

clustering_hclust

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```
In [1]: import pandas as pd
import seaborn as sn
```

0.1 1. Preparing Data

Read data from a specified location

```
In [2]: from IPython.core.interactiveshell import InteractiveShell
InteractiveShell.ast_node_interactivity = "all"

In [3]: raw_df = pd.read_csv( "/Users/Rahul/Documents/Datasets/Hclust_Beer data.csv",
                             sep = ',', na_values = ['', ' '])

raw_df.columns = raw_df.columns.str.lower().str.replace(' ', '_')
raw_df.head()
```

```
Out[3]:
```

	id	beer	cal	sod	alc	cost
0	1	Budweiser	144	15	4.7	0.43
1	2	Schlitz	151	19	4.9	0.43
2	3	Lowenbrau	157	15	4.9	0.48
3	4	Kronenbourg	170	7	5.2	0.73
4	5	Heineken	152	11	5.0	0.77

0.2 2. Extract Features and Standardize

Two ways to extract the features:

- use `pd.filter` and pass the list of features to extract for scaling
- Use `pd.drop` and pass the list of features which need not be extracted

The feature can also be extracted by using `dataframeName[['<name of features>']]`

```
In [4]: #feature_df = raw_df[['cal', 'sod', 'alc', 'cost']]

feature_df = raw_df.drop({'id', 'beer'}, axis = 1)
col_names = feature_df.columns
#col_names

row_index = raw_df.iloc[:,1]
#row_index
```

```
In [5]: from sklearn.preprocessing import StandardScaler
        scaler = StandardScaler()

        feature_scaled_df = pd.DataFrame(scaler.fit_transform( feature_df ))

        feature_scaled_df.columns = col_names
        feature_scaled_df.index = row_index
```

Use rename function, in case renaming of a specific column or index is required

```
In [6]: #feature_scaled_df.rename(index={'Budweiser': 'Bud'}, inplace=True)
```

The referencing of a row or column can be changed by using the below code chunk. Uncomment and change the values within `iloc` to understand how referencing works:

```
In [7]: #ref_row_col = raw_df.iloc[:,:]
        #ref_row_col
```

```
In [8]: feature_scaled_df
```

```
Out [8]:
```

	cal	sod	alc	cost
beer				
Budweiser	0.393336	0.007795	0.351095	-0.470541
Schlitz	0.630693	0.631369	0.621168	-0.470541
Lowenbrau	0.834143	0.007795	0.621168	-0.114071
Kronenbourg	1.274950	-1.239354	1.026278	1.668282
Heineken	0.664602	-0.615780	0.756205	1.953459
Old Mil	0.427244	1.254943	0.216058	-1.539953
Augsburger	1.444491	1.410837	1.431387	-0.684423
Strohs	0.562877	1.878518	0.351095	-0.541835
Miller lite	-1.132535	-0.771673	-0.189051	-0.470541
Bud light	-0.657820	-1.083460	-0.999270	-0.399247
Coors	0.257703	0.475475	0.216058	-0.399247
Coors lite	-1.030811	0.007795	-0.459124	-0.327953
Michelob light	0.088161	-0.615780	-0.324088	0.028518
Becks	0.596785	0.631369	0.351095	1.882165
Kirin	0.562877	-1.395248	0.756205	2.096047
Pabst	-2.183691	0.007795	-2.889782	-0.827012
Hamms	0.122070	0.631369	-0.054015	-0.470541
Heilemans	0.393336	1.410837	0.621168	-0.470541
Olympia	-2.048058	-1.395248	-2.079563	-0.256659
Schlitz lite	-1.200352	-1.239354	-0.324088	-0.185365

0.3 3. Cluster and Visualize

Refer to <http://docs.scipy.org/doc/scipy/reference/generated/scipy.cluster.hierarchy.linkage.html> for reference to available methods, metric.

Rather than standardizing the values above We could have set `z_score` parameter inside the `clustermap` to 1 for standardizing the column values.

```
In [9]: sn.clustermap(feature_scaled_df, method = 'complete', metric = 'euclidean',
    row_cluster=True,col_cluster = False,
    linewidths=.5,figsize =(15,15))
```

```
Out[9]: <seaborn.matrix.ClusterGrid at 0x116372748>
```

