# Diagnostic test



醫學研究部 生物統計小組
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2025/5/6

# 內容大綱

- Hosmer and Lemeshow test (goodness of fit)
- Bland–Altman plot
- Receiver Operating Characteristic (ROC) Curve Analysis

# Hosmer and Lemeshow test

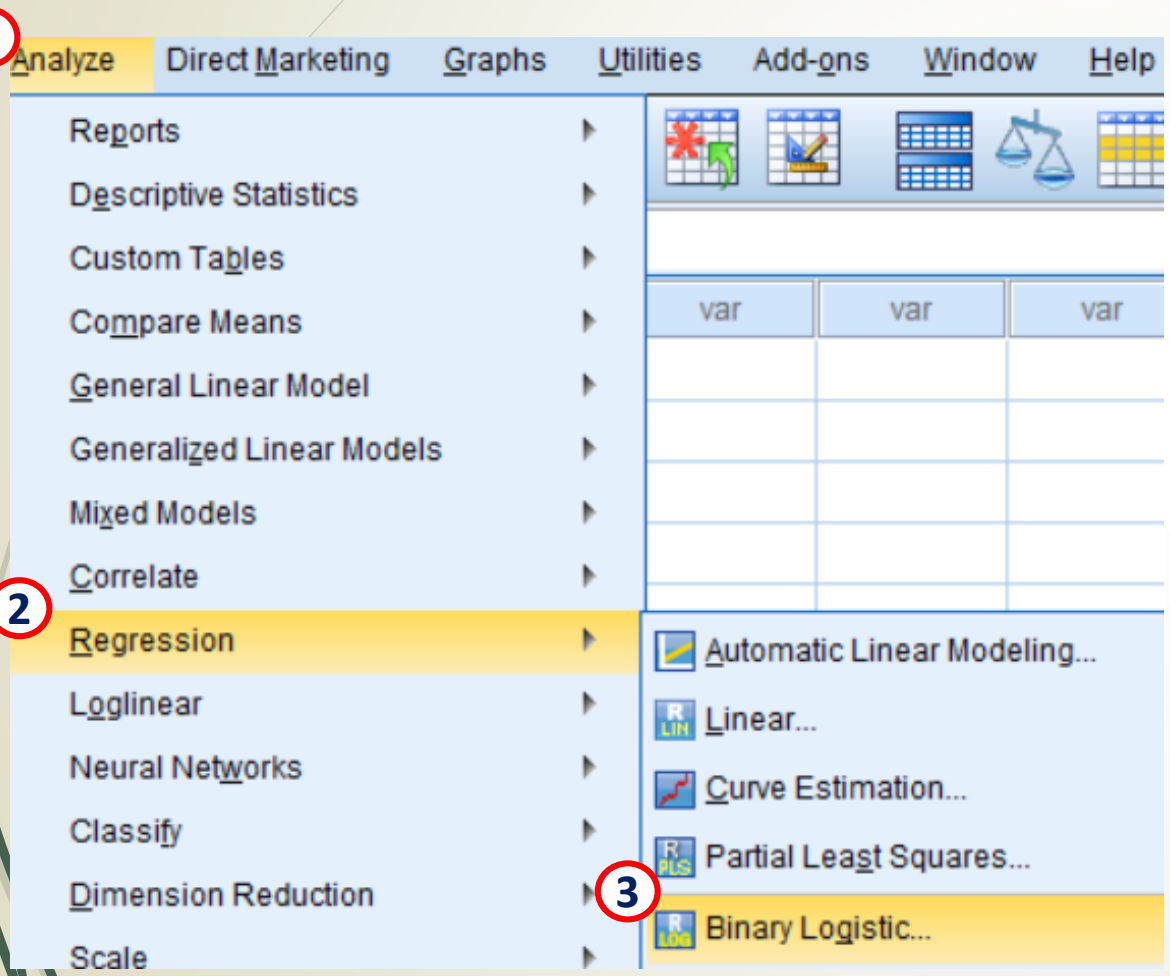
- 對logistic迴歸模型擬合優度的檢定方法
  - 根據預測機率值將資料分成大致相同規模的10個組
  - 將觀測資料按其預測機率做升序排列
    - 第一組機率最小
    - 最後一組估計機率最大

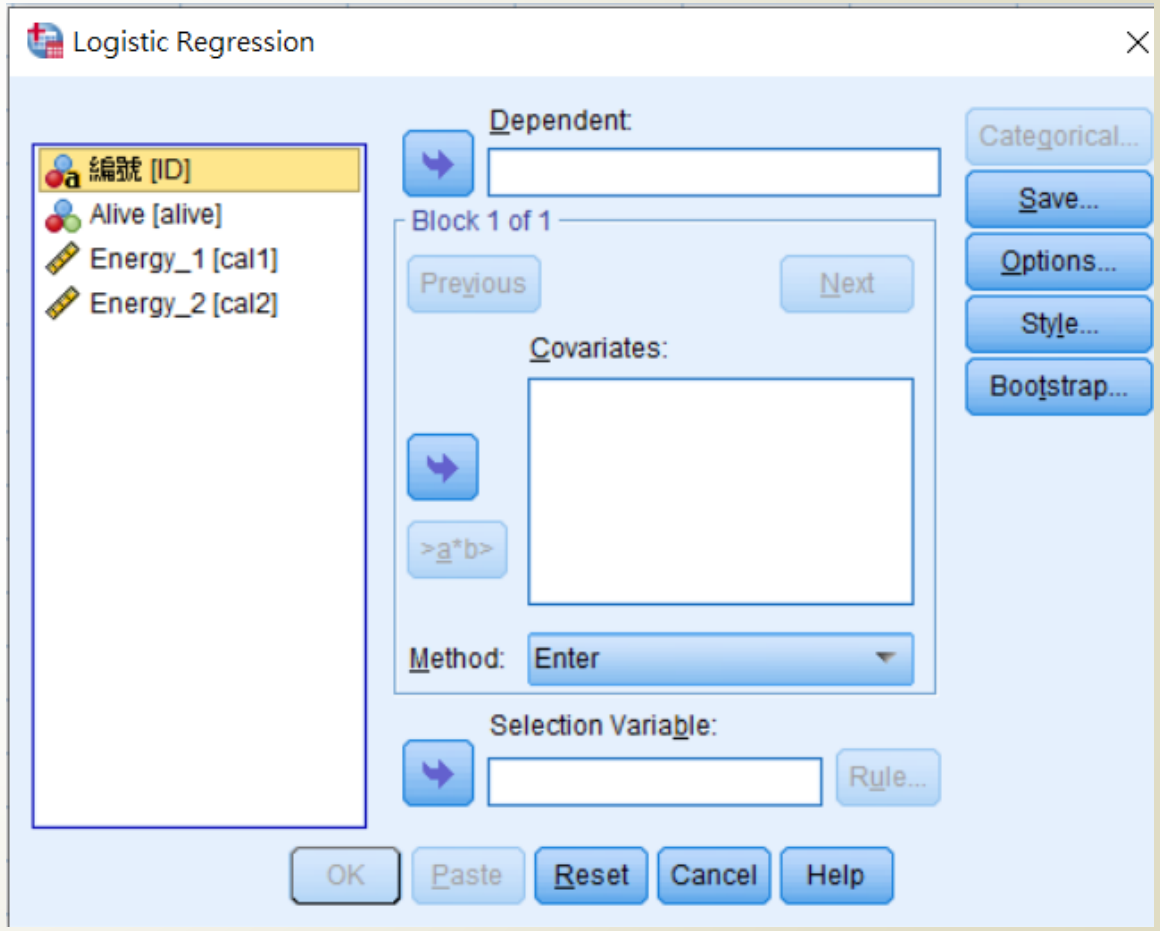
# Hosmer and Lemeshow test

- 類似於Pearson Chi-Square統計量的指標
  - 可從觀測頻數和預測頻數構成的2*G交互表中求得
  - HL指標與Chi-Square分佈相比較
    - $p > 0.05$ (Acceptable Calibration)

# Hosmer and Lemeshow test (SPSS)

- Analyze → Regression → Binary Logistic

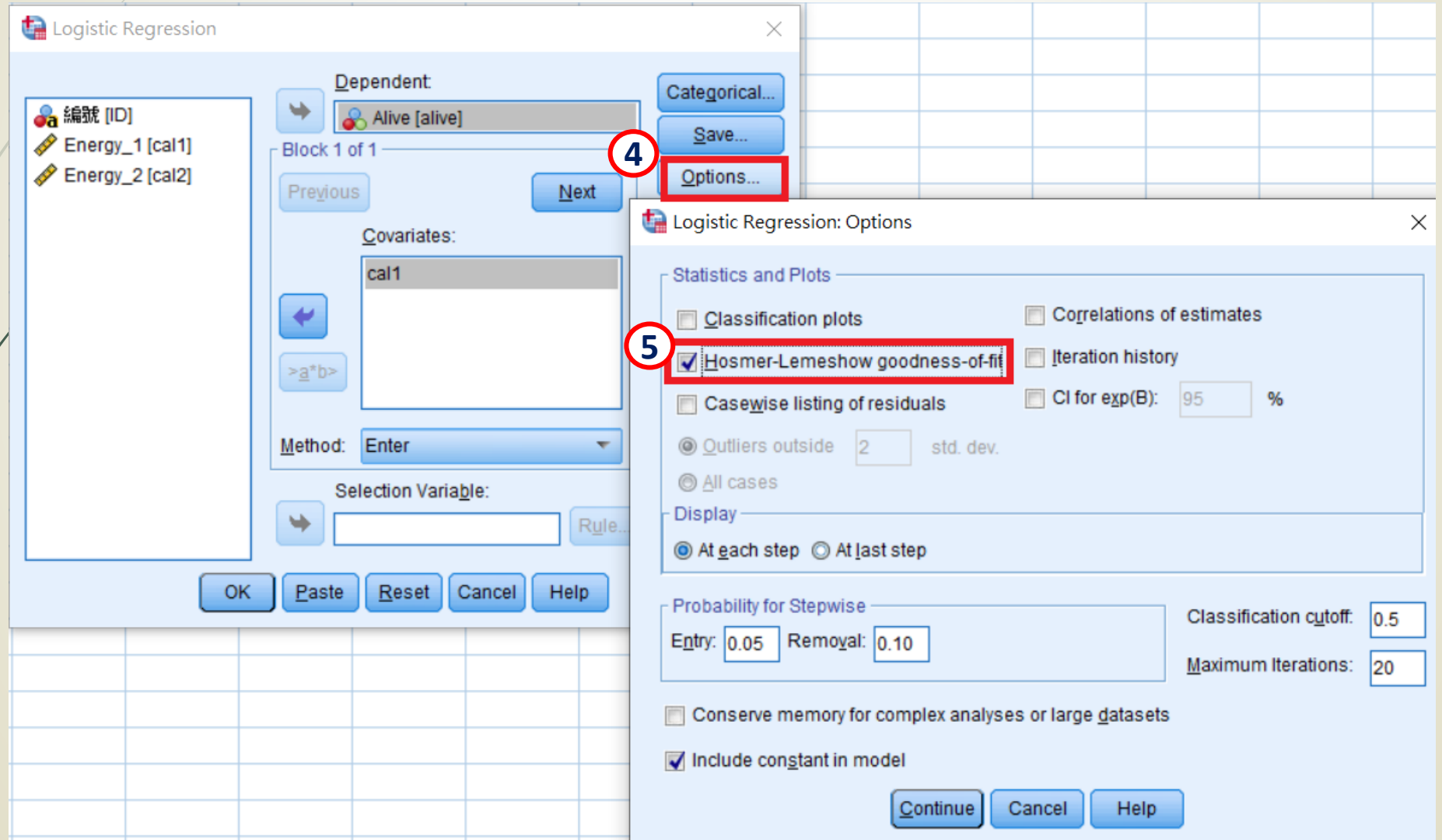



練習範例：ROC ex.sav

# Hosmer and Lemeshow test (SPSS)

- Analyze → Regression → Binary Logistic




練習範例：ROC ex.sav

# Hosmer and Lemeshow test (SPSS)

- Analyze → Regression → Binary Logistic

**Hosmer and Lemeshow Test**

| Step | Chi-square | df | Sig. |
|---|---|---|---|
| 1 | 7.332 | 7 | .395 |

$p > 0.05$
Acceptable calibration

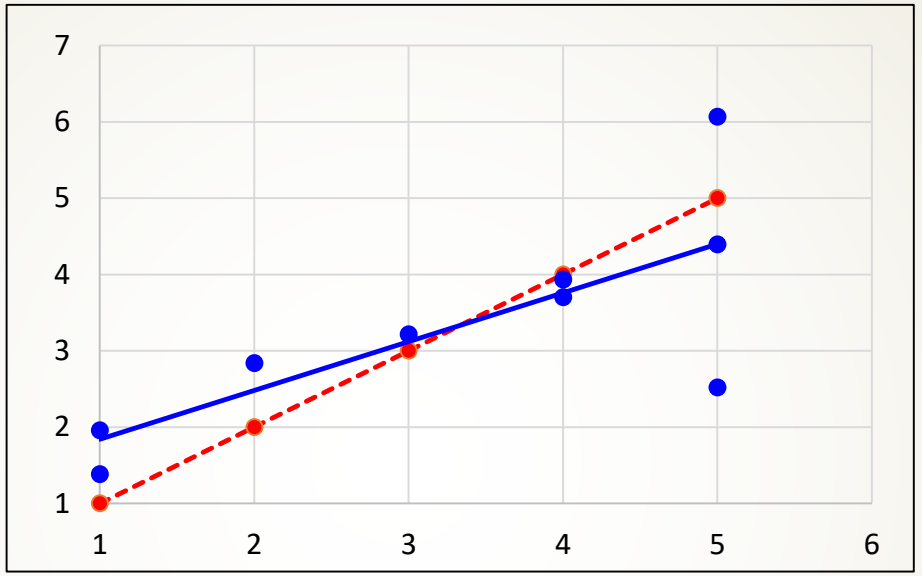
**Contingency Table for Hosmer and Lemeshow Test**

| | | Alive = Death | | Alive = Alive | | Total |
|---|---|---|---|---|---|---|
| | | Observed | Expected | Observed | Expected | |
| Step 1 | 1 | 5 | 4.618 | 1 | 1.382 | 6 |
| | 2 | 5 | 4.041 | 1 | 1.959 | 6 |
| | 3 | 1 | 3.483 | 5 | 2.517 | 6 |
| | 4 | 4 | 3.165 | 2 | 2.835 | 6 |
| | 5 | 3 | 2.785 | 3 | 3.215 | 6 |
| | 6 | 2 | 2.298 | 4 | 3.702 | 6 |
| | 7 | 2 | 2.070 | 4 | 3.930 | 6 |
| | 8 | 1 | 1.606 | 5 | 4.394 | 6 |
| | 9 | 2 | .935 | 5 | 6.065 | 7 |

練習範例：ROC ex.sav

# Hosmer and Lemeshow test (SPSS & Excel)

- Scatter plot
- Bar chart
- Line chart




| Alive = Alive | |
|---|---|
| Observed | Expected |
| 1 | 1.382 |
| 1 | 1.959 |
| 5 | 2.517 |
| 2 | 2.835 |
| 3 | 3.215 |
| 4 | 3.702 |
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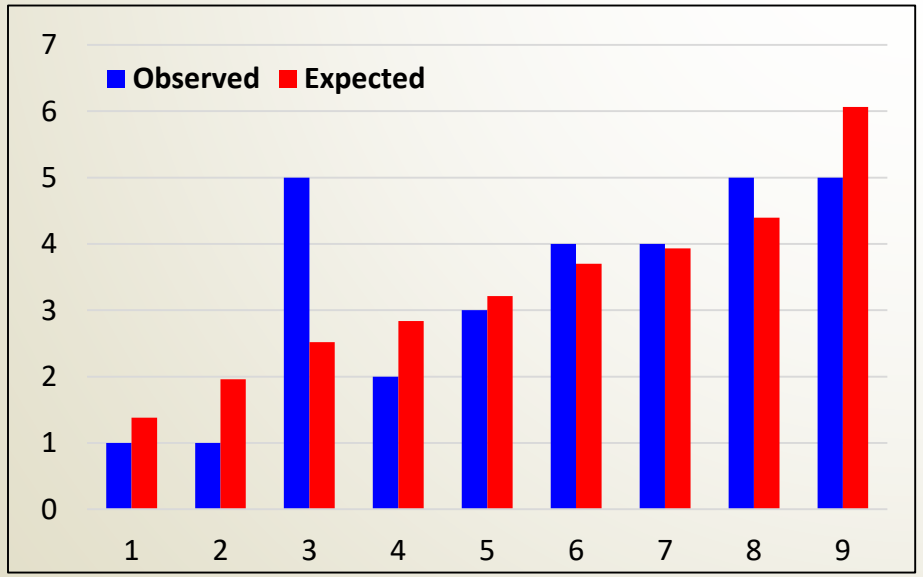


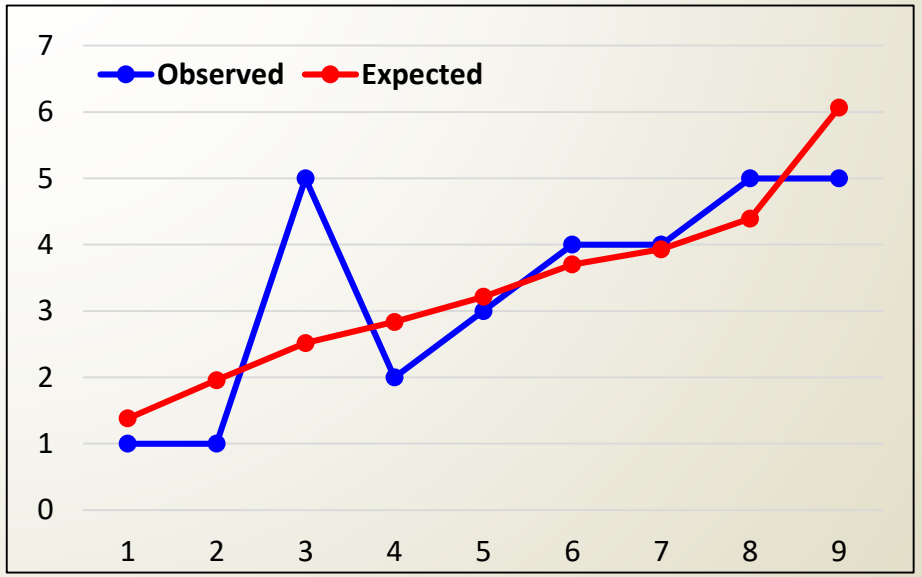


練習範例：ROC ex.sav

# Bland–Altman plot

- The agreement between **two quantitative methods** of measurement
  - correlation coefficient (r)
    - the relationship between one variable and another
    - not the differences (not recommended)
  - Bland–Altman plot
    - In 1983 Altman and Bland (B&A) proposed
    - **Mean difference** and **constructing limits of agreement**

# Bland–Altman plot

- Scatter plot
  - Y axis
    - The difference between the two paired measurements (A-B)
    - Normally distributed (Gaussian) - 95% of differences d ± 1.96s
      - not normally distributed - logarithmic transformation
  - X axis
    - The average of these measures ((A+B)/2)

# Bland–Altman plot

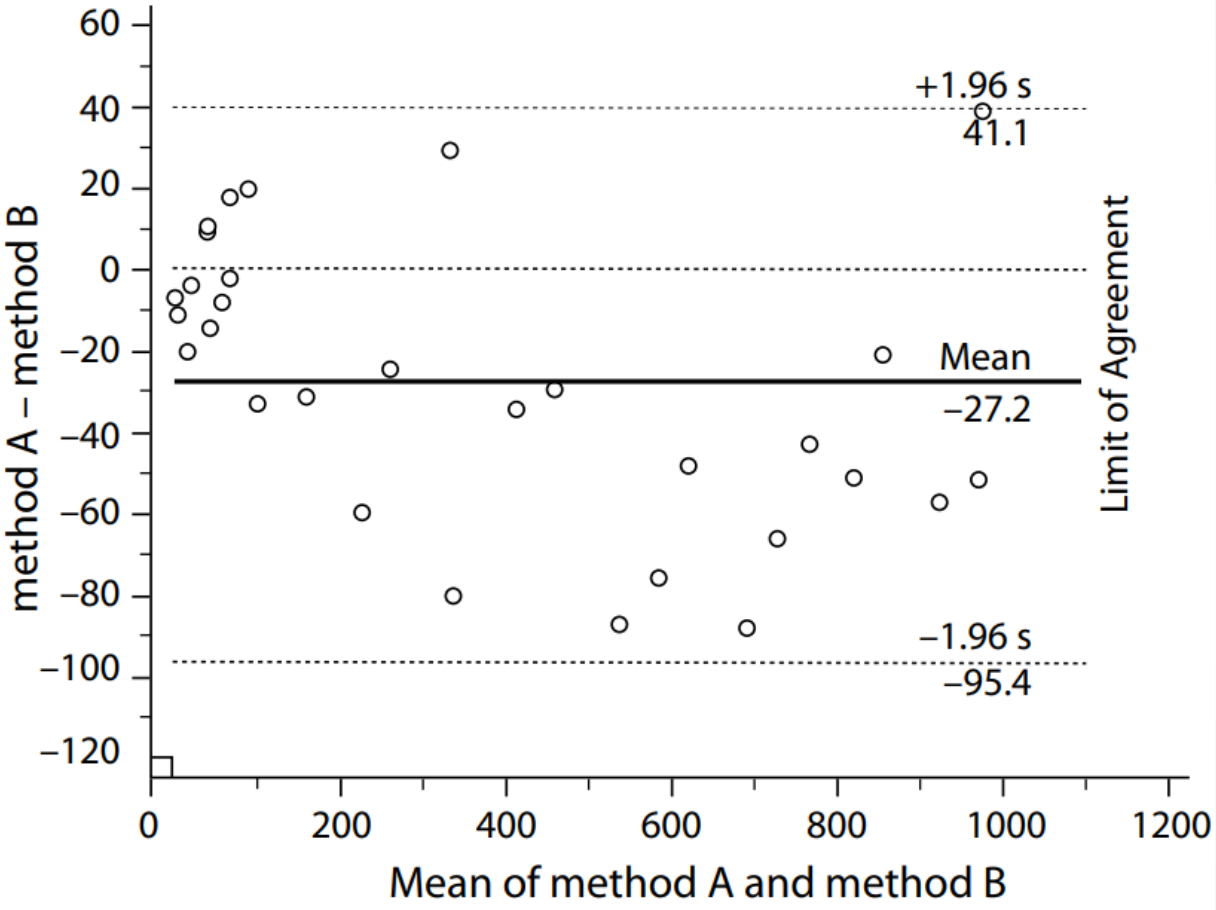


**FIGURE 5.** Bland and Altman plot for data from the table 1, with the representation of the limits of agreement (doted line), from -1.96*s* to +1.96*s*.

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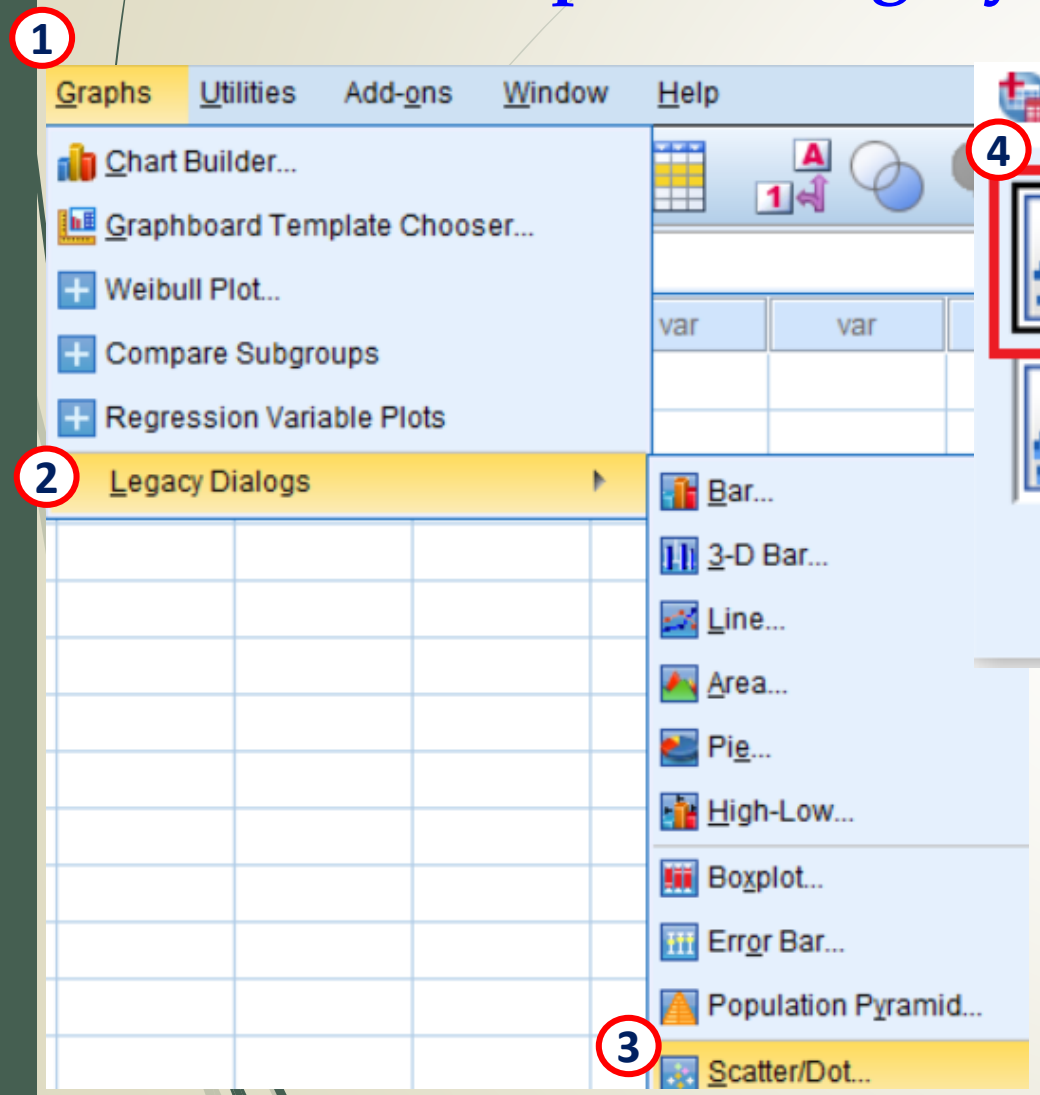
# Bland–Altman plot (SPSS)

- Graphs → Legacy Dialogs → Scatter/Dot



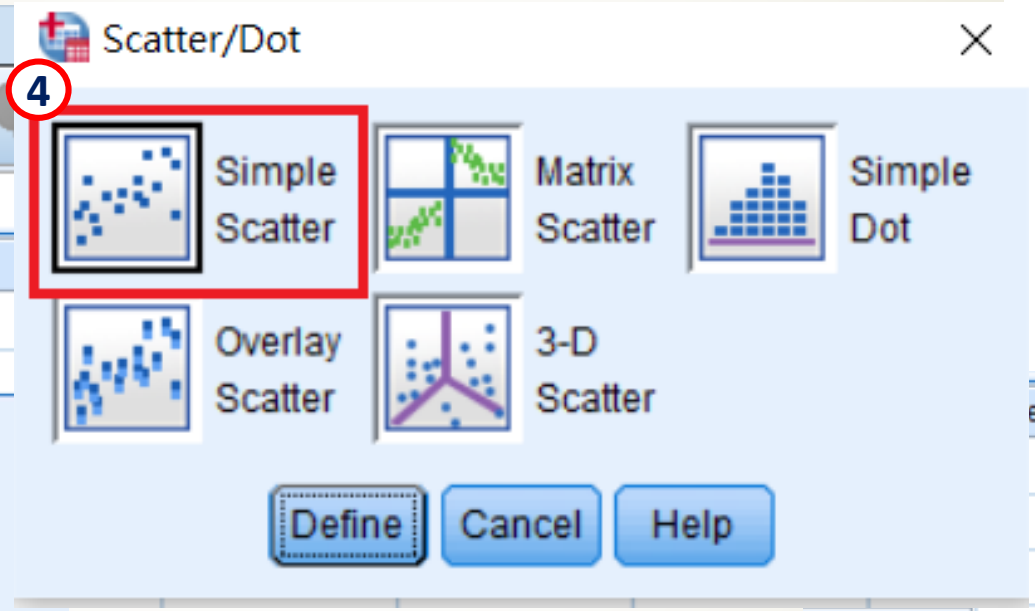




**Table 1.** Hypothetical data of an agreement between two methods (Method A and B).

| Method A (units) | Method B (units) | Mean (A+B)/2 (units) | (A – B) (units) | (A – B)/ Mean (%) |
|---|---|---|---|---|
| 1.0 | 8.0 | 4.5 | -7.0 | -155.6% |
| 5.0 | 16.0 | 10.5 | -11.0 | -104.8% |
| 10.0 | 30.0 | 20.0 | -20.0 | -100.0% |
| 20.0 | 24.0 | 22.0 | -4.0 | -18.2% |
| 50.0 | 39.0 | 44.5 | 11.0 | 24.7% |
| 40.0 | 54.0 | 47.0 | -14.0 | -29.8% |
| 50.0 | 40.0 | 45.0 | 10.0 | 22.2% |
| 60.0 | 68.0 | 64.0 | -8.0 | -12.5% |
| 70.0 | 72.0 | 71.0 | -2.0 | -2.8% |
| 80.0 | 62.0 | 71.0 | 18.0 | 25.4% |
| 90.0 | 122.0 | 106.0 | -32.0 | -30.2% |
| 100.0 | 80.0 | 90.0 | 20.0 | 22.2% |
| 150.0 | 181.0 | 165.5 | -31.0 | -18.7% |
| 200.0 | 259.0 | 229.5 | -59.0 | -25.7% |
| 250.0 | 275.0 | 262.5 | -25.0 | -9.5% |

| | ethodA | MethodB | mean | dif |
|---|---|---|---|---|
| | 1 | 8 | 5 | -7 |
| | 5 | 16 | 11 | -11 |
| | 10 | 30 | 20 | -20 |
| 4 | 20 | 24 | 22 | -4 |
| 5 | 50 | 39 | 45 | 11 |
| 6 | 40 | 54 | 47 | -14 |
| 7 | 50 | 40 | 45 | 10 |
| 8 | 60 | 68 | 64 | -8 |
| 9 | 70 | 72 | 71 | -2 |
| 10 | 80 | 62 | 71 | 18 |

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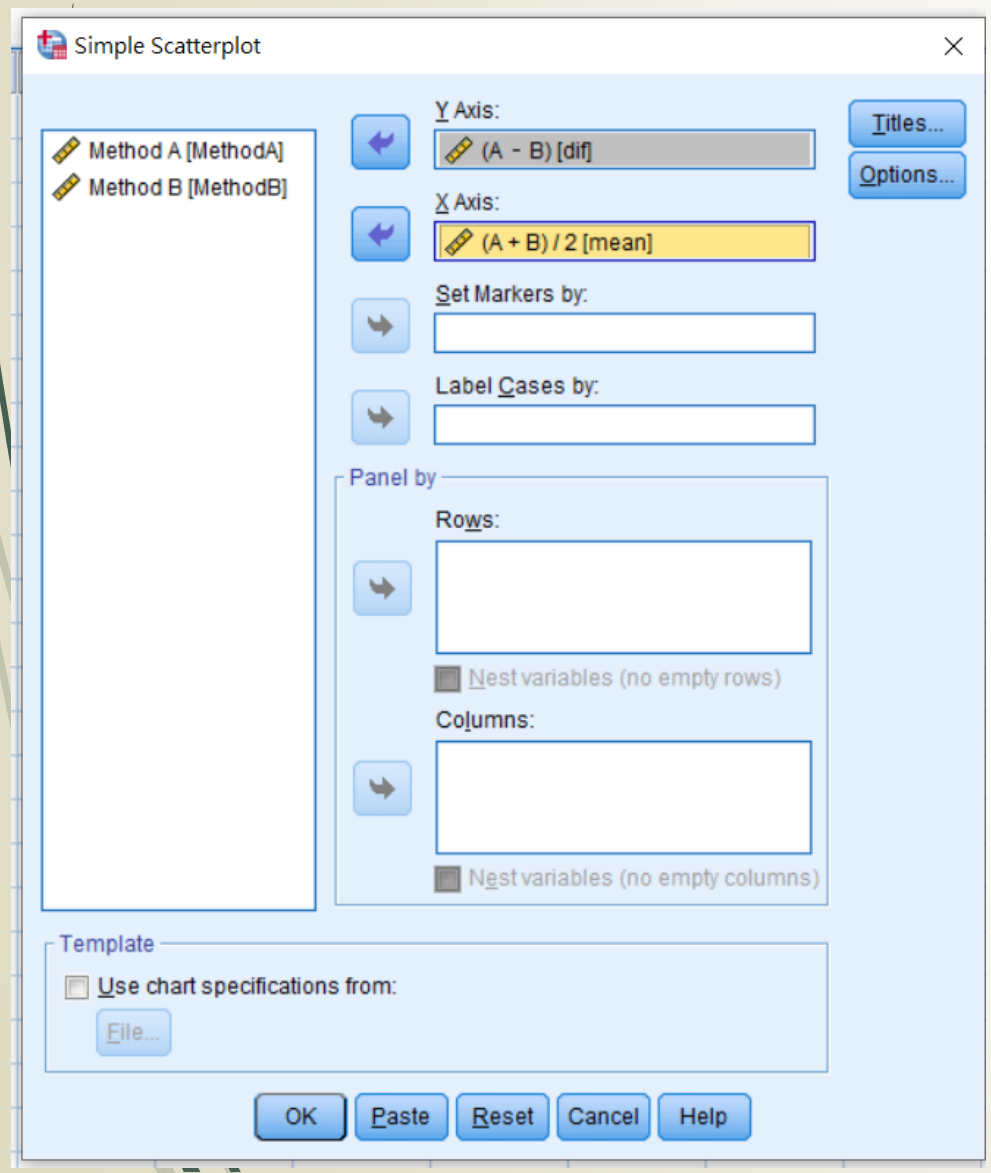
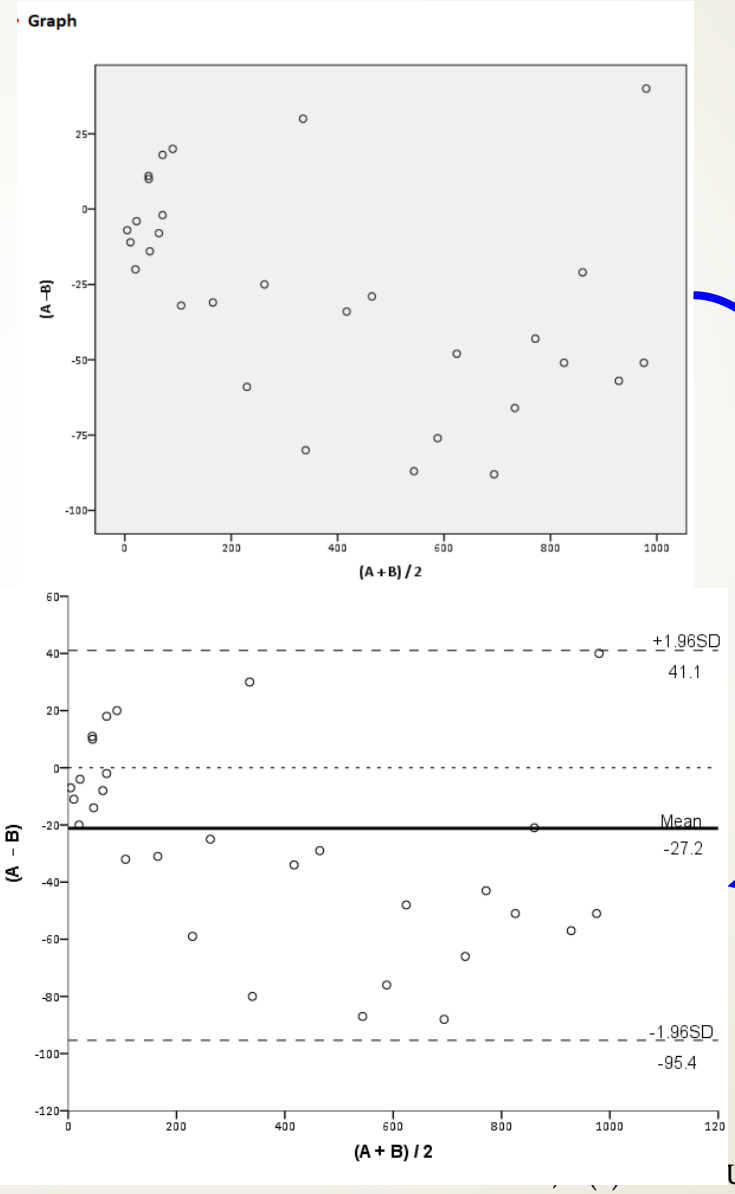
# Bland–Altman plot (SPSS)

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|---|---|---|---|---|
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| 5.0 | 16.0 | 10.5 | -11.0 | -104.8% |
| 10.0 | 30.0 | 20.0 | -20.0 | -100.0% |
| 20.0 | 24.0 | 22.0 | -4.0 | -18.2% |
| 50.0 | 39.0 | 44.5 | 11.0 | 24.7% |
| 40.0 | 54.0 | 47.0 | -14.0 | -29.8% |
| 50.0 | 40.0 | 45.0 | 10.0 | 22.2% |
| 60.0 | 68.0 | 64.0 | -8.0 | -12.5% |
| 70.0 | 72.0 | 71.0 | -2.0 | -2.8% |
| 80.0 | 62.0 | 71.0 | 18.0 | 25.4% |
| 90.0 | 122.0 | 106.0 | -32.0 | -30.2% |
| 100.0 | 80.0 | 90.0 | 20.0 | 22.2% |
| 150.0 | 181.0 | 165.5 | -31.0 | -18.7% |
| 200.0 | 259.0 | 229.5 | -59.0 | -25.7% |
| 250.0 | 275.0 | 262.5 | -25.0 | -9.5% |
| 300.0 | 380.0 | 340.0 | -80.0 | -23.5% |
| 350.0 | 320.0 | 335.0 | 30.0 | 9.0% |
| 400.0 | 434.0 | 417.0 | -34.0 | -8.2% |
| 450.0 | 479.0 | 464.5 | -29.0 | -6.2% |
| 500.0 | 587.0 | 543.5 | -87.0 | -16.0% |
| 550.0 | 626.0 | 588.0 | -76.0 | -12.9% |
| 600.0 | 648.0 | 624.0 | -48.0 | -7.7% |
| 650.0 | 738.0 | 694.0 | -88.0 | -12.7% |
| 700.0 | 766.0 | 733.0 | -66.0 | -9.0% |
| 750.0 | 793.0 | 771.5 | -43.0 | -5.6% |
| 800.0 | 851.0 | 825.5 | -51.0 | -6.2% |
| 850.0 | 871.0 | 860.5 | -21.0 | -2.4% |
| 900.0 | 957.0 | 928.5 | -57.0 | -6.1% |
| 950.0 | 1001.0 | 975.5 | -51.0 | -5.2% |
| 1000.0 | 960.0 | 980.0 | 40.0 | 4.1% |

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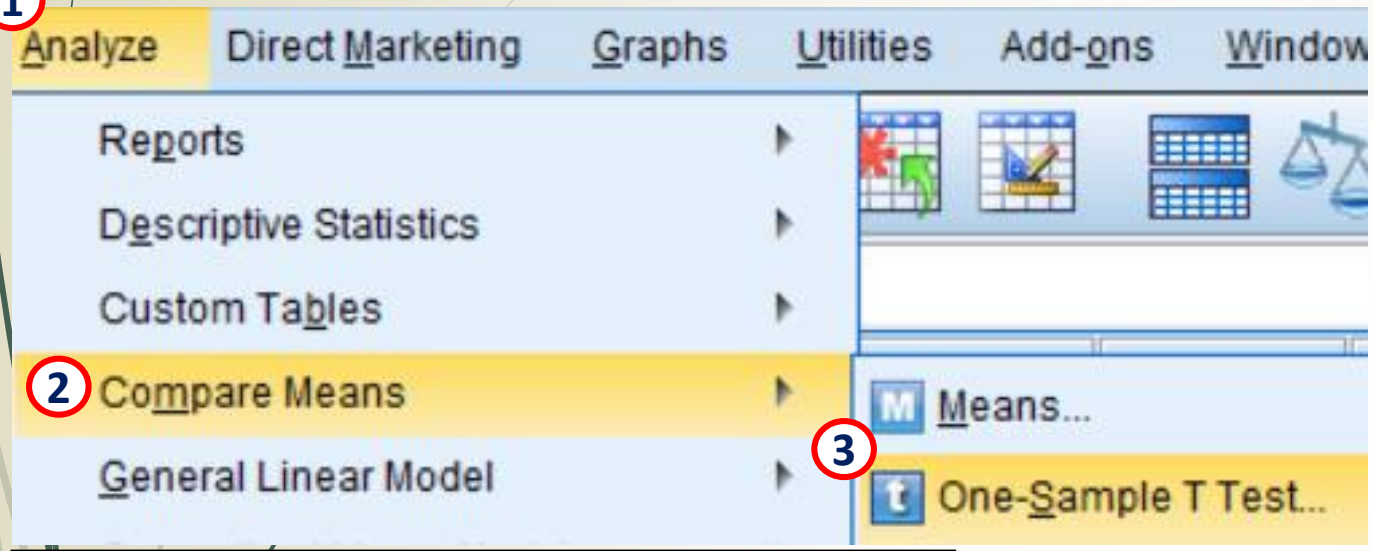
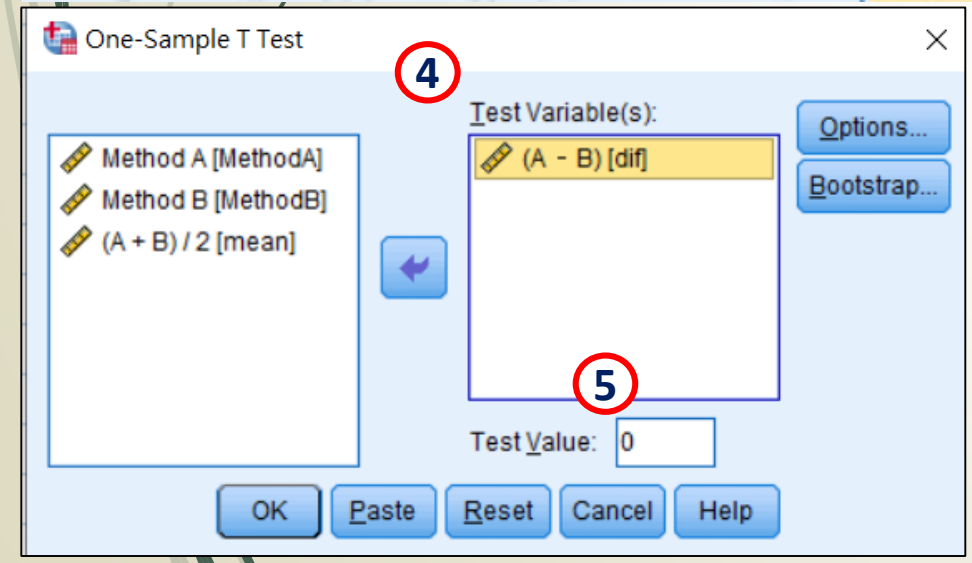
# Bland–Altman plot (SPSS)

- Analyze → Compare Means → One-Sample T test




**T-Test**

**One-Sample Statistics**

| | N | Mean | Std. Deviation | Std. Error Mean |
|---|---|---|---|---|
| (A - B) | 30 | -27.17 | 34.806 | 6.355 |

**One-Sample Test**

| | Test Value = 0 | | | | | |
|---|---|---|---|---|---|---|
| | t | df | Sig. (2-tailed) | Mean Difference | 95% Confidence Interval of the Difference | |
| | | | | | Lower | Upper |
| (A - B) | -4.275 | 29 | .000 | -27.167 | -40.16 | -14.17 |

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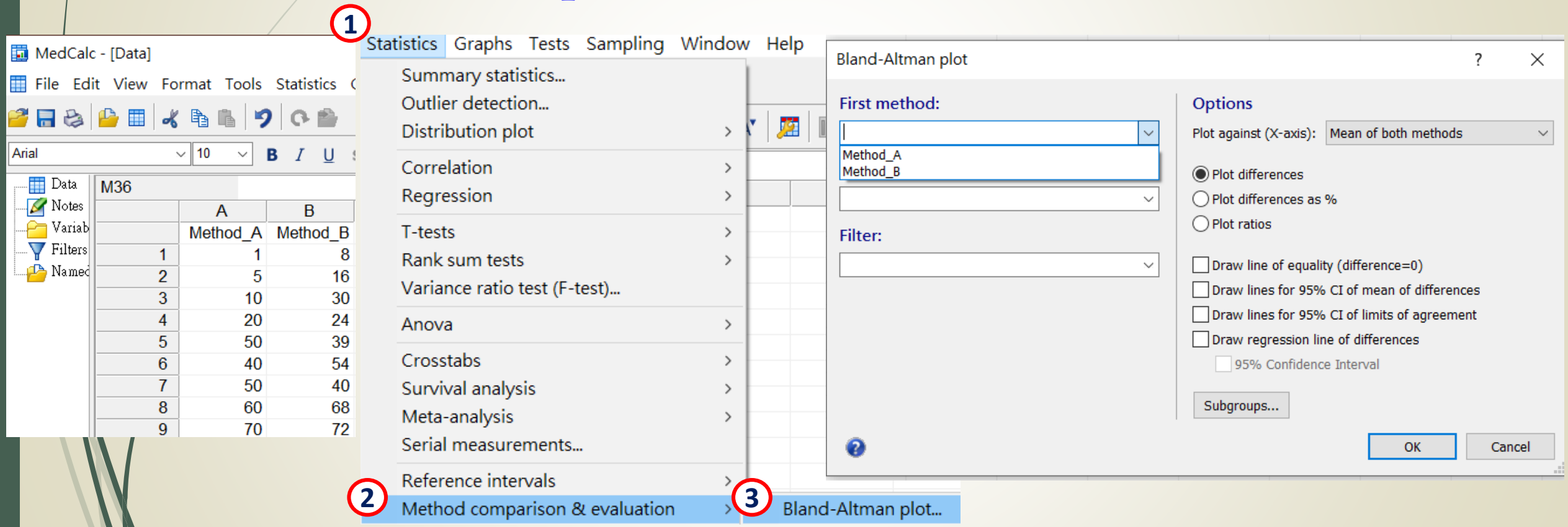
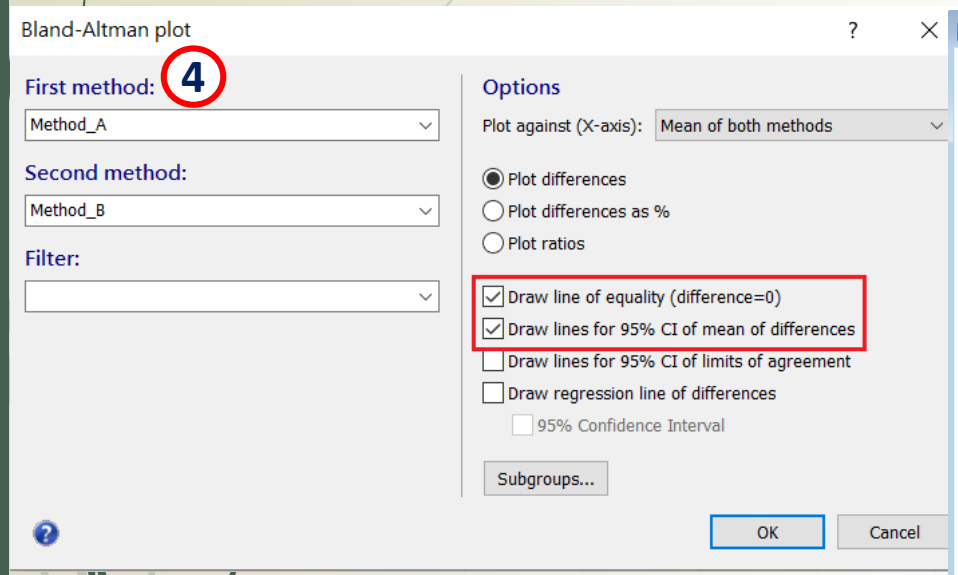
# Bland–Altman plot (MedCalc)

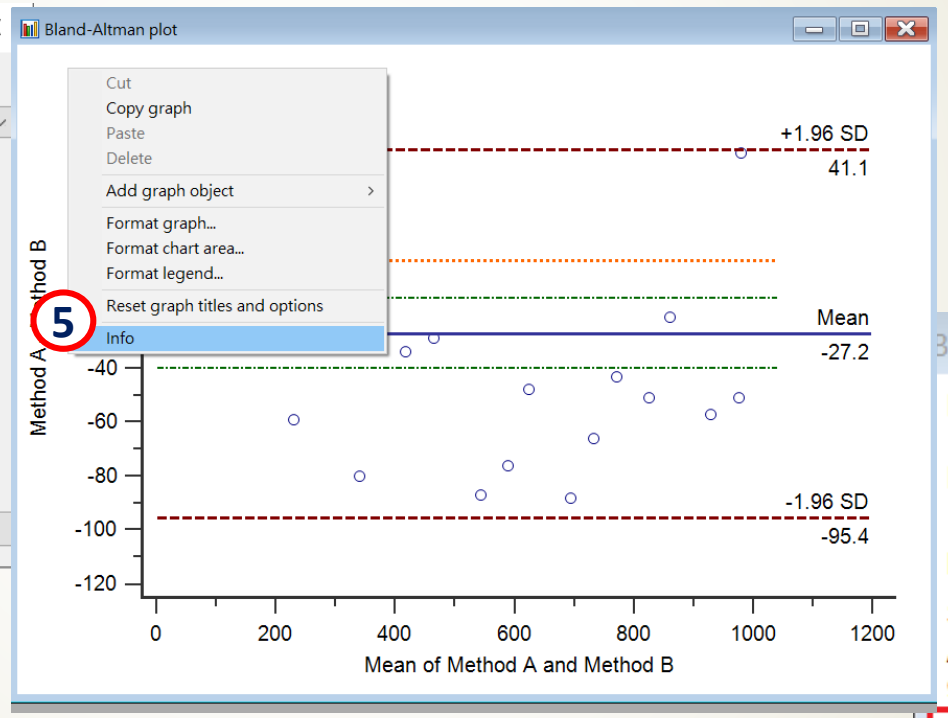
- Statistics → Method comparison & evaluation → Bland–Altman plot

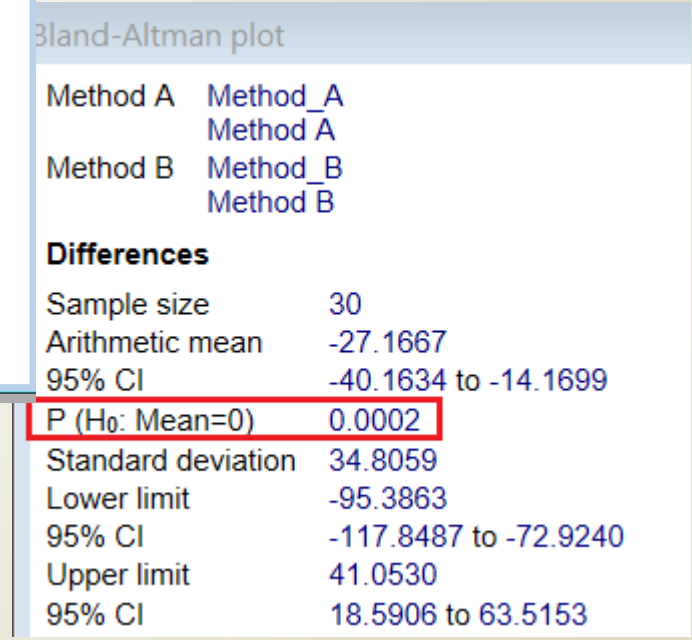


# Bland–Altman plot (MedCalc)

- Statistics → Method comparison & evaluation → Bland–Altman plot

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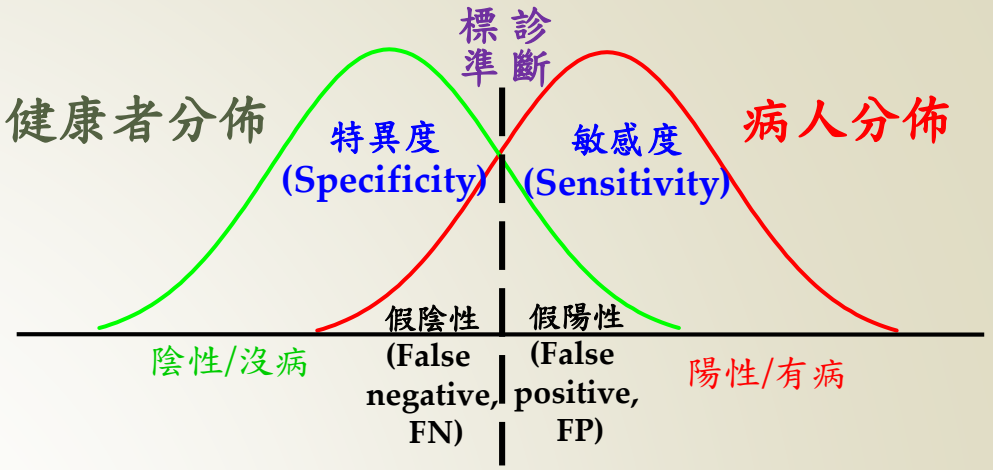
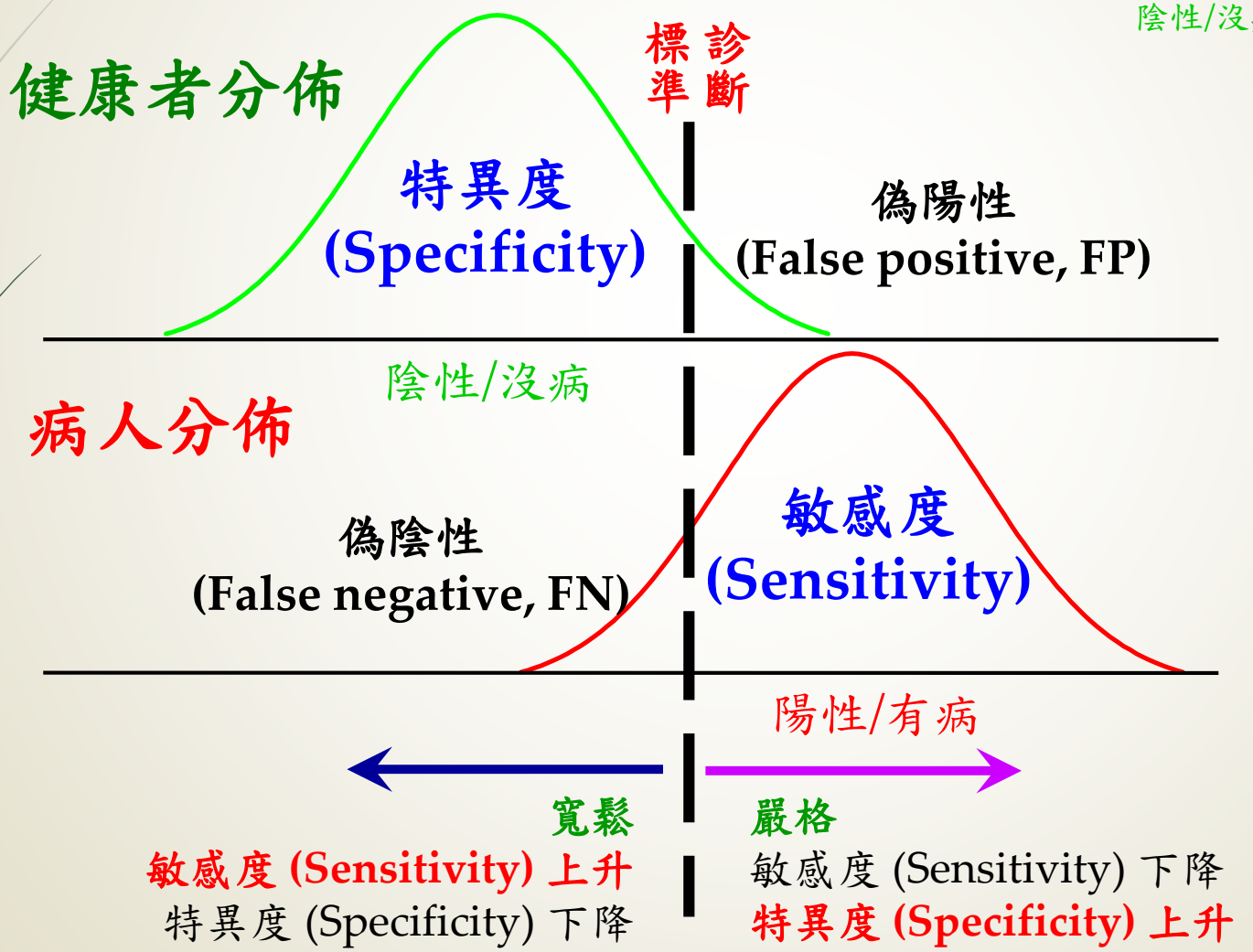
# Diagnostic test



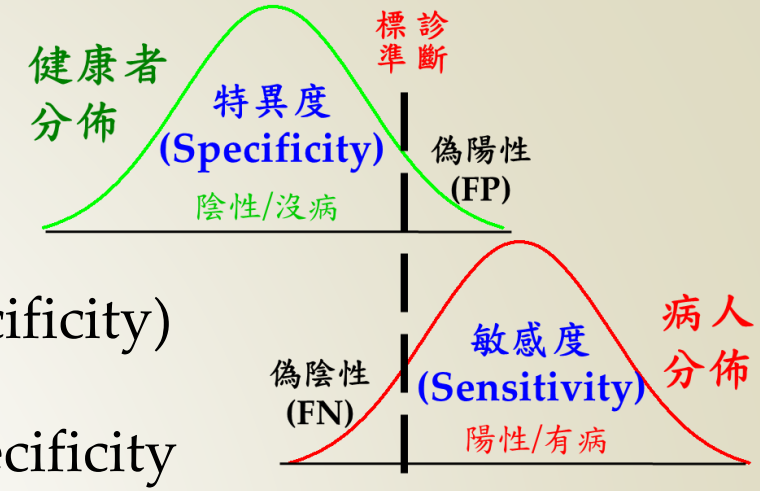



# Diagnostic test

| Screen Test (Hypothesized Class) | | Gold Standard Test (True class): Disease (Positive) | Gold Standard Test (True class): Non-disease (Negative) | |
|---|---|---|---|---|
| | Positive (Yes) | a (True Positive) | b (False Positive) | a + b |
| | Negative (No) | c (False Negative) | d (True Negative) | c + d |
| | | a + c | b + d | a + b + c + d |

- Sensitivity (敏感度) = a / (a + c)
- Specificity (特異度) = d / (b + d)
- Positive predictive value, PPV = a / (a + b)
- Negative predictive value, NPV = d / (c + d)
- Accuracy (精確度) = (a + d) / (a + b + c + d)
- False positive, FP (偽陽性) = b / (a + b)
- False negative, FN (偽陰性) = c / (c + d)

# Diagnostic test




- Likelihood ratio positive, LR+ = Sensitivity / (1 – Specificity)
- Likelihood ratio negative, LR- = (1 – Sensitivity) / Specificity

## 臨床意義

| LR | Interpretation |
|---|---|
| >10 | **Strong** evidence |
| 5-10 | **Moderate** evidence to rule in disease |
| 2-5 | **Weak** evidence |
| 0.5-2.0 | No signification change in the likelihood of disease |
| 0.2-0.5 | **Weak** evidence |
| 0.1-0.2 | **Moderate** evidence to rule out disease |
| < 0.1 | **Strong** evidence |

Source: Sackett, Richardson, Rosenberg, Haynes. Evidence-Based Medicine: How to Practice and Teach EBM. Churchill Livingstone, London, 1997.

# Diagnostic test

- Positive predictive value, PPV = a / (a + b)
- Negative predictive value, NPV = d / (c + d)

| | | Gold Standard Test: Disease | Gold Standard Test: Non-disease | |
|---|---|---|---|---|
| Screen Test | + | a | b | a + b |
| | - | c | d | c + d |
| | | a + c | b + d | a + b + c + d |

$$NPV = \frac{\text{true negative}}{\text{all negative}} = \frac{\text{true negative}}{\text{true negative+false negative}}$$

$$PPV = \frac{\text{true positive}}{\text{all positive}} = \frac{\text{true positive}}{\text{true positive +false positive}}$$

True positive = **all cases (a + c)** * sensitivity
False positive = **all health (b + d)** * (1 – specificity)

All cases = total (a + b + c + d) * prevalence
All health = total (a + b + c + d) * (1 – prevalence)

$$PPV = \frac{(\text{total} * \text{prevalence}) * \text{sensitivity}}{(\text{total} * \text{prevalence}) * \text{sensitivity} + (\text{total} * (1 - \text{prevalence}) * (1 - \text{specificity}))}$$

$$= \frac{\textbf{prevalence} * \text{sensitivity}}{(\textbf{prevalence} * \text{sensitivity}) + (1 - \textbf{prevalence}) * (1 - \text{specificity})}$$

$$NPV = \frac{(1 - \textbf{prevalence}) * \text{specificity}}{(1 - \textbf{prevalence}) * \text{specificity} + \textbf{prevalence} * (1 - \text{sensitivity})}$$

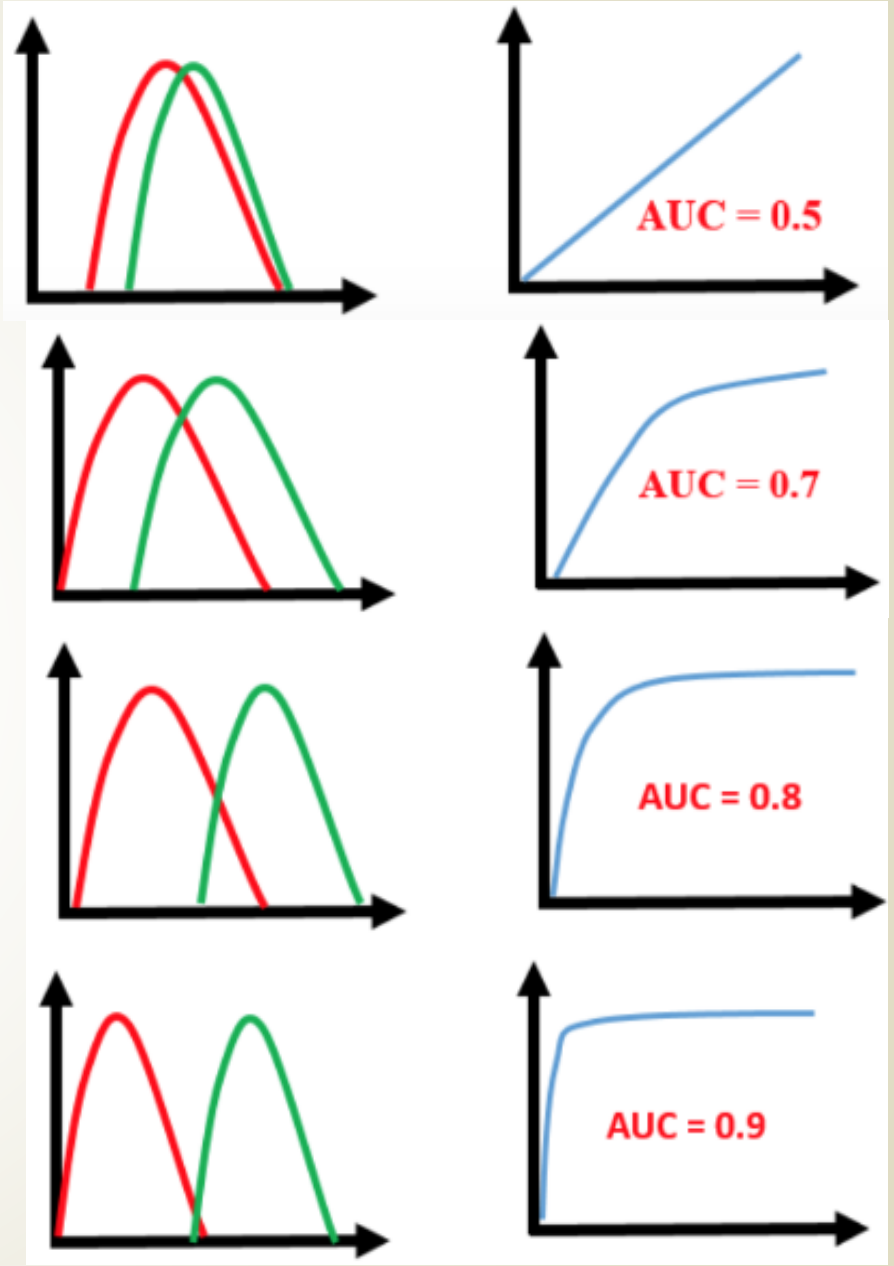
- Prevalence ⬆
  - PPV ⬆ NPV ⬇
- Prevalence ⬇
  - PPV ⬇ NPV ⬆

# ROC Curve Analysis

- 使用時機
  - 當開發新的檢驗方法，無法決定臨界值 (Cut-off value)
  - 利用連續數值預測結果 (二元分類)
- 目的
  - 將連續數值決定臨界值
  - 用來比較不同工具的好壞

# ROC Curve Analysis

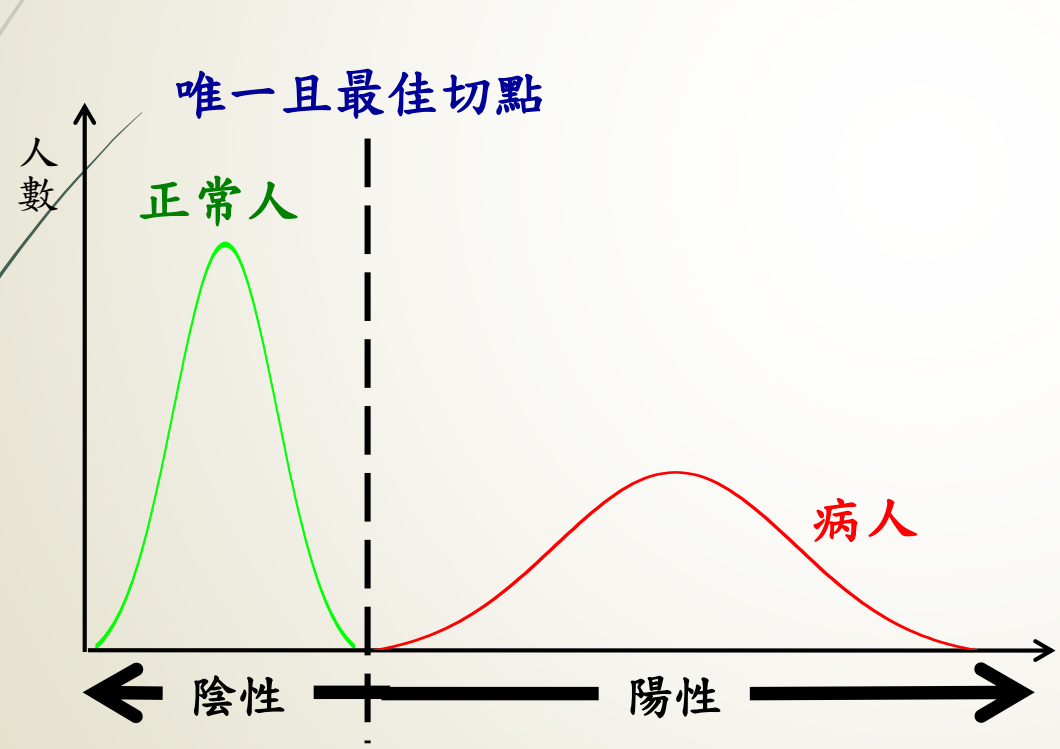
| AUC | Discrimination |
|---|---|
| 0.5 | No discrimination |
| 0.7-0.8 | Acceptable discrimination |
| 0.8-0.9 | Excellent discrimination |
| 0.9-1.0 | Outstanding discrimination |

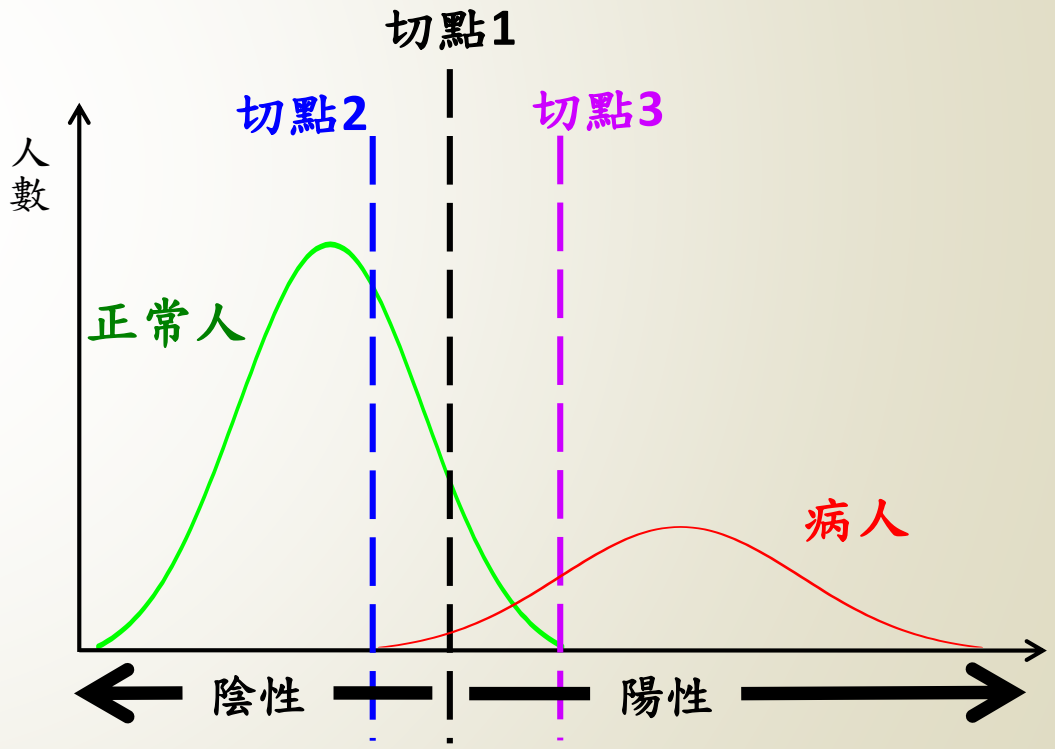



Ref: https://reurl.cc/288Xr9

# ROC Curve Analysis

- Cut-point



# ROC Curve Analysis

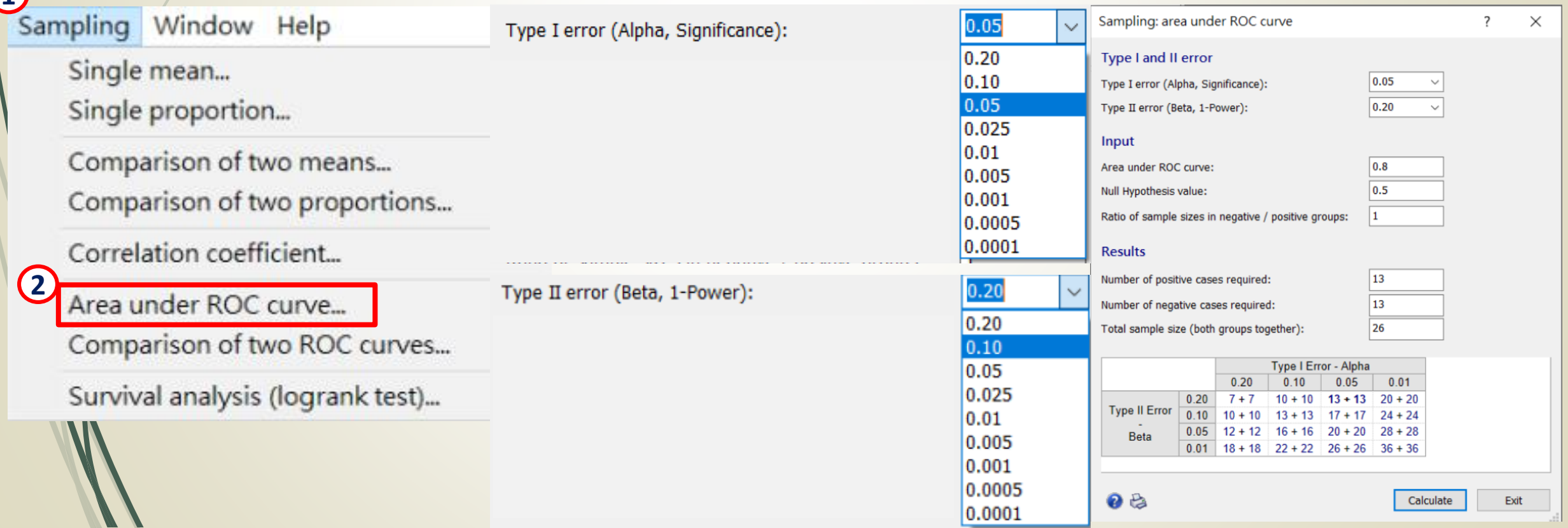
- Youden's index
  - 反映在有疾病和沒有疾病的陽性結果可能機率
  - 公式
    - Sensitivity + Specificity - 1
    - Sensitivity - False positive
  - Range 0-1
  - 不受盛行率影響
  - Maximum
    - Cut-point

# ROC Curve Analysis

- 樣本量-分析結果推論的精確度
  - 假設：AUC = 0.8 、 $\alpha = 0.05$、 $\beta = 0.2$
  - Medcalc計算樣本數
    - **Sampling → Area under ROC curve**
      - Type I error (Alpha, Significance) = 0.05
      - Type II error (Beta, 1-Power) = 0.20
      - Area under ROC curve = 0.80
      - Ratio of sample sizes in negative/positive groups = 1

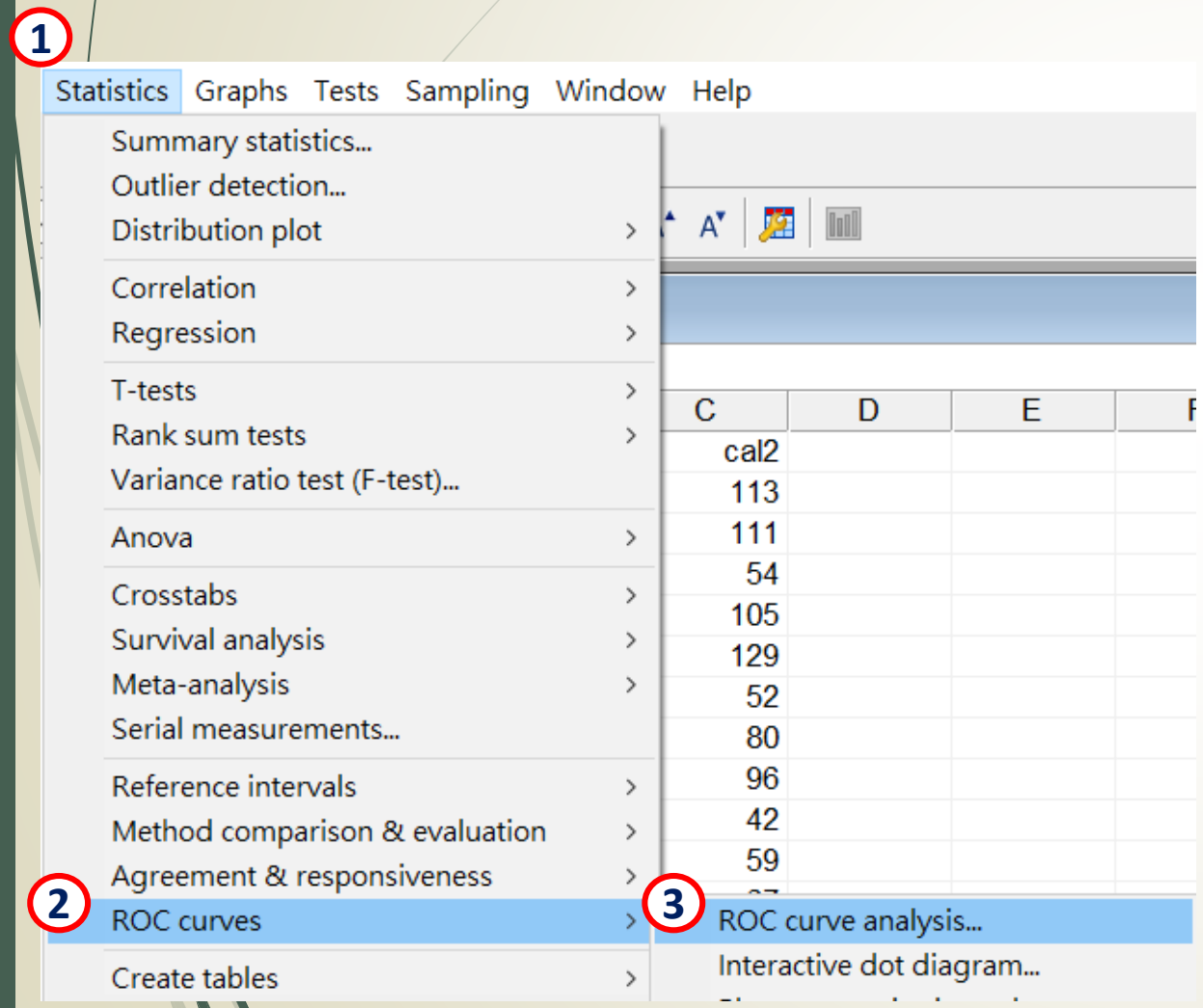
# ROC Curve Analysis

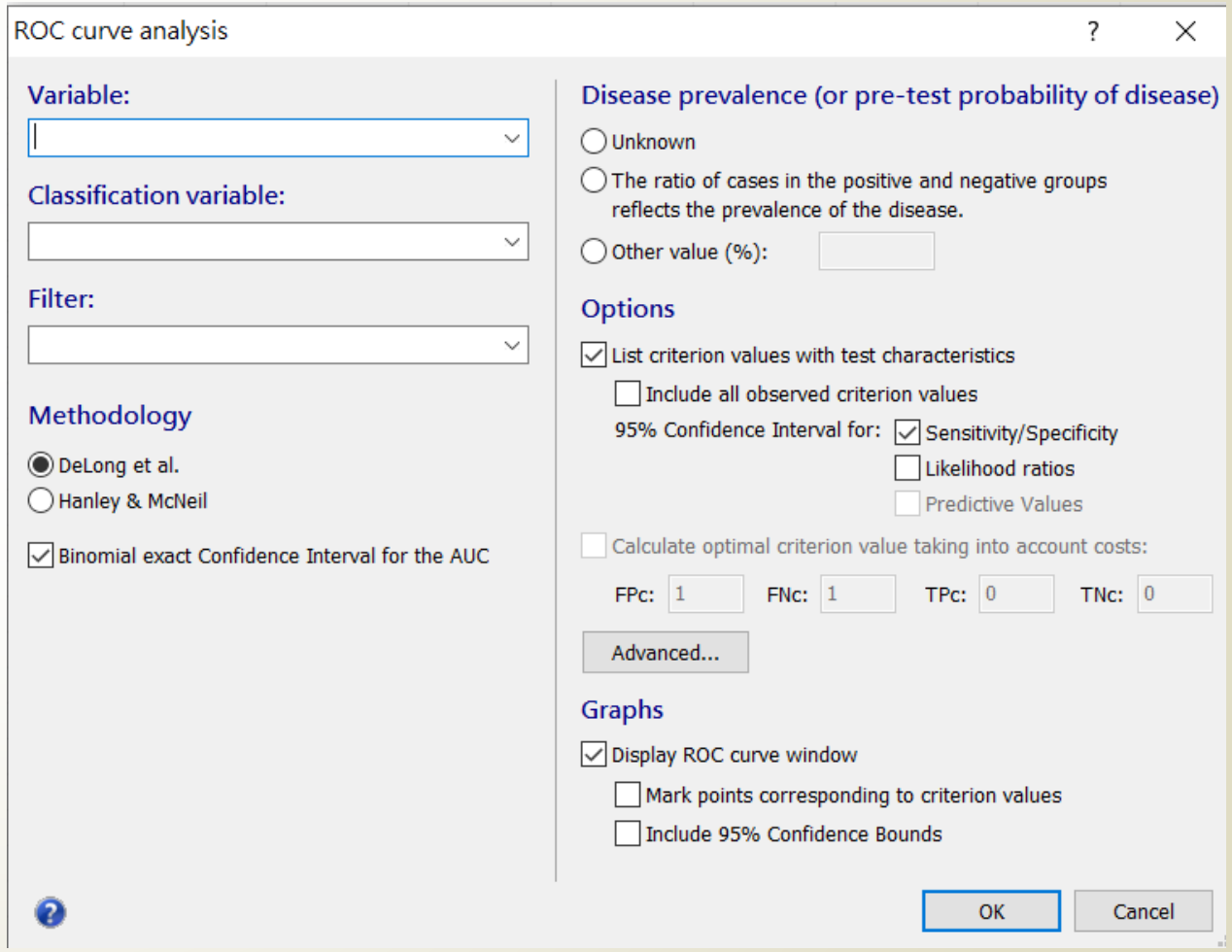
- MedCalc計算樣本數
  - **Sample size → Area under ROC curve**



# ROC Curve Analysis (MedCalc)

- **Statistics → ROC curves → ROC Curve Analysis**



# ROC Curve Analysis (MedCalc)

- Statistics → ROC curves → ROC Curve Analysis

4

ROC curve analysis

Variable:
cal1

Classification variable:
alive
alive
cal1
cal2

Methodology
DeLong et al.
Hanley & McNeil

Binomial exact Confidence Interval for the AUC

Disease prevalence (or pre-test probability of disease)
Unknown
The ratio of cases in the positive and negat
reflects the prevalence of the disease.
Other value (%):

Options
List criterion values with test characteristics
Include all observed criterion values
95% Confidence Interval for: Sensitivit
Likelihood
Predictive
Calculate optimal criterion value taking into
FPc: 1 FNc: 1 TPc: 0
Advanced...

Graphs
Display ROC curve window
Mark points corresponding to criterion v
Include 95% Confidence Bounds

OK Cancel

ROC curve

| | |
|---|---|
| Variable | cal1 |
| Classification variable | alive |

| | | |
|---|---|---|
| Sample size | | 55 |
| Positive group : | alive = 1 | 30 |
| Negative group : | alive = 0 | 25 |

| | |
|---|---|
| Disease prevalence (%) | unknown |

**Area under the ROC curve (AUC)**

| | |
|---|---|
| Area under the ROC curve (AUC) | 0.729 |
| Standard Error[a] | 0.0699 |
| 95% Confidence interval[b] | 0.593 to 0.840 |
| z statistic | 3.283 |
| Significance level P (Area=0.5) | 0.0010 |

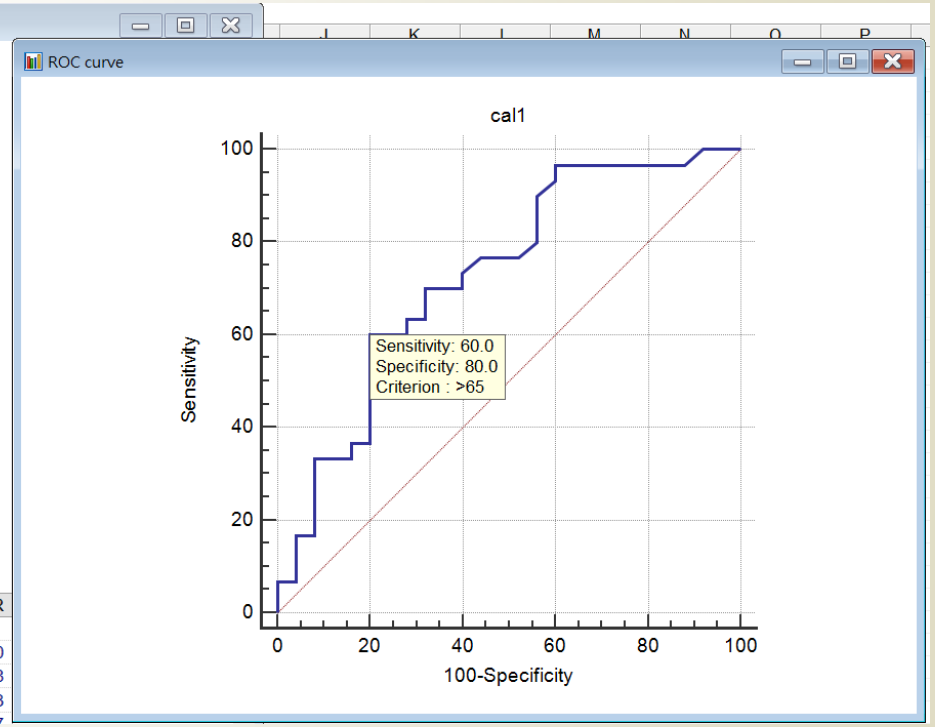
[a] DeLong et al., 1988
[b] Binomial exact

**Youden index**

| | |
|---|---|
| Youden index J | 0.4000 |
| Associated criterion | >65 |
| Sensitivity | 60.00 |
| Specificity | 80.00 |

**Criterion values and coordinates of the ROC curve** [Hide]

| Criterion | Sensitivity | 95% CI | Specificity | 95% CI | +LR | -LR |
|---|---|---|---|---|---|---|
| ≥6 | 100.00 | 88.4 - 100.0 | 0.00 | 0.0 - 13.7 | 1.00 | |
| >16 | 100.00 | 88.4 - 100.0 | 8.00 | 1.0 - 26.0 | 1.09 | 0.00 |
| >19 | 96.67 | 82.8 - 99.9 | 12.00 | 2.5 - 31.2 | 1.10 | 0.28 |
| >35 | 96.67 | 82.8 - 99.9 | 40.00 | 21.1 - 61.3 | 1.61 | 0.083 |



# ROC Curve Analysis (MedCalc)

- **Statistics → ROC curves → ROC Curve Analysis**

ROC curve

| | |
|---|---|
| Variable | test3 |
| Classification variable | Dis |

| | |
|---|---|
| Sample size | 100 |
| Positive group : Dis = 1 | 20 |
| Negative group : Dis = 0 | 80 |

| | |
|---|---|
| Disease prevalence (%) | unknown |

**Area under the ROC curve (AUC)**

| | |
|---|---|
| Area under the ROC curve (AUC) | 0.739 |
| Standard Error[a] | 0.0512 |
| 95% Confidence interval[b] | 0.641 to 0.822 |
| z statistic | 4.660 |
| Significance level P (Area=0.5) | <0.0001 |

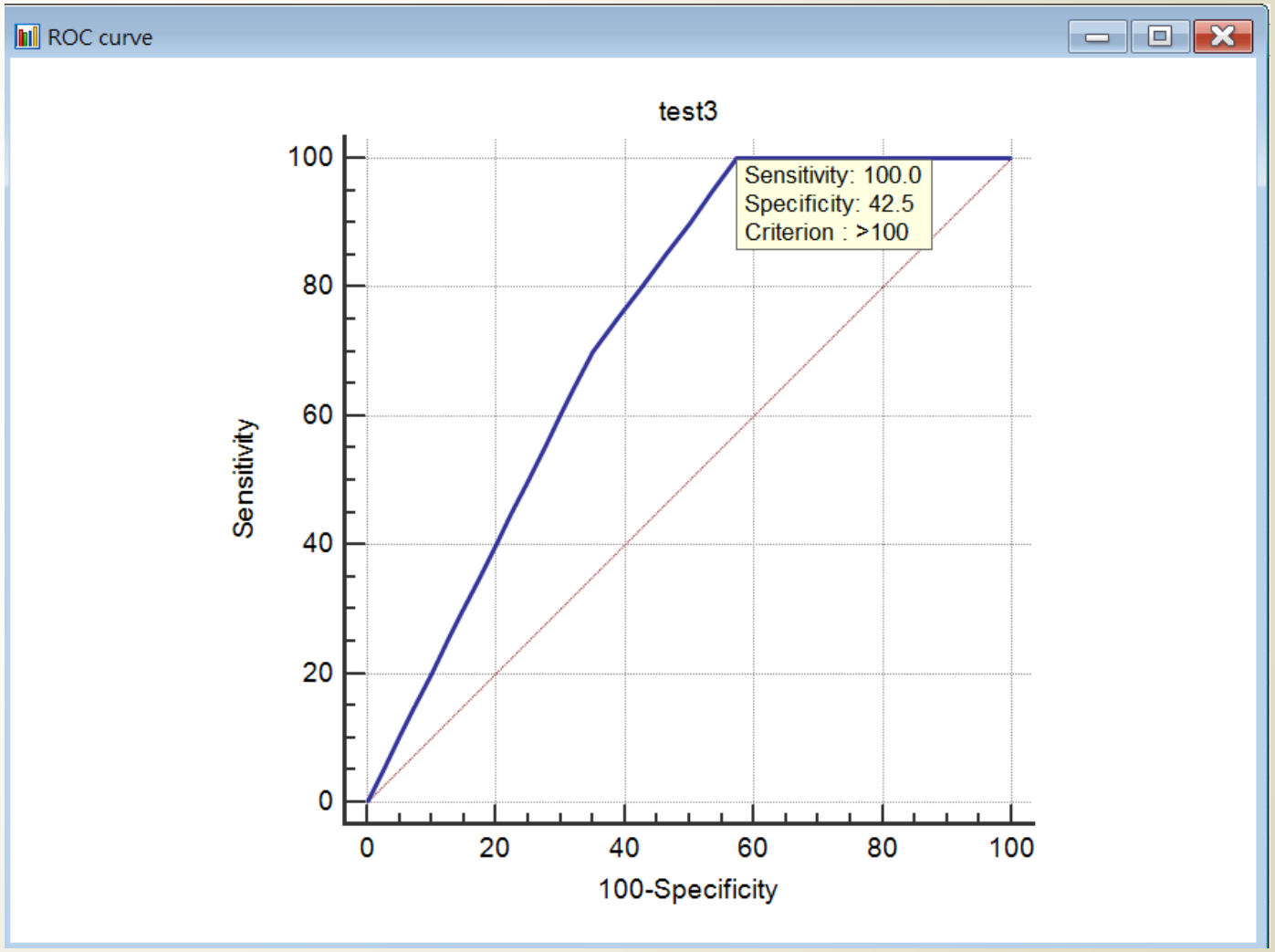
[a] DeLong et al., 1988
[b] Binomial exact

**Youden index**

| | |
|---|---|
| Youden index J | 0.4250 |
| Associated criterion | >100 |
| Sensitivity | 100.00 |
| Specificity | 42.50 |

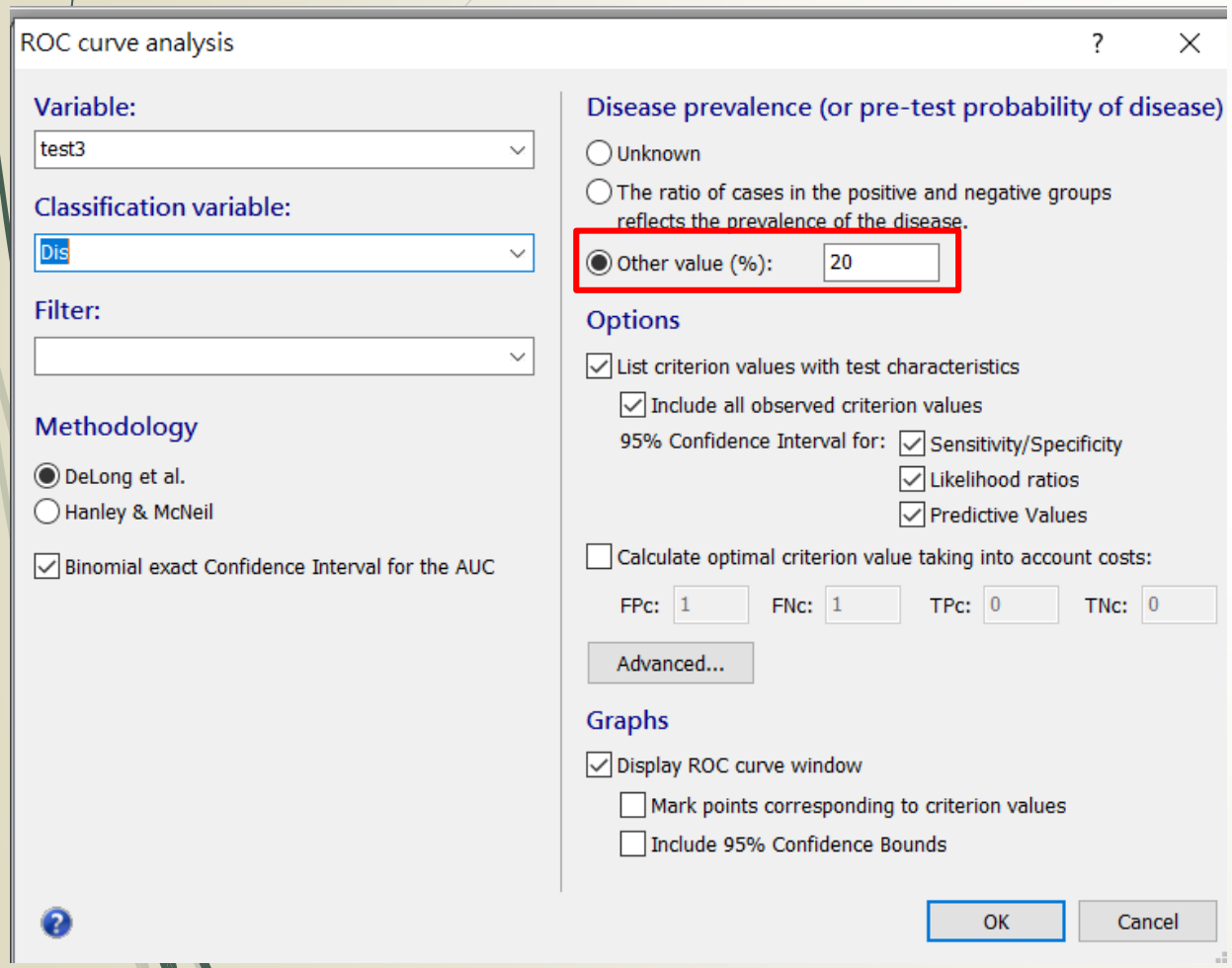
**Criterion values and coordinates of the ROC curve** [Hide]

| Criterion | Sensitivity | 95% CI | Specificity | 95% CI | +LR | -LR |
|---|---|---|---|---|---|---|
| ≥80 | 100.00 | 83.2 - 100.0 | 0.00 | 0.0 - 4.5 | 1.00 | |
| >100 | 100.00 | 83.2 - 100.0 | 42.50 | 31.5 - 54.1 | 1.74 | 0.00 |
| >110 | 95.00 | 75.1 - 99.9 | 46.25 | 35.0 - 57.8 | 1.77 | 0.11 |



# ROC Curve Analysis (MedCalc)

- **Statistics → ROC curves → ROC Curve Analysis**




ROC curve

| | | |
|---|---|---|
| Sample size | | 100 |
| Positive group : | Dis = 1 | 20 |
| Negative group : | Dis = 0 | 80 |

| | |
|---|---|
| Disease prevalence (%) | 20 |

**Area under the ROC curve (AUC)**

| | |
|---|---|
| Area under the ROC curve (AUC) | 0.739 |
| Standard Error[a] | 0.0512 |
| 95% Confidence interval[b] | 0.641 to 0.822 |
| z statistic | 4.660 |
| Significance level P (Area=0.5) | <0.0001 |

[a] DeLong et al., 1988
[b] Binomial exact

**Youden index**

| | |
|---|---|
| Youden index J | 0.4250 |
| Associated criterion | >100 |
| Sensitivity | 100.00 |
| Specificity | 42.50 |

# ROC Curve Analysis (MedCalc)

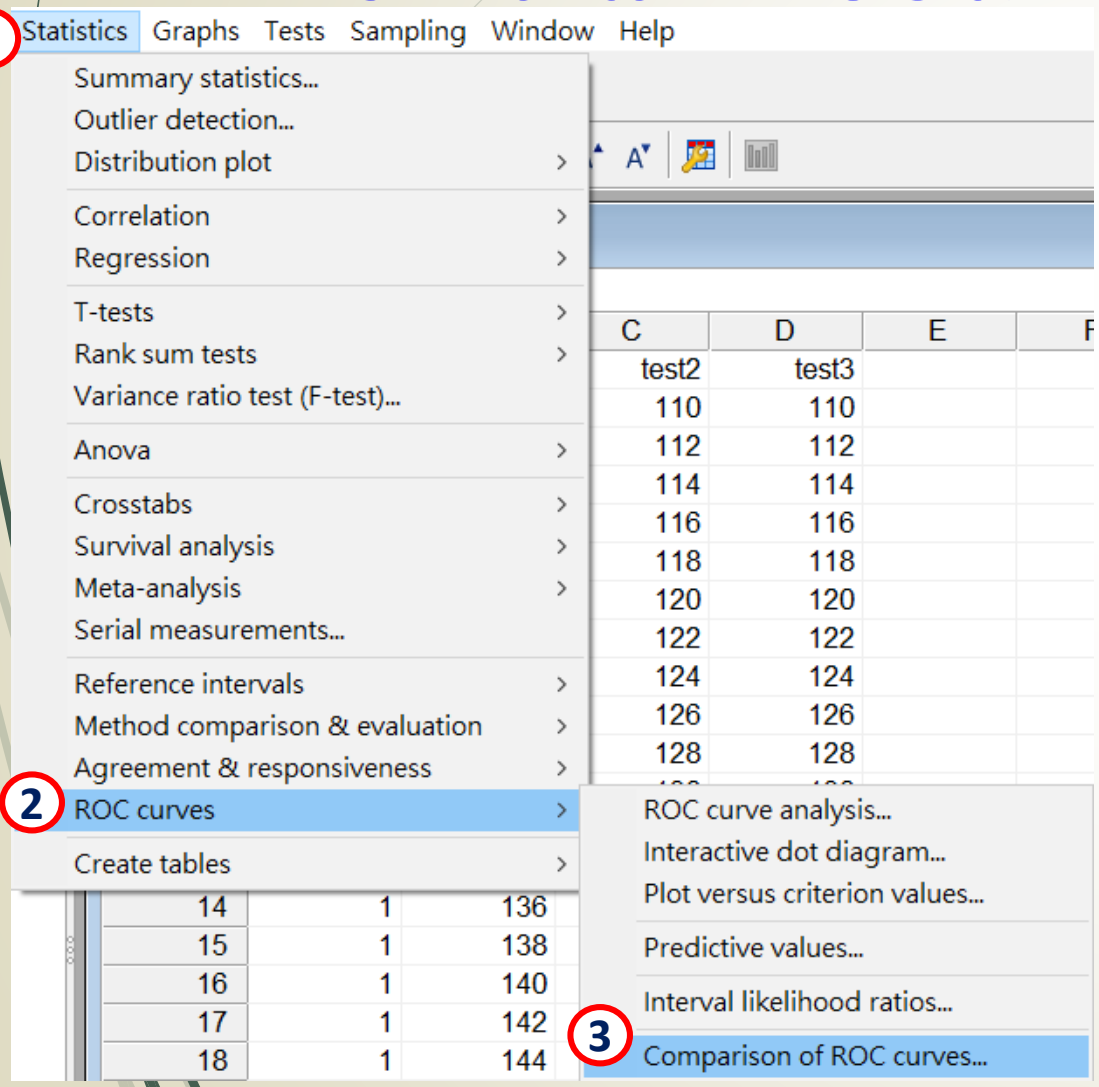
- Statistics → ROC curves → ROC Curve Analysis

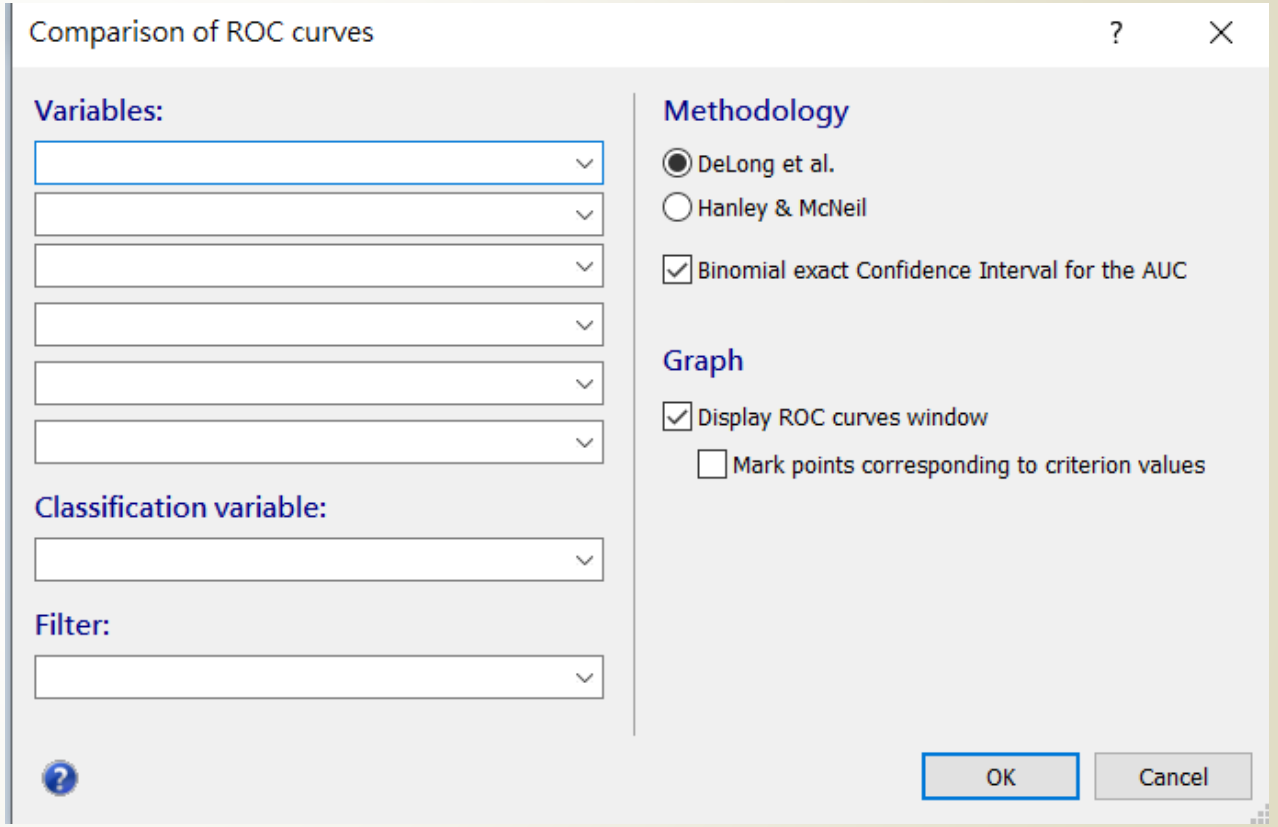
**Criterion values and coordinates of the ROC curve** [Hide]

| Criterion | Sensitivity | 95% CI | Specificity | 95% CI | +LR | 95% CI | -LR | 95% CI | +PV | 95% CI | -PV | 95% CI |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ≥80 | 100.00 | 83.2 - 100.0 | 0.00 | 0.0 - 4.5 | 1.00 | 1.0 - 1.0 | | | 20.0 | 12.7 - 29.2 | | |
| >80 | 100.00 | 83.2 - 100.0 | 2.50 | 0.3 - 8.7 | 1.03 | 1.0 - 1.1 | 0.00 | | 20.4 | 12.9 - 29.7 | 100.0 | 15.8 - 100.0 |
| >82 | 100.00 | 83.2 - 100.0 | 5.00 | 1.4 - 12.3 | 1.05 | 1.0 - 1.1 | 0.00 | | 20.8 | 13.2 - 30.3 | 100.0 | 39.8 - 100.0 |
| >84 | 100.00 | 83.2 - 100.0 | 7.50 | 2.8 - 15.6 | 1.08 | 1.0 - 1.2 | 0.00 | | 21.3 | 13.5 - 30.9 | 100.0 | 54.1 - 100.0 |
| >86 | 100.00 | 83.2 - 100.0 | 10.00 | 4.4 - 18.8 | 1.11 | 1.0 - 1.2 | 0.00 | | 21.7 | 13.8 - 31.6 | 100.0 | 63.1 - 100.0 |
| >88 | 100.00 | 83.2 - 100.0 | 12.50 | 6.2 - 21.8 | 1.14 | 1.1 - 1.2 | 0.00 | | 22.2 | 14.1 - 32.2 | 100.0 | 69.2 - 100.0 |
| >90 | 100.00 | 83.2 - 100.0 | 17.50 | 9.9 - 27.6 | 1.21 | 1.1 - 1.3 | 0.00 | | 23.3 | 14.8 - 33.6 | 100.0 | 76.8 - 100.0 |
| >92 | 100.00 | 83.2 - 100.0 | 22.50 | 13.9 - 33.2 | 1.29 | 1.1 - 1.5 | 0.00 | | 24.4 | 15.6 - 35.1 | 100.0 | 81.5 - 100.0 |
| >94 | 100.00 | 83.2 - 100.0 | 27.50 | 18.1 - 38.6 | 1.38 | 1.2 - 1.6 | 0.00 | | 25.6 | 16.4 - 36.8 | 100.0 | 84.6 - 100.0 |
| >96 | 100.00 | 83.2 - 100.0 | 32.50 | 22.4 - 43.9 | 1.48 | 1.3 - 1.7 | 0.00 | | 27.0 | 17.4 - 38.6 | 100.0 | 86.8 - 100.0 |
| >98 | 100.00 | 83.2 - 100.0 | 37.50 | 26.9 - 49.0 | 1.60 | 1.4 - 1.9 | 0.00 | | 28.6 | 18.4 - 40.6 | 100.0 | 88.4 - 100.0 |
| >100 | 100.00 | 83.2 - 100.0 | 42.50 | 31.5 - 54.1 | 1.74 | 1.4 - 2.1 | 0.00 | | 30.3 | 19.6 - 42.9 | 100.0 | 89.7 - 100.0 |
| >110 | 95.00 | 75.1 - 99.9 | 46.25 | 35.0 - 57.8 | 1.77 | 1.4 - 2.2 | 0.11 | 0.02 - 0.7 | 30.6 | 19.6 - 43.7 | 97.4 | 86.2 - 99.9 |
| >112 | 90.00 | 68.3 - 98.8 | 50.00 | 38.6 - 61.4 | 1.80 | 1.4 - 2.3 | 0.20 | 0.05 - 0.8 | 31.0 | 19.5 - 44.5 | 95.2 | 83.8 - 99.4 |

# ROC Curve Analysis (MedCalc)

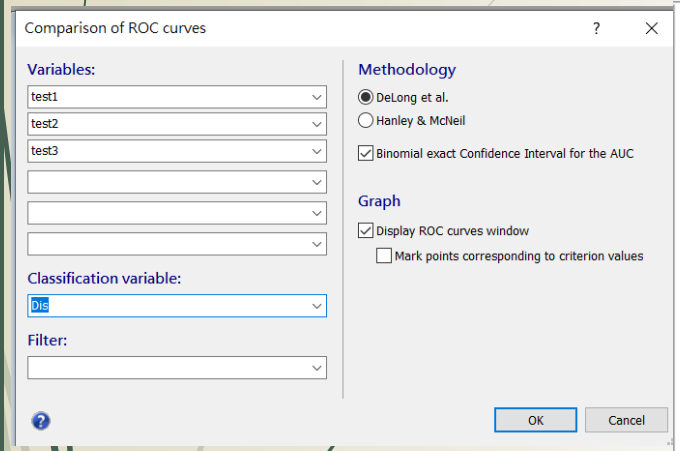
- **Statistics → ROC curves → Comparison of ROC Curves**

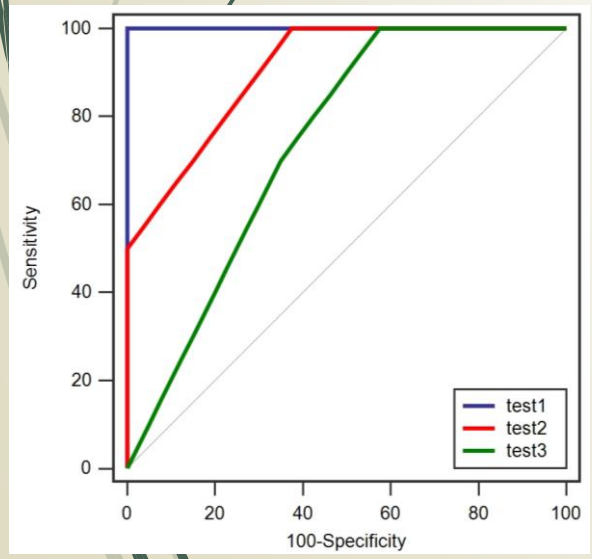


# ROC Curve Analysis (MedCalc)

- **Statistics → ROC curves → Comparison of ROC Curves**




| | |
|---|---|
| Variable 1 | test1 |
| Variable 2 | test2 |
| Variable 3 | test3 |
| Classification variable | Dis |

| | | |
|---|---|---|
| Sample size | | 100 |
| Positive group : | Dis = 1 | 20 |
| Negative group : | Dis = 0 | 80 |

| | AUC | SE [a] | 95% CI [b] |
|---|---|---|---|
| test1 | 1.000 | 0.000 | 0.964 to 1.000 |
| test2 | 0.906 | 0.0324 | 0.831 to 0.955 |
| test3 | 0.739 | 0.0512 | 0.641 to 0.822 |

[a] DeLong et al., 1988
[b] Binomial exact

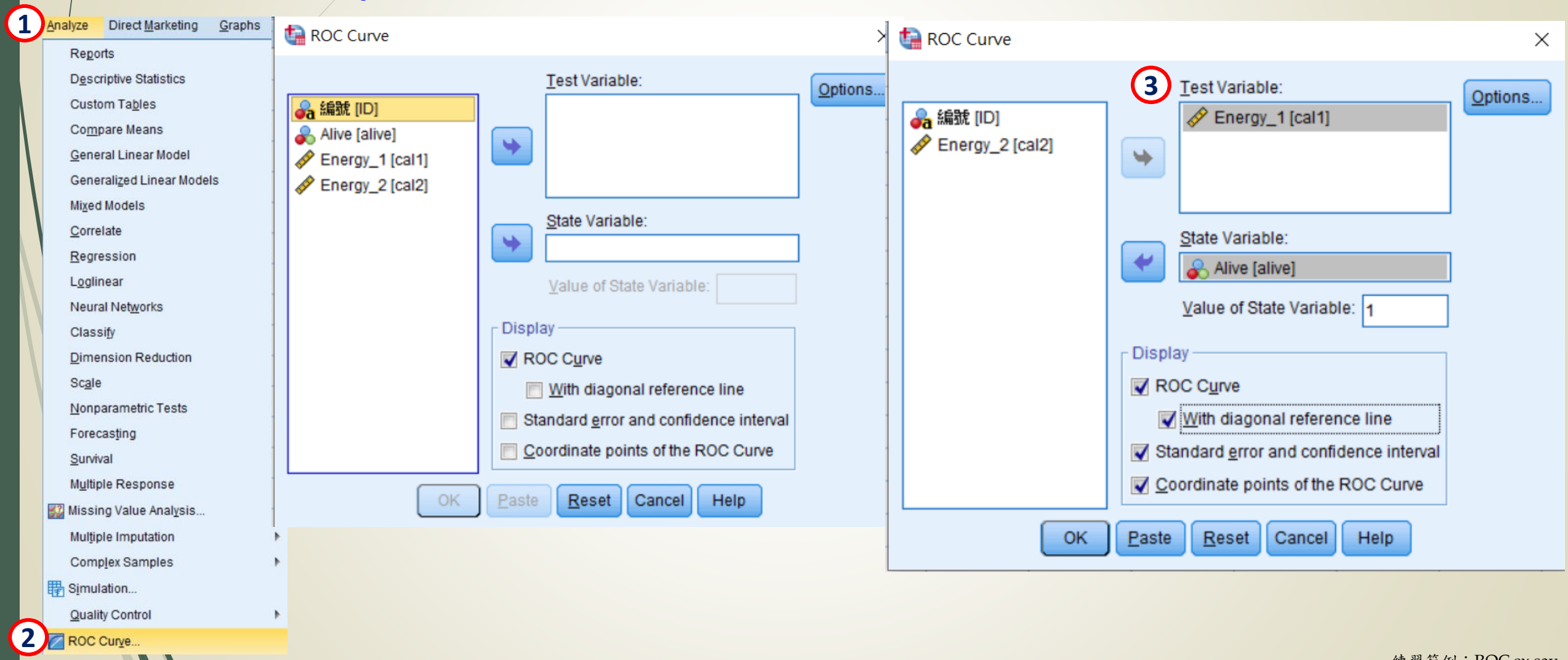
**Pairwise comparison of ROC curves**

| | |
|---|---|
| test1 ~ test2 | |
| Difference between areas | 0.0937 |
| Standard Error[c] | 0.0324 |
| 95% Confidence Interval | 0.0302 to 0.157 |
| z statistic | 2.892 |
| Significance level | P = 0.0038 |
| test1 ~ test3 | |
| Difference between areas | 0.261 |
| Standard Error[c] | 0.0512 |
| 95% Confidence Interval | 0.161 to 0.362 |
| z statistic | 5.099 |
| Significance level | P < 0.0001 |
| test2 ~ test3 | |
| Difference between areas | 0.168 |
| Standard Error[c] | 0.0349 |
| 95% Confidence Interval | 0.0991 to 0.236 |
| z statistic | 4.797 |
| Significance level | P < 0.0001 |

[c] DeLong et al., 1988

# ROC Curve Analysis (SPSS)

- Analyze → ROC curve




練習範例：ROC ex.sav

# ROC Curve Analysis (SPSS)

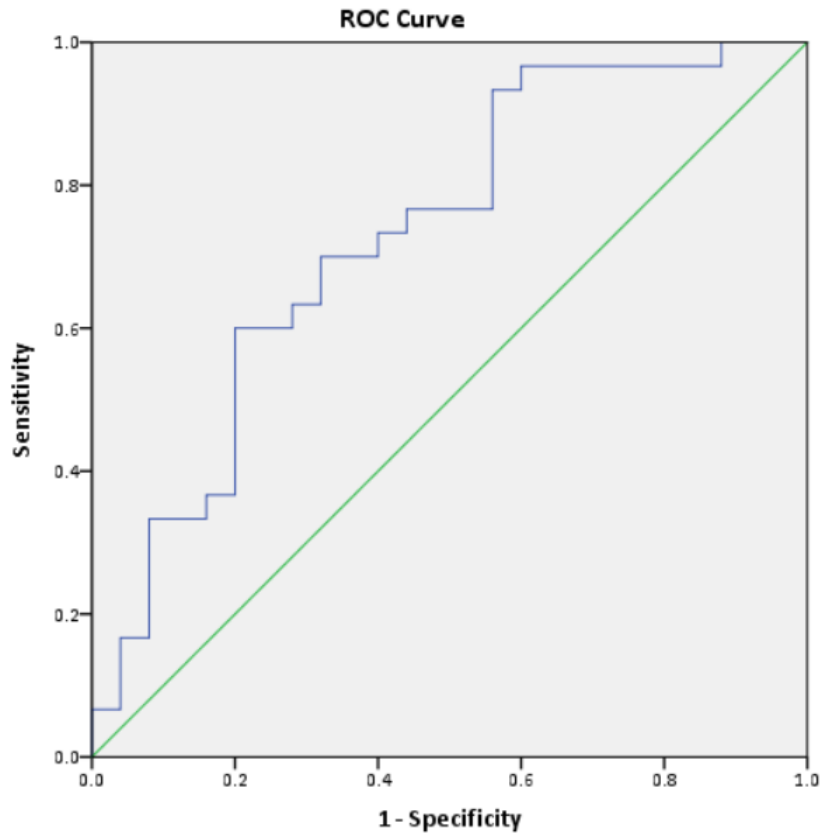
**ROC Curve**

**Case Processing Summary**

| Alive | Valid N (listwise) |
|---|---|
| Positive[a] | 30 |
| Negative | 25 |

Larger values of the test result variable(s) indicate stronger evidence for a positive actual state.

a. The positive actual state is Alive.




**Area Under the Curve**

Test Result Variable(s): Energy_1

| Area | Std. Error[a] | Asymptotic Sig.[b] | Asymptotic 95% Confidence Interval | |
|---|---|---|---|---|
| | | | Lower Bound | Upper Bound |
| .729 | .069 | .004 | .594 | .865 |

a. Under the n

b. Null hypothes

**Co**

Test Result Var

| Positive if Greater Than or Equal To[a] | Sensitivity | 1 - Specificity |
|---|---|---|
| 4.82 | 1.000 | 1.000 |
| 10.68 | 1.000 | .960 |
| 17.07 | 1.000 | .920 |
| 18.76 | 1.000 | .880 |
| 21.61 | .967 | .880 |
| 24.43 | .967 | .840 |
| 25.66 | .967 | .800 |

**AUC = 0.73**
**(0.59-0.87)**
**Acceptable discrimination**

練習範例：ROC ex.sav

# ROC Curve Analysis (SPSS & Excel)

- Cut-point
  - Youden's index (Maximum)
    - Sensitivity + Specificity - 1

IF =B4+D4-1

| | A | B | C | D | E |
|---|---|---|---|---|---|
| 1 | Coordinates of the Curve | | | | |
| 2 | Test Result Variable(s): | | | | |
| 3 | Positive if Greater Than or Equal To[a] | Sensitivity | 1 - Specificity | Specificity | Youden's index |
| 4 | 65.22 | .600 | .200 | 0.800 | =B4+D4-1 |
| 5 | 54.90 | .700 | .320 | 0.680 | 0.380 |
| 6 | 40.99 | .933 | .560 | 0.440 | 0.373 |
| 7 | 36.66 | .967 | .600 | 0.400 | 0.367 |
| 8 | 66.28 | .567 | .200 | 0.800 | 0.367 |
| 9 | 64.15 | .600 | .240 | 0.760 | 0.360 |
| 10 | 60.46 | .633 | .280 | 0.720 | 0.353 |
| 11 | 55.91 | .667 | .320 | 0.680 | 0.347 |
| 12 | 41.64 | .900 | .560 | 0.440 | 0.340 |
| 13 | 53.00 | .700 | .360 | 0.640 | 0.340 |
| 14 | 39.65 | .933 | .600 | 0.400 | 0.333 |
| 15 | 66.95 | .533 | .200 | 0.800 | 0.333 |

# Reference

Supplementary Materials

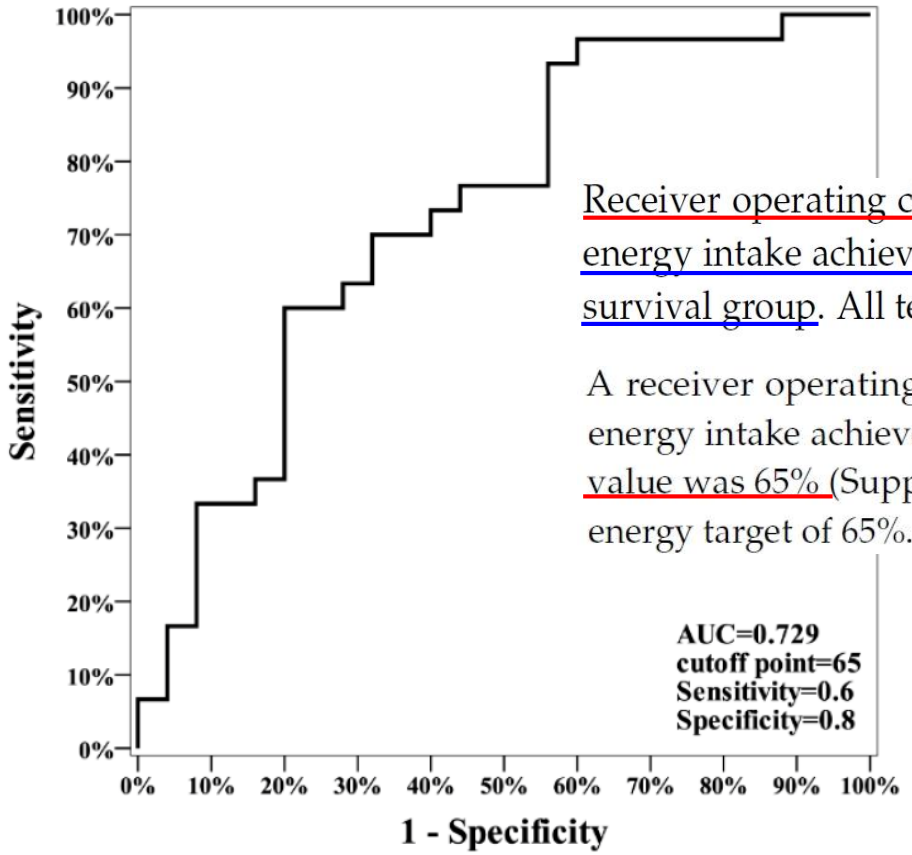



**Figure 1.** Receiver operating characteristic (ROC) curve to determine the cutoff point for the feeding target between surviving and non-surviving malnourished patients administered SBEN.

Receiver operating characteristic (ROC) curves were used to evaluate the discriminative ability of energy intake achievement rates on day 3 after the initiation of small bowel feeding to identify the survival group. All tests were two-sided, with $p < 0.05$ considered significant.

A receiver operating characteristic (ROC) curve was used to evaluate the discriminative ability of energy intake achievement rates 3 days after SBEN initiation to identify the survival group; the cutoff value was 65% (Supplement Figure S1). In the survival group, two-thirds of the patients achieved the energy target of 65%.

Nutrients 2019, 11, 645; Optimal Time and Target for Evaluating Energy Delivery after Adjuvant Feeding with Small Bowel Enteral Nutrition in Critically Ill Patients at High Nutrition Risk

# Reference

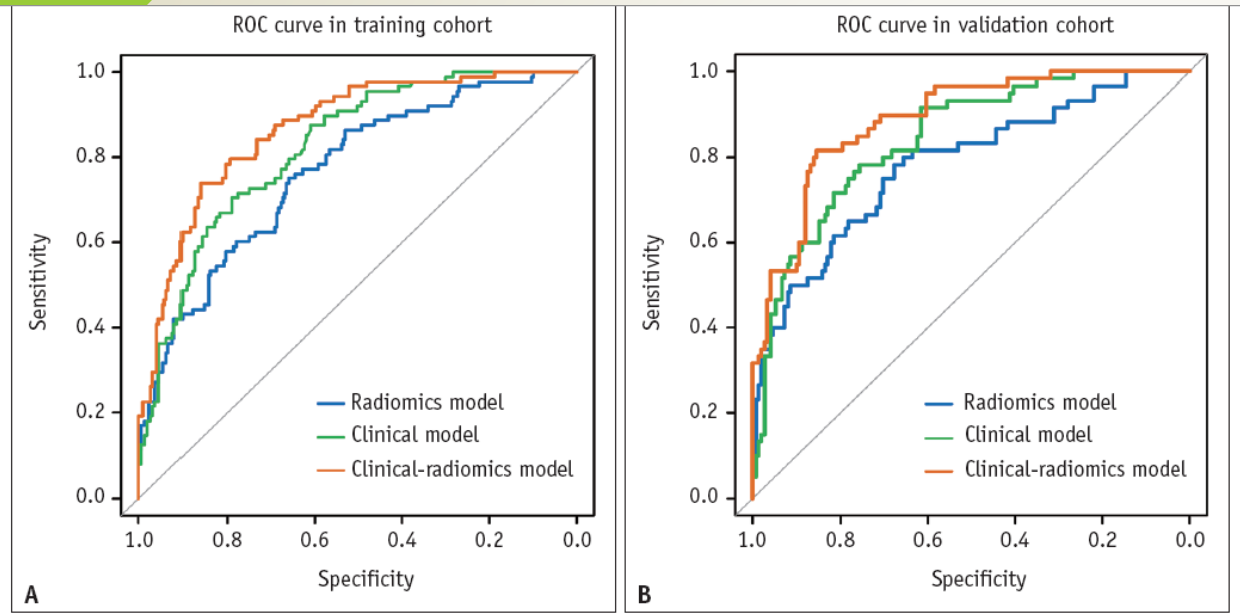



**Fig. 2. ROC curves of the radiomics model, clinical model, and clinical-radiomics model in the training (A) and validation (B) cohorts.** ROC = receiver operating characteristic

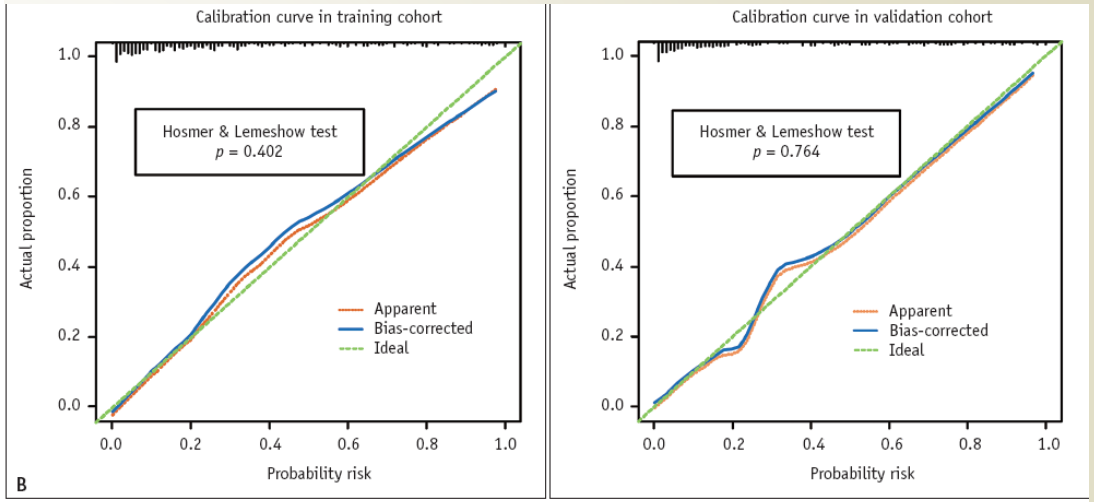



**Fig. 3. The clinical-radiomics nomogram for predicting acute ischemic stroke outcomes.**
**A.** The developed nomogram based on the clinical-radiomics prediction model to predict the risk of poor stroke outcome. Diabetes: 0, no diabetes; 1, diabetes. Sex: 0, female; 1, male. Stroke history: 0, no stroke history; 1, stroke history; $mRS_{baseline}$: 0, ≤ 2; 1, > 2. **B.** Calibration curves for the nomogram in the training and validation cohorts. The green dashed line represents the ideal prediction and the red dashed line represents the predictive ability of the nomogram. The closer the dashed red line fit to the dashed green line, the greater the prediction accuracy of the nomogram. **C.** Decision curve analysis for the nomogram. The black line represents the net benefit of assuming no stroke patients have

The predictive performance of the radiomics, clinical, and clinical-radiomics models was evaluated using **receiver operating characteristic (ROC) curves**. The area under the ROC curve **(AUC)** and balanced **sensitivity** and **specificity** at the cutoff yielding the largest **Youden index** value were calculated. The performance of the three models was tested in the training and validation cohorts. The Delong test was used to compare the AUC between the models.
The calibration curve and **Hosmer–Lemeshow test** were used to assess the calibration performance of the clinicalradiomics nomogram.

Korean J Radiol. 2022 Aug;23(8):811-820. Feasibility of a Clinical-Radiomics Model to Predict the Outcomes of Acute Ischemic Stroke. Yiran Zhou, Di Wu, Su Yan, Yan Xie, Shun Zhang , Wenzhi Lv, Yuanyuan Qin, Yufei Liu, Chengxia Liu, Jun Lu, Jia Li, Hongquan Zhu, Weiyin Vivian Liu, Huan Liu, Guiling Zhang, Wenzhen Zhu

生統小組
統計方法教育訓練

# Thank you

問卷調查

5/6問卷

# For your attention!!