Exercises

In [10]:
```
import pandas as pd
import numpy as np
from matplotlib import pyplot as plt
plt.style.use('ggplot')
%matplotlib inline
diamonds = pd.read_csv('diamonds.csv',index_col=0)
```

Task 1: Basics

- have a look at the diamonds dataset: how many rows do we have?, what are the different columns?
- create a DataFrame consisting only of the x, y and z columns
- access row 5 to 15 in diamonds
- create a DataFrame consisting only of row 5 to 15 and name the rows "A" to "K" (hint: each DataFrame has an .index attribute which can be modified)
- access row "C" in the DataFrame you just created
- use the mixed access operator (.ix) to get the price of the 500th diamond
- group the diamnods by color and compute the mean of the price
- find all the diamonds with more than 2 carat and plot their price distribution in a histogram
- compute and plot the standard deviation of the x dimension for the different cuts

In [11]:
```
# no. rows
len(diamonds)

# x,y,z dataframe
df_xyz = diamonds[ ['x','y','z'] ]

# row 5 to 15
d515 = diamonds.iloc[4:15]

# row 5 by name
a_o = [chr(i) for i in range(65,76)] # generate a list of letters A
-O
d515.index = a_o

# row C
d515.loc["C"]

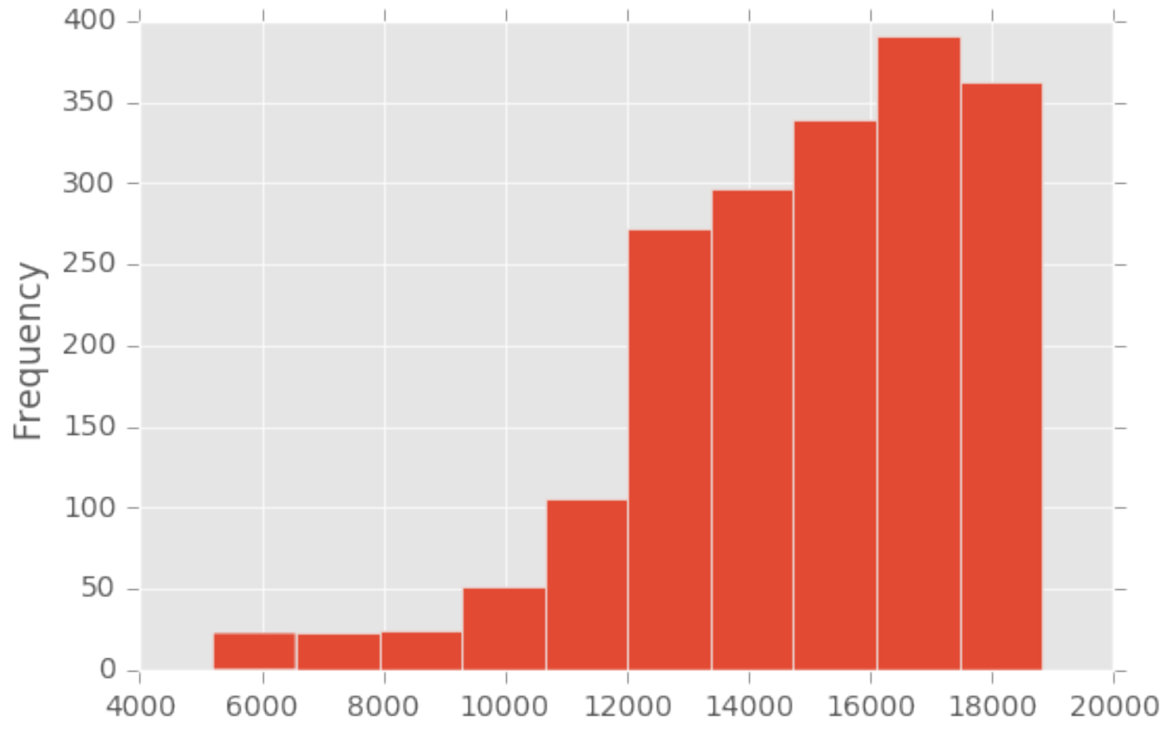
# price of 500th diamond
diamonds.ix[500, 'price']

# price by color
diamonds.groupby("color")["price"].mean()

# diamonds with >2 carat
diamonds[diamonds['carat']>2]['price'].plot(kind='hist')

# std of x for diff. cuts
diamonds.groupby('cut')['x'].std()
```

```
Out[11]: cut
         Fair         0.964317
         Good         1.057301
         Ideal        1.064210
         Premium      1.188252
         Very Good    1.100839
         Name: x, dtype: float64
```



Task 2: Gene expression data

In this exercise we will work with a realistic gene expression data set. Buettner et al. (http://www.nature.com/nbt/journal/v33/n2/full/nbt.3102.html) used single cell RNA-sequencing data, to identify sub-populations of cells with similar gene-expression profiles. RNA-sequencing (RNA seq) data uses next generation sequencing techniques to quantify RNA abundance.

Go to the link given above and download the dataset "Corrected and uncorrected expression values for T-cell data." from the supplementary information section. Have a look at the dataset with Libreoffice and import the second datasheet (Cell-cycle corrected gene expr) as a pandas DataFrame. Use the `read_excel()` function together with the sheetname attribute.

```
In [12]: df_ge_corrected = pd.read_excel( 'nbt.3102-S7.xlsx', sheetname=1 )
```

In the imported table, each column represents a gene, while each row represents a single cell. This table structure is great for an overview, but it is for example not easy to plot a histogramm of the expression of all genes in all cells. For this it would be better to have all expression values in a single column.

Convert the table to a table with 3 columns: `cell_id`, `gene` and `expression`.

Example:

Original table:

	Gnai3	Cdc45	Narf	Klf6
Cell 1	3.2322	3.1981	0.29411	1.7343
Cell 2	1.9832	1.173	0.49389	3.8505
Cell 3	2.2482	3.1705	1.6279	1.6306

converted table:

cell_id	gene	expression
Cell 1	Gnai3	3.2322
Cell 1	Cdc45	3.1981
Cell 1	Narf	0.29411
Cell 1	Klf6	1.7343
Cell 2	Gnai3	1.9832
Cell 2	Cdc45	1.173
...	...	...

this conversion can be done using the function `DataFrame.stack()`, which yields a multi-indexed DataFrame. This multi-indexed DataFrame can be converted to a conventional DataFrame using the method `reset_index()`.

```
In [13]: df_ge_corrected_slim = df_ge_corrected.stack()
         df_ge_corrected_slim = df_ge_corrected_slim.reset_index()
         df_ge_corrected_slim.columns = ('cell_id', 'gene', 'expression')
         df_ge_corrected_slim.head()
```

Out[13]:

	cell_id	gene	expression
0	Cell 1	Gnai3	3.23220
1	Cell 1	Cdc45	3.19810
2	Cell 1	Narf	0.29411
3	Cell 1	Klf6	1.73430
4	Cell 1	Scmh1	0.26642

In the original paper, each cell was assigned to a cluster, based on a principal component analysis of their gene expression profile. The information to which cluster a cell belongs is given in the third sheet of the Excel file (Cluster Assignment). Read in also this sheet and combine the two tables to have expression and cluster assignment in one table.

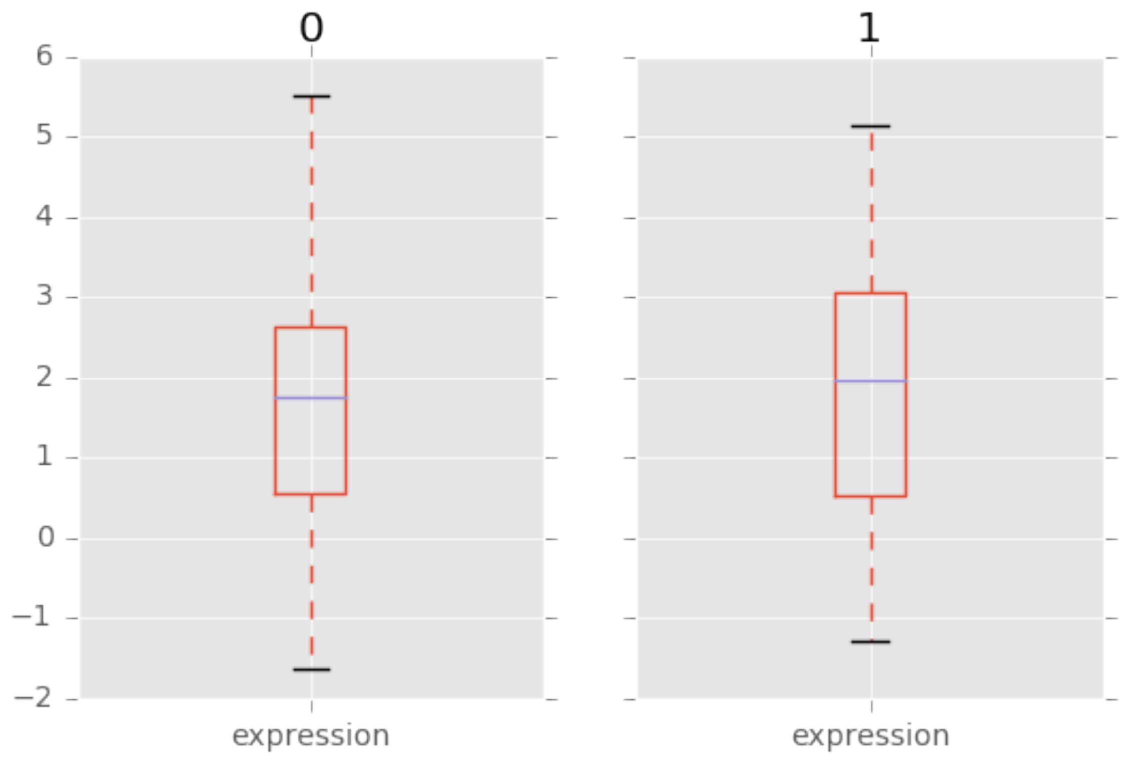
```
In [14]: df_clusters = pd.read_excel( 'nbt.3102-S7.xlsx', sheetname=2 )
         df_clusters.rename(columns={'CellNr': 'cell_id', 'Gata3HighCLuster'
         : 'cluster'}, inplace=True)
         df_merge = pd.merge(df_ge_corrected_slim, df_clusters)
```

Create a boxplot of the expression of all genes for both clusters.

```
In [15]: df_merge.groupby('cluster').boxplot(column='expression')
```

```
/usr/lib/python3/dist-packages/pandas/tools/plotting.py:3082: Futu
reWarning:
The default value for 'return_type' will change to 'axes' in a fut
ure release.
 To use the future behavior now, set return_type='axes'.
 To keep the previous behavior and silence this warning, set retur
n_type='dict'.
  rot=rot, grid=grid, **kwds)
```

```
Out[15]: OrderedDict([(0,
                       {'boxes': [<matplotlib.lines.Line2D at 0x7f12ac10c8d
         0>],
                        'caps': [<matplotlib.lines.Line2D at 0x7f12ac113a58
         >,
                         <matplotlib.lines.Line2D at 0x7f12ac113b70>],
                        'fliers': [<matplotlib.lines.Line2D at 0x7f12ac115b
         e0>],
                        'means': [],
                        'medians': [<matplotlib.lines.Line2D at 0x7f12ac115
         3c8>],
                        'whiskers': [<matplotlib.lines.Line2D at 0x7f12ac10
         3cc0>,
                         <matplotlib.lines.Line2D at 0x7f12ac110cf8>]}),
                      (1,
                       {'boxes': [<matplotlib.lines.Line2D at 0x7f12ac119a9
         0>],
                        'caps': [<matplotlib.lines.Line2D at 0x7f12ac11bb38
         >,
                         <matplotlib.lines.Line2D at 0x7f12ac11ea90>],
                        'fliers': [<matplotlib.lines.Line2D at 0x7f12ac123a
         20>],
                        'means': [],
                        'medians': [<matplotlib.lines.Line2D at 0x7f12ac11e
         ba8>],
                        'whiskers': [<matplotlib.lines.Line2D at 0x7f12ac11
         9c18>,
                         <matplotlib.lines.Line2D at 0x7f12ac11ba20>]})])
```

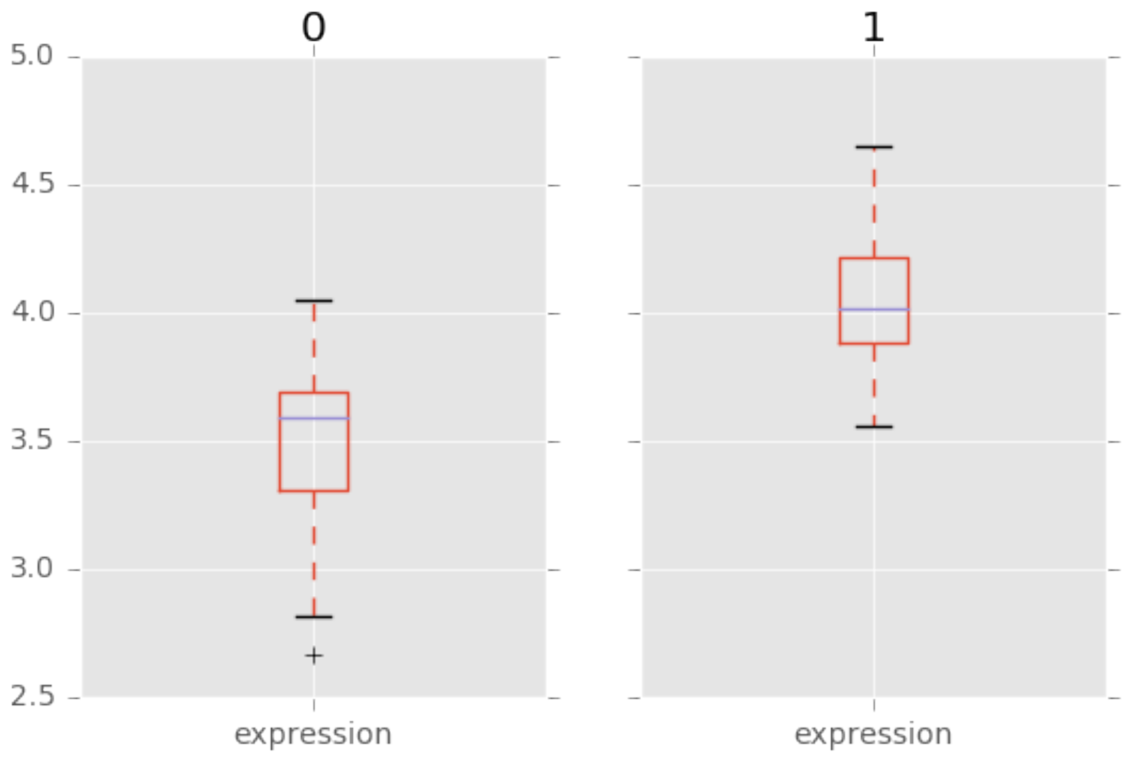


Draw a boxplot of the expression of the different cells in each cluster only for the gene Gata3.

```
In [16]: df_merge[df_merge['gene'] == 'Gata3'].groupby('cluster').boxplot(co
         lumn='expression')
```

```
/usr/lib/python3/dist-packages/pandas/tools/plotting.py:3082: Futu
reWarning:
The default value for 'return_type' will change to 'axes' in a fut
ure release.
 To use the future behavior now, set return_type='axes'.
 To keep the previous behavior and silence this warning, set retur
n_type='dict'.
  rot=rot, grid=grid, **kwds)
```

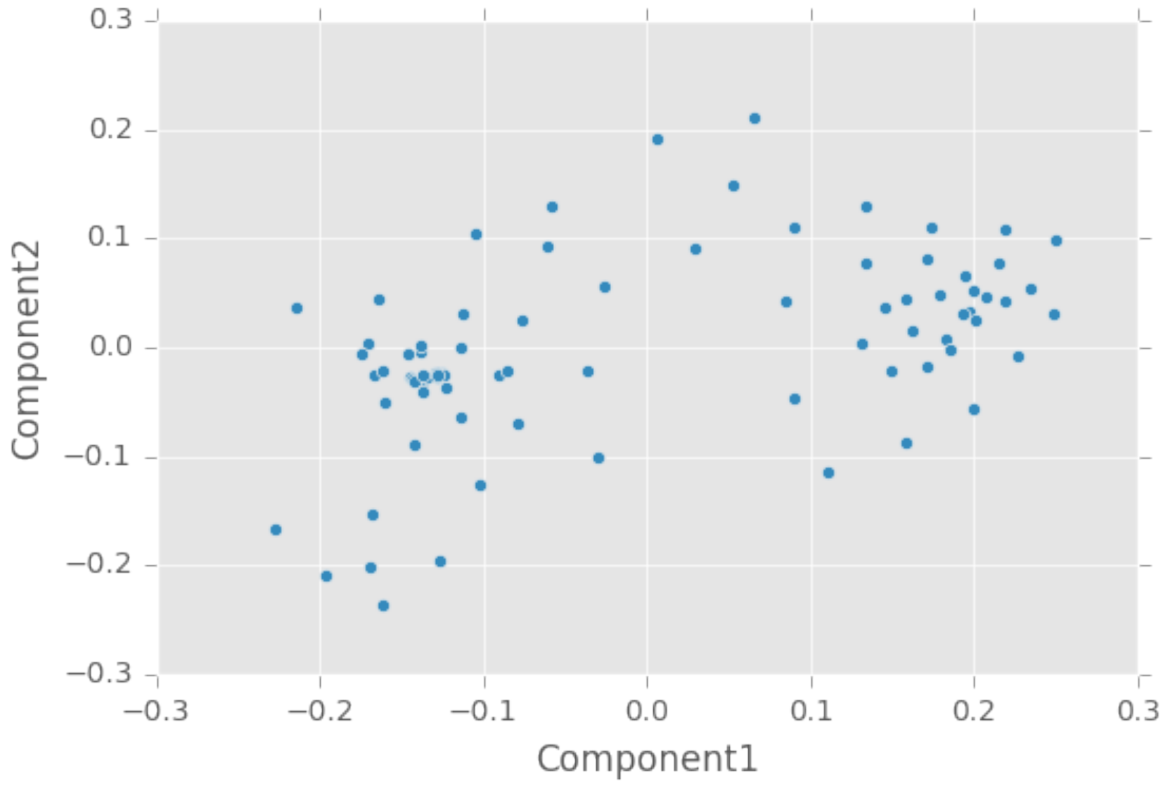
```
Out[16]: OrderedDict([(0,
                        {'boxes': [<matplotlib.lines.Line2D at 0x7f12ac5b61d
         0>],
                         'caps': [<matplotlib.lines.Line2D at 0x7f12ac47afd0
         >,
                          <matplotlib.lines.Line2D at 0x7f12ac129e48>],
                         'fliers': [<matplotlib.lines.Line2D at 0x7f12ac8689
         78>],
                         'means': [],
                         'medians': [<matplotlib.lines.Line2D at 0x7f12ac399
         5c0>],
                         'whiskers': [<matplotlib.lines.Line2D at 0x7f12ac5c
         90b8>,
                          <matplotlib.lines.Line2D at 0x7f12ac49b518>]}),
                       (1,
                        {'boxes': [<matplotlib.lines.Line2D at 0x7f12ac68839
         0>],
                         'caps': [<matplotlib.lines.Line2D at 0x7f12ac5c5ac8
         >,
                          <matplotlib.lines.Line2D at 0x7f12ac5c5be0>],
                         'fliers': [<matplotlib.lines.Line2D at 0x7f12ac3b5b
         70>],
                         'means': [],
                         'medians': [<matplotlib.lines.Line2D at 0x7f12ac3b5
         438>],
                         'whiskers': [<matplotlib.lines.Line2D at 0x7f12ac68
         7b00>,
                          <matplotlib.lines.Line2D at 0x7f12ac687160>]})])
```



Create a scatter-plot of the two principal components for all Gata3 measurements.

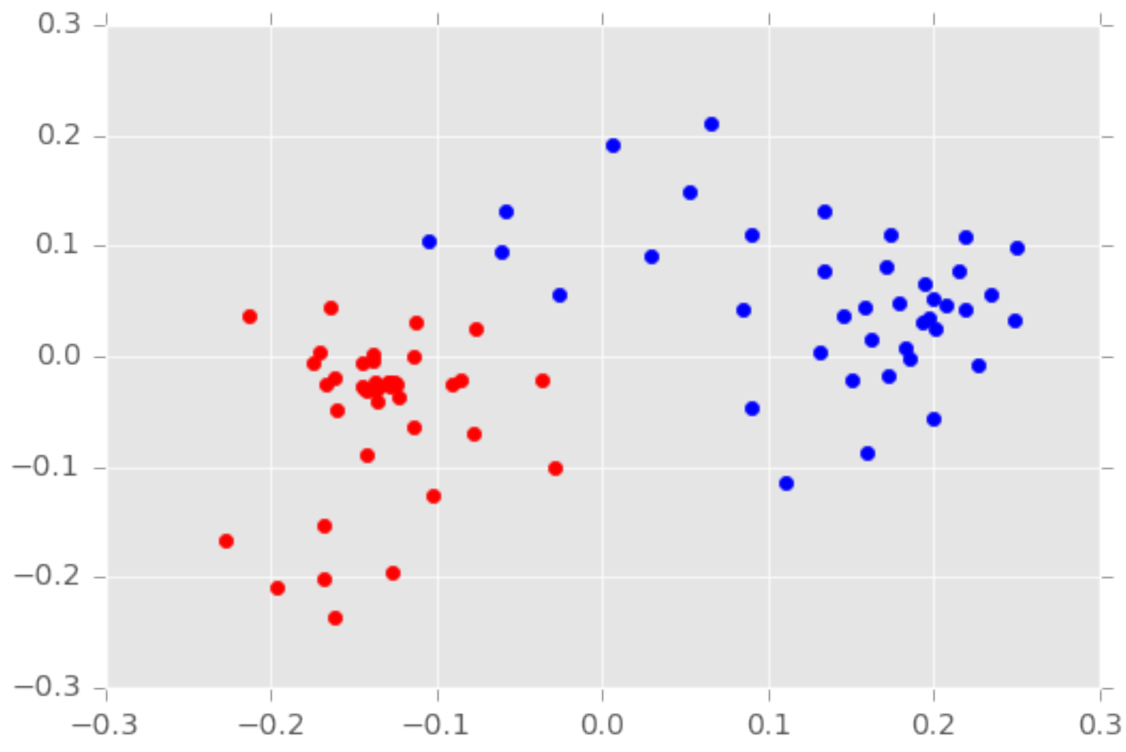
```
In [17]: df_merge[df_merge['gene'] == 'Gata3'].plot(x='Component1', y='Compo
         nent2', kind='scatter' )
```

```
Out[17]: <matplotlib.axes._subplots.AxesSubplot at 0x7f12ac3c9198>
```



Color the points in the scatter plots according to whether they belong to cluster 0 or 1.

```
In [18]: df_gata = df_merge[df_merge['gene'] == 'Gata3']
         c = ['r', 'b']
         for cluster in [0, 1]:
             df_gata_cluster = df_gata[df_gata['cluster'] == cluster]
             plt.scatter(df_gata_cluster['Component1'], df_gata_cluster['Com
         ponent2'], color=c[cluster])
```



```
In [ ]:
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```
In [ ]:
```

```
In [ ]:
```