Data Pre-processing

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Standardization

- Standardization (표준화, Z-score Normalization)
 - ✓ 입력 변수(X)의 정규 분포를 평균이 0이고 표준 편차가 1인 표준 정규 분포로 재조정

$$\mu=0, \sigma=1$$

$$Z$$
-score = $\frac{x-\mu}{\sigma}$

✓ Z-score : 특정 데이터가 평균에서 멀리 떨어진 정도 → outliers (이상치)

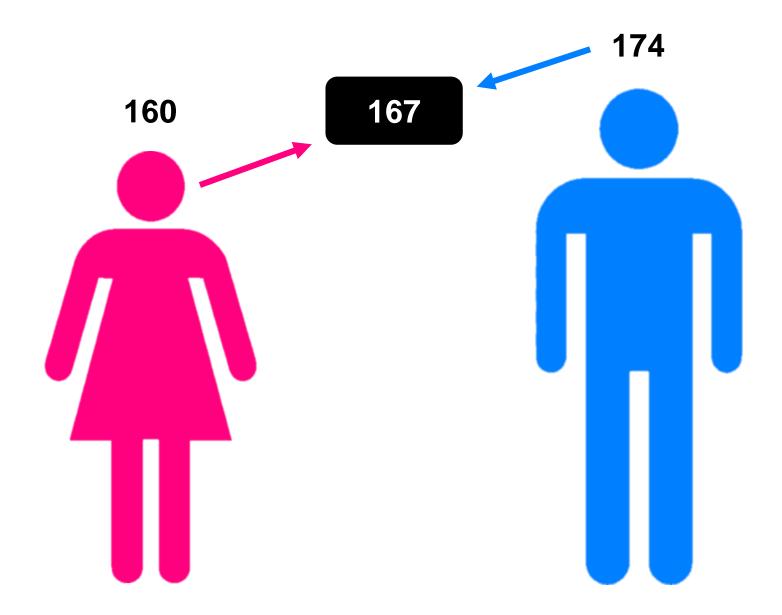
Normalization

- Normalization (정규화)
 - ✓ 모든 입력 변수를 0과 1 사이의 값으로 변환
 - ✓ Min-Max Scaling

$$x' = rac{x - x_{\min}}{x_{\max} - x_{\min}}$$



Reflecting the Characteristics of Each Group



lambda

lambda parameters: indented statement

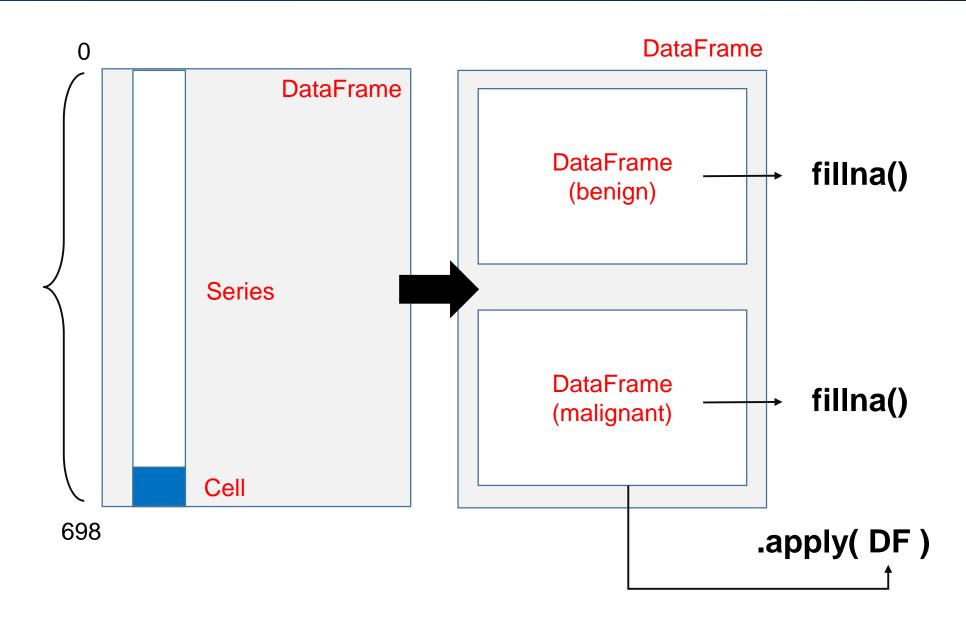
```
def test_ex(x, y):
    return x + y

test_ex(10, 20)
```



(lambda x, y: x + y)(10, 20)

groupby()



Descriptive Statistics

Ⅲ bc_des - DataFrame										
Index	Id	Cl.thickness	Cell.size	Cell.shape	varg.adhesior	Epith.c.size	Bare.nuclei	Bl.cromatin	Iormal.nucleo	Mitoses
count	699	699	699	699	699	699	683	699	699	699
mean	1.0717e+06	4.41774	3.13448	3.20744	2.80687	3.21602	3.54466	3.43777	2.86695	1.58941
std	617096	2.81574	3.05146	2.97191	2.85538	2.2143	3.64386	2.43836	3.05363	1.71508
min	61634	1	1	1	1	1	1	1	1	1
25%	870688	2	1	1	1	2	1	2	1	1
50%	1.17171e+06	4	1	1	1	2	1	3	1	1
75%	1.2383e+06	6	5	5	4	4	6	5	4	1
max	1.34544e+07	10	10	10	10	10	10	10	10	10

Count : the number of available data

Mean : arithmetic mean value

Min : minimum value

Max : maximum value

Q1:~25%

Q2 : ~50% (median)

• Q3 : ~75%

Q4 : ~max

Mode: most frequent value

Std: standard deviation

Min – Max : a range of values

$$\sigma = \sqrt{rac{\sum (x_i - \mu)^2}{N}}$$

 σ = population standard deviation

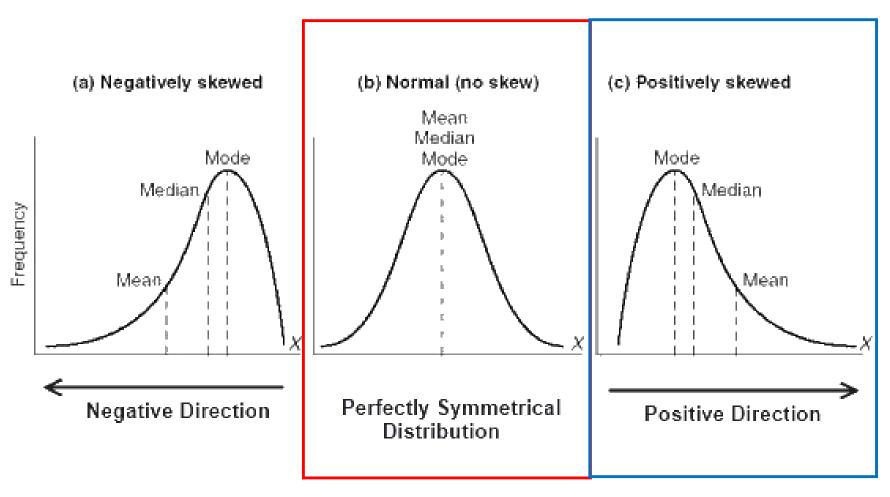
 $oldsymbol{N}$ = the size of the population

 $oldsymbol{x}_i$ = each value from the population

 μ = the population mean

Skewness

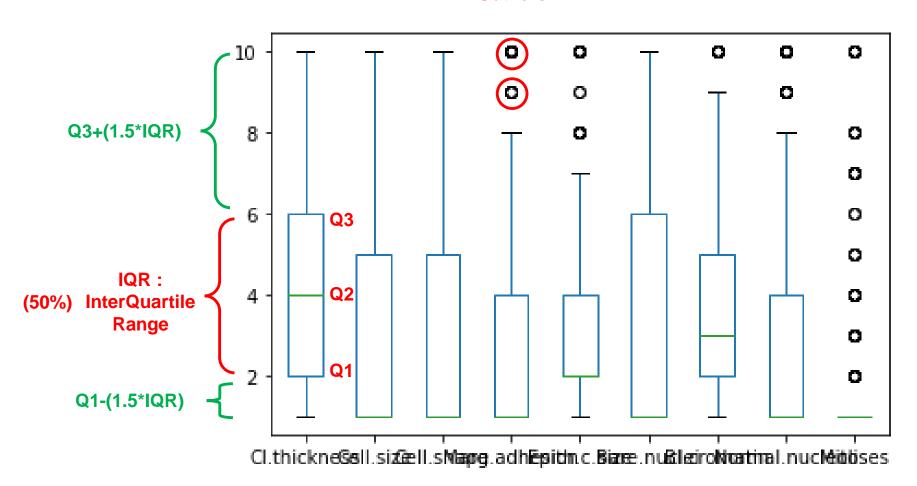
Mean = Median = Mode



BreastCancer Dataset

Boxplot

Outliers



Apply()

