

기술 통계

```
In [1]: import numpy as np
        from scipy import stats
        x = np.random.randint(1, 10, 20)
```

중심 통계량: 데이터의 중심경향을 나타내는 수치

- [평균(Average)]: 표본데이터의 중심무게 (산술평균, 기하평균, 조화평균, 가중평균)
- [중앙값(Median)]: 순서를 가진 표본데이터의 가운데(50%)에 위치한 값
- [최빈값(Mode)]: 표본데이터 중 가장 빈번한 값

평균

```
In [2]: np.mean(x)
```

Out[2]: 5.05

중앙값

```
In [3]: np.median(x)
```

Out[3]: 5.0

최빈값

```
In [4]: stats.mode(x)
```

Out[4]: ModeResult(mode=array([1]), count=array([5]))

변동 통계량: 데이터의 변동성을 나타내는 수치

- 범위(Range): 최대값과 최소값의 차이
- 편차(Deviation): 관측값과 평균의 차이

- 변동(Variation): 편차 제곱의 합
- 분산(Variance): 편차 제곱의 합을 데이터의 수로 나눈 값
- 표준편차(Standard Deviation): $\sqrt{\text{분산}}$

범위

```
In [5]: np.max(x) - np.min(x)
```

```
Out[5]: 8
```

편차 및 변동

```
In [6]: deviation = x - np.mean(x)
variation = sum(deviation ** 2)
```

분산 및 표준편차

```
In [7]: np.var(x)
```

```
Out[7]: 10.0475
```

```
In [8]: np.std(x)
```

```
Out[8]: 3.1697791721190924
```

사분위수

```
In [9]: np.quantile(x, 0.25)
```

```
Out[9]: 1.75
```

```
In [10]: np.quantile(x, 0.5)
```

```
Out[10]: 5.0
```

형태 통계량: 데이터의 분포형태와 왜곡을 나타내는 수치

- 왜도(Skewness): 평균을 중심으로 좌우로 데이터가 편향되어 있는 정도
- 첨도(Kurtosis): 뽕족함 정도
- 이상치(Outlier): 오류로 판단하는 값이지만 기준이 불명확

왜도

```
In [11]: stats.skew(x)
```

```
Out[11]: -0.017496978366576602
```

첨도

```
In [12]: stats.kurtosis(x)
```

```
Out[12]: -1.5873447850750733
```

아웃라이어 (IQR)

```
In [13]: def outlier_detection(x, w = 1.5):  
    Q1 = np.quantile(x, 0.25)  
    Q3 = np.quantile(x, 0.75)  
    IQR = Q3 - Q1  
  
    return np.logical_or(Q1 - w * IQR > x, Q3 + w * IQR < x)
```

```
In [14]: x[-1] = 100  
outlier_detection(x)
```

```
Out[14]: array([False, False, False, False, False, False, False, False, False,  
                False, False, False, False, False, False, False, False,  
                False,  True])
```

가설 검정

예시 및 정리

> 이해문제1: 양치기들이 거짓말쟁이인가?

1) 가설설정

- 대중주장: 현재 대한민국에 있는 양치기들은 일반인 대비 거짓말을 많이 하지 않는다!
- 나의주장: 현재 대한민국에 있는 양치기들은 일반인 대비 거짓말을 많이 한다!

2) 점추정 및 구간추정

- 검정통계량(점추정): $\frac{\text{샘플집단 양치기 거짓말 빈도} - \text{샘플집단 일반인 거짓말 빈도}}{\text{샘플집단 양치기 거짓말 빈도 표준편차}}$ (1회성)
- 신뢰구간(구간추정): 실험을 여러번 반복해서 거짓말차이(검정통계량)의 히스토그램 또는 분포 (반복성)

3) 유의수준 및 유의확률

- 유의수준: (대중주장이 참인 가정에서, 검정통계량 값으로 나의주장이 맞다 오판할 확률)
: 양치기와 일반인이 거짓말 차이가 없다는 전제에서, 양치기들이 일반인보다 거짓말 빈도가 많다 오판할 확률
- 유의확률: (대중주장이 참인 가정에서, 검정통계량 값으로 나의주장이 관찰될 확률)
: 양치기와 일반인이 거짓말 차이가 없다는 전제에서, 양치기들이 일반인보다 거짓말 빈도가 많이 관찰될 확률

4) 의사결정: (유의수준 5%기준)

- 나의주장 참: 5%보다 작은 경우를 희박한 상황이라고 할때, 나의 데이터에서 나의주장이 관찰될 확률(3%)은 희박한 결과를 발견하였으니 양치기들은 거짓말쟁이!
- 대중주장 참: 5%보다 작은 경우를 희박한 상황이라고 할때, 나의 데이터에서 나의주장이 관찰될 확률(7%)은 희박하지 않은 결과를 발견한 것이라 양치기들은 거짓말쟁이가 아님!

등분산 검정

p-value가 낮으면 두 집단 이상의 분산 차이가 존재

```
In [15]: from scipy.stats import levene
a = np.random.normal(100, 1, 1000)
b = np.random.normal(100, 1, 1000)
print(np.var(a), np.var(b))

stat, p = levene(a, b)

stat, p
```

0.9495532722877262 0.9388640228588699

```
Out [15]: (0.14584944355485033, 0.7025743724379527)
```

```
In [16]: from scipy.stats import levene
a = np.random.normal(100, 1, 1000)
b = np.random.normal(100, 10, 1000)
print(np.var(a), np.var(b))

stat, p = levene(a, b)
stat, p
```

1.0119085593907093 102.18348806931758

Out[16]: (1392.0039029661868, 1.173402793950097e-231)

```
In [17]: from scipy.stats import levene
a = np.random.normal(100, 1, 1000)
b = np.random.normal(100, 1, 1000)
c = np.random.normal(100, 10, 1000)
print(np.var(a), np.var(b), np.var(c))

stat, p = levene(a, b, c)
stat, p
```

0.9073400620556052 0.9886939995274929 94.88913973945444

Out[17]: (1323.832703547323, 0.0)

독립 표본 t-test

- p-value가 낮으면 두 집단의 평균 차이가 있음
- 반드시 등분산 검정 후에 사용할 것

`scipy.stats.ttest_ind(a, b, axis=0, equal_var=True, nan_policy='propagate', permutations=None, random_state=None, alternative='two-sided', trim=0)`

- `equal_var`: bool, optional

If True (default), perform a standard independent 2 sample test that assumes equal population variances If False, perform Welch's t-test, which does not assume equal population variance.

- `nan_policy`{'propagate', 'raise', 'omit'}, optional
 - `propagate` : returns nan
 - `raise` : throws an error
 - `omit`: performs the calculations ignoring nan values

```
In [18]: a = np.random.normal(10, 1, 100)
b = np.random.normal(10, 1, 100)

stats.ttest_ind(a, b, equal_var = True)
```

```
Out[18]: Ttest_indResult(statistic=-1.0212913849532985, pvalue=0.30836261766994366)
```

```
In [19]: a = np.random.normal(10, 1, 100)
b = np.random.normal(10, 10, 100)

stats.ttest_ind(a, b, equal_var = False)
```

```
Out[19]: Ttest_indResult(statistic=-0.10412516501227907, pvalue=0.9172757349774978)
```

```
In [20]: a = np.random.normal(10, 1, 100)
b = np.random.normal(15, 1, 100)

stats.ttest_ind(a, b, equal_var = True)
```

```
Out[20]: Ttest_indResult(statistic=-35.174278369876816, pvalue=4.164635776493295e-87)
```

paired t-test

`scipy.stats.ttest_rel(a, b, axis=0, nan_policy='propagate', alternative='two-sided')`

Calculate the t-test on TWO RELATED samples of scores, a and b.

- a와 b의 shape가 반드시 일치해야 함

```
In [21]: a = np.random.normal(10, 1, 100)
b = a + np.random.normal(0, 1, 100)

stats.ttest_rel(a, b)
```

```
Out[21]: Ttest_relResult(statistic=0.9906563880929291, pvalue=0.3242685134244955)
```

정규성 검정

- p-value가 0.05 이상인 경우에는 정규분포를 따른다고 봐도 무방함

```
In [22]: # 정규 분포를 따르는 경우
from scipy import stats
x = np.random.normal(100, 10, 100)
k2, p = stats.normaltest(x)
print(p)
```

0.16440012751371216

```
In [23]: # 정규 분포를 따르지 않는 경우
from scipy import stats
x = np.random.random(10000)
k2, p = stats.normaltest(x)
print(p)
```

0.0

일원분산분석

- 정규성 검정을 한 뒤에 수행할 것 (정규성 만족못하면 Kruskal-Wallis H Test 수행)

```
In [24]: import pandas as pd
import numpy as np
import statsmodels.formula.api as smf
import statsmodels.api as sm
from statsmodels.stats.anova import AnovaRM
from scipy import stats
```

```
In [25]: # 데이터 준비
# information on experimental design
group_list = ['control', 'patient1', 'patient2']
subs_list = ['01', '02', '03', '04', '05', '06', '07', '08', '09', '10']

# read data into dataframe
df_1way = pd.DataFrame(columns=["group", "my_value"])
my_row = 0
for ind_g, group in enumerate(group_list):
    for sub in subs_list:
        # generate random value here as example
        my_val = np.random.normal(ind_g, 1, 1)[0]
        df_1way.loc[my_row] = [group, my_val]
        my_row = my_row + 1
```

```
In [26]: df_1way.head()
```

```
Out[26]:
```

	group	my_value
0	control	0.907117
1	control	0.471981
2	control	0.148081
3	control	0.318889
4	control	-0.049459

statsmodel을 활용

```
In [27]: # generate model for linear regression
my_model = smf.ols(formula='my_value ~ group', data=df_1way)

# fit model to data to obtain parameter estimates
my_model_fit = my_model.fit()

# show anova table
anova_table = sm.stats.anova_lm(my_model_fit, typ=2)
print(anova_table)

# group - F, PR (p-value)만 확인하면 됨
```

	sum_sq	df	F	PR(>F)
group	19.105558	2.0	15.193014	0.000038
Residual	16.976555	27.0	NaN	NaN

scipy stats을 활용

```
In [28]: F, p = stats.f_oneway(df_1way[df_1way['group'] == 'control'].my_value, df_1way[df_1way['group'] == 'patient1'].my_value, df_1way[df_1way['group'] == 'patient2'].my_value)
print(F, p)

15.193013869948365 3.797760762024205e-05
```

이원분산분석 & 교호작용분석

```
In [29]: # information on experimental design
group_list = ['control', 'patient1', 'patient2']
language_list = ['English', 'German', 'French']
```



```

subs_list = ['01', '02', '03', '04', '05', '06', '07', '08', '09', '10']

# read data into dataframe
df_2way = pd.DataFrame(columns=["group", "language", "my_value"])
my_row = 0
for ind_g, group in enumerate(group_list):
    for ind_l, lan in enumerate(language_list):
        for sub in subs_list:
            # generate random value here as example
            my_val = np.random.normal(ind_g + ind_l, 1, 1)[0]
            df_2way.loc[my_row] = [group, lan, my_val]
            my_row = my_row + 1

df_2way.head()

```

Out[29]:

	group	language	my_value
0	control	English	0.246734
1	control	English	1.052874
2	control	English	-0.474547
3	control	English	-0.769478
4	control	English	-0.372473

In [30]:

```

# fit model to data to obtain parameter estimates
# formula = Y ~ 인자 * 인자
my_model_fit = smf.ols(formula='my_value ~ group * language', data=df_2way).fit()

# show anova table
print(sm.stats.anova_lm(my_model_fit, typ=2))

# group, language은 유효
# group*language의 p-value는 0.25로 유효하지 않음 --> 두 독립 변수의 교호작용은 없음!

```

	sum_sq	df	F	PR(>F)
group	82.481682	2.0	42.847287	2.022200e-13
language	49.828294	2.0	25.884623	2.033270e-09
group: language	9.053971	4.0	2.351662	6.091095e-02
Residual	77.963119	81.0	NaN	NaN

kruskal test (정규성 검정 실패시, 사용하는 One-way ANOVA)

scipy.stats.kruskal(sample1,sample2,...)

- p value가 작을수록 차이가 있음

```
In [31]: from scipy import stats
x = [1, 3, 5, 7, 9]
y = [2, 4, 6, 8, 10]
stats.kruskal(x, y)
```

```
Out[31]: KruskalResult(statistic=0.2727272727272734, pvalue=0.6015081344405895)
```

```
In [32]: from scipy import stats
x = [1,2,3,4,5]
y = [1,2,3,4,5]
z = [1,2,3,4,5]
stats.kruskal(x, y, z)
```

```
Out[32]: KruskalResult(statistic=0.0, pvalue=1.0)
```

교차 분석

p가 작을수록 독립

```
In [33]: from scipy.stats import chi2_contingency
df = pd.DataFrame({'Gender' : ['M', 'M', 'M', 'F', 'F'] * 10,
                   'isSmoker' : ['Smoker', 'Smoker', 'Smoker', 'Non-Smoker', 'Non-Smoker'] * 10})
df.head()
```

```
Out[33]:
```

	Gender	isSmoker
0	M	Smoker
1	M	Smoker
2	M	Smoker
3	F	Non-Smoker
4	F	Non-Smoker

```
In [34]: contingency= pd.crosstab(df['Gender'], df['isSmoker'])
contingency
```

Out [34]: isSmoker Non-Smoker Smoker

Gender		
F	20	0
M	0	30

In [35]: *# Chi-square test of independence.*
c, p, dof, expected = chi2_contingency(contingency)
Print the p-value
print(p)

1.2317319065658562e-11

상관분석

In [36]: **from** scipy.stats **import** pearsonr
from scipy.stats **import** spearmanr

```
x1 = np.random.random(100)
x2 = np.random.random(100)
```

```
print(pearsonr(x1, x2))
print(spearmanr(x1, x2))
```

(-0.009913368485027201, 0.922019862002112)
SpearmanrResult(correlation=-0.016393639363936393, pvalue=0.8713954941535211)

요인분석 및 주성분분석

sklearn.decomposition.FactorAnalysis(n_components=None, *, tol=0.01, copy=True, max_iter=1000, noise_variance_init=None, svd_method='randomized', iterated_power=3, rotation=None, random_state=0)

sklearn.decomposition.PCA(n_components=None, *, copy=True, whiten=False, svd_solver='auto', tol=0.0, iterated_power='auto', random_state=None)

회귀분석

데이터 준비

In [37]: **import** statsmodels.api **as** sm

```
X = pd.DataFrame(np.random.random((100, 5)), columns = ["X1", "X2", "X3", "X4", "X5"])
Y = X["X1"] + X["X2"] + np.random.random(100) / 10
```

회귀모델 기초

모델링

In [38]: `X = sm.add_constant(X) # adding a constant (1로만 구성된 변수가 추가됨)`

```
model = sm.OLS(Y, X).fit() # Y, X 순서임을 확인
predictions = model.predict(X) # X에 대한 예측치 (Series)
```

```
print_model = model.summary()
print(print_model)
```

OLS Regression Results

```
=====
Dep. Variable:          y      R-squared:                0.995
Model:                OLS      Adj. R-squared:           0.995
Method:             Least Squares      F-statistic:           3816.
Date:                Thu, 19 Aug 2021    Prob (F-statistic):       7.06e-107
Time:                14:34:29      Log-Likelihood:          217.82
No. Observations:      100      AIC:                   -423.6
Df Residuals:          94      BIC:                   -408.0
Df Model:              5
Covariance Type:      nonrobust
=====
```

	coef	std err	t	P> t	[0.025	0.975]
const	0.0437	0.013	3.425	0.001	0.018	0.069
X1	0.9952	0.010	98.338	0.000	0.975	1.015
X2	1.0091	0.011	91.522	0.000	0.987	1.031
X3	-0.0045	0.010	-0.438	0.663	-0.025	0.016
X4	0.0084	0.010	0.799	0.426	-0.012	0.029
X5	0.0061	0.010	0.613	0.541	-0.014	0.026

```
=====
Omnibus:                27.854      Durbin-Watson:           2.298
Prob(Omnibus):           0.000      Jarque-Bera (JB):         5.636
Skew:                   -0.051      Prob(JB):                 0.0597
Kurtosis:               1.841      Cond. No.                  9.08
=====
```

Notes:

[1] Standard Errors assume that the covariance matrix of the errors is correctly specified.

해석 필요

- Standard error가 가지는 의미: The standard error is an estimate of the standard deviation of the coefficient, the amount it varies across cases. It can be thought of as a measure of the precision with which the regression coefficient is measured.
- $P > |t|$: p-value (0.05미만이면 유의)
- [0.025 0.975]: 신뢰 구간
- Prob (F-statistic): the probability that the null hypothesis for the full model is true (i.e., that all of the regression coefficients are zero)

회귀모델 가정 검토

선형성

- 응답 변수가 예측 변수와 선형 회귀 계수의 선형 조합으로 표현 가능함을 의미
- 상관계수, scatter plot으로 검토

scatter plot

```
In [39]: from matplotlib import pyplot as plt
fig = plt.figure(figsize = (6, 10))
for i in range(1, 6):
    plt.subplot(3, 2, i)
    plt.title("X{}~Y".format(i))
    plt.scatter(X["X{}".format(i)], Y)
fig.tight_layout()
```

상관계수

```
In [40]: from scipy import stats
for i in range(1, 6):
    print(i, stats.pearsonr(X["X" + str(i)], Y)[0])
```

```
1 0.7169488074770946
2 0.6999618891342666
3 -0.1159727038320417
4 0.12254363846193096
5 -0.09733277938669578
```

독립성

- 다중공선성이 없어야 함
- 다중공선성을 일으키는 변수 (VIF 10이상)를 제거하거나, 변수선택법을 이용하여 해결

```
In [41]: from statsmodels.stats.outliers_influence import variance_inflation_factor
pd.Series([variance_inflation_factor(X.values, i)
           for i in range(X.shape[1])],
           index=X.columns)
```

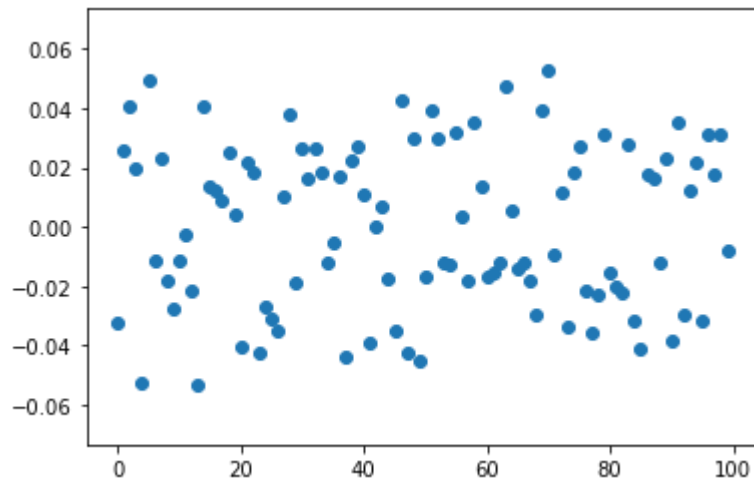
```
Out[41]: const    20.407675
X1         1.002517
X2         1.097224
X3         1.042954
X4         1.057066
X5         1.036779
dtype: float64
```

잔차 등분산성

잔차 그림

```
In [42]: # 잔차가 -0.06부터 0.06까지 고르게 퍼져 있음
# 정상적인 잔차그림은 0을 중심으로 예측 값에 관계없이 일정 범위 내에서 특정한 패턴을 가지지 않게 분포됩니다.
res = model.resid
plt.scatter(range(len(res)), res.values)
```

```
Out[42]: <matplotlib.collections.PathCollection at 0x17f1cf60c88>
```



Bresuch-Pagan test

- The null hypothesis (H0): Homoscedasticity (등분산성) is present
- The alternative hypothesis: (Ha): Homoscedasticity is not present

```
In [43]: from statsmodels.compat import lzip
import statsmodels.stats.api as sms

names = ['Lagrange multiplier statistic', 'p-value', 'f-value', 'f p-value']

test = sms.het_breuschpagan(model.resid, model.model.exog)
lzip(names, test)

# p-value가 0.05 미만이 아니므로, 등분산성이 존재한다고 볼 수 있음
# 등분산성 가정을 만족하지 않으면 제곱항 추가, 변수 변환 등 고려가 필요
```

```
Out[43]: [('Lagrange multiplier statistic', 4.379630030338111),
 ('p-value', 0.49614819719458125),
 ('f-value', 0.8610826814043929),
 ('f p-value', 0.5103673804157989)]
```

잔차 정규성

```
In [44]: # 정규 분포를 따르지 않음
from scipy import stats
k2, p = stats.normaltest(res)
print(p)
```

```
8.946146855803877e-07
```

잔차 독립성

- durbin_watson 테스트: 1.5와 2.5 사이에 있으면 정상

```
In [45]: from statsmodels.stats.stattools import durbin_watson

#perform Durbin-Watson test
durbin_watson(model.resid)
```

```
Out[45]: 2.298391259795813
```

변수선택법

$$AIC = 2K - 2\ln(L)$$

- K is the number of independent variables used
- L is the log-likelihood estimate (a.k.a. the likelihood that the model could have produced your observed y-values).

전진선택법

```
In [46]: def processSubset(X,y,feature_set):
    model = sm.OLS(y,X[list(feature_set)]) # Modeling
    regr = model.fit() # model fitting
    AIC = regr.aic # model's AIC
    return {"model" : regr, "AIC" : AIC}
```

```
In [47]: def forward(X,y,predictors):
    # predictor - 현재 선택되어있는 변수

    remaining_predictors = [p for p in X.columns.difference(['const']) if p not in predictors]
    results = []
    for p in remaining_predictors :
        results.append(processSubset(X=X,y=y,feature_set=predictors+[p]+'const'))

    models = pd.DataFrame(results)

    # AIC가 가장 낮은 것을 선택
    best_model = models.loc[models['AIC'].argmin()]
    print("Selected predictors:",best_model["model"].model.exog_names,"AIC: ",best_model[0].aic)
    return best_model

### 전진선택법 모델
def forward_model(X,y):
    Fmodels = pd.DataFrame(columns=["AIC","model"])

    # 미리 정의된 데이터 변수
    predictors = []

    for i in range(1,len(X.columns.difference(['const']))+1):
        Forward_result = forward(X=X,y=y,predictors=predictors)
        if i > 1 :
            if Forward_result["AIC"] > Fmodel_before:
                break
            Fmodels.loc[i] = Forward_result
            predictors = Fmodels.loc[i]["model"].model.exog_names
            Fmodel_before = Fmodels.loc[i]["AIC"]
            predictors = [k for k in predictors if k != 'const']

    return Fmodels['model'][len(Fmodels['model'])]
```


In [48]:

```
# 상수가 반드시 포함되어 있어야 함: X = sm.add_constant(X)
print(forward_model(X,Y).summary())
```

Selected predictors: ['X1', 'const'] AIC: 27.990661502147674

Selected predictors: ['X1', 'X2', 'const'] AIC: -428.4013516846708

Selected predictors: ['X1', 'X2', 'X4', 'const'] AIC: -426.98009592720234

OLS Regression Results

```
=====
Dep. Variable:          y      R-squared:                0.995
Model:                  OLS    Adj. R-squared:           0.995
Method:                 Least Squares    F-statistic:       9721.
Date:                   Thu, 19 Aug 2021    Prob (F-statistic):   1.77e-112
Time:                   14:34:30    Log-Likelihood:      217.20
No. Observations:       100    AIC:                -428.4
Df Residuals:           97    BIC:                -420.6
Df Model:                2
Covariance Type:        nonrobust
=====
```

	coef	std err	t	P> t	[0.025	0.975]
X1	0.9947	0.010	99.345	0.000	0.975	1.015
X2	1.0109	0.010	96.949	0.000	0.990	1.032
const	0.0481	0.007	6.643	0.000	0.034	0.063

```
=====
Omnibus:                 37.979    Durbin-Watson:           2.315
Prob(Omnibus):            0.000    Jarque-Bera (JB):         6.300
Skew:                    -0.048    Prob(JB):                 0.0428
Kurtosis:                 1.774    Cond. No.                  5.30
=====
```

Notes:

[1] Standard Errors assume that the covariance matrix of the errors is correctly specified.

후진선택법

In [49]:

```
import itertools
def backward(X,y,predictors):
    results = []

    # 데이터 변수들이 미리 정의된 predictors 조합 확인

    for combo in itertools.combinations(predictors, len(predictors) - 1):
        results.append(processSubset(X=X,y=y,feature_set=list(combo)+['const']))
    models = pd.DataFrame(results)

    # 가장 낮은 AIC를 가진 모델을 선택
    best_model = models.loc[models['AIC'].argmin()]
```

```

print("Selected predictors:",best_model['model'].model.exog_names,' AIC:',best_model[0].aic)
return best_model

def backward_model(X,y) :
    Bmodels = pd.DataFrame(columns=["AIC","model"], index = range(1,len(X.columns)))
    predictors = X.columns.difference(['const'])
    Bmodel_before = processSubset(X,y,predictors)['AIC']
    while (len(predictors) > 1):
        Backward_result = backward(X=X, y= y,predictors=predictors)
        if Backward_result['AIC'] > Bmodel_before :
            break
        Bmodels.loc[len(predictors) -1] = Backward_result
        predictors = Bmodels.loc[len(predictors) - 1]['model'].model.exog_names
        Bmodel_before = Backward_result["AIC"]
        predictors = [k for k in predictors if k != 'const']
    return (Bmodels["model"].dropna().iloc[0])

```

In [50]:

```

# 상수가 반드시 포함되어 있어야 함: X = sm.add_constant(X)
print(backward_model(X,Y).summary())

```

Selected predictors: ['X1', 'X2', 'X4', 'X5', 'const'] AIC: -425.44443485780164
 Selected predictors: ['X1', 'X2', 'X4', 'const'] AIC: -426.98009592720234
 Selected predictors: ['X1', 'X2', 'const'] AIC: -428.4013516846708
 Selected predictors: ['X1', 'const'] AIC: 27.990661502147674

OLS Regression Results

```

=====
Dep. Variable:          y      R-squared:                0.995
Model:                  OLS    Adj. R-squared:           0.995
Method:                 Least Squares    F-statistic:       9721.
Date:                  Thu, 19 Aug 2021    Prob (F-statistic): 1.77e-112
Time:                  14:34:30    Log-Likelihood:    217.20
No. Observations:      100    AIC:                -428.4
Df Residuals:          97    BIC:                -420.6
Df Model:               2
Covariance Type:       nonrobust
=====

```

	coef	std err	t	P> t	[0.025	0.975]
X1	0.9947	0.010	99.345	0.000	0.975	1.015
X2	1.0109	0.010	96.949	0.000	0.990	1.032
const	0.0481	0.007	6.643	0.000	0.034	0.063

```

=====
Omnibus:                 37.979    Durbin-Watson:           2.315
Prob(Omnibus):            0.000    Jarque-Bera (JB):         6.300
Skew:                    -0.048    Prob(JB):                 0.0428
Kurtosis:                 1.774    Cond. No.                  5.30
=====

```

Notes:

[1] Standard Errors assume that the covariance matrix of the errors is correctly specified.

단계적 선택법

In [51]:

```

def Stepwise_model(X,y):
    Stepmodels = pd.DataFrame(columns = ["AIC","model"])
    predictors = []
    Smodel_before = processSubset(X,y,predictors + ['const'])['AIC']

    # 변수 1~10개 0-9 -> 1-10
    for i in range(1,len(X.columns.difference(['const']))+1):
        Forward_result = forward(X=X,y=y,predictors = predictors) # constant added
        Stepmodels.loc[i] = Forward_result

        predictors = Stepmodels.loc[i]['model'].model.exog_names
        predictors = [k for k in predictors if k != 'const']
        Backward_result = backward(X=X,y=y,predictors = predictors)
        if Backward_result["AIC"] < Forward_result["AIC"]:
            Stepmodels.loc[i] = Backward_result
            predictors = Stepmodels.loc[i]["model"].model.exog_names
            Smodel_before = Stepmodels.loc[i]["AIC"]

```

```

    predictors = [k for k in predictors if k != "const"]
    print('backward')
    if Stepmodels.loc[i]["AIC"] > Smodel_before:
        break
    else :
        Smodel_before = Stepmodels.loc[i]["AIC"]
    return Stepmodels["model"][len(Stepmodels["model"])]

```

```
In [52]: print(Stepwise_model(X,Y).summary())
```

```

Selected predictors: ['X1', 'const'] AIC: 27.990661502147674
Selected predictors: ['const'] AIC: 98.14853540392605
Selected predictors: ['X1', 'X2', 'const'] AIC: -428.4013516846708
Selected predictors: ['X1', 'const'] AIC: 27.990661502147674
Selected predictors: ['X1', 'X2', 'X4', 'const'] AIC: -426.98009592720234
Selected predictors: ['X1', 'X2', 'const'] AIC: -428.4013516846708
backward
Selected predictors: ['X1', 'X2', 'X4', 'const'] AIC: -426.98009592720234
Selected predictors: ['X1', 'X2', 'const'] AIC: -428.4013516846708
backward
Selected predictors: ['X1', 'X2', 'X4', 'const'] AIC: -426.98009592720234
Selected predictors: ['X1', 'X2', 'const'] AIC: -428.4013516846708
backward

```

OLS Regression Results

```

=====
Dep. Variable:          y      R-squared:                0.995
Model:                  OLS      Adj. R-squared:         0.995
Method:                 Least Squares      F-statistic:       9721.
Date:                  Thu, 19 Aug 2021      Prob (F-statistic):   1.77e-112
Time:                  14:34:30      Log-Likelihood:      217.20
No. Observations:      100      AIC:                -428.4
Df Residuals:          97      BIC:                -420.6
Df Model:               2
Covariance Type:        nonrobust
=====

```

	coef	std err	t	P> t	[0.025	0.975]
X1	0.9947	0.010	99.345	0.000	0.975	1.015
X2	1.0109	0.010	96.949	0.000	0.990	1.032
const	0.0481	0.007	6.643	0.000	0.034	0.063

```

=====
Omnibus:                 37.979      Durbin-Watson:           2.315
Prob(Omnibus):            0.000      Jarque-Bera (JB):        6.300
Skew:                    -0.048      Prob(JB):                0.0428
Kurtosis:                 1.774      Cond. No.                 5.30
=====

```

Notes:

[1] Standard Errors assume that the covariance matrix of the errors is correctly specified.

다항 회귀

`class sklearn.preprocessing.PolynomialFeatures(degree=2, *, interaction_only=False, include_bias=True, order='C')`

For example, if an input sample is two dimensional and of the form $[a, b]$, the degree-2 polynomial features are $[1, a, b, a^2, ab, b^2]$.

In [53]:

```
from sklearn.preprocessing import PolynomialFeatures
polynomial_features = PolynomialFeatures(degree=2, interaction_only = False)

A = pd.DataFrame({"X1": [1, 2, 3], "X2": [2, 3, 4]})
xp = polynomial_features.fit_transform(A)
xp.shape # bias, X1, X2, X1^2, X2^2, X1X2

# xp로 모델링하면 됨
```

Out[53]: (3, 6)

로지스틱 회귀 분석

데이터 준비

In [54]:

```
from sklearn.datasets import make_classification
X, Y = make_classification(n_features = 5)
```

기초

- Pseudo R-squ. is a substitute for R-squared. It also measures the amount of outcome variable variance, which is explained by the model. Pseudo R-squared can be interpreted in the same way as R-squared; the higher the better, with a maximum of 1.
- LL-null and LLR p-value are equivalent to the F-statistic and F-proba of linear regression, and are interpreted in the same manner for comparing models. The higher the value for LL-null the better. Low values for LLR p-value (<0.05) mean you can reject the null hypothesis that the model based on the intercept (all coefficients = 0) is better than the full model. Hence, our model is relevant.
- The z-statistic plays the same role as the t-statistic in the linear regression output and equals the coefficient divided by its standard error. The lower, the better.

```
In [55]: from statsmodels.discrete.discrete_model import Logit
model = Logit(Y, X)
model = model.fit()
print(model.summary())
```

```
Optimization terminated successfully.
Current function value: 0.138469
Iterations 9
```

Logit Regression Results

```
=====
Dep. Variable:          y      No. Observations:          100
Model:                Logit   Df Residuals:           96
Method:                MLE    Df Model:              3
Date:                Thu, 19 Aug 2021   Pseudo R-squ.:        0.8002
Time:                14:34:31   Log-Likelihood:       -13.847
converged:              True    LL-Null:              -69.315
Covariance Type:      nonrobust   LLR p-value:         6.902e-24
=====
```

	coef	std err	z	P> z	[0.025	0.975]
x1	0.6468	nan	nan	nan	nan	nan
x2	0.2020	nan	nan	nan	nan	nan
x3	4.5396	7.6e+06	5.97e-07	1.000	-1.49e+07	1.49e+07
x4	0.5489	0.546	1.005	0.315	-0.522	1.620
x5	-1.9118	1.26e+07	-1.52e-07	1.000	-2.47e+07	2.47e+07

```
=====
```