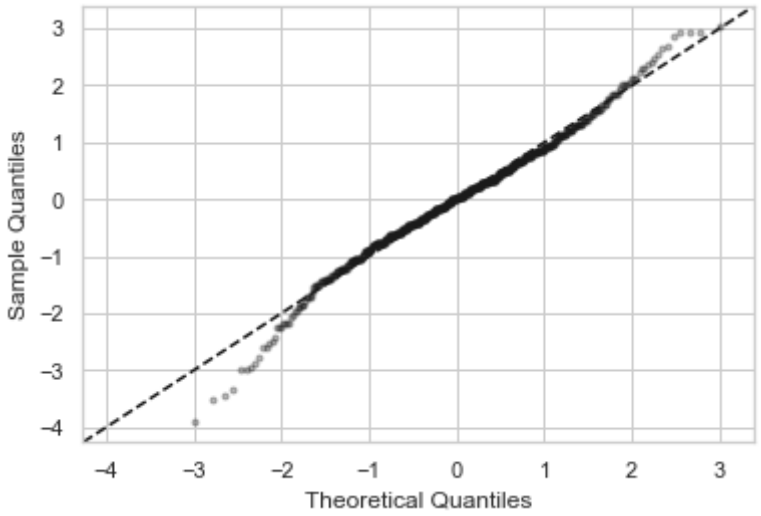


In [57]:
```
grouped_df = pd.DataFrame(
             {
                 'weight' : non_smoking['wt1'],
                 'smoking': ['Non-Smokers' for i in non_smoking['wt1']]
             }
)
grouped_df1 = pd.DataFrame(
             {
                 'weight' : smoking['wt1'],
                 'smoking': ['Smokers' for i in smoking['wt1']]
             }
)
cdf = pd.concat([grouped_df, grouped_df1])
sns.boxplot(x ='smoking', y ='weight', data = cdf)
```

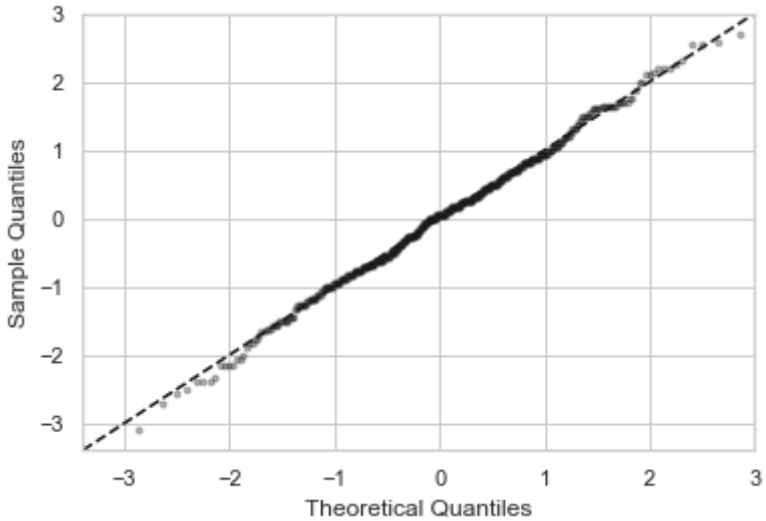
Out[57]: <matplotlib.axes._subplots.AxesSubplot at 0x116596710>



In [58]:
```
#QQ plot for non smoking
test = non_smoking['wt1']
pp = sm.ProbPlot(test, fit=True)
qq = pp.qqplot(marker='.', markerfacecolor='k', markeredgecolor='k', alpha=
sm.qqline(qq.axes[0], line='45', fmt='k--')
plt.show()
```



In [59]:
```
#QQ plot for smoking
test = smoking['wt1']
pp = sm.ProbPlot(test, fit=True)
qq = pp.qqplot(marker='.', markerfacecolor='k', markeredgecolor='k', alpha=
sm.qqline(qq.axes[0], line='45', fmt='k--')
plt.show()
```



Data Validation

We found non-smoking group's data is not normally distributed. We will process a normality check for our smoking at pregnant birth weight data set and non-smoker babies' birth weight group via Chi-Square GOF test

In [60]:
```
k2, p = stats.normaltest(non_smoking['wt1'])

alpha = 1e-3
print("p = {:g}".format(p))
if p < alpha:
    print("The null hypothesis can be rejected,")
else:
    print("The null hypothesis cannot be rejected,  the dataset is normally
```

```
p = 2.50963e-05
The null hypothesis can be rejected,
```

In [62]:
```
k2, p = stats.normaltest(smoking['wt1'])

alpha = 1e-3
print("p = {:g}".format(p))
if p < alpha:  # null hypothesis: x comes from a normal distribution
    print("The null hypothesis can be rejected,")
else:
    print("The null hypothesis cannot be rejected,  the dataset is normally
```

```
p = 0.948874
The null hypothesis cannot be rejected,  the dataset is normally distribu
ted
```

T test

test the mean difference of two data sets

In [63]:
```
print('p-val is', stats.ttest_ind(non_smoking['wt1'], smoking['wt1'], equal
```

```
p-val is 3.5241301163155265e-17
```

Low Weight cut-off point w/ Chi-square independence Test

https://www.chop.edu/conditions-diseases/low-birthweight (https://www.chop.edu/conditions-diseases/low-birthweight), The weight is compared with the baby's gestational age and recorded in the medical record. A birthweight less than 2,500 grams (88.1849 ounces) is diagnosed as low birthweight. Babies weighing less than 1,500 grams (52.91094 ounces) at birth are considered very low birthweight.

cut-off point validation by chi-square test

In [66]:
```
def catogorize(non_smoking, smoking, low_weight):
    non_smoking_nlow = len([i for i in non_smoking if i <= low_weight])
    smoking_nlow = len([i for i in smoking if i <= low_weight])
    non_smoking_nn = len([i for i in non_smoking if i > low_weight])
    smoking_nn = len([i for i in smoking if i > low_weight])
    output = pd.DataFrame({
            'low weight': [non_smoking_nlow, smoking_nlow],
            'normal weight:': [non_smoking_nn, smoking_nn]}, index = ['non
    )
    return output
```

In [84]:
```
lst = []
pvals = []
for i in range(75,116, 5):
    contingency_table = catogorize(non_smoking['wt1'], smoking['wt1'], i)
    f_obs = np.array([contingency_table.iloc[0][0:].values,
                      contingency_table.iloc[1][0:].values])
    lst += [i]
    pvals += [stats.chi2_contingency(f_obs)[0:3][1]]
output = pd.DataFrame(
        {
            'p-value': pvals
        }, index = lst
)
output.index.name = 'Cut-off point'
output.to_csv('chi-square_set1.csv')
output
```

Out[84]:

Cut-off point	p-value
75	1.483697e-01
80	1.193173e-01
85	3.455917e-02
90	2.999904e-04
95	2.950961e-07
100	1.410511e-12
105	6.779451e-16
110	4.794657e-15
115	1.442709e-13

In [72]:
```
non_smoking_n = len(non_smoking['wt1'])
non_smoking_ln = len([i for i in non_smoking['wt1'] if i <= 88.1849])
smoking_n = len(smoking['wt1'])
smoking_ln = len([i for i in smoking['wt1'] if i <= 88.1849])

non_smoking_lprop = non_smoking_ln / non_smoking_n
smoking_lprop = smoking_ln / smoking_n
```

In [73]:
```
smoking_lprop
```

Out[73]:
```
0.08264462809917356
```

In [74]:
```
non_smoking_lprop
```

Out[74]:
```
0.03099730458221024
```

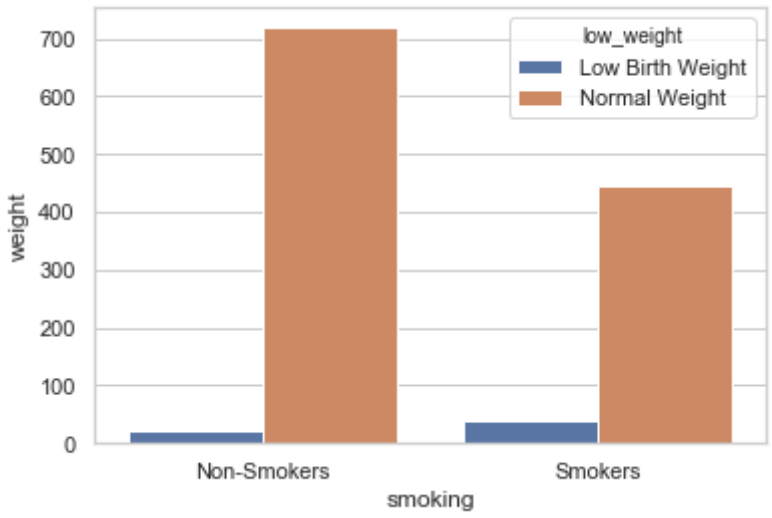
use cut-off point of 88.2 as low weight. To see the distribution plot.

low weight graph for original data set

In [75]:
```
proportion_low_weight_table = pd.DataFrame(
                            {
                                'Non-Smokers': non_smoking_lprop,
                                'Smokers': smoking_lprop
                            }
,index = ['Proportion'])
```

In [76]:
```
cdf['low_weight'] = cdf['weight'].apply(lambda x: 'Low Birth Weight' if x <
cdf1 = cdf.groupby(['low_weight','smoking']).count().reset_index()
```

In [77]:
```
sns.set(style="whitegrid")
tips = sns.load_dataset("tips")
ax = sns.barplot(x="smoking", y="weight", hue="low_weight", data=cdf1)
```



performing proportion test for original data set with cut-off lower weight 88.1849

In [78]:
```
freq = np.array([cdf1['weight'][0], cdf1['weight'][1]])
sample = np.array([cdf1['weight'][0]+cdf1['weight'][2], cdf1['weight'][1]+c
stat, pval = proportions_ztest(freq, sample)
pval
```

Out[78]: 6.236909061746852e-05

Comparison Set 2

Non smoking vs. Smoking but not in pregnancy

denoted as Non-Smokers and Smokers

In [26]:
```
non_smoking = data_2.loc[(data_2['smoke'] == 0)]
smoking = data_2.loc[(data_2['smoke'] > 1) & (data_2['smoke'] < 9)]
non_smoking.to_csv('non_smoking_all_time.csv')
smoking.to_csv('smoking_all_time.csv')
```

Stats Overview

In [27]:
```
baby_weights = pd.DataFrame(
        {
            "Babies' Birth Weights born to Non-smoking mothers (in ounce)"
            "Babies' Birth Weights born to smoking mothers (in ounce)": smo
        }
)
baby_weights
```

Out[27]:

	Babies' Birth Weights born to Non-smoking mothers (in ounce)	Babies' Birth Weights born to smoking mothers (in ounce)
count	544.000000	198.000000
mean	122.777574	123.787879
std	17.109661	18.193139
min	55.000000	62.000000
25%	113.000000	112.000000
50%	124.000000	123.000000
75%	132.250000	137.000000
max	176.000000	170.000000

In [28]:
```
smoking['wt1'].skew()
```

Out[28]: -0.3539445104412361

In [29]:
```
non_smoking['wt1'].skew()
```

Out[29]:
```
-0.12179028083493815
```

In [30]:
```
stats.kurtosis(smoking['wt1'], fisher = False)
```

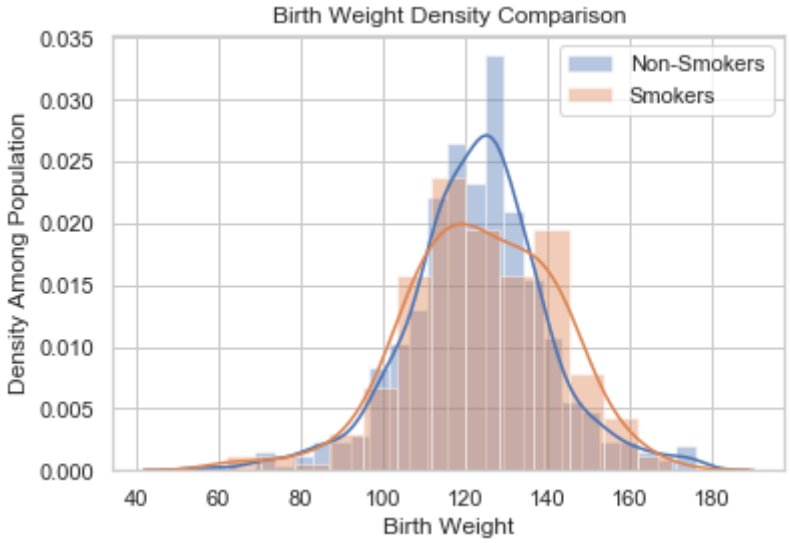
Out[30]:
```
3.4517687297202033
```

In [31]:
```
stats.kurtosis(non_smoking['wt1'], fisher = False)
```

Out[31]:
```
4.310783478561745
```

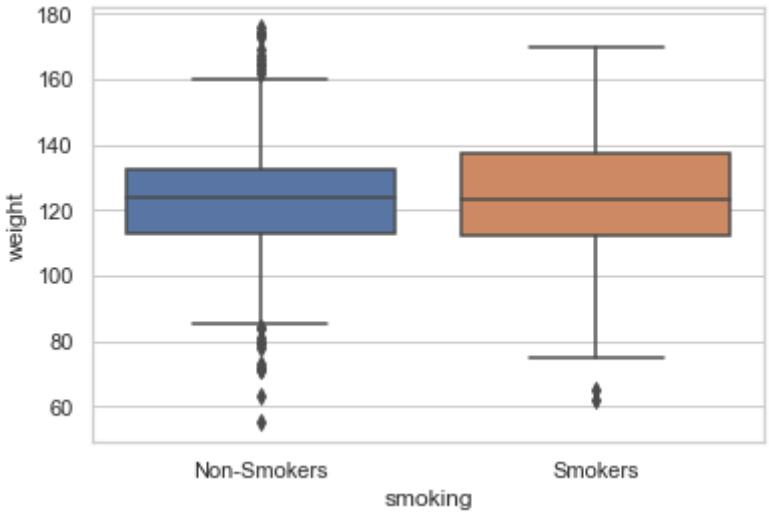
In [32]:
```
sns.distplot(non_smoking['wt1'], label="Non-Smokers")
sns.distplot(smoking['wt1'], label="Smokers")
plt.legend()
plt.title('Birth Weight Density Comparison')
plt.xlabel('Birth Weight')
plt.ylabel('Density Among Population')
```

Out[32]:
```
Text(0, 0.5, 'Density Among Population')
```



In [33]:
```
grouped_df = pd.DataFrame(
             {
                 'weight' : non_smoking['wt1'],
                 'smoking': ['Non-Smokers' for i in non_smoking['wt1']]
             }
)
grouped_df1 = pd.DataFrame(
             {
                 'weight' : smoking['wt1'],
                 'smoking': ['Smokers' for i in smoking['wt1']]
             }
)
cdf = pd.concat([grouped_df, grouped_df1])
sns.boxplot(x ='smoking', y ='weight', data = cdf)
```

Out[33]: <matplotlib.axes._subplots.AxesSubplot at 0x116c276a0>



In [34]:
```
k2, p = stats.normaltest(non_smoking['wt1'])

alpha = 1e-3
print("p = {:g}".format(p))
if p < alpha:  # null hypothesis: x comes from a normal distribution
    print("The null hypothesis can be rejected,")
else:
    print("The null hypothesis cannot be rejected, the dataset is normally
```

```
p = 8.48975e-05
The null hypothesis can be rejected,
```

In [35]:
```
k2, p = stats.normaltest(smoking['wt1'])

alpha = 1e-3
print("p = {:g}".format(p))
if p < alpha:  # null hypothesis: x comes from a normal distribution
    print("The null hypothesis can be rejected,")
else:
    print("The null hypothesis cannot be rejected, the dataset is normally
```

```
p = 0.0490721
The null hypothesis cannot be rejected, the dataset is normally distribut
ed
```

T test for mean

In [36]:
```
stats.ttest_ind(non_smoking['wt1'], smoking['wt1'], equal_var = False)[1]
```

Out[36]:
```
0.49720854479542087
```

In [37]:
```
# fail to reject
```

Chi-square test to validate low weight cut-off

In [38]:
```
lst = []
pvals = []
for i in range(75,100):
    contingency_table = catogorize(non_smoking['wt1'], smoking['wt1'], i)
    f_obs = np.array([contingency_table.iloc[0][0:].values,
                      contingency_table.iloc[1][0:].values])
    lst += [i]
    pvals += [stats.chi2_contingency(f_obs)[0:3][1]]
output = pd.DataFrame(
        {
            'p-value': pvals
        }, index = lst
)
output.index.name = 'Cut-off point'
output.to_csv('chi-square_set1.csv')
output
```

88	0.862166
89	0.937247
90	0.895917
91	0.834903
92	0.924728
93	0.949936
94	0.967193
95	0.886804
96	0.972409

In [39]:
```
## Proportion
```

In [40]:
```
non_smoking_n = len(non_smoking['wt1'])
non_smoking_ln = len([i for i in non_smoking['wt1'] if i <= 88.1849])
smoking_n = len(smoking['wt1'])
smoking_ln = len([i for i in smoking['wt1'] if i <= 88.1849])

non_smoking_lprop = non_smoking_ln / non_smoking_n
smoking_lprop = smoking_ln / smoking_n
```

In [41]:
```
proportion_low_weight_table = pd.DataFrame( {
                                'Non-Smokers': non_smoking_lprop,
                                'Smokers': smoking_lprop
                            }
,index = ['Proportion'])
proportion_low_weight_table
```

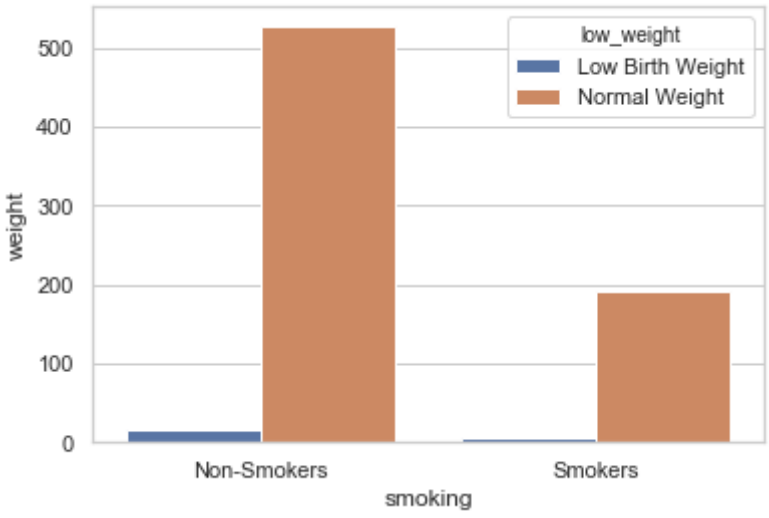
Out[41]:

	Non-Smokers	Smokers
Proportion	0.03125	0.030303

In [42]:
```
grouped_df = pd.DataFrame(
             {
                 'weight' : non_smoking['wt1'],
                 'smoking': ['Non-Smokers' for i in non_smoking['wt1']]
             }
)
grouped_df1 = pd.DataFrame(
             {
                 'weight' : smoking['wt1'],
                 'smoking': ['Smokers' for i in smoking['wt1']]
             }
)
cdf = pd.concat([grouped_df, grouped_df1])
```

In [43]:
```
cdf['low_weight'] = cdf['weight'].apply(lambda x: 'Low Birth Weight' if x <
cdf1 = cdf.groupby(['low_weight','smoking']).count().reset_index()
```

In [44]:
```
sns.set(style="whitegrid")
tips = sns.load_dataset("tips")
ax = sns.barplot(x="smoking", y="weight", hue="low_weight", data=cdf1)
```



In [45]:
```
# Proportion test for low weight
```

In [46]:
```
freq = np.array([cdf1['weight'][0], cdf1['weight'][1]])
sample = np.array([cdf1['weight'][0]+cdf1['weight'][2], cdf1['weight'][1]+c
stat, pval = proportions_ztest(freq, sample)
pval
```

Out[46]:
```
0.9475110159453997
```

In [93]:
```
# fail to reject, they are the same
```

In [ ]:
```

```