# 1. 군집화 분석 수행

- Absenteeism at work dataset
- Clustering task를 위한 numerical attribute type의 데이터를 조건으로 설정하였습니다. Attribute는 10~100개, instance는 100~1000개 사이를 원한다는 데이터 조건도 추가하였더니 옆 사진과 같이 11개의 데이터 셋이 나왔습니다.
- 그 중, 직장 결근(absenteeism at work)과 관련된 데이터 셋이 흥미로운 주제라고 생각하여 선택하였습니다.
- 군집화 분석 수행 과제를 ver1과 ver2로 진행하였습니다. 두 버전의 코드와 실행화면을 설명할 예정입니다.

# 군집화 분석 수행 Ver.1

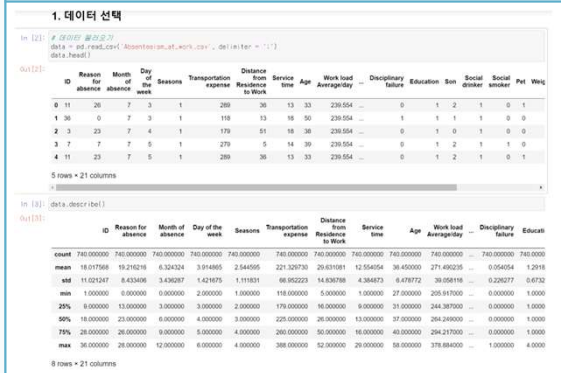
- 필요한 패키지, 라이브러리 설치
- 데이터 불러오기 (csv) ☞ data
- describe(), isnull(), dtypes 실행
- → 결측치 없음

기계학습 과제#1

Absenteeism at work dataset - EDA & Machine Learning Model

```
In [1]: # 설치되지 않은 라이브러리(오류..)은 anaconda prompt에서 pip install ~

import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import matplotlib.style as style

%matplotlib inline
import plotly.offline as py
import plotly.graph_objs as go
from plotly.offline import download_plotlyjs, init_notebook_mode, plot, iplot
import plotly.tools as tls
import plotly.figure_factory as ff
py.init_notebook_mode(connected=True)
import squarify

# import 클러스터링 위한 라이브러리
import sklearn
from sklearn.preprocessing import StandardScaler
from sklearn.cluster import KMeans
from sklearn.metrics import silhouette_score
from scipy.cluster.hierarchy import linkage
from scipy.cluster.hierarchy import dendrogram
from scipy.cluster.hierarchy import cut_tree
```

```
In [4]: # 결측치 확인
data.isnull().sum().sort_values(ascending = False)

Out[4]: ID                               0
Disciplinary failure                0
Body mass index                     0
Height                              0
Weight                              0
Pet                                 0
Social smoker                       0
Social drinker                      0
Son                                 0
Education                           0
Hit target                          0
Reason for absence                  0
Work load Average/day               0
Age                                 0
Service time                        0
Distance from Residence to Work     0
Transportation expense              0
Seasons                             0
Day of the week                     0
Month of absence                    0
Absenteeism time in hours           0
dtype: int64
```



1. 데이터 선택

```
In [2]: # 데이터 불러오기
data = pd.read_csv('Absenteeism_at_work.csv', delimiter = ';')
data.head()
```

Out[2]:

| | ID | Reason for absence | Month of absence | Day of the week | Seasons | Transportation expense | Distance from Residence to Work | Service time | Age | Work load Average/day | ... | Disciplinary failure | Education | Son | Social drinker | Social smoker | Pet | Weig |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 0 | 11 | 26 | 7 | 3 | 1 | 289 | 36 | 13 | 33 | 239.554 | ... | 0 | 1 | 2 | 1 | 0 | 1 | |
| 1 | 36 | 0 | 7 | 3 | 1 | 118 | 13 | 18 | 50 | 239.554 | ... | 1 | 1 | 1 | 1 | 0 | 0 | |
| 2 | 3 | 23 | 7 | 4 | 1 | 179 | 51 | 18 | 38 | 239.554 | ... | 0 | 1 | 0 | 1 | 0 | 0 | |
| 3 | 7 | 7 | 7 | 5 | 1 | 279 | 5 | 14 | 39 | 239.554 | ... | 0 | 1 | 2 | 1 | 1 | 0 | |
| 4 | 11 | 23 | 7 | 5 | 1 | 289 | 36 | 13 | 33 | 239.554 | ... | 0 | 1 | 2 | 1 | 0 | 1 | |

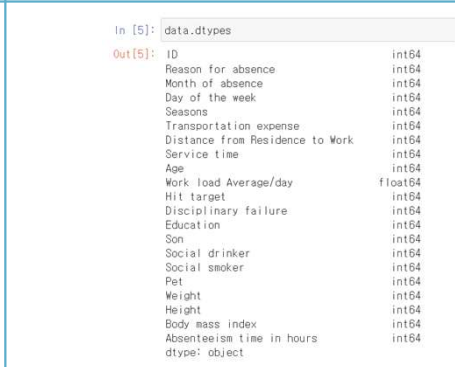
5 rows × 21 columns

```
In [3]: data.describe()
```

Out[3]:

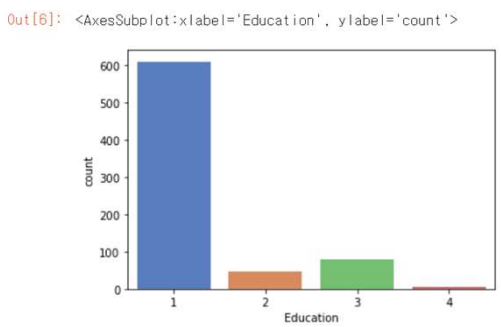
| | ID | Reason for absence | Month of absence | Day of the week | Seasons | Transportation expense | Distance from Residence to Work | Service time | Age | Work load Average/day | ... | Disciplinary failure | Educati |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| count | 740.000000 | 740.000000 | 740.000000 | 740.000000 | 740.000000 | 740.000000 | 740.000000 | 740.000000 | 740.000000 | 740.000000 | ... | 740.000000 | 740.0000 |
| mean | 18.017568 | 19.216216 | 6.324324 | 3.914865 | 2.544595 | 221.329730 | 29.631081 | 12.554054 | 36.450000 | 271.490235 | ... | 0.054054 | 1.2918 |
| std | 11.021247 | 8.433406 | 3.436287 | 1.421675 | 1.111831 | 66.952223 | 14.836788 | 4.384873 | 6.478772 | 39.058116 | ... | 0.226277 | 0.6732 |
| min | 1.000000 | 0.000000 | 0.000000 | 2.000000 | 1.000000 | 118.000000 | 5.000000 | 1.000000 | 27.000000 | 205.917000 | ... | 0.000000 | 1.0000 |
| 25% | 9.000000 | 13.000000 | 3.000000 | 3.000000 | 2.000000 | 179.000000 | 16.000000 | 9.000000 | 31.000000 | 244.387000 | ... | 0.000000 | 1.0000 |
| 50% | 18.000000 | 23.000000 | 6.000000 | 4.000000 | 3.000000 | 225.000000 | 26.000000 | 13.000000 | 37.000000 | 264.249000 | ... | 0.000000 | 1.0000 |
| 75% | 28.000000 | 26.000000 | 9.000000 | 5.000000 | 4.000000 | 260.000000 | 50.000000 | 16.000000 | 40.000000 | 294.217000 | ... | 0.000000 | 1.0000 |
| max | 36.000000 | 28.000000 | 12.000000 | 6.000000 | 4.000000 | 388.000000 | 52.000000 | 29.000000 | 58.000000 | 378.884000 | ... | 1.000000 | 4.0000 |

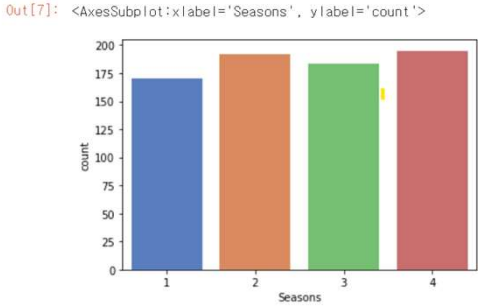
8 rows × 21 columns

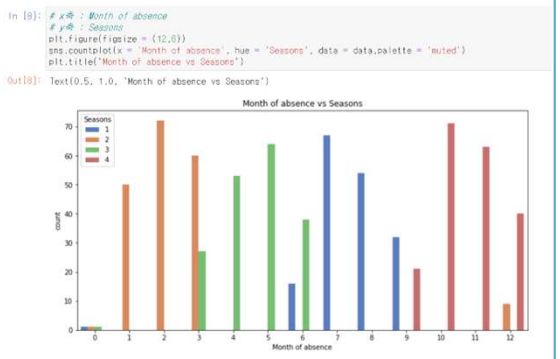


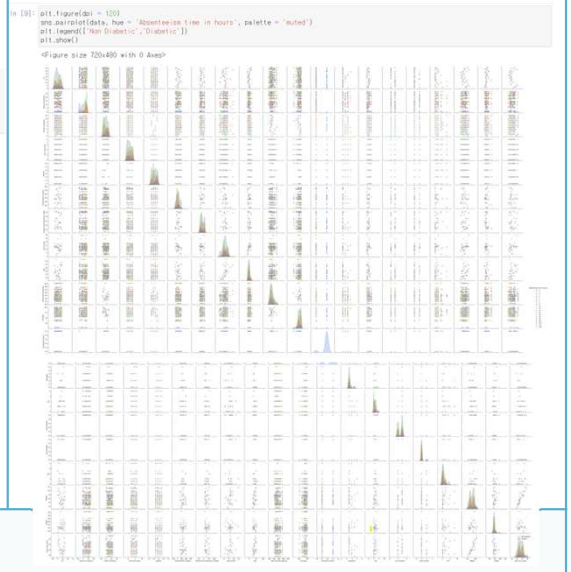
```
In [5]: data.dtypes

Out[5]: ID                               int64
Reason for absence                  int64
Month of absence                    int64
Day of the week                     int64
Seasons                             int64
Transportation expense              int64
Distance from Residence to Work     int64
Service time                        int64
Age                                 int64
Work load Average/day             float64
Hit target                          int64
Disciplinary failure                int64
Education                           int64
Son                                 int64
Social drinker                      int64
Social smoker                       int64
Pet                                 int64
Weight                              int64
Height                              int64
Body mass index                     int64
Absenteeism time in hours           int64
dtype: object
```

- data의 Education, Seasons attribute 에 대한 countplot 그리기
- Month of absence vs Seasons countplot 그리기
- pairplot 그려보기
- pairplot : 데이터의 각 컬럼(열)들의 모든 상관관계 출력, 그리드(grid) 형태로 각 집합의 조합에 대해 히스토그램과 분포도 그린다. 3차원 이상의 데이터라면 pairplot 함수를 사용해 분포도 그린다.

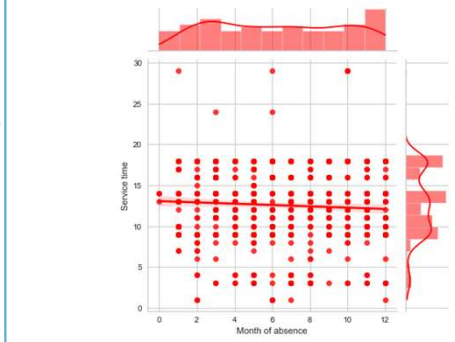


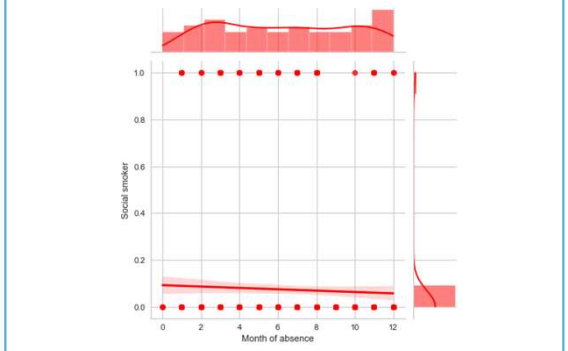



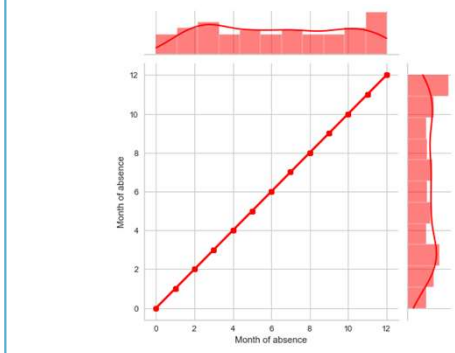



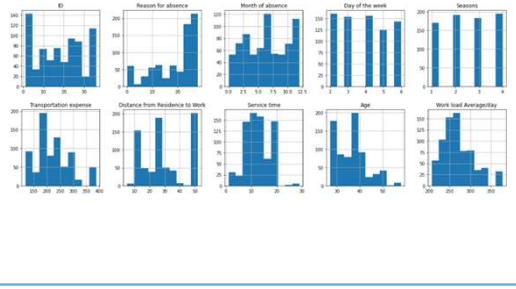
- 변수 간 상관관계 확인 → Joint plot (Month of Absence with Other Variables) 그려보기
- i != 'Glucose' and i != 'Outcome'
- print(f"Correlation between Month of absence and {i} ==> ", data.corr().loc['Month of absence'][i])
  ☞ **변수 간 상관성 문장 출력**
- 총 21개의 그래프와 상관성 도출, 그 중 일부

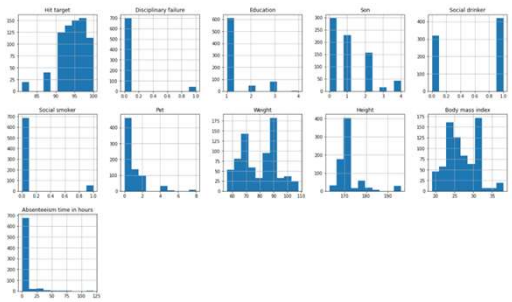



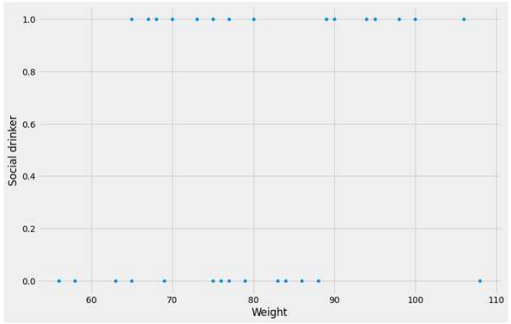



- 데이터 분포 관찰 위한 시각화 진행 (hist)
- scatterplot 함수 정의
- → scatterplot 그려보기
- data의 column 확인
- customized_scatterplot(data['Social drinker'], data['Weight'])

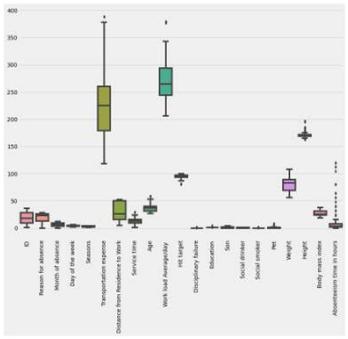


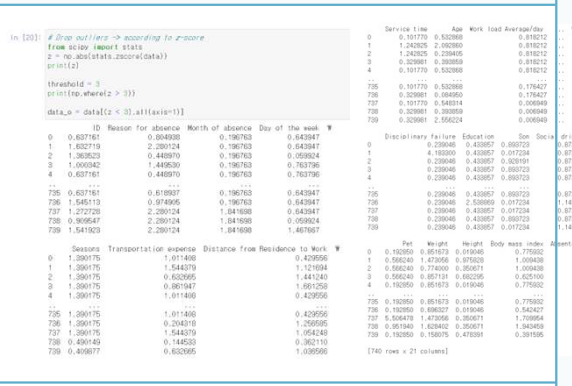

```
In [12]: data['Social drinker'].value_counts()
Out[12]: 1    420
         0    320
         Name: Social drinker, dtype: int64

In [13]: from plotly.offline import download_plotlyjs, init_notebook_mode, plot, iplot
         import plotly.graph_objs as go

         # tolist : array를 list로 변환
         vals = data['Social drinker'].value_counts().tolist()
         labels = [0,1]

         df = [go.Bar(x = labels, y = vals, marker = dict(color="#F7CF6A"))]

         layout = go.Layout(title = "Count by Social drinker")

         fig = go.Figure(data = df, layout = layout)

         iplot(fig, filename = 'basic-bar')

In [14]: # 함수 정의
         def customized_scatterplot(y, x):
             ## plot sizing
             style.use('fivethirtyeight')
             plt.subplots(figsize = (12,8))
             # 인풋 변수 plotting - 종속 변수
             sns.scatterplot(y = y, x = x);

In [15]: data.columns
Out[15]: Index(['ID', 'Reason for absence', 'Month of absence', 'Day of the week',
                'Seasons', 'Transportation expense', 'Distance from Residence to Work',
                'Service time', 'Age', 'Work load Average/day ', 'Hit target',
                'Disciplinary failure', 'Education', 'Son', 'Social drinker',
                'Social smoker', 'Pet', 'Weight', 'Height', 'Body mass index',
                'Absenteeism time in hours'],
               dtype='object')
```

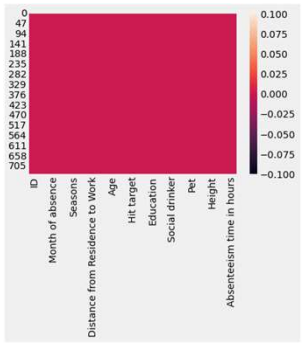


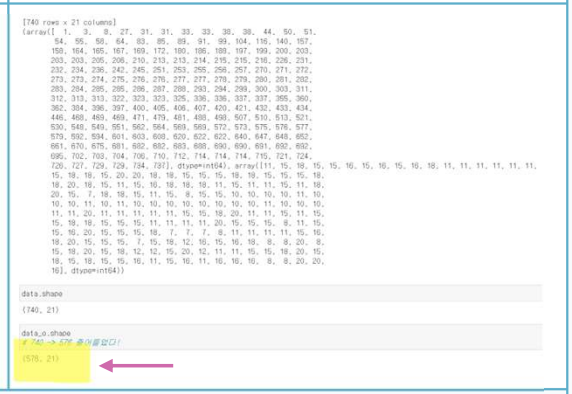



- outlier 확인 위해 boxplot 사용
- 누락/null 값 확인 위해 heatmap 사용
- data의 outlier를 drop한 data_o
- → data의 shape (740,21)에 비해 data_o의 shape (576,21) 줄어들었다!





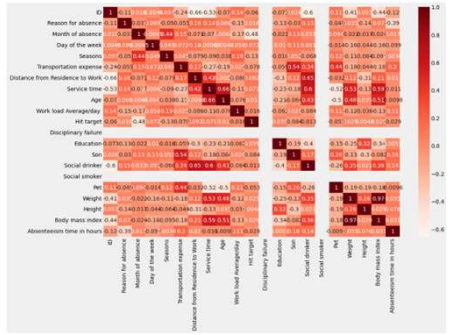


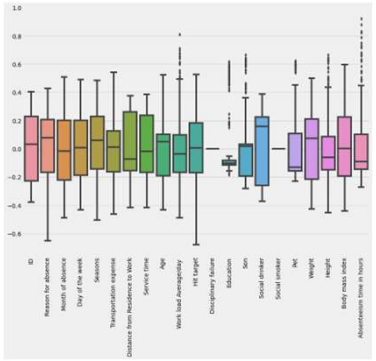



- 정규화 진행 Normalization
- scaler에 data_o 채우고 normalize 진행, numpy array → DataFrame 변환
- 정규화된 데이터 boxplot 그리기
- heatmap 그리기
- 높은 상관성을 갖는 feature 도출

In [23]:
```
# Normalize
from sklearn import preprocessing
from sklearn.preprocessing import StandardScaler, normalize

# 컬럼명
names = data_o.columns

# Create Scaler object
scaler = preprocessing.StandardScaler()

# Fit data on the scaler object
scaled_df = scaler.fit_transform(data_o)
scaled_df = pd.DataFrame(scaled_df, columns=names)

# Normalizing the Data
normalized_df = normalize(scaled_df)

# Converting the numpy array -> pandas DataFrame
normalized_df = pd.DataFrame(normalized_df,columns=names)
```

In [24]:
```
plt.figure(figsize = (13,10))
sns.boxplot(data = normalized_df)
plt.xticks(rotation = 90)
```

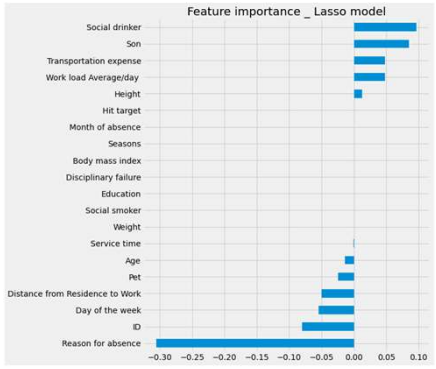


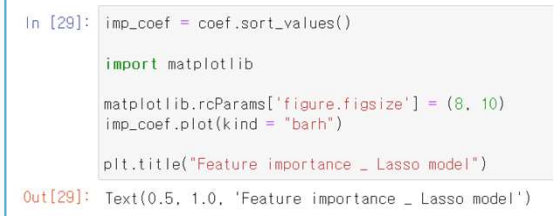


In [26]:
```
# Correlation with output variable
cor_target = abs(cor["Absenteeism time in hours"])

# Selecting highly correlated features
relevant_features = cor_target[cor_target>0.5]
relevant_features
```

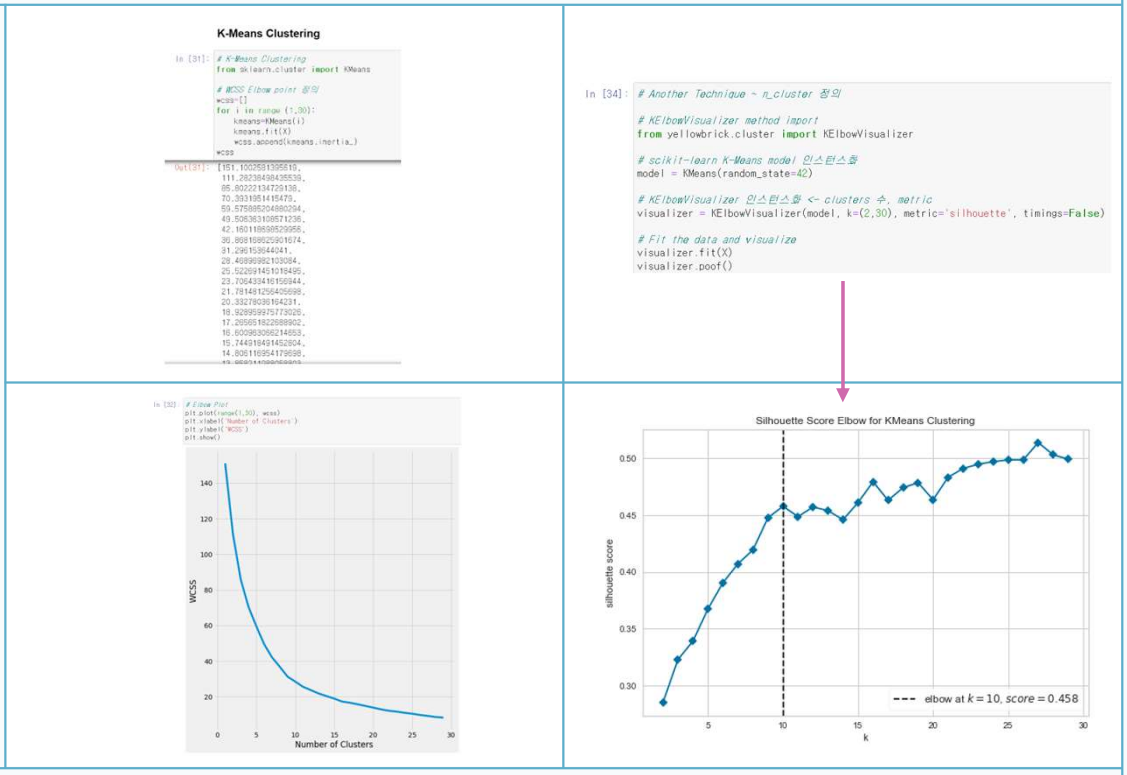
Out[26]:
```
Absenteeism time in hours    1.0
Name: Absenteeism time in hours, dtype: float64
```

- 1-1. LassoCV 회귀분석 진행
- "정규화 선형회귀의 일종으로, 선형회귀 계수에 대한 제약 조건을 추가하여 모델이 과도하게 최적화하는 현상(과적합 overfitting)을 막는 분석 방법"
- feature 선택 후 LassoCV() 진행
- best alpha, score? (LassoCV) 도출
- variable, eliminated variables? 도출
- Lasso 모델에서의 feature importance plot
- X에서 attribure drop → X 갱신


- 1-2. K-Means Clustering ① 진행
- "비지도 학습의 클러스터링 모델 중 하나, K는 클러스터의 개수, K-means Clustering의 목적은 유사한 데이터 포인트끼리 grouping 하여 패턴을 찾아내는 것"
- Elbow method : works by finding WCSS
- "WCSS(Within-Cluster Sum of Square) is the sum of the squared distance between each point and the centroid in a cluster."
- elbow plot 그리기 + silhouette score elbow kmeans clustering plot
- !pip install -U scikit-learn
- 오류 해결 과정에서 stackoverflow 참고!



- k_means_new ☜ 10개로 군집화
- cluster_new, fit_predict
- 클러스터 모양 3d 시각화
- cluster_new data로 plot 그리기
- lmplot : seaborn.lmplot, column 간의 선형관계 확인에 용이, 각 데이터셋의 분포(산점도)와 회귀선을 동시에 나타내도록 시각화 출력 가능

In [35]:
```
k_means_new = KMeans(10)
kmeans.fit(X)
cluster_new = X.copy()
cluster_new['cluster_pred'] = k_means_new.fit_predict(X)
cluster_new.head()
```

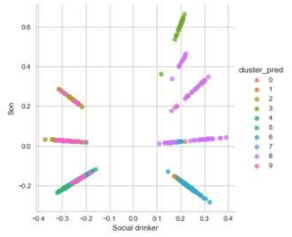
Out[35]:

| | Transportation expense | Work load Average/day | Son | Social drinker | Height | cluster_pred |
|---|---|---|---|---|---|---|
| 0 | 0.328957 | -0.254351 | 0.324561 | 0.294374 | 0.120332 | 8 |
| 1 | -0.177749 | -0.214543 | -0.217476 | 0.248302 | -0.069948 | 6 |
| 2 | 0.329408 | -0.254699 | 0.325005 | 0.294778 | 0.120497 | 8 |
| 3 | -0.165427 | -0.199670 | -0.202400 | 0.231089 | -0.065099 | 6 |
| 4 | 0.377743 | -0.140836 | 0.018475 | 0.162997 | 0.066629 | 8 |

In [36]:
```
# Visualize cluster shapes (3d)

cluster1=cluster_new.loc[cluster_new['cluster_pred'] == 0]
cluster2=cluster_new.loc[cluster_new['cluster_pred'] == 1]
cluster1=cluster_new.loc[cluster_new['cluster_pred'] == 2]
cluster2=cluster_new.loc[cluster_new['cluster_pred'] == 3]
cluster1=cluster_new.loc[cluster_new['cluster_pred'] == 4]
cluster2=cluster_new.loc[cluster_new['cluster_pred'] == 5]
cluster1=cluster_new.loc[cluster_new['cluster_pred'] == 6]
cluster2=cluster_new.loc[cluster_new['cluster_pred'] == 7]
cluster1=cluster_new.loc[cluster_new['cluster_pred'] == 8]
cluster2=cluster_new.loc[cluster_new['cluster_pred'] == 9]
```

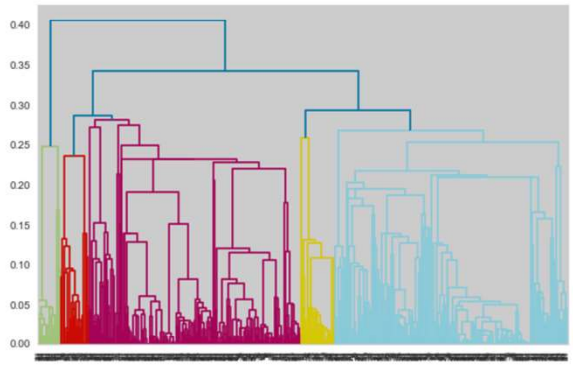
In [37]:
```
import seaborn as sns

# plot data with seaborn
facet = sns.lmplot(data = cluster_new, x = 'Social drinker', y = 'Son',
                   hue = 'cluster_pred', fit_reg = False, legend = True, legend_out = True)
```

```
C:\Users\jwoo\anaconda3\lib\site-packages\seaborn\regression.py:592: UserWarning:

legend_out is deprecated from the `lmplot` function signature. Please update your code to pass
```



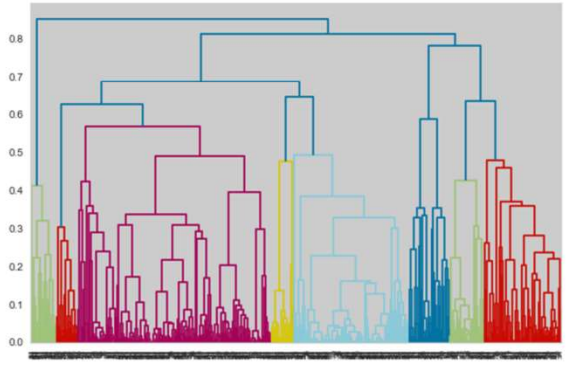
## Hierachical Clustering

In [38]:
```
import scipy.cluster.hierarchy as hcluster
from sklearn.cluster import AgglomerativeClustering

from scipy.cluster.hierarchy import linkage
from scipy.cluster.hierarchy import dendrogram
from scipy.cluster.hierarchy import cut_tree

# single linkage
mergings = linkage(X, method = "single", metric = 'euclidean')
dendrogram(mergings) # 덴드로그램
plt.show()
```



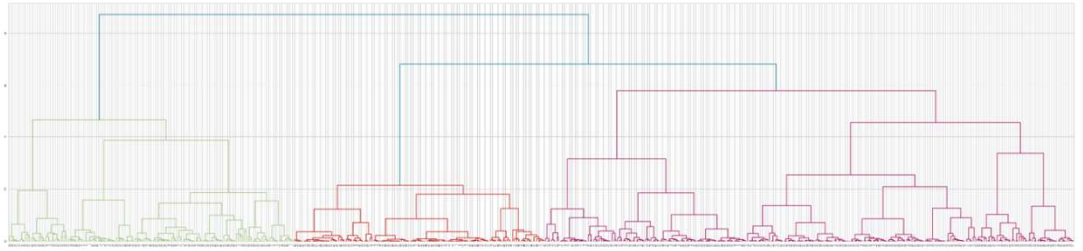

In [39]:
```
features = normalized_df.columns
```

In [40]:
```
# average linkage
mergings = linkage(X, method = "average", metric = 'euclidean')
dendrogram(mergings)
plt.show()
```




- 1-3. Hierarchical clustering ② 진행
- "계층적 트리 모형을 이용해 개별 개체들을 순차적, 계층적으로 유사한 개체 내지 그룹과 통합하여 군집화를 수행하는 알고리즘", dendrogram 덕분에 군집 수를 사전에 정하지 않아도 학습 수행 가능
- Dendrogram : 개체들이 결합되는 순서를 나타내는 트리형태의 구조
- Single/average method linkage ☞ dendrogram
- Dendrogram plot

In [41]:
```
# dendogram plot
plt.figure(figsize=(50, 12))
dend = hcluster.dendrogram(hcluster.linkage(X, method = 'ward'))
```

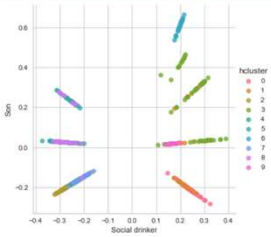


- 1-4. Agglomearative Hierarchical clustering
- "각 데이터가 모두 나뉘어져 있는 상태에서, 작은 단위로부터 클러스터링을 시작하여 모든 데이터를 묶을 때까지 반복하는 Bottom-Up 방식으로 클러스터링 진행"
- hcluster_df ☞ Implot 그리기
- Silhouette analysis ☞ 각 n_cluster에 대한 Silhouette 점수
- n_clusters=10 실루엣 점수(0.77358..)가 가장 높다!

→ "실루엣 점수"는 개체가 다른 클러스터에 비해 자신의 클러스터와 얼마나 유사한 지 측정

- 실루엣 범위는 -1에서 +1까지, 값이 높으면 객체가 자체 클러스터와 잘 일치하고 인접 클러스터와 잘 일치하지 않음을 나타낸다.
- 대부분의 개체에 높은 값이 있으면 클러스터링 구성이 적합하다. 많은 포인트의 값이 낮거나 음수이면 클러스터링 구성에 클러스터가 너무 많거나 적을 수 있다.

```
In [44]: facet = sns.lmplot(data=hcluster_df, x = 'Social drinker', y = 'Son',
                            hue = 'hcluster', fit_reg = False, legend = True, legend_out = True)
C:\Users\jwoo\anaconda3\lib\site-packages\seaborn\regression.py:592: UserWarning:
legend_out is deprecated from the `lmplot` function signature. Please update your code to p
```




```
In [42]: # Agglomearative Hierarchical clustering -> label
hcluster = AgglomerativeClustering(n_clusters = 10, affinity = 'euclidean', linkage = 'ward')
hcluster.fit_predict(X)
hcluster_label = hcluster.labels_

In [43]: hcluster_df = pd.DataFrame(X)

# adding hcluster labels in hcluster_df
hcluster_df['hcluster'] = hcluster_label

hcluster_df.head()
```

Out[43]:

| | Transportation expense | Work load Average/day | Son | Social drinker | Height | hcluster |
|---|---|---|---|---|---|---|
| 0 | 0.328857 | -0.254351 | 0.324561 | 0.294374 | 0.120332 | 3 |
| 1 | -0.177749 | -0.214543 | -0.217476 | 0.248302 | -0.069948 | 0 |
| 2 | 0.329408 | -0.254699 | 0.325005 | 0.294778 | 0.120497 | 3 |
| 3 | -0.165427 | -0.199670 | -0.202400 | 0.231089 | -0.065099 | 0 |
| 4 | 0.377743 | -0.140836 | 0.018475 | 0.162997 | 0.066629 | 3 |

Silhouette analysis

```
In [45]: # Silhouette analysis
range_n_clusters = [2, 3, 4, 5, 6, 7, 8,9,10,11]

for num_clusters in range_n_clusters:
    hcluster = AgglomerativeClustering(n_clusters = num_clusters, affinity = 'euclidean', linkage = 'ward')
    hcluster.fit_predict(X)
    hcluster_label = hcluster.labels_

    # silhouette 분석
    silhouette_avg = silhouette_score(X, hcluster_label)
    print("For n_clusters={0}, the silhouette score is {1}".format(num_clusters, silhouette_avg))
```

```
For n_clusters=2, the silhouette score is 0.543143159868007
For n_clusters=3, the silhouette score is 0.5773067650765904
For n_clusters=4, the silhouette score is 0.5846954848661825
For n_clusters=5, the silhouette score is 0.6068500727548206
For n_clusters=6, the silhouette score is 0.6391201129904711
For n_clusters=7, the silhouette score is 0.6868206206856714
For n_clusters=8, the silhouette score is 0.6804154084759017
For n_clusters=9, the silhouette score is 0.7418258484483151
For n_clusters=10, the silhouette score is 0.7735890174965222
For n_clusters=11, the silhouette score is 0.8628685653950439
```

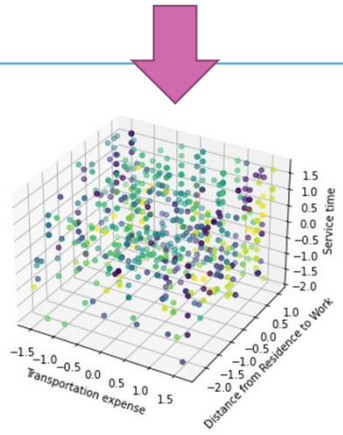
- 1-5. Affinity Propagation Clustering ④ 진행
- "모든 데이터가 특정한 기준에 따라 자신을 대표할 대표 데이터를 선택한다. 만약 스스로가 자기 자신을 대표하게 되면 클러스터의 중심이 된다."
- scaled data에 affinity propagation 알고리즘 적용 with 선택된 hyperparameter
- 각 data point의 cluster label?
- 시각화 위해 3D scatter plot
- plot에 있는 data point 색칠 위해 cluster label 사용

**Affinity Propagation Clustering**

In [3]:
```
import pandas as pd
from sklearn.cluster import AffinityPropagation
from sklearn.preprocessing import StandardScaler

data = pd.read_csv("Absenteeism_at_work.csv", sep=";")

# Separate the target variable (absenteeism time in hours)
target = data["Absenteeism time in hours"]
data.drop("Absenteeism time in hours", axis = 1, inplace = True)

# Scale the data
scaler = StandardScaler()
data_scaled = scaler.fit_transform(data)

# Affinity Propagation 클러스터링
aff_prop = AffinityPropagation(damping = 0.5, preference = -50)
aff_prop.fit(data_scaled)

# Get the cluster labels
cluster_labels = aff_prop.labels_

# Print the cluster labels for each data point
print("Cluster labels : \n", cluster_labels)
```

```
Cluster labels :
 [18  4  2 17 18 39 51  0 15 30  0  0  0  2  2 24 39  2 40 41 29  2 51 27
 18 51 18 16 18  2  2  1 30  1  2 51 18 31  1 27 26 50  2 28 15 50  2 31
 27 34 37 37 36  3 37  4 36  6 37  5  6 27  6  3  4 47  6 26  3 36  5 34
  6 36 27 34 36 34 35 27  6 36  6 25 34 11 36 34 36 11 36 25 36 27  5 36
 34 34  5  3 46 22 36 27  3 35 36 27 36 35  3 24 26  9  7  7 11  9  9  9
  9  7  9  7  7  7  7  7  8 38  7  9  7  7  9 38  9 12 10 11  9 27 38
 12 12  9  9  8  9  9 29 29  9  9 12  0 16 25 12  0  8 41 27 25 15  0 11
 38 25 27  9 17 10  9  9  8  9  9 10 17  9 41  9 34  9 11 12 11  9 27 10
 46 12 12 34 41 27 38 11 13 38 22 14 38 11 11 10  9  9 11 10 38 37 48 23
 48 10 46 51 12 35 12 12 12 10 11 12 46 22 46 46 13 10 32  9 15 46 50 50
 29 47 15 29 29 16 51 18 39 18 18  0 18 16 18 42 17 17 27 18 41 29 47 46
 41 30 46 30 51 40 19 19 31 20 19 31 20 37 19 31 19 31 31 28 46 20 34 34
 19 34 22 34 34  4 20 21  3 33  6 21 20 34 27 20 28 28 46 34 21 46 35 37
 37 37 21 21 46  3  5  6 27 34 13 15 28 48 22  3 22  6 12 34 12  6  0 27
 23 37  6 36  6  6 22 46 27 34  6  6 21  3 22  6 28 30 27 16  2 18  9  7
 11 30 11 38 12 28 46 39 39  7 39 40 38 27 39 43 39 39 24 39 40 43 24 24
 16 39 39 24 39 39  7 24 24 27 43 30 25 13 43 51 37 30 46 46 46 48 37  4
 39 38  0 24 43 27 44 33 41 29 43 46 46 17 27 43 50 28 41 33 47 43 51 27
 25 25 42 26 29  8  3 30 47  3 43  3 26 27 20 34 43 24 43 28  2 26 46  2
  8 24 29 30 47 26  0 29 29 50  0 50 17  1 24 40  2 46 51 18 28 24 31 17
  2 25 24 50 18 28 31  2 25 29 30 24 50 31  0 31 31 50 15 31 47  5  2 26
  8 33 35 32 21 34 32 34  3 32 34 36 33 33 36 33  6 42 34 33 36 33 26 36
 21  5 37 36  6  3 29  6  3 34 21 26 35 34  3 36  6  3  3 36 37 37  5 20
 26 33 35  6 34 36 47 26 36 35 25 28 49 21 36 36 36 15  8  8 25 25  8 25
 32 25  8 11  8 39 38 39 39 43 40 41 39 26 39 47 45 39 49 43 40 39 39 26
  8 25 39 49  8 39 39 39 15 44 43 40 43 41 26 39 39 44 43 41 42 41 42 43
 26 39 26 47 44 51 43 43 39 47 43 41 43 40 43 18 42 43 41 39 47 39 43 25
 15 43 39  8 18 33 40  3 51  5 26 47 33 25 46 51 50 30 47 26 44 47 11 26
 46 47 30 45 44  3 28 47 24 45 17 45 47 46 46  3  4 47 23 25 15 44 24 25
 40 29 44 24 47 35 15 25 15 40 25 47 50  3 13 46 49 47 14 48 46 47 34  8
 50 49 50 50 49 28 49 42 50 42 18 50 51 26 33 18 30 38 38 12]
```

In [5]:
```
import matplotlib.pyplot as plt
from mpl_toolkits.mplot3d import Axes3D

# Plot the clusters
fig = plt.figure()
ax = Axes3D(fig)
ax.scatter(data_scaled[:, 0], data_scaled[:, 1], data_scaled[:, 2], c=cluster_labels)
ax.set_xlabel('Transportation expense')
ax.set_ylabel('Distance from Residence to Work')
ax.set_zlabel('Service time')
plt.show()
```



# 군집화 분석 수행 Ver.2

기계학습 과제#1 ver2

**Absenteeism at work dataset - EDA & Machine Learning Model**

```
In [1]: import pandas as pd
        import numpy as np
        import matplotlib.pyplot as plt
        import seaborn as sns

        from sklearn.model_selection import ShuffleSplit, GridSearchCV
        from sklearn.ensemble import RandomForestClassifier, RandomForestRegressor
        from sklearn.preprocessing import StandardScaler, OneHotEncoder, MinMaxScaler
        from sklearn.pipeline import Pipeline
        from sklearn.compose import ColumnTransformer
        from sklearn.cluster import KMeans
        from sklearn.manifold import TSNE

        import plotly.express as px
        from sklearn.decomposition import PCA
        from sklearn.inspection import permutation_importance
        from sklearn.cluster import AgglomerativeClustering
        from sklearn.metrics import silhouette_samples, silhouette_score, homogeneity_score,
        completeness_score, v_measure_score, adjusted_rand_score, adjusted_mutual_info_score, fowlkes_mallows_score

        from scipy.cluster import hierarchy
        from scipy.spatial import distance_matrix
        from sklearn.cluster import DBSCAN
        import matplotlib.cm as cm
```

**ANALYSING DATA**

```
In [2]: data = pd.read_csv("Absenteeism_at_work.csv", sep=';', index_col='ID')
        data.head()
```

Out[2]:

| ID | Reason for absence | Month of absence | Day of the week | Seasons | Transportation expense | Distance from Residence to Work | Service time | Age | Work load Average/day | Hit target | Disciplinary failure | Education | Son | Social drinker | Social smoker | Pet | Wei |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 11 | 26 | 7 | 3 | 1 | 289 | 36 | 13 | 33 | 239.554 | 97 | 0 | 1 | 2 | 1 | 0 | 1 | |
| 36 | 0 | 7 | 3 | 1 | 118 | 13 | 18 | 50 | 239.554 | 97 | 1 | 1 | 1 | 1 | 0 | 0 | |
| 3 | 23 | 7 | 4 | 1 | 179 | 51 | 18 | 38 | 239.554 | 97 | 0 | 1 | 0 | 1 | 0 | 0 | |
| 7 | 7 | 7 | 5 | 1 | 279 | 5 | 14 | 39 | 239.554 | 97 | 0 | 1 | 2 | 1 | 1 | 0 | |
| 11 | 23 | 7 | 5 | 1 | 289 | 36 | 13 | 33 | 239.554 | 97 | 0 | 1 | 2 | 1 | 0 | 1 | |

```
In [3]: data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 740 entries, 11 to 35
Data columns (total 20 columns):
 #   Column                           Non-Null Count  Dtype
---  ------                           --------------  -----
 0   Reason for absence               740 non-null    int64
 1   Month of absence                 740 non-null    int64
 2   Day of the week                  740 non-null    int64
 3   Seasons                          740 non-null    int64
 4   Transportation expense           740 non-null    int64
 5   Distance from Residence to Work  740 non-null    int64
 6   Service time                     740 non-null    int64
 7   Age                              740 non-null    int64
 8   Work load Average/day            740 non-null    float64
 9   Hit target                       740 non-null    int64
 10  Disciplinary failure             740 non-null    int64
 11  Education                        740 non-null    int64
 12  Son                              740 non-null    int64
 13  Social drinker                   740 non-null    int64
 14  Social smoker                    740 non-null    int64
 15  Pet                              740 non-null    int64
 16  Weight                           740 non-null    int64
```

```
In [4]: data.describe()
```

Out[4]:

| | Reason for absence | Month of absence | Day of the week | Seasons | Transportation expense | Distance from Residence to Work | Service time | Age | Work load Average/day | Hit target | Disciplinary failure | Education |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| count | 740.000000 | 740.000000 | 740.000000 | 740.000000 | 740.000000 | 740.000000 | 740.000000 | 740.000000 | 740.000000 | 740.000000 | 740.000000 | 740.000000 |
| mean | 19.216216 | 6.324324 | 3.914865 | 2.544595 | 221.329730 | 29.631081 | 12.554054 | 36.450000 | 271.490235 | 94.587838 | 0.054054 | 1.291892 |
| std | 8.433406 | 3.436287 | 1.421675 | 1.111831 | 66.952223 | 14.836788 | 4.384873 | 6.478772 | 39.058116 | 3.779313 | 0.226277 | 0.673238 |
| min | 0.000000 | 0.000000 | 2.000000 | 1.000000 | 118.000000 | 5.000000 | 1.000000 | 27.000000 | 205.917000 | 81.000000 | 0.000000 | 1.000000 |
| 25% | 13.000000 | 3.000000 | 3.000000 | 2.000000 | 179.000000 | 16.000000 | 9.000000 | 31.000000 | 244.387000 | 93.000000 | 0.000000 | 1.000000 |
| 50% | 23.000000 | 6.000000 | 4.000000 | 3.000000 | 225.000000 | 26.000000 | 13.000000 | 37.000000 | 264.249000 | 95.000000 | 0.000000 | 1.000000 |
| 75% | 26.000000 | 9.000000 | 5.000000 | 4.000000 | 260.000000 | 50.000000 | 16.000000 | 40.000000 | 294.217000 | 97.000000 | 0.000000 | 1.000000 |
| max | 28.000000 | 12.000000 | 6.000000 | 4.000000 | 388.000000 | 52.000000 | 29.000000 | 58.000000 | 378.884000 | 100.000000 | 1.000000 | 4.000000 |

```
In [5]: categorical_atts = ['Reason for absence','Month of absence','Day of the week',
                          'Seasons','Disciplinary failure', 'Education', 'Social drinker',
                          'Social smoker', 'Pet', 'Son']
        numerical_atts = data.drop(columns=categorical_atts).columns.to_list()

        # update types of categorical columns
        #for cat in categorical_atts:
        #    data[cat] = data[cat].astype('category')
```

```
In [6]: # number of unique values in categorical atts
        data[categorical_atts].nunique()
```

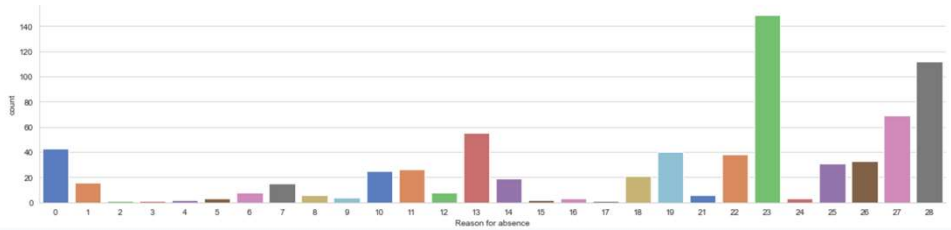
Out[6]:

```
Reason for absence    28
Month of absence      13
Day of the week        5
Seasons                4
Disciplinary failure   2
Education              4
Social drinker         2
Social smoker          2
Pet                    6
Son                    5
dtype: int64
```

```
In [7]: # plot distribution of "reason for absence" column
        sns.set_style("whitegrid")
        sns.catplot(data=data, x='Reason for absence', kind= 'count',size=4, aspect=4, palette='muted')
```

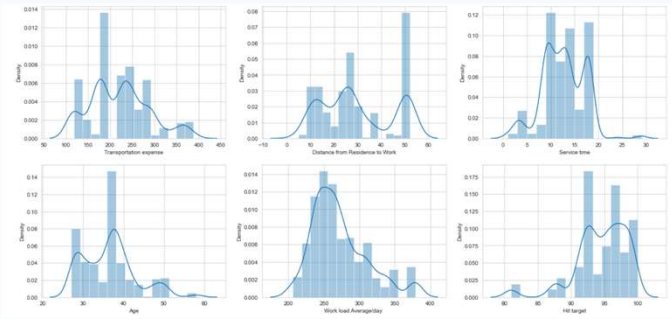
```
C:₩Users₩jwoo₩anaconda3₩lib₩site-packages₩seaborn₩categorical.py:3750: UserWarning: The `size` parameter has been renamed to `height
`; please update your code.
  warnings.warn(msg, UserWarning)
```

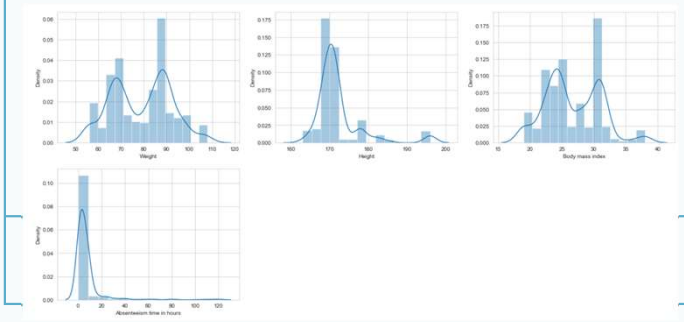
Out[7]: <seaborn.axisgrid.FacetGrid at 0x1c1924e25e0>



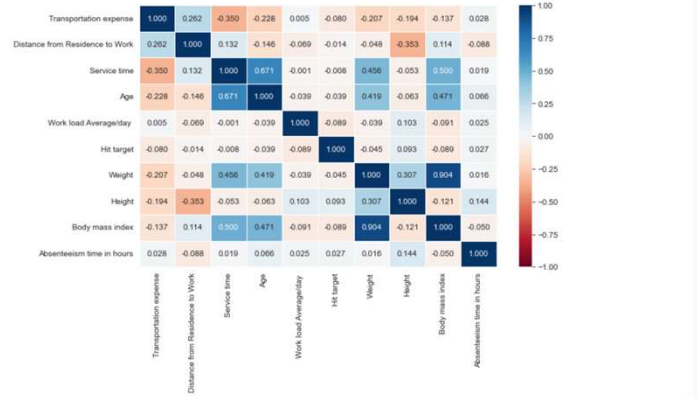

- import 라이브러리, 패키지
- data (index_col을 ID로!)
- info, describe, nunique
- catplot : 범주형 변수와 수치형 변수 간 관계 시각화

```
In [8]: # plot distribution of numerical attributes
num_df = data[numerical_atts]
plt.figure(figsize=(20,20))
for i in range(1, 11):
    plt.subplot(4, 3, i)
    sns.distplot(num_df[num_df.columns[i-1]],bins=14)
```

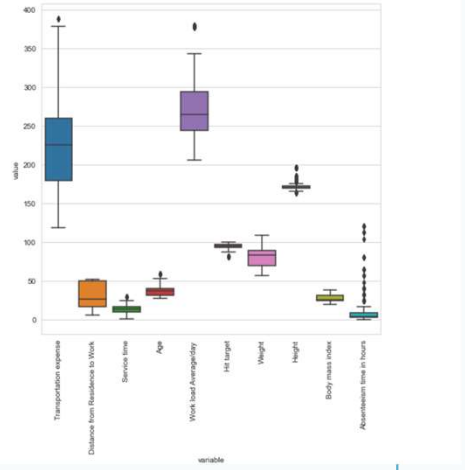




```
In [9]: # correlation matrix
num_corr = num_df.corr()
plt.figure(figsize=(10,6))
sns.heatmap(num_corr, annot=True, fmt=".3f",vmin=-1, vmax=1, linewidths=.5, cmap = sns.color_palette("RdBu", 100))
plt.yticks(rotation=0)
plt.show()
```




```
In [10]: # display boxlots
plt.figure(figsize=(8,8))
sns.boxplot(x="variable", y="value", data=pd.melt(num_df))
plt.xticks(rotation=90)
plt.show()
```



- subplot : 2개 이상의 그래프 한 figure에 출력 가능
- distplot : 분포 표현, 히스토그램 그려준다
- heatmap
- boxplot

- outlier 확인 위해 제1분위수(Q1), 제3분위수(Q3)로 min, max 확인
- outlier 값들을 → mean 값으로 대체
- 정규화 진행
- best parameters?
- → grid.best_estimator_.feature_importances_ 대해 pie chart 그려보기

**OUTLIER DETECTION**

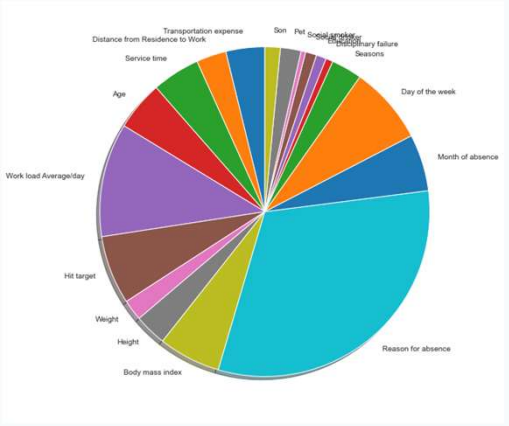
```
In [11]: # Check for outliers using boxplots and drop them
for num_att in numerical_atts:
    # Getting 75 and 25 percentile of variable "i"
    Q3, Q1 = np.percentile(data[num_att], [75,25])
    MEAN = data[num_att].mean()

    # Calculating Interquartile range
    IQR = Q3 - Q1

    # Calculating upper extream and lower extream
    minimum = Q1 - (IQR*1.5)
    maximum = Q3 + (IQR*1.5)

    # Replacing all the outliers value to Mean
    data_clean=data.drop(data.loc[data[num_att]< minimum,num_att].index)
    data_clean=data.drop(data.loc[data[num_att]> maximum,num_att].index)

In [12]: # size reduced to 150 from 740
len(data_clean)

Out[12]: 150
```

**FEATURE SELECTION**

**1. w Random Forest importances:**

- Train a RF model to see feature importances. It's ok, we are already have target attribute in the dataset.

```
In [14]: # X, y splitting (we dont need train test splitting since this model is just for feature importances)
y_original = data_pp[:,-1].reshape(-1, 1)
y = np.round(MinMaxScaler((0,2)).fit_transform(y_original)).ravel()
X = np.delete(data_pp,-1,1)

# cross-validation with 10 splits
cross_val = ShuffleSplit(n_splits=10, random_state = 42)

# define model
rf = RandomForestClassifier(random_state = 0,max_features=None,n_jobs=-1)

# parameters
parameters = {
                "n_estimators":[1000],
                #'max_depth': list(range(1,11)),
                #"criterion": ["gini","entropy"],
                #"criterion": ["mse","mae"],
                #"class_weight": [None, "balanced"],
                #"max_features":["auto", None, "log2"],
                }

# grid search for parameters
grid = GridSearchCV(estimator=rf, param_grid=parameters, cv=cross_val, n_jobs=-1)#multithreading: all cores are used
grid.fit(X,y)

# print best scores
print("The best parameters are %s with a score of %0.4f"
      % (grid.best_params_, grid.best_score_))

The best parameters are {'n_estimators': 1000} with a score of 0.7133
```

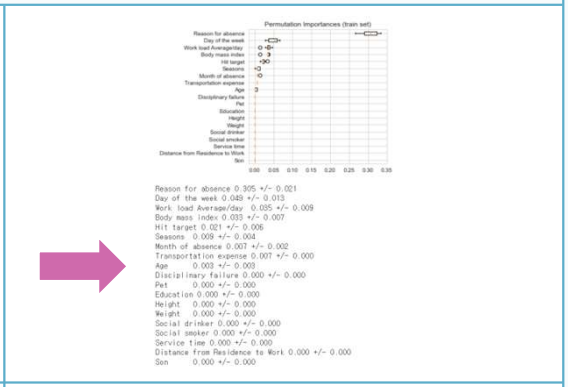


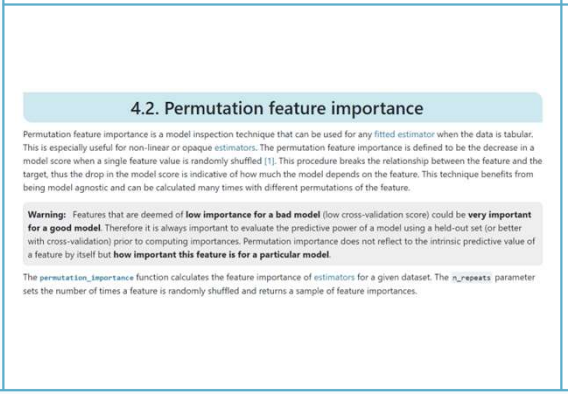

**NORMALIZATION**

```
In [13]: # transform data
numeric_transformer = MinMaxScaler()
#categorical_transformer = OneHotEncoder(sparse=False, handle_unknown='ignore')

# exclude target attr,bute
numerical_atts = [x for x in numerical_atts if x not in ['Absenteeism time in hours']]
preprocessor = ColumnTransformer(
    transformers=[
        ('num', numeric_transformer, numerical_atts),
        ('cat', 'passthrough', categorical_atts)
    ], remainder='passthrough')
data_pp = preprocessor.fit_transform(data_clean)
```

```
In [15]: # pie-chart
atts = numerical_atts+categorical_atts
plt.figure(figsize=(10,10))
plt.pie(grid.best_estimator_.feature_importances_, labels=atts, shadow=True, startangle=90)
```

- permutation feature importance 변수 중요도 확인
- '특정 모델에 특화된(Model-specific)'이 아닌, '어느 모델이든(Model-agnostic) 학습시킨 후(Post-hoc)'에 적용
- "Black-box 모델에 대하여, 특정 feature를 안 썼을 때, 이것이 성능 손실에 얼마만큼의 영향을 주는지를 통해 그 feature의 중요도를 파악하는 방법"
- ☞ 재학습 필요 없다! 그러나 무작위로 섞기 때문에 실행마다 결과 달라질 수 있다
- 변수 중요도 각각 확인 후 attribute 9개 선택



SEE HTTPS://SCIKIT-LEARN.ORG/STABLE/MODULES/PERMUTATION_IMPORTANCE.HTML#PERMUTATION-IMPORTANCE

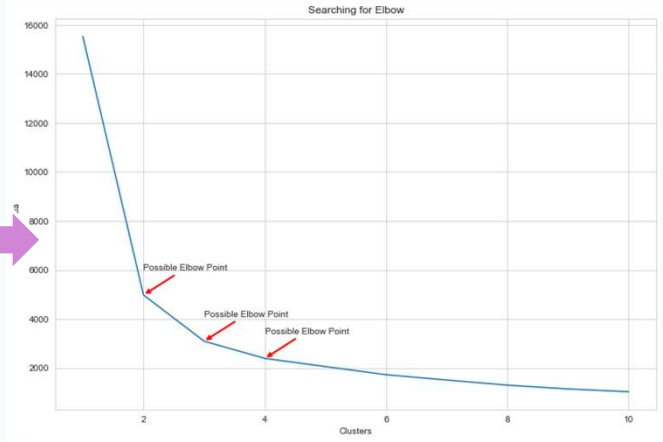
# 2-1. K-MEANS CLUSTERING ①

**1. K-means:**

"inertia_" attribute provides sum of squared distances of samples to their closest cluster center. Wen can plot it and decide on the parameter "n_clusters" by using elbow method.

see https://scikit-learn.org/stable/modules/generated/sklearn.cluster.KMeans.html

In [18]:
```
# run k-means for range of 10 clusters then analyse with elbow method
clusters = []

for i in range(1, 11):
    km = KMeans(n_clusters=i).fit(X_selected)
    clusters.append(km.inertia_)

fig, ax = plt.subplots(figsize=(12, 8))
sns.lineplot(x=list(range(1, 11)), y=clusters, ax=ax)
ax.set_title('Searching for Elbow')
ax.set_xlabel('Clusters')
ax.set_ylabel('Inertia')

# Annotate arrow
ax.annotate('Possible Elbow Point', xy=(4, clusters[3]), xytext=(4, clusters[3]+1000), xycoords='data',
            arrowprops=dict(arrowstyle='->', connectionstyle='arc3', color='red', lw=2))

ax.annotate('Possible Elbow Point', xy=(3,clusters[2] ), xytext=(3, clusters[2]+1000), xycoords='data',
            arrowprops=dict(arrowstyle='->', connectionstyle='arc3', color='red', lw=2))

ax.annotate('Possible Elbow Point', xy=(2,clusters[1] ), xytext=(2, clusters[1]+1000), xycoords='data',
            arrowprops=dict(arrowstyle='->', connectionstyle='arc3', color='red', lw=2))

plt.show()
```




**Notes**

The k-means problem is solved using either Lloyd's or Elkan's algorithm.

The average complexity is given by O(k n T), where n is the number of samples and T is the number of iteration.

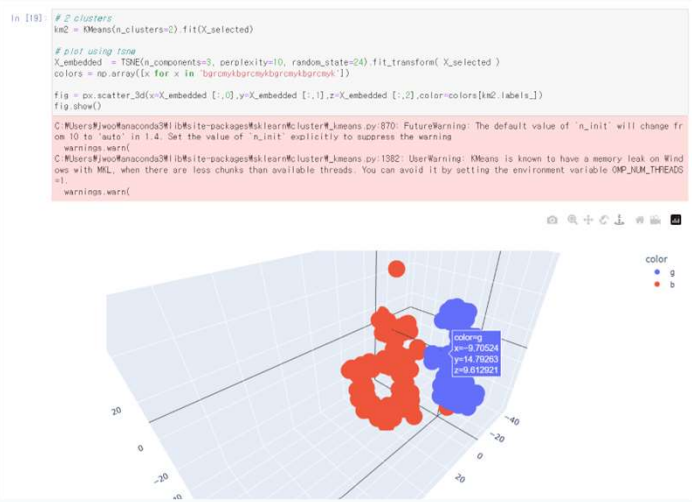
The worst case complexity is given by O(n^(k+2/p)) with n = n_samples, p = n_features. Refer to "How slow is the k-means method?" D. Arthur and S. Vassilvitskii - SoCG2006. for more details.

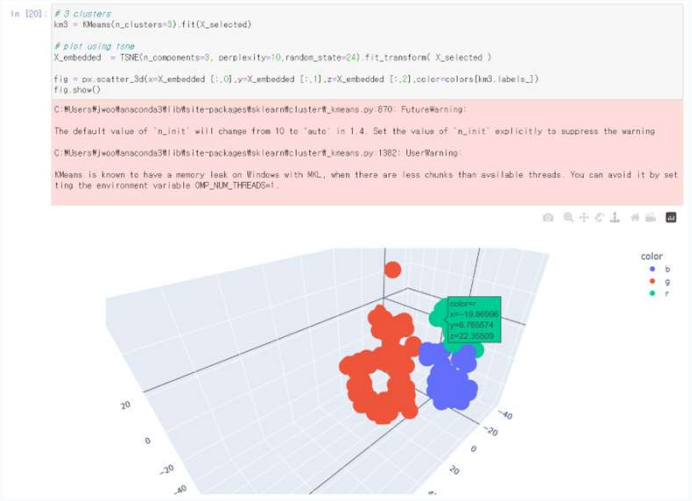
In practice, the k-means algorithm is very fast (one of the fastest clustering algorithms available), but it falls in local minima. That's why it can be useful to restart it several times.

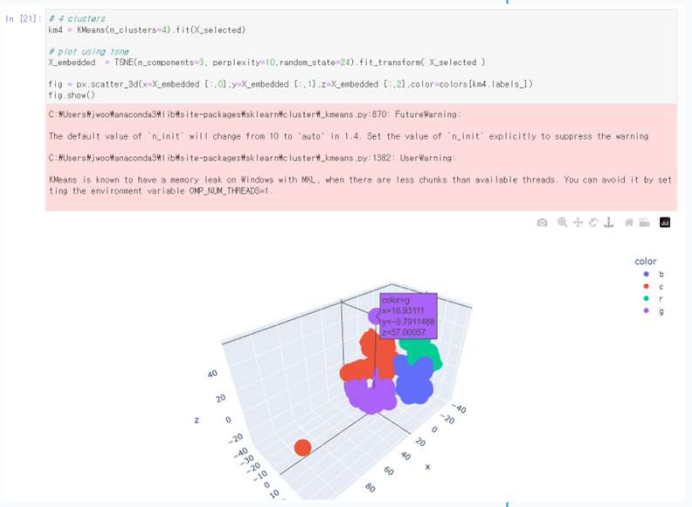
If the algorithm stops before fully converging (because of `tol` or `max_iter`), `labels_` and `cluster_centers_` will not be consistent, i.e. the `cluster_centers_` will not be the means of the points in each cluster. Also, the estimator will reassign `labels_` after the last iteration to make `labels_` consistent with `predict` on the training set.

SEE HTTPS://SCIKIT-LEARN.ORG/STABLE/MODULES/GENERATED/SKLEARN.CLUSTER.KMEANS.HTML

I TRIED POSSIBLE ELBOW POINTS BY CREATING PLOTS. USED T-SNE FOR VISUALIZING DATA ON 3D SPACE.
SEE HTTPS://SCIKIT-LEARN.ORG/STABLE/MODULES/GENERATED/SKLEARN.MANIFOLD.TSNE.HTML



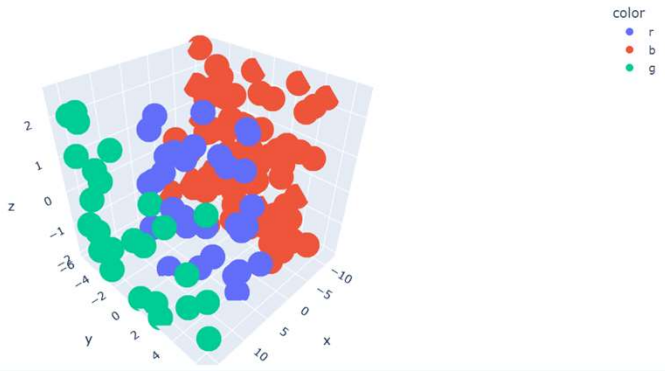




☞ It seems like 4 clusters work best. Let's try the same process again with 2-2. **PCA + K-means**.

FOR PCA SEE HTTPS://SCIKIT-LEARN.ORG/STABLE/MODULES/GENERATED/SKLEARN.DECOMPOSITION.PCA.HTML

```
In [22]: # PCA for reducing dimensions to 3
pca = PCA(n_components=3)
pca_results = pca.fit_transform(X_selected)

# running k-means on resuts of pca
km_pca = KMeans(n_clusters=3).fit(pca_results)
fig = px.scatter_3d(x=pca_results [:,0],y=pca_results [:,1],z=pca_results [:,2],color=colors[km_pca.labels_])
fig.show()
```

```
C:₩Users₩jwoo₩anaconda3₩lib₩site-packages₩sklearn₩cluster₩_kmeans.py:870: FutureWarning:

The default value of `n_init` will change from 10 to 'auto' in 1.4. Set the value of `n_init` explicitly to suppress the warning

C:₩Users₩jwoo₩anaconda3₩lib₩site-packages₩sklearn₩cluster₩_kmeans.py:1382: UserWarning:

KMeans is known to have a memory leak on Windows with MKL, when there are less chunks than available threads. You can avoid it by set
ting the environment variable OMP_NUM_THREADS=1.
```




→ Lost most of valuable information about data with **PCA(차원축소)**. So, resulting graph seems incomplete.

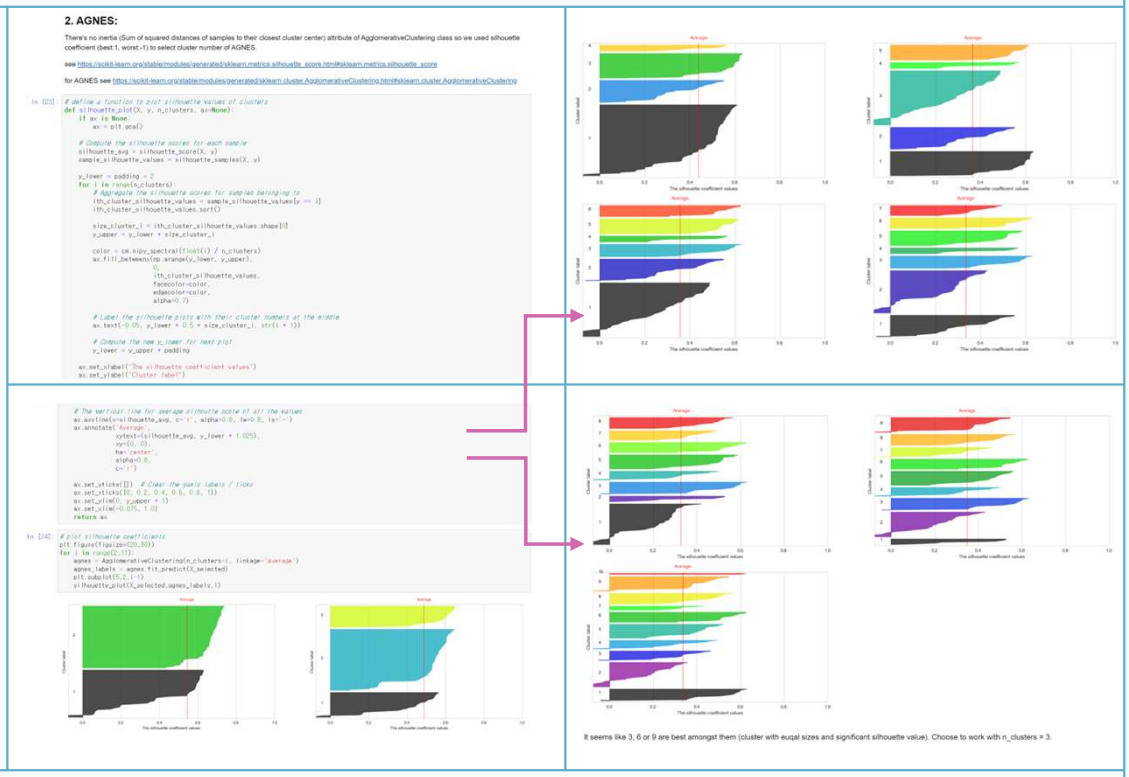
- **T-SNE**
- 매니폴드(manifold) 학습의 하나, 복잡한 데이터의 시각화가 목적
- 높은 차원의 데이터를 2차원 또는 3차원으로 축소시켜 시각화
- ☞ 높은 차원 공간에서 비슷한 데이터 구조는 낮은 차원 공간에서 가깝게 대응, 비슷하지 않은 데이터 구조는 멀리 떨어져 대응되는 결과 도출!

→ USING K-MEANS ON ORIGINAL 7-DIMENSIONAL DATA THEN PLOTTING WITH T-SNE GIVES BETTER RESULTS.

SEE

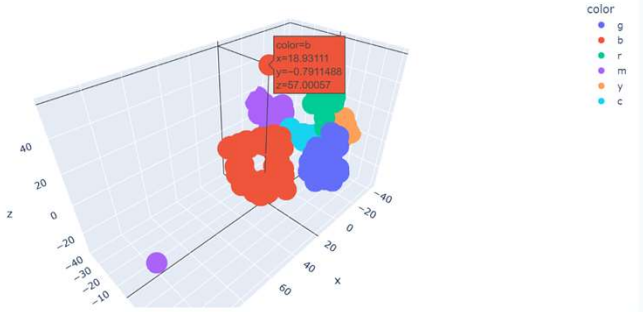
HTTPS://SCIKIT-LEARN.ORG/STABLE/MODULES/GENERATED/SKLEARN.CLUSTER.AGGLOMERATIVECLUSTERING.HTML#SKLEARN.CLUSTER.AGGLOMERATIVECLUSTERING

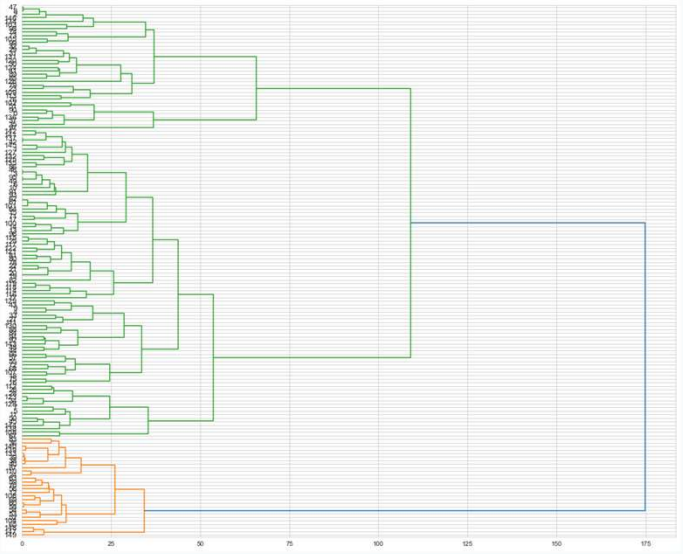
- 2-3. AGNES (Agglomerative Clustering)
- silhouette coefficient 사용 (best : 1, worst : -1) → to select cluster number of AGNES.
- 클러스터의 실루엣 값 plot 함수 정의
- Silhouette Score 종합
- 실루엣 coefficient plot
- It seems like 3, 6 or 9 are best amongst them
- → Choose to work with n_clusters = 3.




SEE https://scikit-learn.org/stable/modules/generated/sklearn.metrics.silhouette_score.html#sklearn.metrics.silhouette_score

```
In [25]: # 6 clusters
agnes6 = AgglomerativeClustering(n_clusters=6, linkage='average').fit(X_selected)

# plot using tsne
X_embedded  = TSNE(n_components=3, perplexity=10,random_state=24).fit_transform( X_selected )

fig = px.scatter_3d(x=X_embedded [:,0],y=X_embedded [:,1],z=X_embedded [:,2],color=colors[agnes6.labels_])
fig.show()
```



- TSNE 이용하여 **3d plot** 그리기
- 가능한 clustering 대해 dendrogram 그려보기

Let's plot the complete dendrogram to see the possible clusterings.

```
In [26]: # there's no inertia in attribute of AgglomerativeClustering class so we use scipy's distance matrix
dist = distance_matrix(X_selected, X_selected)

# dendrogram
Z = hierarchy.linkage(dist, 'average')
plt.figure(figsize=(18, 15))
dendro = hierarchy.dendrogram(Z, leaf_rotation=0, leaf_font_size=12, orientation='right')
```

**3. DBSCAN:**

eps: The maximum distance between two samples for one to be considered as in the neighborhood of the other (default: 0.5).

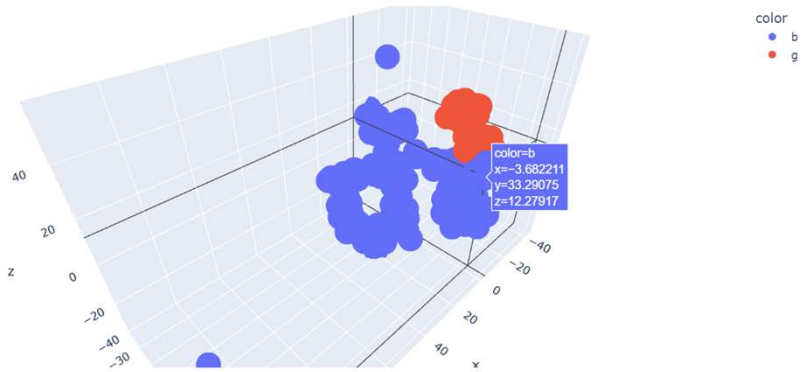
min_samples: The number of samples (or total weight) in a neighborhood for a point to be considered as a core point. This includes the point itself (default: 5).

see https://scikit-learn.org/stable/modules/generated/sklearn.cluster.DBSCAN.html

In [27]:
```
# search for best parameters by using silhouette_score
score_list=[]
for eps in np.arange(0.5,20,0.5):
    for min_samples in range(3,20):
        db = DBSCAN(eps=eps, min_samples=min_samples).fit(X_selected)
        labels = db.labels_
        n = len(np.unique(labels))
        if n>1:
            score=silhouette_score(X_selected, labels)
            score_list.append((score,(eps,min_samples)))

biggest_score = sorted(score_list)[-1]
best_eps, best_min_spamles = biggest_score[1]
best_eps, best_min_spamles
```

Out[27]: (5.0, 11)

In [28]:
```
# best model for DBSCAN
db_best = DBSCAN(eps=best_eps, min_samples=best_min_spamles).fit(X_selected)

# plot using tsne
X_embedded  = TSNE(n_components=3, perplexity=10,random_state=24).fit_transform( X_selected )

fig = px.scatter_3d(x=X_embedded [:,0],y=X_embedded [:,1],z=X_embedded [:,2],color=colors[db_best.labels_])
fig.show()
```




## 2-4. DBSCAN clustering ③

(Density-Based-Spatial Clustering of Applications with Noise)

- DBSCAN : "서로 인접한 데이터들은 같은 클러스터 내에 있다는 것을 가정한 알고리즘"
- 가깝게 인접해 있는 데이터들은 같은 클러스터라 가정하고 인접한 데이터를 잘 찾아서 클러스터 할당 (K-Means 약점 극복)
- 특정 데이터를 중심으로 밀도가 높은 곳에 포함된 데이터에는 클러스터를 할당하고, 밀도가 낮으면 그 데이터를 노이즈로 취급!
- Silhouette score 이용하여 최선의 parameter 탐색
- best model for DBSCAN?

SEE HTTPS://SCIKIT-LEARN.ORG/STABLE/MODULES/GENERATED/SKLEARN.CLUSTER.DBSCAN.HTML

# Evaluation METRICS FOR

## K-MEANS
## PCA+K-MEANS
## AGNES
## DBSCAN

- Compare best models by using **8 metrics**:
- **1) Estimated number of clusters Estimated number of noise points**
- **2) Homogeneity**: For perfect clustering, each cluster contains only members of a single class.
- **3) Completeness**: For perfect clustering, all members of a given class are assigned to the same cluster.
- **4) V-measure**: Harmonic mean of Homogeneity and Completeness.
- **5) Adjusted Rand Index**: Given the knowledge of the ground truth class, the adjusted Rand index is a function that measures the similarity of the two assignments, ignoring permutations and with chance normalization:
- **6) Adjusted Mutual Information**: Given the knowledge of the ground truth class, the Mutual Information is a function that measures the agreement of the two assignments, ignoring permutations.
- **7) Fowlkes-Mallows score**: Geometric mean of precision and recall.
- **8) Silhouette Coefficient**: If the ground truth labels are not known, the Silhouette Coefficient is calculated using the mean intra-cluster distance (a) and the mean nearest-cluster distance (b) for each sample by (b - a) / max(a, b)

SEE HTTPS://SCIKIT-LEARN.ORG/STABLE/MODULES/CLUSTERING.HTML#CLUSTERING-PERFORMANCE-EVALUATION

# 군집화 분석 결과 평가

```
In [29]: # print metric for chosen models
models = [km4, km_pca, agnes6, db_best]
names = ["K-MEANS:","PCA + K-MEANS:","AGNES:", "DBSCAN:"]

for i, model in enumerate(models):
    labels = model.labels_
    n = len(np.unique(labels))
    y = np.round(MinMaxScaler((0,n)).fit_transform(y_original)).ravel()

    # Number of clusters in labels, ignoring noise if present.
    n_clusters_ = len(set(labels)) - (1 if -1 in labels else 0)
    n_noise_ = list(labels).count(-1)

    print(names[i])
    print('Estimated number of clusters: %d' % n_clusters_)
    print('Estimated number of noise points: %d' % n_noise_)
    print("Homogeneity: %0.3f" % homogeneity_score(y, labels))
    print("Completeness: %0.3f" % completeness_score(y, labels))
    print("V-measure: %0.3f" % v_measure_score(y, labels))
    print("Adjusted Rand Index: %0.3f" % adjusted_rand_score(y, labels))
    print("Adjusted Mutual Information: %0.3f" % adjusted_mutual_info_score(y, labels))
    print("Fowlkes-Mallows score: %0.3f" % fowlkes_mallows_score(y, labels))
    print("Silhouette Coefficient: %0.3f" % silhouette_score(X, labels))
    print("₩n")
```

```
K-MEANS:
Estimated number of clusters: 4
Estimated number of noise points: 0
Homogeneity: 0.157
Completeness: 0.133
V-measure: 0.144
Adjusted Rand Index: 0.075
Adjusted Mutual Information: 0.121
Fowlkes-Mallows score: 0.344
Silhouette Coefficient: 0.330

PCA + K-MEANS:
Estimated number of clusters: 3
Estimated number of noise points: 0
Homogeneity: 0.147
Completeness: 0.176
V-measure: 0.160
Adjusted Rand Index: 0.077
Adjusted Mutual Information: 0.143
Fowlkes-Mallows score: 0.423
Silhouette Coefficient: 0.437

AGNES:
Estimated number of clusters: 6
Estimated number of noise points: 0
Homogeneity: 0.211
Completeness: 0.188
V-measure: 0.199
Adjusted Rand Index: 0.110
Adjusted Mutual Information: 0.156
Fowlkes-Mallows score: 0.348
Silhouette Coefficient: 0.276

DBSCAN:
Estimated number of clusters: 2
Estimated number of noise points: 0
Homogeneity: 0.029
Completeness: 0.045
V-measure: 0.035
Adjusted Rand Index: -0.035
Adjusted Mutual Information: 0.024
Fowlkes-Mallows score: 0.557
Silhouette Coefficient: 0.518
```

- ① Only metric doesn't reqire ground-truth(실측계수) labels is Silhouette Coefficient.
- For it → DBSCAN > PCA+KMEANS > K-MEANS > AGNES. ② Its results are correlated with Fowlkes-Mallows score although they require different inputs with only difference of swapping AGNES and K-MEANS.
- ③ For Homogeneity and Completeness principles → AGNES > PCA+KMEANS > K-MEANS > DBSCAN. ④ The results are similar for Mutual Information.
- ⑤ For Rand Index → AGNES > K-MEANS > PCA+KMEANS > DBSCAN.