main

December 10, 2019

0.1 Please set below variable `running` to `1` if you run this notebook.

Its purpose is to ensure that interactive functions will display their outputs if you open the notebook on github (without downloading). If you run the notebook without setting `running` to `1` all interactive functions will display twice.

```
In [129]: running = 0
```

`field` is a slice of response table you want to analyse
`feature` is a single column name of responders table
`group` is a slice of people, i.e. men/female/left-handed/right-handed

1 Table of content

1. Data preparation
2. Searching for correlations
   - Principal component analysis for `fields` **(interactive)**
   - Correlations with a chosen `feature` **(interactive)**
   - Searching for interesting correlations
3. Clustering
   - Hierarchical clustering for a chosen `field` **(interactive)**
   - K-means clustering for a chosen `field` **(interactive)**
   - T-SNE **(interactive)**
   - Finding outliners **(interactive)**
4. Other
   - BMI distribution within `genders`
   - `Feature's` distribution between `groups` **(interactive)**

```
In [130]: %matplotlib inline
          import matplotlib.pyplot as plt
          import matplotlib
          import pandas as pd
          import numpy as np
          import scipy.cluster.hierarchy as sch
```

```
        import ipywidgets as widgets
        from sklearn.cluster import KMeans
        from sklearn.preprocessing import scale, StandardScaler
        from pylab import rcParams
        from numpy.random import RandomState
        from IPython.display import display
        from ipywidgets import interact, interactive, fixed, interact_manual, Dropdown, IntSl
        from sklearn.manifold import TSNE
```

Define two functions for cluster analysis visualisation

```
In [131]: from itertools import cycle, islice
          from pandas.plotting import parallel_coordinates


          def pd_centers(featuresUsed, centers):

              colNames = list(featuresUsed)
              colNames.append('prediction')

              # Zip with a column called 'prediction' (index)
              Z = [np.append(A, index) for index, A in enumerate(centers)]

              # Convert to pandas for plotting
              P = pd.DataFrame(Z, columns=colNames)
              P['prediction'] = P['prediction'].astype(int)
              return P

          def parallel_plot(data, size):

              my_colors = list(islice(cycle(['b', 'r', 'g', 'y', 'k']), None, len(data)))
              plt.figure(figsize=size).gca().axes.set_ylim([1,5])
              parallel_coordinates(data, 'prediction', color = my_colors, marker='o')
              plt.xticks(rotation=75)
              plt.ylabel('centers of clusters')
```

1.1 1. Data preparation

```
In [132]: responses = pd.read_csv("responses.csv")

          responses.at[676,'Height'] += 100 # repair a value
```

Divide dataset onto severall parts

```
In [133]: music = responses.loc[:,'Dance':'Opera']
          movies = responses.loc[:,'Horror':'Action']
          hobbies = responses.loc[:,'History':'Pets']
          phobias = responses.loc[:,'Flying':'Fear of public speaking']
          personality = responses.loc[:,'Daily events':'Spending on healthy eating'].select_dty
```

Create a path to relate to variables using their names

```
In [134]: field_name = {'music':music, 'movies':movies, 'hobbies':hobbies, 'phobias':phobias,
```

1.1.1 Define two new features: `braveness` and `BMI`

Negation of 'breaveness' is a scaled sum of individual's ratings of all phobias.
Note: highter value = more brave.
'BMI' stands for 'Body Mass Index'

```
In [135]: braveness = (50-phobias.sum(axis=1)) / 10 + 1
          bmi = round(responses['Weight'] / (responses['Height'] / 100)**2, 2)


          responses_ = responses.copy()
          responses_.insert(0, "Braveness", braveness.to_list(), True)
          responses_.insert(0, "BMI", bmi.to_list(), True)

          # braveness.plot.hist(bins=40, alpha=0.5, density = True)
```

Filter responses leaving only numerical values

```
In [136]: responses_int = responses_.select_dtypes(include=['int','float'])
          print(responses_.shape, responses_int.shape)
```

```
(1010, 152) (1010, 141)
```

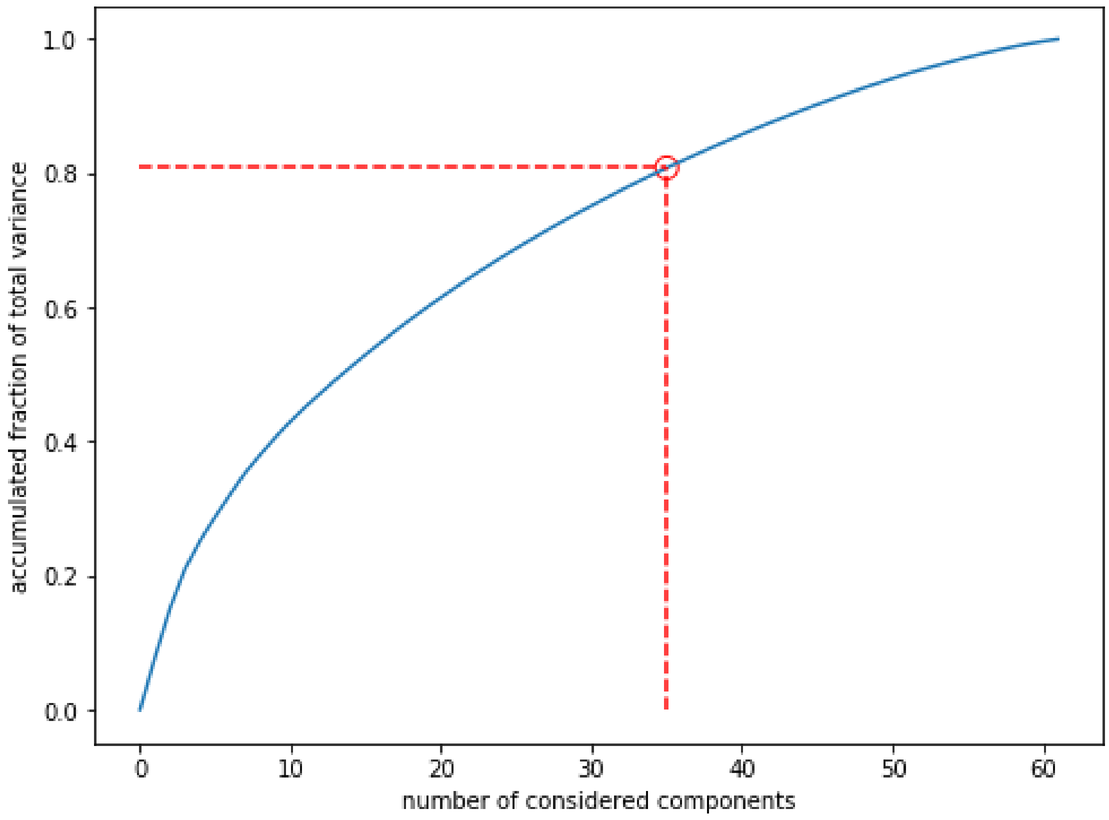
1.2 2. Search for correlations

1.2.1 2.1. Principal Component analysis (PCA) for `fields`

For a chosen `field` analyse impact of `number of most relevant components` took into consideration for quality of representing data.

```
In [137]: @interact(field = ['personality','phobias','music','movies','hobbies'], noOfComponen
          def PCA(field, noOfComponents):
              field = field_name[field]

              df = field.dropna()
              df_np = np.array(df)

              # Calculate covarriance matrix for all features (columns) in TYPE

              Sigma = np.cov(df_np, rowvar=0, bias=1)

              # Calculate eigenvectors of covarriance matrix

              eigenvalues, eigenvectors = np.linalg.eigh(Sigma)
```

```
        plt.figure(figsize=(8,6))
        plt.plot([0]+[sum(eigenvalues[-i:]) / sum(eigenvalues) for i in range(1, field.sl
        plt.xlabel('number of considered components')
        plt.ylabel('accumulated fraction of total variance')

        x = noOfComponents
        y = (lambda i: sum(eigenvalues[-i:]) / sum(eigenvalues))(noOfComponents)
        plt.scatter([x], [y], s=100, edgecolors='r', facecolors = 'none')
        plt.plot([x,x], [0,y], c='r', linestyle='dashed')
        plt.plot([0,x], [y,y], c='r', linestyle='dashed')
        plt.show()
        print('Amount of total variance covered by {} most impactful components: {}'.forr

    if running == 0:
        PCA('personality', 35)
```



```
Amount of total variance covered by 35 most impactful components: 0.8079
```

Comment 1:

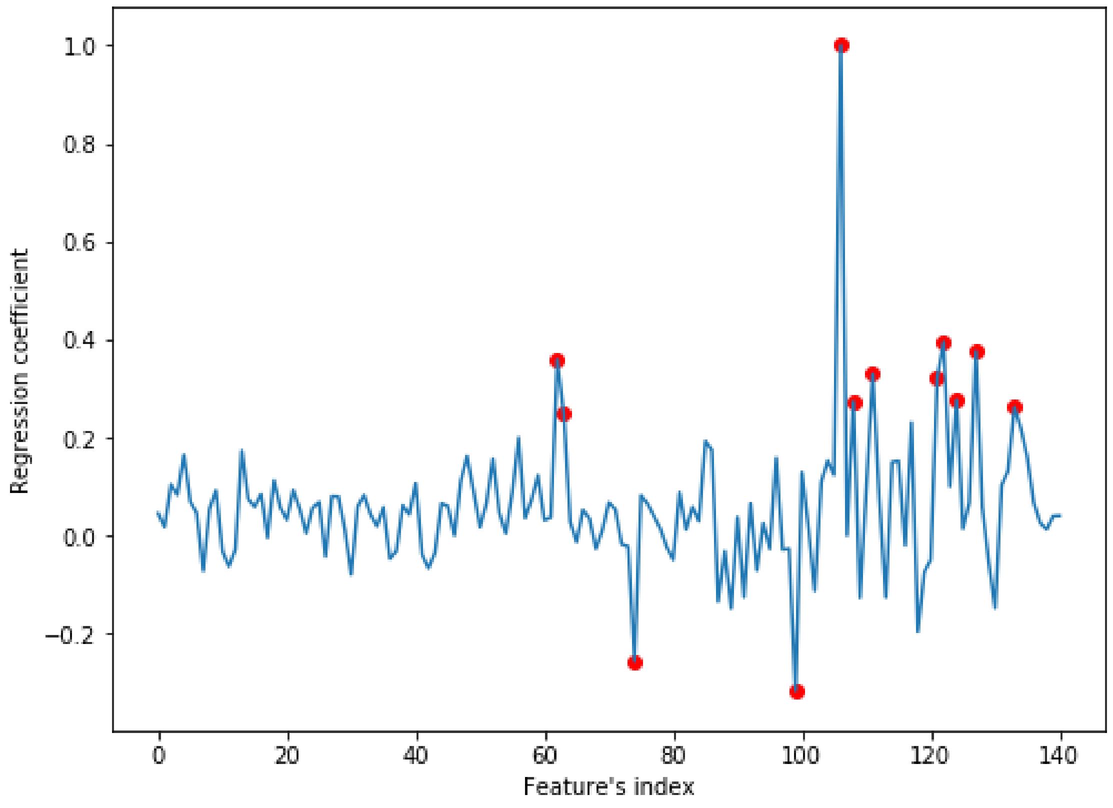
For `field = personality` 5 most impactful personality features (components) occupy only 29% of total variance, what means that features are **not very correlated (rather independent)**. To cover up 80% of total variance it's necessarily to take 35 most impactful features out of total 61.

1.2.2 2.2. Correlations with a chosen `feature`, restricted to a specified `group`

```
In [138]: @interact(feature = IntSlider(106,0,139,1), group = ['all', 'male', 'female', 'right
          def Correlate_with(feature, group):

              cols = responses_int.columns.to_list()
              feature = cols[feature]

              # Filter responses according to `group`

              if group == 'all':
                  responses_int_filtered = responses_int
              if group in {'male', 'female'}:
                  responses_int_filtered = responses_int[responses['Gender'] == group]
              if group in {'left handed', 'right handed'}:
                  responses_int_filtered = responses_int[responses['Left - right handed'] == g

              # Select 1 columns from correlation's table for specified `group`

              correlations = [responses_int_filtered[feature].corr(responses_int_filtered[f])

              # Filter, leaving only interesting correlations

              df = pd.DataFrame(correlations, columns = ['Correlations'])
              df = df[abs(df['Correlations']) > 0.25]

              # Make pretty visialisation for selected column

              corr_features = [cols[f] for f in df.index]
              corr = responses_int_filtered[corr_features].corr().loc[:,feature]

              print("Features correlated with '{}':".format(feature))
              corr_ = {'Feature\'s name':corr.index, 'Coefficient':round(corr,3).to_list()}
              corr_ = pd.DataFrame(corr_, index = df.index)
              corr_ = corr_[corr_['Feature\'s name'] != feature]
              display(corr_)

              # Visualise the plot

              plt.figure(figsize=(8,6))
              plt.plot(correlations)
              plt.xlabel('Feature\'s index')
              plt.ylabel('Regression coefficient')
              plt.scatter(df.index, np.array(corr), c='r')
```

```
            plt.show()
            print("Red dots correspond to features correlated with '{}'".format(feature))

        if running == 0:
            Correlate_with(106, 'all')
```

```
Features correlated with 'Number of friends':


              Feature's name  Coefficient
62          Fun with friends        0.359
63         Adrenaline sports        0.250
74   Fear of public speaking       -0.257
99                Loneliness       -0.317
108          New environment        0.273
111              Socializing        0.329
121        Happiness in life        0.321
122            Energy levels        0.394
124              Personality        0.276
127      Interests or hobbies        0.376
133   Entertainment spending        0.262
```



```
Red dots correspond to features correlated with 'Number of friends'
```

1.2.3 2.2. Search for interesting correlations

Consider `men` and `women` independently.

Find what features have most correlations with any of 'personality' features. But focus on features which lead to correlations with similar Pearson's value for **both men and women treated separently**. This approach is crucial, because i.e. if `men` are more likely to be interested in `cars` than `women` and at the same time, `men` are statisticaly `heigher` that `women`, then without considering gender independence we would get a correlation between `cars` and `height`, which is a nonsense.

```
In [139]: # Index _1 stands for men, index_2 stands for women

          for feature in personality.columns:

              cols = responses_int.columns.to_list()

              # Select 1 column from correlation's table for specified `group`, per group

              responses_male = responses_[responses_['Gender'] == 'male']
              responses_female = responses_[responses_['Gender'] == 'female']
              correlations_1 = [responses_male[feature].corr(responses_male[f]) for f in cols ]
              correlations_2 = [responses_female[feature].corr(responses_female[f]) for f in co

              # Filter, leaving only interesting correlations

              df_1 = pd.DataFrame(correlations_1, columns = ['Correlations'])
              df_1 = df_1[ abs(df_1['Correlations']) > 0.25]
              df_2 = pd.DataFrame(correlations_2, columns = ['Correlations'])
              df_2 = df_2[ abs(df_2['Correlations']) > 0.25]

              # Catch feature's index value

              features_index = df_1[df_1['Correlations'] > 0.99].index[0]

              # Preparations for pretty visualisation

              corr_features_1 = [cols[f] for f in df_1.index]
              corr_features_2 = [cols[f] for f in df_2.index]

              corr_1 = responses_male[corr_features_1].corr().loc[:,feature].drop([feature])
              corr_2 = responses_female[corr_features_2].corr().loc[:,feature].drop([feature])

              # Find set of features that lead to correlations in both genders
              set_ = set(corr_1.index) & set(corr_2.index)

              # If at least 5 distinct correlation are found
```

```
            if len(corr_1) > 0 and len(set_) > 5:

                corr_ = {'Correlated feature\'s name':list(set_)
                         , 'Coefficient for Men':round(corr_1,3).loc[set_].tolist()
                         , 'Coefficient for Women':round(corr_2,3).loc[set_].tolist()}

                corr_ = pd.DataFrame(corr_)
                corr_ = corr_.style.set_caption("Feature\'s name: {}".format(feature)).hide_
                print("Feature\'s name ({}): {}:".format(features_index, feature))
                display(corr_)
```

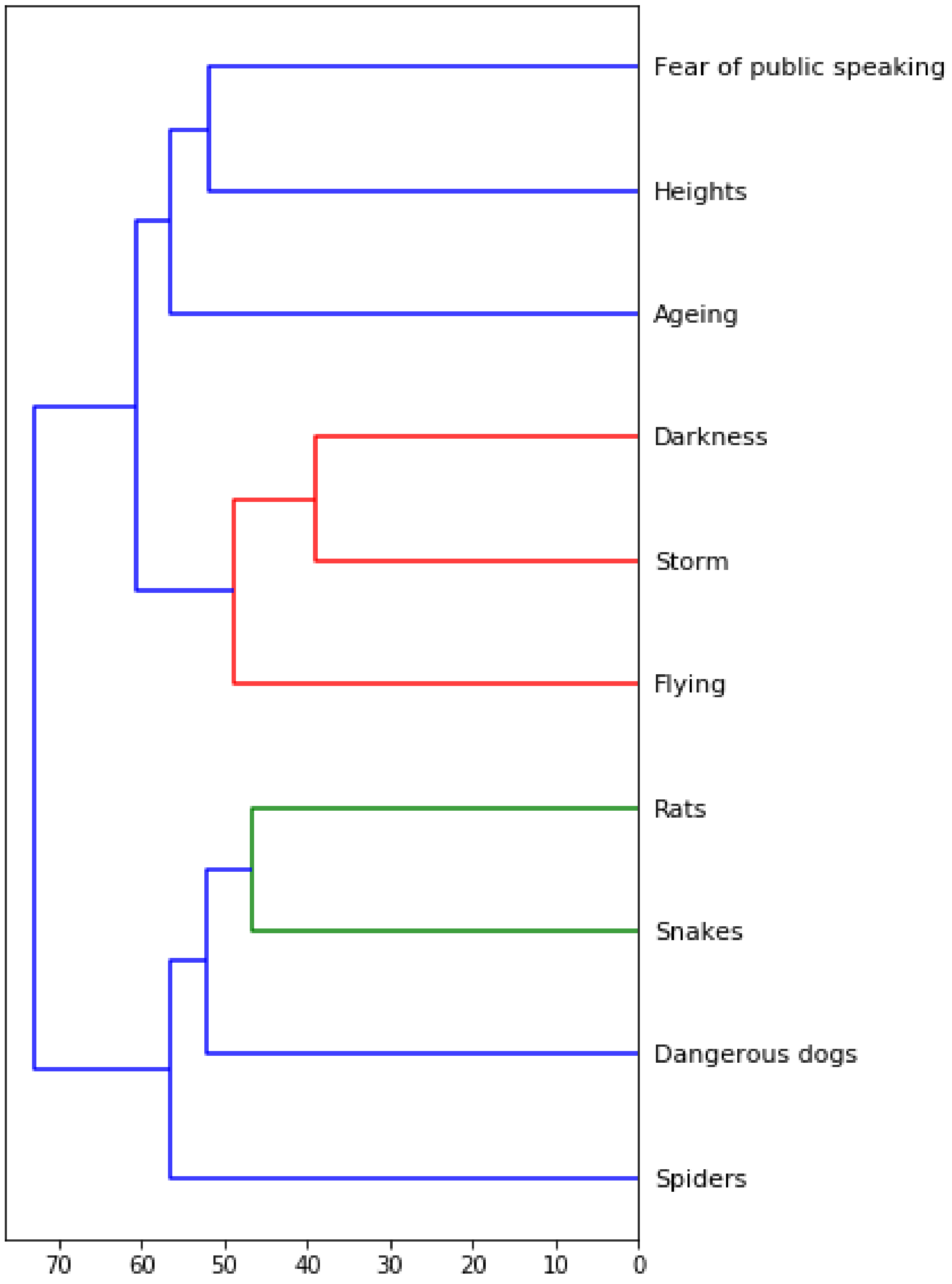
```
Feature's name (106): Number of friends:


<pandas.io.formats.style.Styler at 0x7f52150157b8>


Feature's name (122): Energy levels:


<pandas.io.formats.style.Styler at 0x7f52142983c8>


Feature's name (134): Spending on looks:


<pandas.io.formats.style.Styler at 0x7f5214280940>
```

1.3 3. Clustering

1.3.1 3.1. Hierarchical clustering for a chosen `field`

```
In [140]: @interact(field = ['phobias','music','movies','hobbies','personality'])
          def Hierarchical_cluster(field):
              field = field_name[field]

              df_select = field.copy(deep=True).dropna()
              x = df_select.to_numpy().T

              # Adjust figure size to accommodate the full tree

              rcParams['figure.figsize'] = 5, 10

              # Do a hierarchical clustering using Ward's method

              z = sch.linkage(x, method='ward')

              # Display dendrogram
```

```
    names = df_select.columns.tolist()
    info = sch.dendrogram(z, orientation='left', labels=names, leaf_font_size=11)
    plt.show()

if running == 0:
    Hierarchical_cluster('phobias')
```



Comment 1: `phobias` seem to have 3 distinct types: - animals (Rats, Snakes, Dangerous dogs, Spiders) - nature (Darkness, Storm, Flying) - social (Fear of public speaking, Heights, Ageing)

Comment 2: `music` clusters in 5 distinct types: - **old music**: rock n roll, jazz, alternative - **metal-**

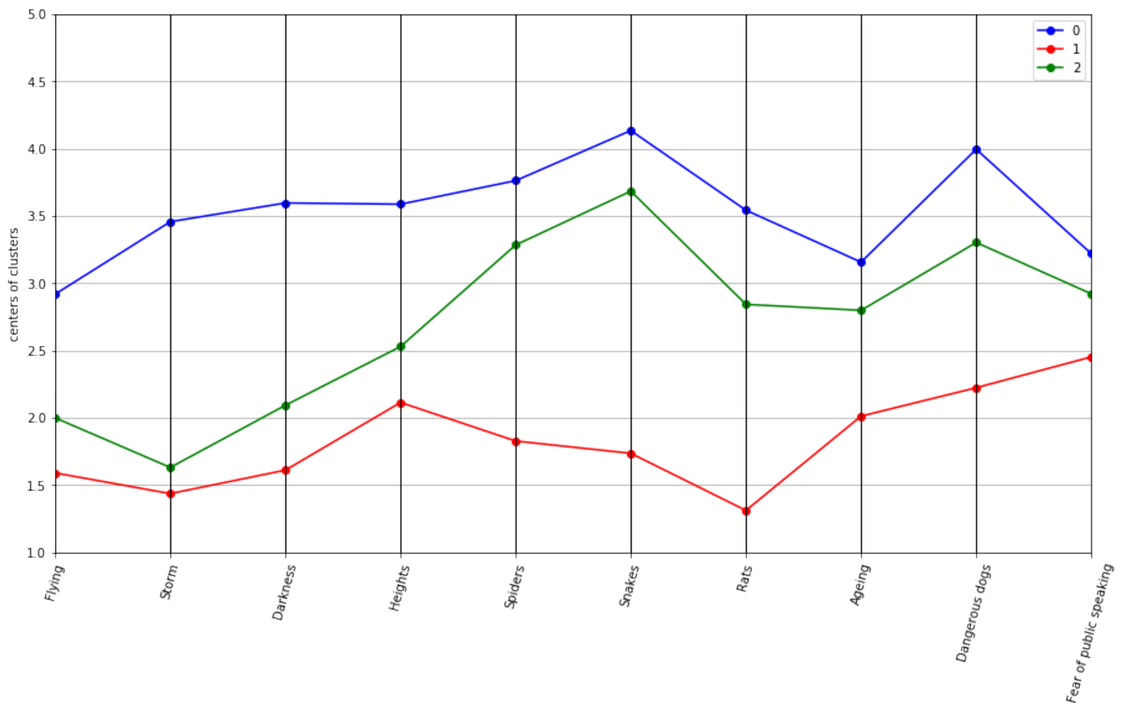
like music: rockˆ, punk, metal - **instrumental music**": opera, classical, country, folk - **popular music**: latino, musical, pop, dance - **rap-like music**: reggae, hiphip, techno

ˆ although rock was assigned to 'yellow label', it's not too far from 'magenta label', which seems more logical

1.3.2 3.2. K-means clustering for a chosen `field`

```
In [141]: @interact(field = ['phobias','music','movies','hobbies','personality'], noOfClusters
                          randomstate = IntSlider(745,0,10000,10))
          def K_means_cluster(field, noOfClusters, randomstate):

              field = field_name[field]
              df_select = field.copy(deep=True).dropna()

              # Perform scaling on the dataframe containing the field's features

              scaler_x = StandardScaler()
              data = scaler_x.fit_transform(df_select)

              # Perform K-Means

              model = KMeans(init='k-means++', n_clusters=noOfClusters, n_init=20, random_state

              print("Total sum of squares of distances:", round(model.inertia_))
              print(90*'_')
              print("\nCount of people in each cluster")
              print(90*'_')
              print(pd.value_counts(model.labels_, sort=False))

              # Display plot showing centers of clusters

              P = pd_centers(featuresUsed=field.columns.to_list(),
                             centers=scaler_x.inverse_transform(model.cluster_centers_))
              parallel_plot(P, (15, 8))
              plt.show()

          if running == 0:
              K_means_cluster('phobias', 3, 745)
```

```
Total sum of squares of distances: 7088.0
__________________________________________________________________________________________

Count of people in each cluster
__________________________________________________________________________________________
0    223
1    384
2    383
dtype: int64
```



Comment 1:
For `phobias` with `3 clusters` people seem to divide in following types:

- people scared of nothing.
- people scared of various animals.
- people scared of everything.

Using `4 clusters` reveals an additional group, without changing centers of previous `3 clusters`:

- people scared of everything except of animals.

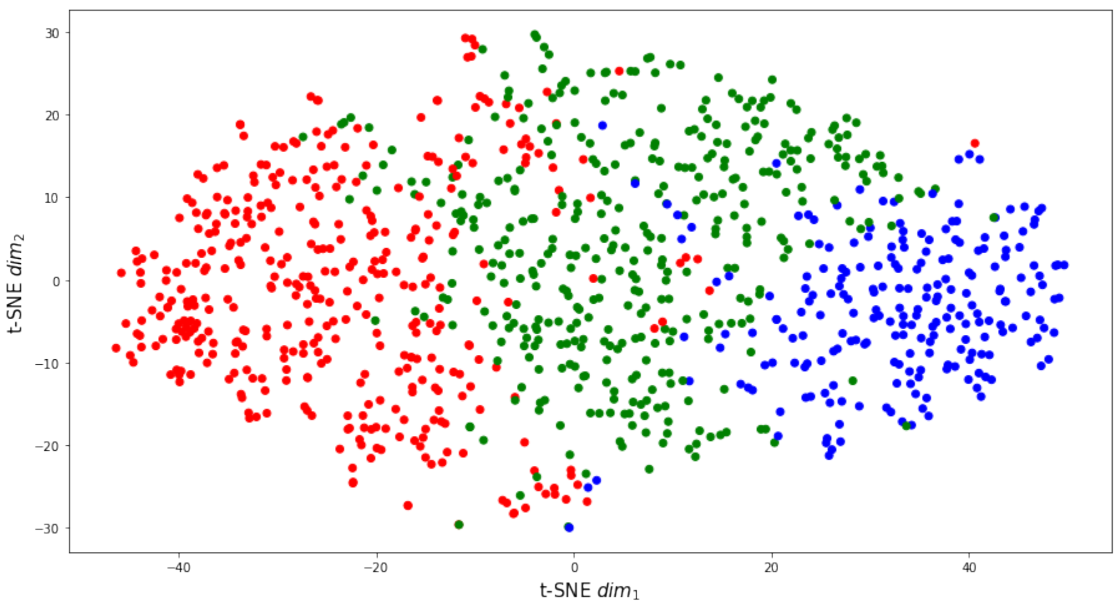
Using `5 clusters` modifies some of previous cluster's centers.

1.3.3 3.3. t-SNE

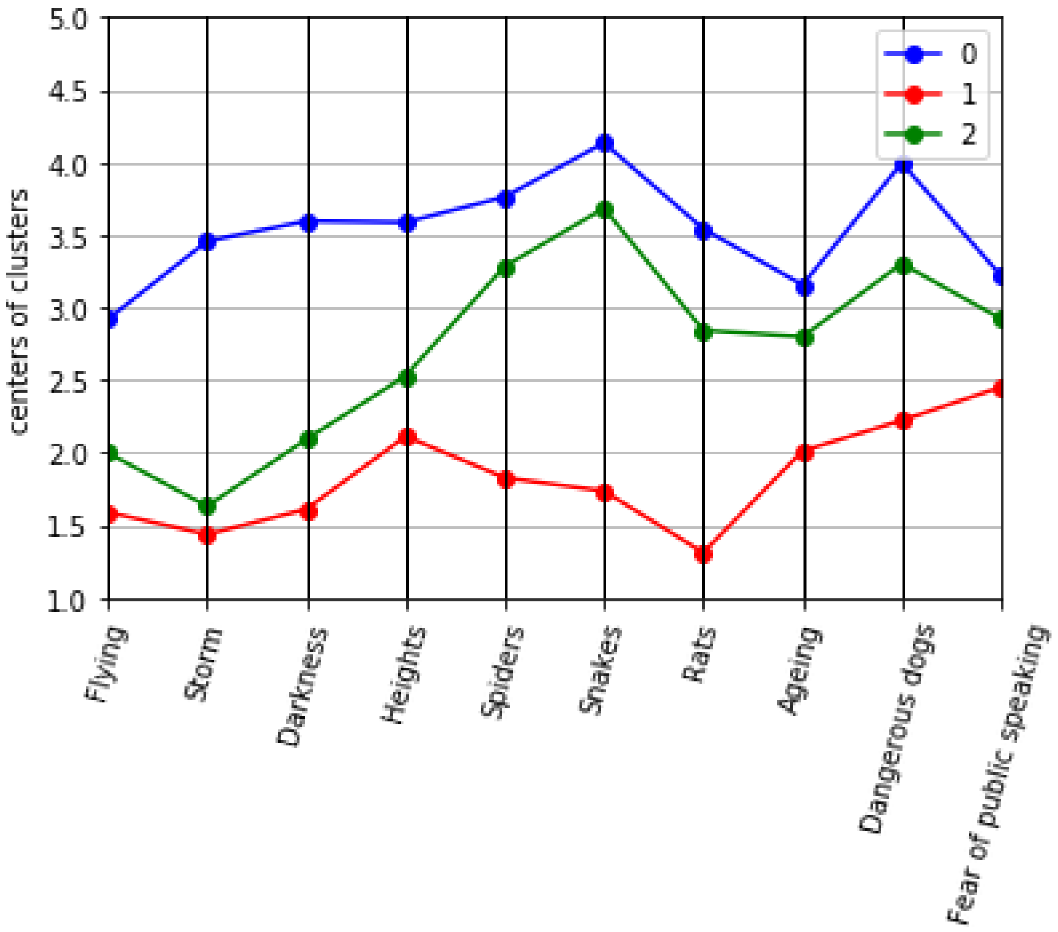
Visualise data of specified `field` by reducing its dimensions to 2D space, using `t-distributed stochastic neighbor embedding`.

```
In [142]: @interact(field = ['phobias','music','movies','hobbies','personality'], noOfClusters
                    randomstate = IntSlider(745,0,10000,10))
          def T_SNE_cluster(field, noOfClusters, randomstate):

              field = field_name[field]
```

```
    df_select = field.copy(deep=True).dropna()

    # Compute K-means to get labels

    scaler_x = StandardScaler()
    data = scaler_x.fit_transform(df_select)
    model = KMeans(init='k-means++', n_clusters=noOfClusters,
                   n_init=20, random_state=randomstate).fit(data)

    a = [0, 1, 2, 3, 4, 5, 6]
    b = ['b', 'r', 'g', 'y', 'k', 'm']
    dict_ = dict(zip(a,b))
    colors = [dict_[i] for i in model.labels_]

    # Show result of T-SNE

    plt.figure(figsize=(15,8))
    X_embedded = TSNE(n_components=2, random_state=randomstate).fit_transform(data)
    plt.scatter(X_embedded[:,0], X_embedded[:,1], color = colors)
    plt.xlabel('t-SNE $dim_1$', size=15)
    plt.ylabel('t-SNE $dim_2$', size=15)
    plt.show()

    # Show result of K-means for labels colors

    P = pd_centers(featuresUsed=field.columns.to_list(),
                   centers=scaler_x.inverse_transform(model.cluster_centers_))
    parallel_plot(P, (6, 4))
    plt.show()

if running == 0:
    T_SNE_cluster('phobias', 3, 745)
```



t-SNE dim_2
t-SNE dim_1



centers of clusters
0
1
2
Flying
Storm
Darkness
Heights
Spiders
Snakes
Rats
Ageing
Dangerous dogs
Fear of public speaking

Comment 1:

For phobias, using coloring from K-means algorithm, we notice that for 3 clusters data is well separated, but for 4 clusters two of the clusters are mixed. This suggests that 3 is trully an appropriate number of clusters.

However, cluster regions are tangential with their bondaries, which means that there exist people who's preferences are on the middle, instead belonging purely to one distinct cluster.

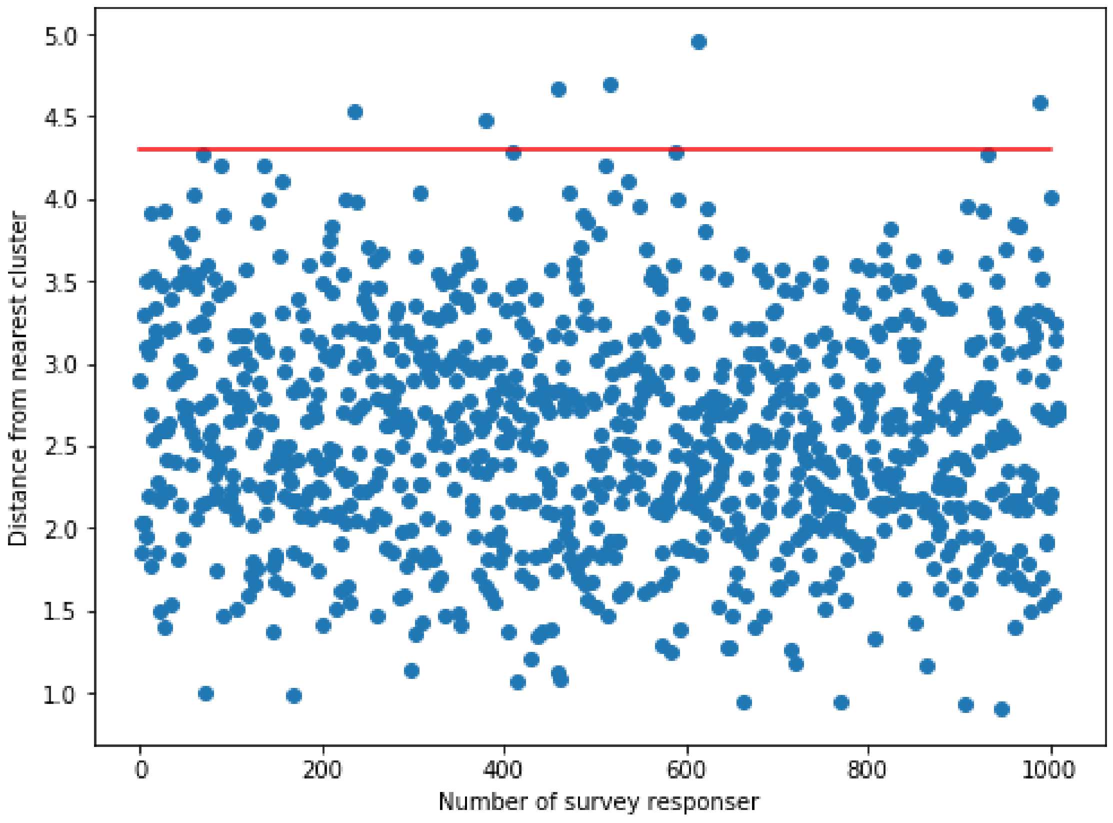
1.3.4 3.4. Finding outliners

People who likely cheated by answering randomly.

allowed_dist is maximum allowed distance from nearest cluster to not be considered as an outliner

```
In [143]: @interact(field = ['phobias','music','movies','hobbies','personality'], noOfClusters
                    randomstate = IntSlider(745,0,10000,10), allowed_dist = FloatSlider(value=4
          def Find_outliners(field, noOfClusters, randomstate, allowed_dist):

              field = field_name[field]
              df_select = field.copy(deep=True).dropna()

              # Compute K-means

              scaler_x = StandardScaler()
              data = scaler_x.fit_transform(df_select)
              model = KMeans(init='k-means++', n_clusters=noOfClusters,
                             n_init=20, random_state=randomstate).fit(data)

              centers = model.cluster_centers_

              # Plot distance from nearest cluster for all points for which cluster analysis w

              plt.figure(figsize=(8,6))
              x = df_select.index.tolist()
              y = [min([np.linalg.norm(a-b) for a in centers]) for b in data[:] ]
              plt.scatter(x,y)
              plt.plot([0,1000], [allowed_dist, allowed_dist], 'red') # Above this line are ou
              plt.xlabel("Number of survey responser")
              plt.ylabel("Distance from nearest cluster")
              plt.show()

              # Find which points are far away from any cluster. Print their indexies and meas

              outliners = []
              for i in range(len(y)):
                  if y[i] > allowed_dist:
                      outliners.append((x[i], y[i], df_select.index[i]))
```

```
    print("Number of people above the red line: {}".format(len(outliners)))
    print("Number of survey responser and its distance from nearest cluster (max 10)
    for outliner in outliners[:min(10, len(outliners))]:
        print(outliner[0], "\t", round(outliner[1], 3))

    # Gather all informations about found ouliners, being carefull on index (notice 

    filter_ = np.full(responses.shape[0], False)
    for outliner in outliners:
        filter_[outliner[2]] = True
    df_ = responses[filter_]

    # Select and display only columns including strings

    df_cols = set(df_.columns) - set(df_.select_dtypes(include=['int','float']).colu
    print( "\nAll non-numeric informations about surveyors detected as outliners (ma
    display(df_[df_cols][:min(10, df_.shape[0])])

if running == 0:
    Find_outliners('phobias', 3, 745, 4.3)
```



```
Number of people above the red line: 6
Number of survey responser and its distance from nearest cluster (max 10):

236          4.531
378          4.472
458          4.666
516          4.704
614          4.957
989          4.582

All non-numeric informations about surveyors detected as outliners (max 10):


            Alcohol Only child House - block of flats  Gender Village - town  \
236     drink a lot        yes         block of flats  female           city
378     drink a lot         no         block of flats  female           city
458  social drinker         no        house/bungalow  female        village
516           never         no         block of flats    male           city
614  social drinker         no        house/bungalow  female        village
989     drink a lot         no        house/bungalow  female        village

                 Punctuality         Education           Internet usage  \
236         i am often early  secondary school  less than an hour a day
378  i am often running late  secondary school          few hours a day
458  i am often running late  secondary school          few hours a day
516       i am always on time  secondary school          few hours a day
614         i am often early  secondary school          few hours a day
989         i am often early    masters degree          most of the day

                          Lying         Smoking Left - right handed
236                   sometimes   tried smoking        right handed
378                   sometimes   tried smoking        right handed
458  only to avoid hurting someone   tried smoking        right handed
516                   sometimes   tried smoking        right handed
614                   sometimes  current smoker        right handed
989                   sometimes   former smoker        right handed
```

Comment 1:
Seems like most of the outliners are woman. Possibly, woman tend to be more undecisive than men, not necessary being 'cheaters'.

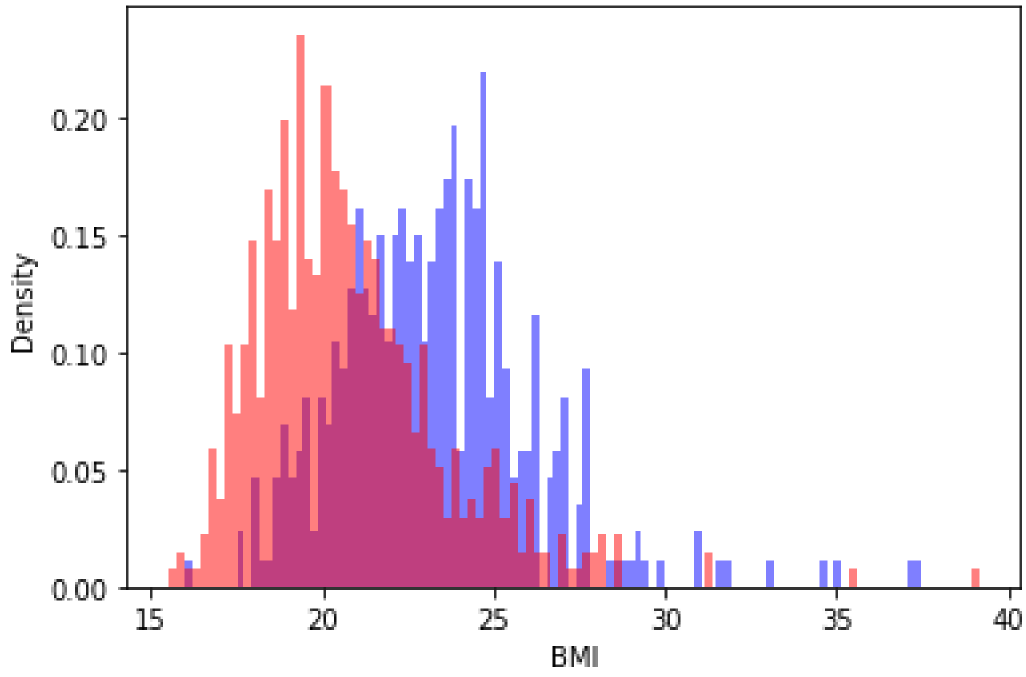
1.4 4. Other

1.4.1 4.1. BMI (body mass index) distribution within genders

```
In [144]: plt.figure(figsize=(6,4))

          responses_male = responses_[responses_['Gender'] == 'male']
```

```
responses_female = responses_[responses_['Gender'] == 'female']

responses_male['BMI'].plot.hist(bins=100, alpha=0.5, color = 'blue', density = True)
responses_female['BMI'].plot.hist(bins=100, alpha=0.5, color = 'red', density = True

plt.xlabel('BMI')
plt.ylabel('Density')
```

```
Out[144]: Text(0, 0.5, 'Density')
```



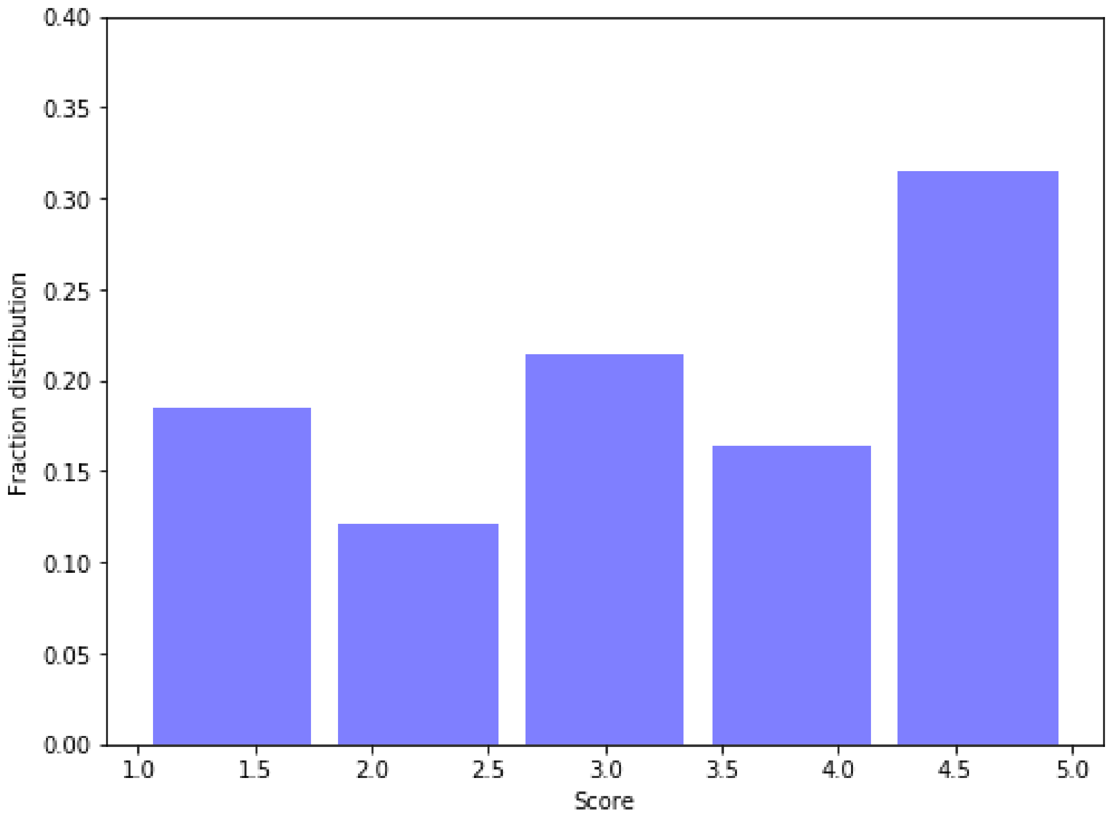
Comment 1:
both genders have gaussian-like distribution of BMI values, however their mean values differ:
- women's average BMI is around 20 - men's average BMI is around 24

1.4.2 4.2. Feature's distribution between groups.

```
In [145]: @interact(feature = IntSlider(103,0,139,1), group = ['all', 'male', 'female', 'right
          def Compare(feature, group):

              cols = responses_int.columns.to_list()
              feature = cols[feature]

              # Filter responses according to `group`

              if group == 'all':
                  responses_int_filtered = responses_int
```

```
            if group in {'male', 'female'}:
                responses_int_filtered = responses_int[responses['Gender'] == group]
            if group in {'left handed', 'right handed'}:
                responses_int_filtered = responses_int[responses['Left - right handed'] == gr

            # Nan values are not plotted, so disclude them in counting

            n = sum(responses_int_filtered[feature] == responses_int_filtered[feature])

            print("Fraction distribution for '{}' in group '{}':".format(feature, group))
            display(responses_int_filtered[feature].value_counts(normalize=True).sort_index()

            plt.figure(figsize=(8,6))
            responses_int_filtered[feature].plot.hist(bins=5, alpha=0.5, color='b',
                                                     weights = [1./n for i in range(0,n)], 
            plt.xlabel('Score')
            plt.ylabel('Fraction distribution')
            plt.ylim(0,0.4)
            plt.show()

        if running == 0:
            Compare(103, 'all')
```

```
Fraction distribution for 'God' in group 'all':


1.0    0.185516
2.0    0.121032
3.0    0.214286
4.0    0.163690
5.0    0.315476
Name: God, dtype: float64
```



Comment 1:

Woman are more likely to be religious. - 36% of woman and 25% of men are strongly religious (5.0 points in survey). - 15% of woman and 24% of men are atheist-like (1.0 point in survey).