# P3_Creating_Customer_Segments

April 3, 2016

## 1 P3 Creating Customer Segments

In this project you, will analyze a dataset containing annual spending amounts for internal structure, to understand the variation in the different types of customers that a wholesale distributor interacts with.

Instructions:

- Run each code block below by pressing **Shift+Enter**, making sure to implement any steps marked with a TODO.
- Answer each question in the space provided by editing the blocks labeled "Answer:".
- When you are done, submit the completed notebook (.ipynb) with all code blocks executed, as well as a .pdf version (File > Download as).

In [1]:
```
# Import libraries: NumPy, pandas, matplotlib
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
from   matplotlib import rc

# Tell iPython to include plots inline in the notebook
%matplotlib inline

# Set styles for seaborn
%config InlineBackend.figure_formats = {'png', 'retina'}
rc_sns = {'lines.linewidth': 2,
          'axes.labelsize': 14,
          'axes.titlesize': 14,
          'axes.facecolor': 'DFDFE5'}
sns.set_context('notebook', font_scale=1.2, rc=rc_sns, )
sns.set_style  ('darkgrid', rc=rc_sns)

# Read dataset
data = pd.read_csv("wholesale-customers.csv")
print "Dataset has {} rows, {} columns".format(*data.shape)
print data.head()  # print the first 5 rowsdata.describe()
```

```
Dataset has 440 rows, 6 columns
   Fresh  Milk  Grocery  Frozen  Detergents_Paper  Delicatessen
0  12669  9656     7561     214              2674          1338
1   7057  9810     9568    1762              3293          1776
2   6353  8808     7684    2405              3516          7844
3  13265  1196     4221    6404               507          1788
4  22615  5410     7198    3915              1777          5185
```

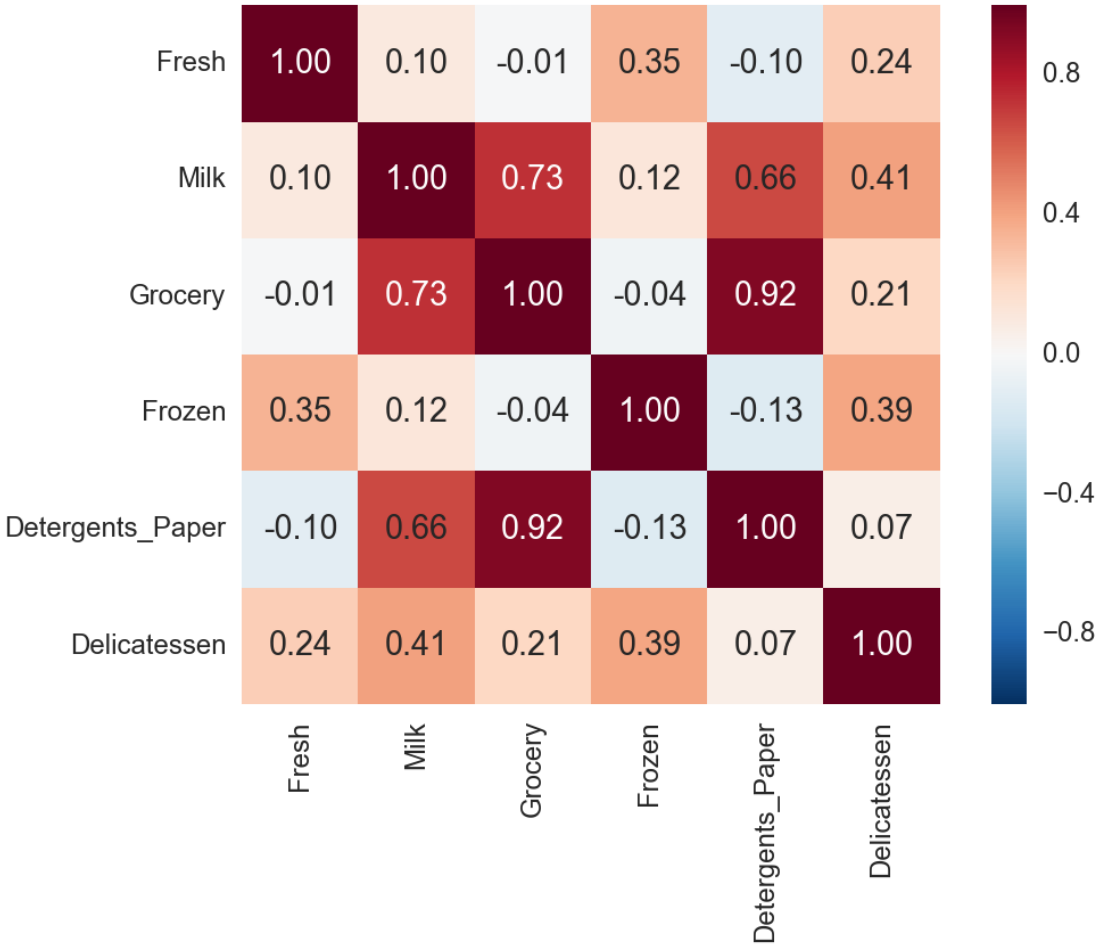
## 1.1 Data Exploration

Explore the dataset with correlation matrix.

In [2]:
```
from sklearn.cross_validation import train_test_split
from sklearn.preprocessing import StandardScaler, MinMaxScaler

sc    = StandardScaler()
X_std = sc.fit_transform(data)

cols = list(data.columns)
sns.heatmap(np.corrcoef(X_std.T),
            cbar=True, square=True, annot=True, fmt='.2f',
            xticklabels=cols, yticklabels=cols)
data.describe()
```

Out[2]:

| | Fresh | Milk | Grocery | Frozen | Detergents_Paper | Delicatessen |
|---|---|---|---|---|---|---|
| count | 440.000000 | 440.000000 | 440.000000 | 440.000000 | 440.000000 | 440.000000 |
| mean | 12000.297727 | 5796.265909 | 7951.277273 | 3071.931818 | 2881.493182 | 1524.870455 |
| std | 12647.328865 | 7380.377175 | 9503.162829 | 4854.673333 | 4767.854448 | 2820.105937 |
| min | 3.000000 | 55.000000 | 3.000000 | 25.000000 | 3.000000 | 3.000000 |
| 25% | 3127.750000 | 1533.000000 | 2153.000000 | 742.250000 | 256.750000 | 408.250000 |
| 50% | 8504.000000 | 3627.000000 | 4755.500000 | 1526.000000 | 816.500000 | 965.500000 |
| 75% | 16933.750000 | 7190.250000 | 10655.750000 | 3554.250000 | 3922.000000 | 1820.250000 |
| max | 112151.000000 | 73498.000000 | 92780.000000 | 60869.000000 | 40827.000000 | 47943.000000 |




## 1.2 Feature Transformation

**1)** In this section you will be using PCA and ICA to start to understand the structure of the data. Before doing any computations, what do you think will show up in your computations? List one or two ideas for what might show up as the first PCA dimensions, or what type of vectors will show up as ICA dimensions.

Answer:

PCA seeks to find orthogonal directions (principle components) that maximize variances. According to the table above, "Fresh" and "Grocery" have the largest variance, thus more likely to show up in the first PCA dimension.

For ICA, non-normality of the marginal densities are maximized to discover latent variables (independent components) underlying the dataset.[1] The vectors showing up after ICA would be the "source" that can generate the observed dataset. According to the correlation matrix generated above, "Fresh" and "Frozen" have less correlation with other variables, thus more likely to show up as the first ICA dimension.

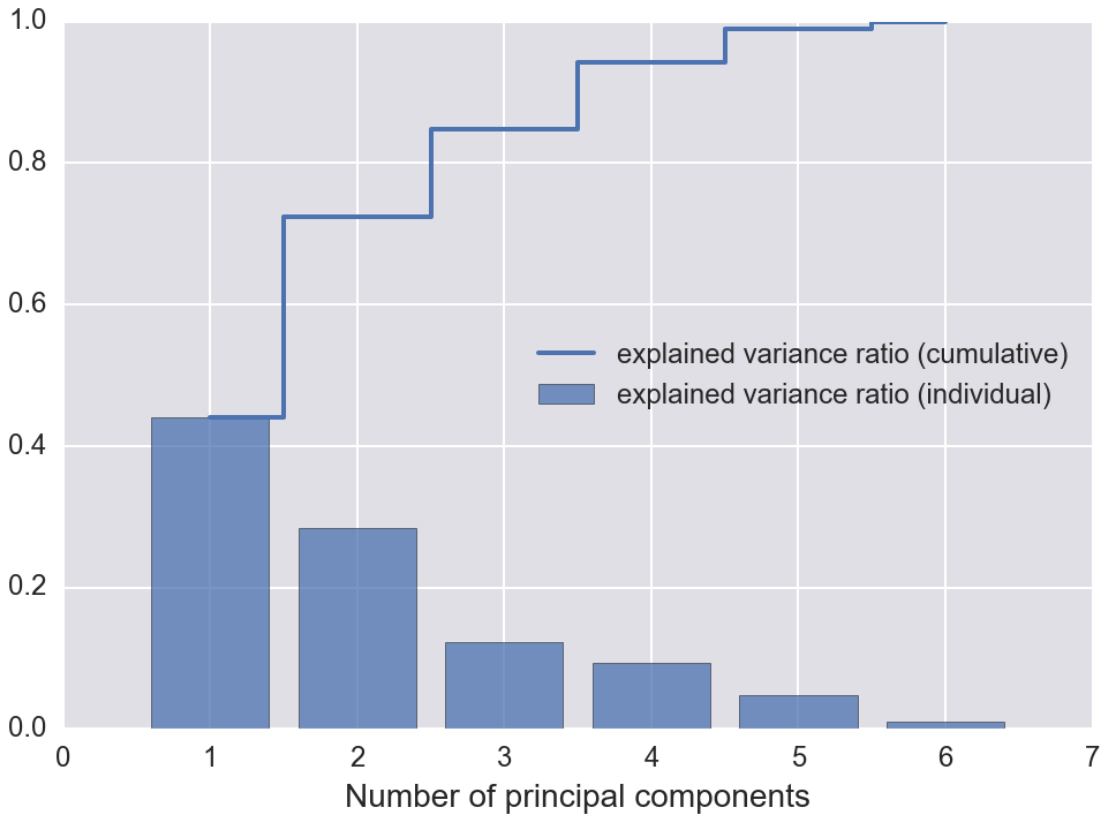
[1] http://research.ics.aalto.fi/ica/icademo/

### 1.2.1 PCA

```
In [3]: # TODO: Apply PCA with the same number of dimensions as variables in the dataset
        from sklearn.decomposition import PCA
        from sklearn.preprocessing import StandardScaler
```

```
        # Standardize input data
        sc    = StandardScaler()
        X     = data.values.astype(np.float64)
        X_std = sc.fit_transform(X)

        # Perform PCA analysis
        pca       = PCA(n_components=None)
        X_std_pca = pca.fit_transform(X_std)

        # Print the components and the amount of variance in the data contained in each dimension
        print('Principal components (pc) :')
        print(pca.components_)

        print('\nExplained variance ratios (EVR):')
        print(pca.explained_variance_ratio_)

        print('\nEVR of the 1st and 2nd pc: %.3f' % sum(pca.explained_variance_ratio_[:2]))
        print('EVR of the 3rd and 4th pc: %.3f' % sum(pca.explained_variance_ratio_[2:4]))
        print('EVR of the first four  pc: %.3f' % sum(pca.explained_variance_ratio_[:4]))

        # visualization of indivudual and cumulative explained variance ratio
        # code adapted from p132 of S. Raschka "Python Machine Learning" 2015
        n_pca   = pca.n_components_
        evr     = pca.explained_variance_ratio_
        cum_evr = np.cumsum(evr)

        plt.bar (range(1, n_pca+1), evr, alpha=0.75,
                 align='center', label='explained variance ratio (individual)')

        plt.step(range(1, n_pca+1), cum_evr,
                 where='mid',    label='explained variance ratio (cumulative)')

        plt.legend(loc='best')
        plt.xlabel('Number of principal components')
        rc('font', weight='bold')
```

```
Principal components (pc) :
[[-0.04288396 -0.54511832 -0.57925635 -0.05118859 -0.5486402  -0.24868198]
 [-0.52793212 -0.08316765  0.14608818 -0.61127764  0.25523316 -0.50420705]
 [-0.81225657  0.06038798 -0.10838401  0.17838615 -0.13619225  0.52390412]
 [-0.23668559 -0.08718991  0.10598745  0.76868266  0.17174406 -0.55206472]
 [ 0.04868278 -0.82657929  0.31499943  0.02793224  0.33964012  0.31470051]
 [ 0.03602539  0.03804019 -0.72174458  0.01563715  0.68589373  0.07513412]]

Explained variance ratios (EVR):
[ 0.44082893  0.283764    0.12334413  0.09395504  0.04761272  0.01049519]

EVR of the 1st and 2nd pc: 0.725
EVR of the 3rd and 4th pc: 0.217
EVR of the first four  pc: 0.942
```




**2)** How quickly does the variance drop off by dimension? If you were to use PCA on this dataset, how many dimensions would you choose for your analysis? Why?

Answer:

The explained variance ratio drops off pretty fast after the first two principle components, which account for **72.5%** of the total variance while the third and fourth constitute around **21.7%**.

It would be reasonable to choose a total of **four dimensions** for analysis since the first four principle components accounts for around **94.2%** of the variance.

**3)** What do the dimensions seem to represent? How can you use this information?

```
In [4]: pd.DataFrame(pca.components_, columns=cols, index=['PC %d' %idx for idx in range(1, len(cols)+1
```

Out[4]:

| | Fresh | Milk | Grocery | Frozen | Detergents_Paper | Delicatessen |
|---|---|---|---|---|---|---|
| PC 1 | -0.042884 | -0.545118 | -0.579256 | -0.051189 | -0.548640 | -0.248682 |
| PC 2 | -0.527932 | -0.083168 | 0.146088 | -0.611278 | 0.255233 | -0.504207 |
| PC 3 | -0.812257 | 0.060388 | -0.108384 | 0.178386 | -0.136192 | 0.523904 |
| PC 4 | -0.236686 | -0.087190 | 0.105987 | 0.768683 | 0.171744 | -0.552065 |
| PC 5 | 0.048683 | -0.826579 | 0.314999 | 0.027932 | 0.339640 | 0.314701 |
| PC 6 | 0.036025 | 0.038040 | -0.721745 | 0.015637 | 0.685894 | 0.075134 |

Answer:

The dimensions represent linear combinations of the original features, which capture the variances between data points in decreasing order. For example, as shown in the table above, the first principle component (PC) will take the original dataset and transform it to lie along an axis that assigns more absolute weight to features such as **Milk** , **Grocery** and **Detergents_Paper** compared to **Fresh** and **Frozen**. For the second PC, more absolute weight is assigned to **Fresh**, **Frozen** and **Delicatessen** compared to **Grocery** and **Milk**.

The transformed dataset might prove to be a better representation of the original dataset, thus potentially making clustering results more relevant. Throwing out the principal components with low variance might also help reduce the "curse of dimensionality".

### 1.2.2 ICA

```
In [10]: # TODO: Fit an ICA model to the data
         # Note: Adjust the data to have center at the origin first!
         from sklearn.decomposition import FastICA

         ica   = FastICA(n_components=None, whiten=True, random_state=0)
         X_ica = ica.fit_transform(X_std)


         print('The unmixing matrix:')
         pd.set_option('display.precision', 4)
         pd.DataFrame(ica.components_, columns=cols, index=['IC %d' %idx for idx in range(1, len(cols)+
```

The unmixing matrix:

Out[10]:

| | Fresh | Milk | Grocery | Frozen | Detergents_Paper | Delicatessen |
|---|---|---|---|---|---|---|
| IC 1 | 0.0026 | -0.0130 | 0.0642 | 0.0018 | -0.0079 | -0.0047 |
| IC 2 | 0.0037 | -0.0168 | -0.1130 | 0.0071 | 0.1342 | 0.0159 |
| IC 3 | -0.0019 | -0.0728 | 0.0544 | 0.0018 | -0.0146 | 0.0172 |
| IC 4 | -0.0502 | 0.0064 | 0.0065 | 0.0033 | -0.0104 | 0.0029 |
| IC 5 | -0.0049 | -0.0016 | -0.0055 | -0.0024 | 0.0023 | 0.0509 |
| IC 6 | 0.0109 | 0.0010 | -0.0073 | -0.0541 | 0.0026 | 0.0169 |

**4)** For each vector in the ICA decomposition, write a sentence or two explaining what sort of object or property it corresponds to. What could these components be used for?

Answer:

Each row vector in **ica.components_** represents a row in the un-mixing matrix. After transforming the original standardized dataset with **X_std.dot(ica.components_.T)**, each new dimension (customer behaviors) would be as statistically independent as possible. The transformed data can then be used for clustering analysis and identification of customer categories.

Description of independent components (IC) or customer behaviors: * IC1 corresponds to the behavior - spending more on **Grocery** but average on other categories. Negative sign can be interpreted as anti-correlations. When the weight magnitude of a certain category is small (less than 10% of the largest weight in that IC), it means average spending on that category, thus omitted in the discussions. * IC2 behavior - spending more on **Detergents_Paper** but much less on **Grocery**, as can be seen from the anti-correlation between the two categories. * IC3 behavior - spending more on **Grocery** and **Delicatessen** but less on **Milk** and **Detergents_Paper**. * IC4 behavior - spending less on **Fresh** and **Detergents_Paper**. * IC5 behavior - spending more on **Delicatessen** and average on other categories. * IC6 behavior - spending more on **Fresh** but less on **Frozen**.

## 1.3 Clustering

In this section you will choose either K Means clustering or Gaussian Mixed Models clustering, which implements expectation-maximization. Then you will sample elements from the clusters to understand their significance.

### 1.3.1 Choose a Cluster Type

**5)** What are the advantages of using K Means clustering or Gaussian Mixture Models?

Answer:

**KMeans** * advantage: reasonably fast performance. * disadvantages: 1) assumes spherical cluster; 2) can't handle unevenly sized clusters well; 3) need to specify number of clusters. 4) smoother decision boundaries compared to K-means. [2][5]

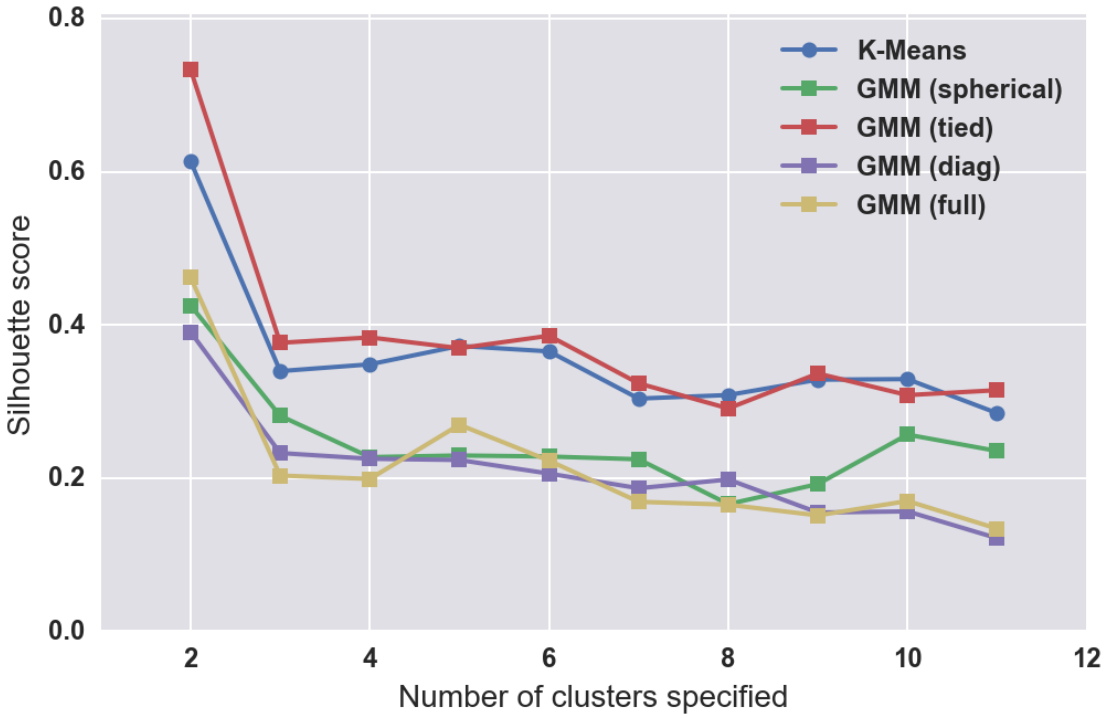
**Gaussian Mixture Model** * advantage: 1) performs fuzzy membership assignment; 2) accommodates clusters with vastly different sizes as well as correlation structures; 3) provides more structural information about the cluster such as cluster width. * disadvantages: 1) need to specify number of Gaussian mixtures; 2) sometimes can be stuck in local minimums; 3) can be problematic while handling non-Gaussian clusters such as ring structures. [3] [4]

For this case, GMM might be more appropriate since the cluster size might not be evenly distributed.

**6)** Below is some starter code to help you visualize some cluster data. The visualization is based on this demo from the sklearn documentation.

In [6]:
```
# Generate a plot for silhouette scores vs number of specified clusters
# in order to aid selection of optimal cluster size

# Import clustering modules
import itertools
import matplotlib.gridspec as gridspec
from mlxtend.evaluate import plot_decision_regions
from sklearn.cluster  import KMeans
from sklearn.mixture  import GMM
from sklearn.metrics  import silhouette_score

# Use silhouette score to select the number of clusters for K-means and GMM
n_cluster_min = 2
n_cluster_max = 11
cluster_range = range(n_cluster_min, n_cluster_max+1)

# Compute silhouette scores
km_silhouette  = []
cov_types      = ['spherical', 'tied', 'diag', 'full']
empty_list     = [[] for i in cov_types]
gmm_silhouette = dict(zip(cov_types, empty_list))

for i in cluster_range:
    y_km  = KMeans(n_clusters=i, random_state=0).fit_predict(X_std)
    km_silhouette.append (silhouette_score(X_std, y_km,  metric='euclidean'))

    for cov_type in cov_types:
        y_gmm = GMM(n_components=i, random_state=0, covariance_type= cov_type).fit_predict(X_st
        gmm_silhouette[cov_type].append(silhouette_score(X_std, y_gmm, metric='euclidean'))

# Plot silhouette score vs number of clusters chosen
plt.figure(figsize=(8, 5), dpi=300)

plt.plot(cluster_range, km_silhouette,  marker='o', label = 'K-Means')
for cov_type in cov_types:
    plt.plot(cluster_range, gmm_silhouette[cov_type], marker='s', label = 'GMM (%s)' %cov_type

plt.xlabel('Number of clusters specified')
plt.ylabel('Silhouette score')
plt.xlim(n_cluster_min-1, n_cluster_max+1)
plt.ylim(0, 0.805)
plt.yticks(np.arange(0, 0.805, 0.2))
```

```
plt.legend(loc='upper right')
rc('font', weight='bold')
```

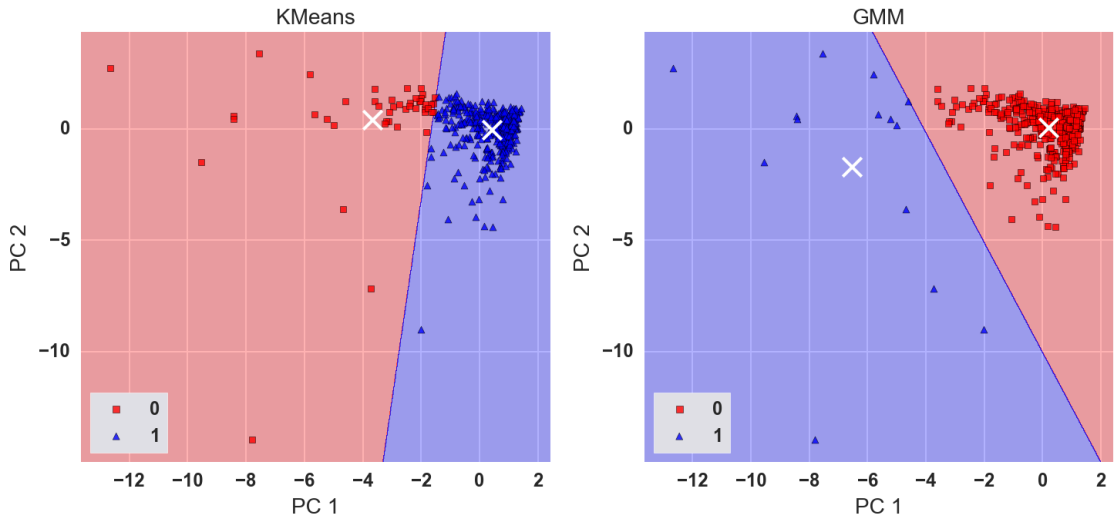



From the plot shown above, GMM clustering algorithm with a covariance type of **tied** and **n_components=2** provides the best silhouette-score of **0.733**, which is around **19.3%** better compared to K-means(n_cluster=2).

In [7]:
```
# TODO: First we reduce the data to two dimensions using PCA to capture variation
pca_reduced       = PCA(n_components=2)
X_std_pca_reduced = pca_reduced.fit_transform(X_std)
print('=================================================================================')
print('First 5 elements after transformation with the first two principle components:')
print(X_std_pca_reduced[:5])
print('=================================================================================')

# TODO: Implement your clustering algorithm here,
# and fit it to the reduced data for visualization

# initializing clustering algorithms KMeans/GMM and centroids
clus      = [KMeans(n_clusters=2), GMM(n_components=2, covariance_type='tied')]
centroids = {}

# plotting decision regions for KMeans and GMM
gs   = gridspec.GridSpec(1, 2)
grds = itertools.product([0, 1], repeat=1)

fig = plt.figure(figsize=(12, 5))
for clu, grd in zip(clus, grds):
```

```
            # fit to the reduced reduced data
            y_clu = clu.fit_predict(X_std_pca_reduced)

            clu_name = clu.__class__.__name__
            if   clu_name=='KMeans': centroids[clu_name] = clu.cluster_centers_
            elif clu_name=='GMM':    centroids[clu_name] = clu.means_

            print('%s:\n%s' % (clu_name, clu))
            print('================================================================================')

            # plotting the decision boundaries with mlxtend.evaluate.plot_decision_regions
            # http://rasbt.github.io/mlxtend/user_guide/evaluate/plot_decision_regions/
            ax  = plt.subplot(gs[grd[0]])
            fig = plot_decision_regions(X=X_std_pca_reduced, y=y_clu, clf=clu)
            fig.legend(loc='lower left', frameon=True)

            # plotting the centroids of the clusters
            plt.scatter(centroids[clu_name][:, 0], centroids[clu_name][:, 1],
                        marker='x', s=150, linewidths=2, color='w', zorder=2)
            plt.title (clu_name)
            plt.xlabel('PC 1')
            plt.ylabel('PC 2')
```

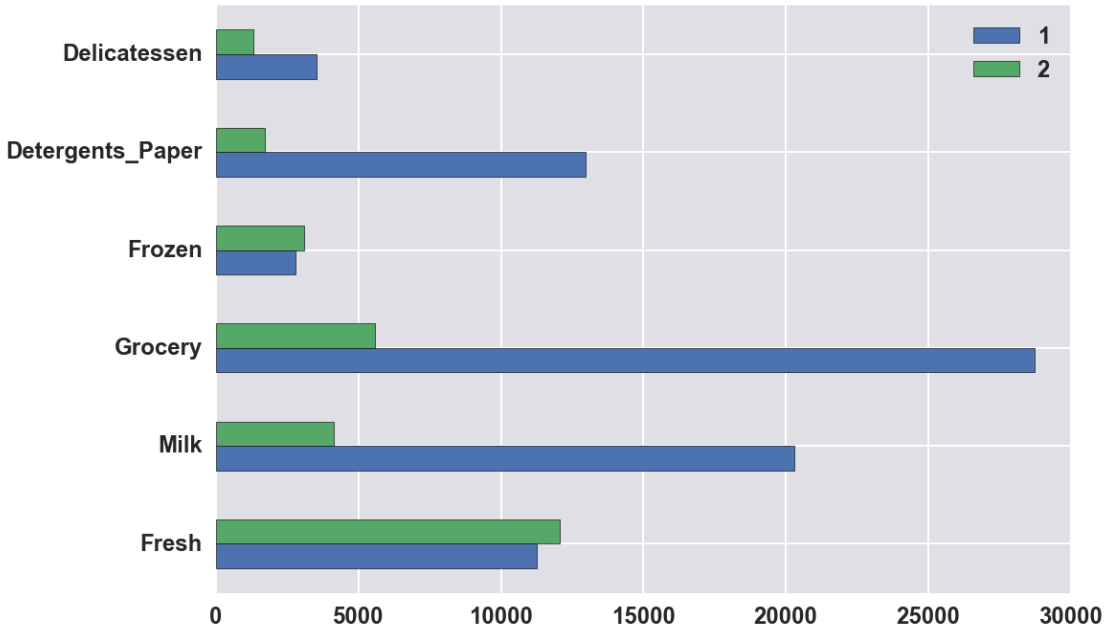
```
================================================================================
First 5 elements after transformation with the first two principle components:
[[-0.19329055  0.30509996]
 [-0.4344199   0.32841262]
 [-0.81114323 -0.8150957 ]
 [ 0.77864783 -0.65275373]
 [-0.16628726 -1.27143372]]
================================================================================
KMeans:
KMeans(copy_x=True, init='k-means++', max_iter=300, n_clusters=2, n_init=10,
    n_jobs=1, precompute_distances='auto', random_state=None, tol=0.0001,
    verbose=0)
================================================================================
GMM:
GMM(covariance_type='tied', init_params='wmc', min_covar=0.001,
  n_components=2, n_init=1, n_iter=100, params='wmc', random_state=None,
  thresh=None, tol=0.001, verbose=0)
================================================================================
```




**7)** What are the central objects in each cluster? Describe them as customers.

```
In [8]: print('Centroids of KMeans:')
        print(centroids['KMeans'])

        print('\nMeans of GMM:')
        print(centroids['GMM'])

        pd.set_option('precision', 4)
        print('\nCustomer types based on KMeans centroids:')
        pd.DataFrame(sc.inverse_transform(pca_reduced.inverse_transform(centroids['KMeans'])),
                     columns=cols, index=range(1,3)).T.plot(kind='barh')
```

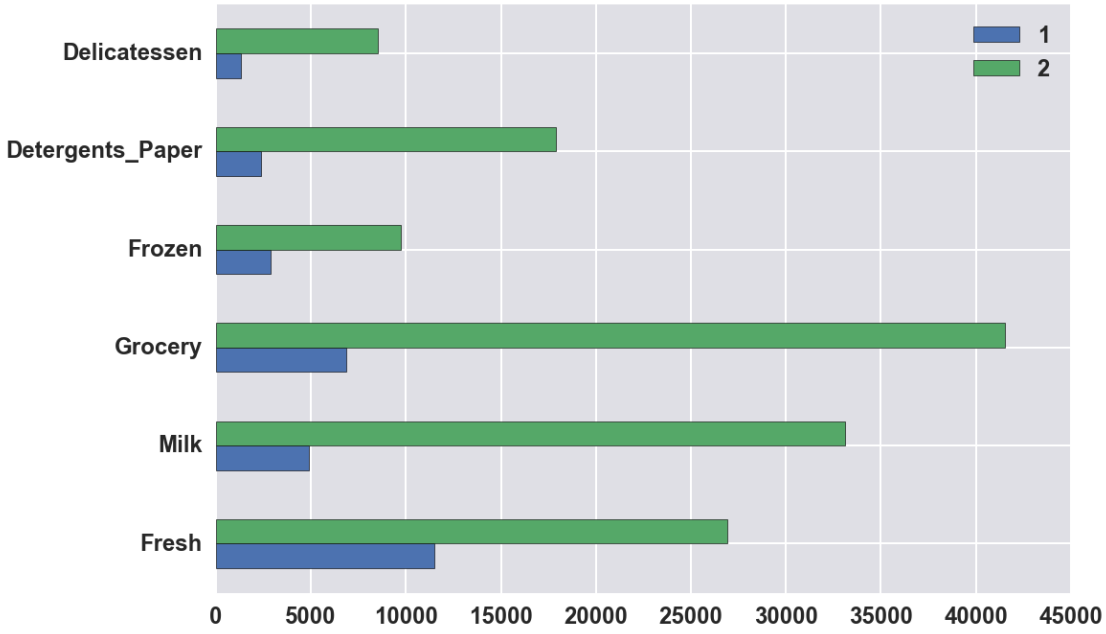
```
Centroids of KMeans:
[[-3.67428358  0.40751388]
 [ 0.41858927 -0.04642563]]

Means of GMM:
[[ 0.21094239  0.05500227]
 [-6.53677134 -1.70443345]]

Customer types based on KMeans centroids:

Out[8]: <matplotlib.axes._subplots.AxesSubplot at 0x11a7cbd90>
```




In [9]:
```
print('Customer types based on GMM means:')
pd.DataFrame(sc.inverse_transform(pca_reduced.inverse_transform(centroids['GMM'])),
             columns=cols, index=range(1,3)).T.plot(kind='barh')
```

```
Customer types based on GMM means:
```

Out[9]: <matplotlib.axes._subplots.AxesSubplot at 0x119704ad0>



Answer:

The centroids returned by both KMeans and GMM are listed above. For KMeans, the data points just to the left of the upper decision boundaries might not be suitably classified. Visually, the decision boundaries produced by GMM seems to be more plausible.

According to **KMeans**, 1. customer type 1 would buy less amount of Milk, Grocery, Detergents_Paper and Delicatessen compared to customer type 2; 2. customer type 1 & 2 would buy similar amount of Fresh and Frozen.

According to **GMM**, 1. customer type 1 would spend more on all categories - high volume buyers; 2. customer type 2 would spend less on all categories, especially Milk and Grocery - low volume buyers.

### 1.3.2 Conclusions

**8)** Which of these techniques felt like it fit naturally with the data?

**Answer:** In my opinion, PCA and GMM clustering provide a suitable framework for customer type discovery. * First, PCA projects the original dataset onto a new feature space with each orthogonal dimension ordered by descending explained variance ratio (EVR). If the EVR of a dimension is small compared to a pre-defined threshold, the corresponding dimension can be discarded to help alleviate the "curse of dimensionality" and potentially increase the performance of the subsequent clustering step. To aid visualization, we have chosen the number of components to be 2, which may not be optimal for clustering performance. * Compared to K-means, GMM can be considered as a soft clustering method utilizing expectation maximization. In GMM, each cluster can be interpreted as Gaussian density with a centroid and covariance matrix. Each observation (data point) is assigned a weight for each cluster instead of a binary cluster membership. Even though the decision boundaries for K-means and GMM are similar, those for GMM are usually smoother. [5] After empirical verification, GMM(n_component=2, cov_type='tied') is found to offer 19.3% better silhouette score compared to K-means.

[5] Trevor et al. P463, The Elements of Statistical Learning 2e, 2011.

**9)** How would you use that technique to assist if the company conducted an experiment?

**Answer:** With GMM clustering model, we can separate the existing customer base into two types and perform targeted experiments. For each type of customers, we can first randomly divide them into two groups, one of which will receive existing service and serve as the control while the other will be the experimental group, receiving a variation of the service. Responses/sales from each group of customers can then be recorded and analyzed, which can help the company to decide whether to change the service for a particular type of customers.

**10)** How would you use that data to predict future customer needs?

**Answer:** After performing some experiments using the methodology outlined above, the responses/sales can be organized into a binary target variable (better/worse) or a continuous target variable (percent difference compared to the average of the matching control group).

For each case, we can use existing data to train and validate a supervised classification/regression model with, for example, KNN or Logistic Regression. When a new customer's data becomes available, we can use the model to predict whether the customer will respond favorably to the change in service or predict the magnitude of response in terms of sales.