## 10.5.2 Hierarchical Clustering

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Here we are going to use scipy. First we will do the same as the last exercise. It will all be made in one cell. For details please see 10.5.1

```
In [3]: # conventional way to import pandas
        import pandas as pd
        # conventional way to import seaborn
        import seaborn as sns
        from sklearn.cluster import KMeans
        import numpy as np
        import matplotlib.pyplot as plt
        np.random.seed(0)
        X = np.random.standard_normal(size=(25,2))
        for row in X:
            row[0] = row[0] + 3
            row[1] = row[1]-4
        kmeans2 = KMeans(n_clusters=2, random_state=0,n_init=20).fit(X)
        kmeans3 = KMeans(n_clusters=3, random_state=0,n_init=20).fit(X)
  Here comes the interresting part...
In [4]: from scipy.cluster import hierarchy
        fig, (ax1,ax2,ax3) = plt.subplots(3,1, figsize=(15,18))
        for linkage, cluster, ax in zip([hierarchy.complete(X), hierarchy.average(X), hierarchy.
                                         [ax1,ax2,ax3]):
            cluster = hierarchy.dendrogram(linkage, ax=ax, color_threshold=0)
        ax1.set_title('Complete Linkage')
        ax2.set_title('Average Linkage')
        ax3.set_title('Single Linkage');
```

