



羅吉斯迴歸分析

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Logistic regression



- 主要在探討以自變項 (Independent variable) 的變化來預測或解釋結果變項 (Dependent variable) 的變化。
- 目的要建立變數間的因果關係，以利預測結果
- 依變項為二元分類資料 (0 or 1) → 預測 1 的機率
 - 年齡與有無特定慢性病的關係
 - 吸菸與有無肺癌的關係
 - 嚼檳榔與有無口腔癌的關係
 - 醫師年資與手術成功與否的關係
- 自變項為類別變數或連續變數

Logistic regression

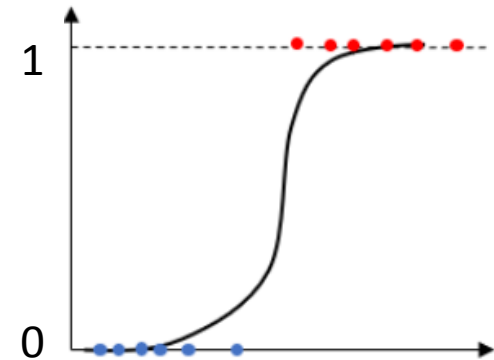
- 單變項迴歸表示式

$$\ln \frac{p}{1-p} = \beta_0 + \beta_1 X$$

- 多變項迴歸表示式

$$\ln \frac{p}{1-p} = \beta_0 + \beta_1 X + \beta_2 X_2 + \dots + \beta_k X_k$$

- 自變數 (X) 對依變數 (Y) 的影響是以指數的方式做變動，因此不需要常態分配的假設
- 使用「最大概似函數估計法 (Maximum Likelihood Estimation)」做參數估計



Odds ratio (OR)



		Outcome	
		Lung cancer	Control
Exposure	Smoking	a	b
	Non Smoking	c	d

$$OR = \frac{a/c}{b/d} = \frac{ad}{bc}$$

Odds ratio	意義
OR=1	抽菸與肺癌無關
OR>1	抽菸可能為肺癌的危險因子
OR<1	抽菸可能為肺癌的保護因子

Logistic regression example-1



- 經由ELISA 和CIA探討dsDNA抗體檢測不一致的風險因素

Table 5. Logistic regression of risk factors for inconsistency of anti-dsDNA antibody tests by ELISA and CIA.

	Univariate			Multivariable		
	Odds Ratio	95%CI	<i>p</i> -Value	Odds Ratio	95%CI	<i>p</i> -Value
Age	1.03	(1.01–1.05)	0.010 *			
Female	Reference					
Male	1.75	(0.72–4.22)	0.215			
Creatine < 1.4 (mg/dL)	Reference					
Creatine ≥ 1.4 (mg/dL)	1.67	(0.81–3.47)	0.165			
UPCR < 500 (mg/g)	Reference					
UPCR ≥ 500 (mg/g)	0.66	(0.37–1.17)	0.157			
ANA < 1:80	Reference					
ANA 1:80–1:640	1.47	(0.30–7.14)	0.632			
ANA ≥ 1:640	0.76	(0.16–3.58)	0.724			
ANA Homogeneous (<i>n</i> = 281)	0.59	(0.26–1.34)	0.206			
C3 ≥ 87 (mg/dL)	Reference			Reference		
C3 < 87 (mg/dL)	0.40	(0.24–0.67)	0.001 **	0.93	(0.40–2.13)	0.861
C4 ≥ 19 (mg/dL)	Reference			Reference		
C4 < 19 (mg/dL)	0.45	(0.27–0.77)	0.003 **	1.04	(0.43–2.51)	0.930
CIC < 10.8 (μg Eq/mL)	Reference			Reference		
CIC ≥ 10.8 (μg Eq/mL)	0.44	(0.24–0.79)	0.006 **	0.42	(0.18–0.94)	0.036 *
Anti-dsDNA antibody by CIA (IU/mL)	0.98	(0.98–0.99)	<0.001 **			
Anti-dsDNA antibody by ELISA (WHO units/mL)	0.98	(0.98–0.99)	<0.001 **	0.98	(0.98–0.99)	<0.001 **
SLEDAI < 4	Reference			Reference		
SLEDAI ≥ 4	0.22	(0.12–0.39)	<0.001 **	0.33	(0.14–0.79)	0.013 *

Logistic regression. * $p < 0.05$, ** $p < 0.01$. Anti-dsDNA antibodies: anti-double-stranded DNA antibodies; UPCR: urine protein/creatinine ratio; ANA: anti-nuclear antibodies; CIC: anti-C1q circulating immune complexes antibody; CIA: chemiluminescent immunoassay; ELISA: enzyme-linked immunosorbent assay; SLEDAI: Systemic Lupus Erythematosus Disease Activity Index.

Logistic regression SPSS dataset



Outcome (0 or 1)

	caseno	Inconsistency	Age	Sex	Creatinine_1.4gp
1	1	0	69.4	0	0
2	2	0	53.4	0	0
3	3	0	55.4	0	0
4	4	0	36.1	0	0
5	5	0	35.9	0	0
6	6	0	48.7	0	0
7	7	0	66.1	0	0
8	8	0	48.9	0	0
9	9	0	37.1	1	0
10	10	0	42.1	0	0
11	11	0	57.2	0	0
12	12	0	40.7	0	0

Variable	Code
Sex	
Female	0
Male	1
Creatinine_1.4gp	
<1.4	0
≥1.4	1
UPCR_500gp	
<500	0
≥500	1
ANA_gp	
<1:80	1
1:80-1:640	2
≥1:640	3
C3_87gp	
<87	0
≥87	1
C4_19gp	
<19	0
≥19	1
CIC_10.8gp	
<10.8	0
≥10.8	1
SLEDAI_4gp	
<4	0
≥4	1

Logistic regression SPSS analysis-1



分析>迴歸>二元Logistic

The image shows the SPSS software interface. The 'Analyze' menu is open, and the 'Regression' option is selected, which has opened a submenu. In the submenu, 'Binary Logistic...' is highlighted. The background shows a data viewer with columns labeled '1.4gp', 'UPCR_500gp', 'ANA_gp', and 'Diff'. The data rows are as follows:

1.4gp	UPCR_500gp	ANA_gp	Diff
0	0	.	.
0	1	2	2
0	0	3	3
0	0		

Logistic regression SPSS analysis-2



The main dialog box for Logistic Regression. The dependent variable is 'Inconsistency'. The list of variables on the left includes caseno, Age, Sex, Creatinine_1.4gp, UPCR_500gp, ANA_gp, Diffuse_Homogeneous, C3_87gp, C4_19gp, CIC_10.8gp, Bio-flash (IU/mL) (>35, Positiv..., ELISA (WHO) (>139, Positive) [...], and SLEDAI_4gp. The 'Covariates' list contains C3_87gp, C4_19gp, CIC_10.8gp, ELISA, and SLEDAI_4gp. The 'Method' is set to 'Enter'. The 'Options...' button is highlighted with a red box.

The 'Define Categorical Variables' dialog box. The 'Covariates' list contains 'ELISA'. The 'Categorical Covariates' list contains C3_87gp(Indicator), C4_19gp(Indicator), CIC_10.8gp(Indicator(first)), and SLEDAI_4gp(Indicator(first)). The 'Change Contrast' section is highlighted with a red box, showing 'Contrast' set to 'Indicator' and 'Reference Category' set to 'First'.

The 'Options' dialog box. The 'Statistics and Plots' section is highlighted with a red box, showing 'CI for exp(B)' checked and set to 95%. Other options include 'Classification plots', 'Correlations of estimates', 'Hosmer-Lemeshow goodness-of-fit', 'Iteration history', 'Casewise listing of residuals', 'Outliers outside 2 std. dev.', 'All cases', 'Display' (At each step), 'Probability for Stepwise' (Entry: 0.05, Removal: 0.10), 'Classification cutoff: 0.5', 'Maximum Iterations: 20', 'Conserve memory for complex analyses or large datasets', and 'Include constant in model'.

Logistic regression SPSS output



OR

Variables in the Equation

		B	S.E.	Wald	df	Sig.	Exp(B)	95% C.I. for EXP(B)	
								Lower	Upper
Step 1 ^a	C3_87gp(1)	.074	.424	.031	1	.861	1.077	.469	2.473
	C4_19gp(1)	-.040	.449	.008	1	.930	.961	.399	2.315
	CIC_10.8gp(1)	-.878	.419	4.400	1	.036	.415	.183	.944
	ELISA	-.017	.003	42.615	1	.000	.983	.978	.988
	SLEDAI_4gp(1)	-1.114	.449	6.150	1	.013	.328	.136	.792
	Constant	4.064	.749	29.416	1	.000	58.196		

a. Variable(s) entered on step 1: C3_87gp, C4_19gp, CIC_10.8gp, ELISA, SLEDAI_4gp.

經多變項調整後，

SLEDAI ≥ 4 比 < 4 有 0.328 倍的風險發生不一致情形且達統計差異 (p=0.013)，代表 SLEDAI ≥ 4 比 < 4 ，較不會發生不一致情形。

Logistic regression example-2



- 探討Brain Image對於大腦皮質下區域失智症的影響
 - Adjusted model
 - age, sex and CCI

TABLE 5 | Associations of imaging variables with subcortical vascular dementia, *N* = 57.

	Dementia	
	OR (95%CI)	<i>p</i>
MARS		
Infratentorial	1.00 (0.93–1.07)	0.963
Deep	1.03 (0.99–1.08)	0.161
Lobar	1.00 (0.99–1.02)	0.739
Total	1.00 (0.99–1.01)	0.580
ARWMC		
Infratentorial	0.53 (0.10–2.80)	0.458
Basal ganglia	1.67 (0.74–3.78)	0.221
Subcortical	2.03 (1.24–3.32)	0.005*
Total	1.43 (1.09–1.89)	0.011*
PVSE		
Centrum semiovale	0.72 (0.36–1.42)	0.339
Basal ganglia	1.10 (0.44–2.74)	0.837
Lesion quantity		
ICH	1.00 (0.75–1.34)	1.000
Lacune	1.18 (1.02–1.35)	0.023*
Lesion burden score		
CAA-SVD score	2.33 (1.01–5.40)	0.047*
C1†	1.41 (1.09–1.83)	0.009*
C2‡	1.38 (1.08–1.76)	0.010*

ICH, intracerebral hemorrhage; *MARS*, Microbleed anatomical rating scale; *ARWMC*, Age-related White Matter Change; *PVSE*, enlargement of the perivascular space; *CAA*, cerebral amyloid angiopathy; *SVD*, small vessel disease; *OR*, odd's ratio.

ORs determined by multivariate logistic regression, adjusted for age, sex, and CCI; **p* < 0.05.

†Sum of total MARS score and total ARWMC scale.

‡Sum of total MARS score, total ARWMC scale, BG PVSE (≥20), and lacune (≥5).

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Logistic regression SPSS dataset



	caseno	Dementia	CCI	Gender	Age	Infratentor_MARS	Deep_MARS	Lobar_MARS	Total_MARS
1	1	1	4	1	87	6	4	11	21
2	2	0	6	1	99
3	3	0	5	1	72	0	2	10	12
4	4	0	2	0	82	14	10	17	41
5	5	0	1	1	80	1	7	5	13
6	6	0	3	1	54	12	21	120	153
7	7	1	2	1	64	0	12	56	68
8	8	1	4	1	61	6	5	1	12
9	9	0	5	1	72	37	43	176	256
10	10	0	3	1	63	1	1	1	3
11	11	0	1	0	89	3	3	5	11
12	12	0	2	1	88	8	19	5	32

Logistic regression SPSS analysis



Logistic Regression

Dependent: Dementia

Block 1 of 1

Covariates: CCI, Gender, Age, Subcortical_ARWMC

Method: Enter

Selection Variable:

OK Paste Reset Cancel Help

Logistic Regression: Define Categorical Variables

Covariates: CCI, Age, Subcortical_ARWMC

Categorical Covariates: Gender(Indicator(first))

Change Contrast

Contrast: Indicator

Reference Category: Last, First

Continue Cancel Help

Logistic Regression: Options

Statistics and Plots

- Classification plots
- Hosmer-Lemeshow goodness-of-fit
- Casewise listing of residuals
- Outliers outside 2 std. dev.
- All cases
- Correlations of estimates
- Iteration history
- CI for exp(B): 95 %

Display

At each step At last step

Probability for Stepwise

Entry: 0.05 Removal: 0.10

Classification cutoff: 0.5

Maximum iterations: 20

Conserve memory for complex analyses or large datasets

Include constant in model

Continue Cancel Help

Logistic regression SPSS output



Variables in the Equation

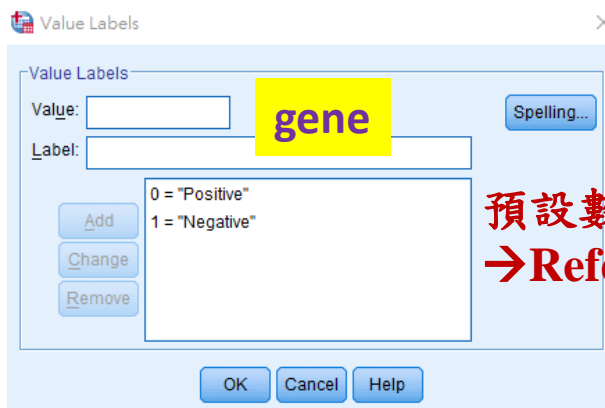
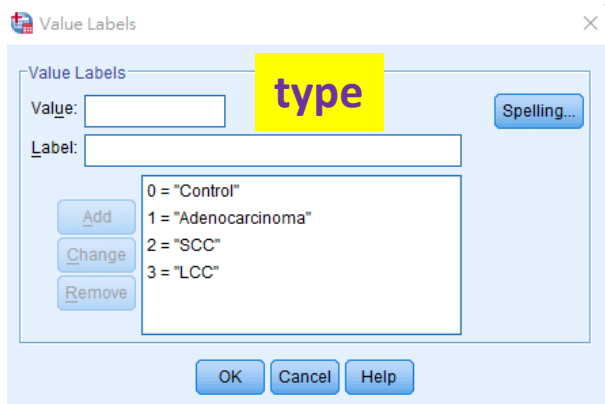
	B	S.E.	Wald	df	Sig.	Exp(B)	95% C.I. for EXP(B)	
							Lower	Upper
Step 1 ^a								
CCI	-.119	.295	.163	1	.687	.888	.498	1.583
Gender(1)	.287	.824	.122	1	.727	1.333	.265	6.700
Age	.005	.036	.022	1	.883	1.005	.936	1.079
Subcortical_ARWMC	.708	.251	7.920	1	.005	2.029	1.240	3.322
Constant	-5.365	3.040	3.114	1	.078	.005		

a. Variable(s) entered on step 1: CCI, Gender, Age, Subcortical_ARWMC.

經性別、年齡和CCI調整後，
Subcortical_ARWMC每增加1個單位罹患失智症的風險增加 2.029 倍
且達統計差異 (p=0.005)。

Multinomial Logistic Regression SPSS dataset

- 依變項為類別變數，而且超過兩種以上
- 自變項為類別變數或連續變數
- 探討基因突變對不同組織類型的肺癌發生風險的關係



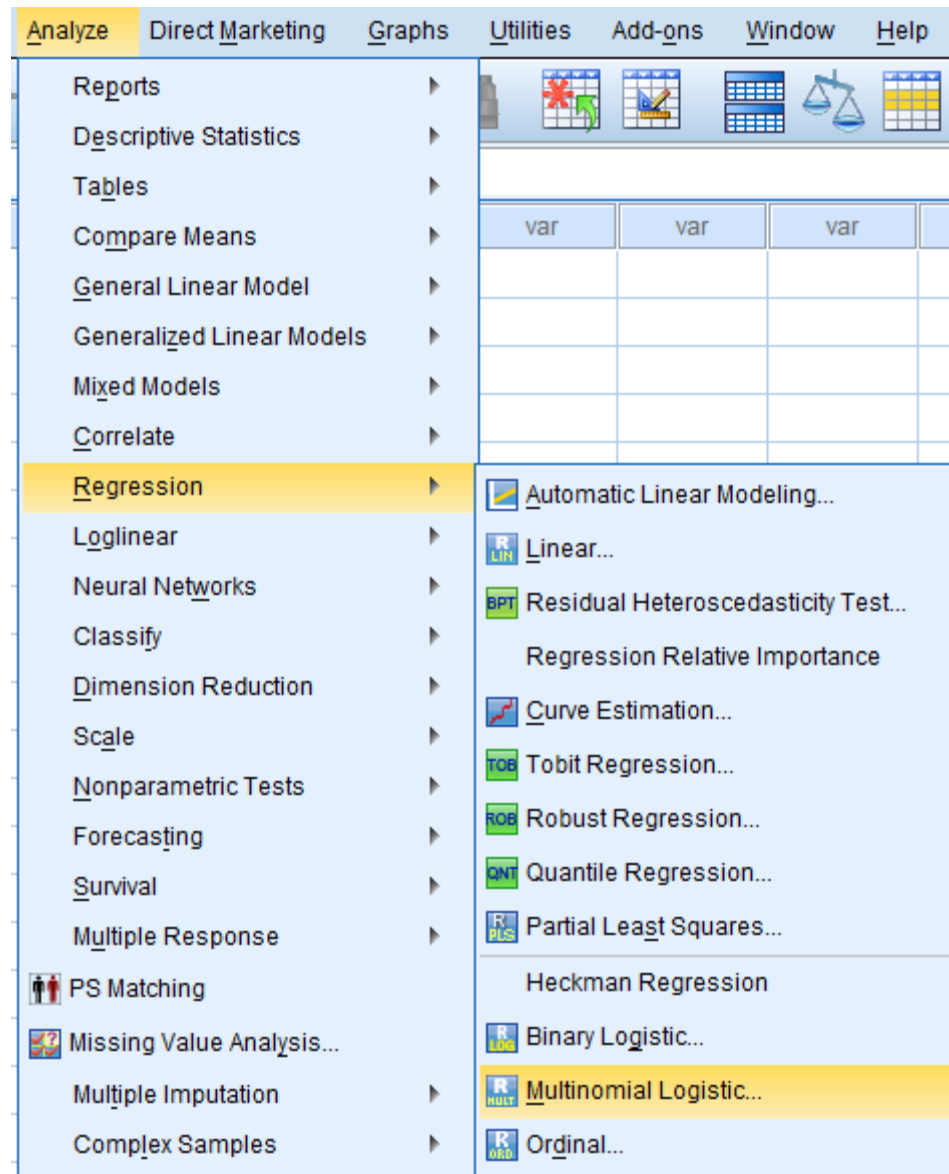
預設數值大
→ Reference

	ID	type	gene
1	1	1	0
2	2	1	0
3	3	1	0
4	4	1	0
5	5	1	0
6	6	1	0
7	7	1	0
8	8	1	0
9	9	1	0
10	10	1	0
11	11	1	0
12	12	1	0
13	13	1	0
14	14	1	0
15	15	1	0

Multinomial Logistic Regression SPSS analysis-1



分析>迴歸>多項式Logistic



Multinomial Logistic Regression SPSS analysis-2



The image displays two overlapping SPSS dialog boxes for Multinomial Logistic Regression. The primary dialog box on the left has the following settings:

- Dependent:** type(First)
- Reference Category:** (highlighted with a red box and a red arrow pointing to the secondary dialog)
- Factor(s):** gene
- Covariate(s):** (empty)

The secondary dialog box on the right, titled "Multinomial Logistic Regre...", shows the following options:

- Reference Category:**
 - First Category
 - Last Category
 - Custom
- Category Order:**
 - Ascending
 - Descending

Buttons at the bottom of the secondary dialog include "Continue", "Cancel", and "Help". The primary dialog box has buttons for "OK", "Paste", "Reset", "Cancel", and "Help" at the bottom.

Multinomial Logistic Regression SPSS output



Parameter Estimates

OR

type ^a		B	Std. Error	Wald	df	Sig.	Exp(B)	95% Confidence Interval for Exp (B)	
								Lower Bound	Upper Bound
Adenocarcinoma	Intercept	-1.769	.279	40.117	1	.000			
	[gene=0]	2.686	.441	37.044	1	.000	14.667	6.177	34.827
	[gene=1]	0 ^b	.	.	0
SCC	Intercept	-.788	.191	17.096	1	.000			
	[gene=0]	1.299	.412	9.948	1	.002	3.667	1.635	8.221
	[gene=1]	0 ^b	.	.	0
LCC	Intercept	-1.587	.259	37.634	1	.000			
	[gene=0]	2.193	.442	24.576	1	.000	8.963	3.766	21.331
	[gene=1]	0 ^b	.	.	0

a. The reference category is: Control.

b. This parameter is set to zero because it is redundant.

有基因突變比沒有基因突變，
發生風險分別為腺癌有 14.667 倍、鱗狀細胞癌有 3.667 倍、
大細胞癌有 8.963 倍且皆達統計差異。

From log odds to probability



Here's the equation of a logistic regression model with 1 predictor X:

a.k.a. **Log Odds**
or **Logit**

$$\log\left(\frac{P}{1-P}\right) = \beta_0 + \beta_1 X$$

Intercept

A blue box surrounds the left side of the equation, $\log\left(\frac{P}{1-P}\right)$. A blue arrow points from the text "a.k.a. Log Odds or Logit" to the box. Another blue arrow points from the text "Intercept" to the β_0 term in the equation.

Where **P is the probability** of having the outcome and **P / (1-P) is the odds** of the outcome.

When $X = 0$, the intercept β_0 is the log of the odds of having the outcome

From log odds to probability

$$\ln \frac{p}{1-p} = \beta_0 + \beta_1 X \quad \longrightarrow \quad \frac{p}{1-p} = e^{\beta_0 + \beta_1 X}$$

$$p = e^{\beta_0 + \beta_1 X} - p e^{\beta_0 + \beta_1 X}$$

$$p(1 + e^{\beta_0 + \beta_1 X}) = e^{\beta_0 + \beta_1 X}$$

$$p = \frac{e^{\beta_0 + \beta_1 X}}{1 + e^{\beta_0 + \beta_1 X}}$$

SPSS dataset probability



➤ SPSS dataset probability

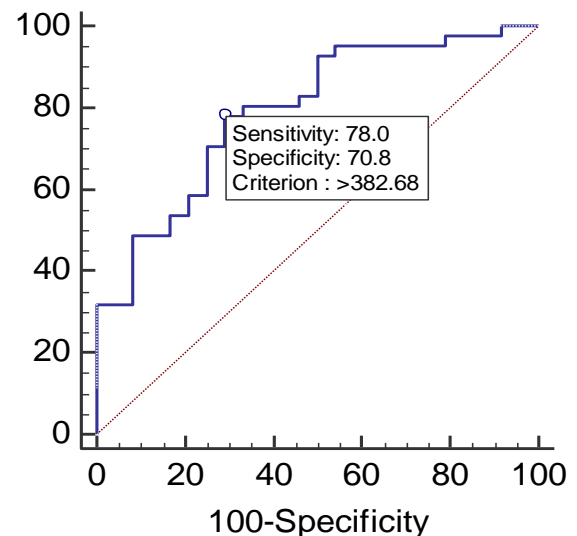
	caseno	Inconsistency	Age	PRE_1
1	1	0	69.4	.60618
2	2	0	53.4	.49037
3	3	0	55.4	.50477
4	4	0	36.1	.36660
5	5	0	35.9	.36528
6	6	0	48.7	.45612
7	7	0	66.1	.58241
8	8	0	48.9	.45726
9	9	0	37.1	.37362
10	10	0	42.1	.40845
11	11	0	57.2	.51823
12	12	0	40.7	.39827



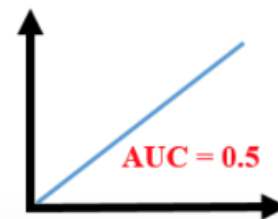
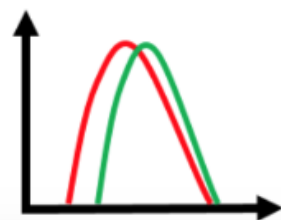
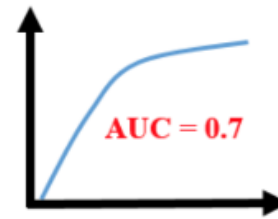
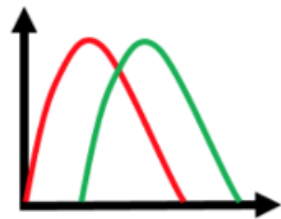
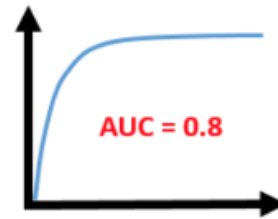
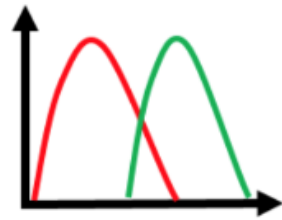
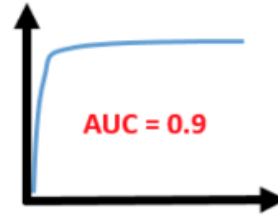
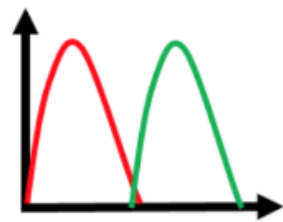
ROC curve

- 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)
 - 比較不同Biomarker (A β 42/t-tau) 預測認知功能有無下降
- 目的
 - 將連續數值決定臨界值
 - 用來比較不同工具的好壞
- 最適切點 (Youden Index = Sensitivity + Specificity - 1)
 - Sensitivity + Specificity 最大的點
 - 0-1 之間，越接近 1 越好

AUC	Discrimination
0.5	沒有鑑別力
0.7+	可接受的鑑別力
0.8+	好的鑑別力
0.9+	非常好的鑑別力



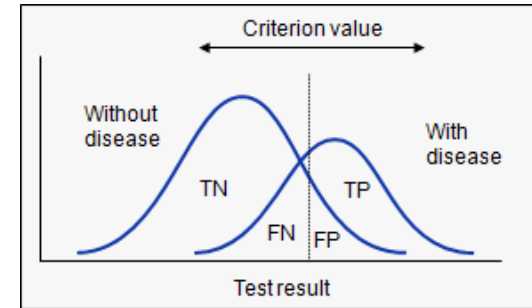
Area under the ROC Curve



診斷工具指標



	Gold Standard Test		Total
	Disease	Control	
Screen test			
Positive	a	b	a+b
Negative	c	d	c+d
Total	a+c	b+d	a+b+c+d



Ref: <https://www.medcalc.org/manual/roc-curves.php>

$$\text{Sensitivity} = \frac{a}{a+c}$$

$$\text{Specificity} = \frac{d}{b+d}$$

$$\text{False positive} = \frac{b}{b+d}$$

$$\text{False negative} = \frac{c}{a+c}$$

$$\text{Positive Predictive Value} = \frac{a}{a+b}$$

$$\text{Negative Predictive Value} = \frac{d}{c+d}$$

$$\text{Likelihood ratio positive} = \frac{\text{Sensitivity}}{1-\text{specificity}}$$

$$\text{Likelihood ratio negative} = \frac{1-\text{sensitivity}}{\text{specificity}}$$

Likelihood ratio



概似比的臨床意義

Likelihood ratio	Interpretation
>10	Strong evidence to rule in disease
5~10	Moderate evidence to rule in disease
2~5	Weak evidence to rule in disease
0.5~2.0	No signification change in the likelihood of disease
0.2~0.5	Weak evidence to rule out disease
0.1~0.2	Moderate evidence to rule out disease
<0.1	Strong evidence to rule out disease

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

ROC example

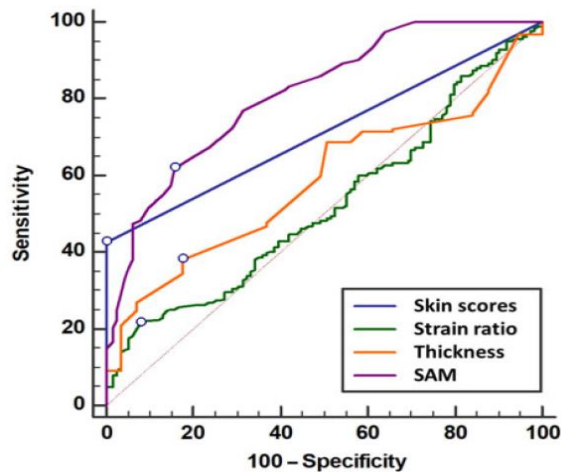


- 利用高光譜影像評估皮膚狀況是否預測硬皮症

TABLE 3 ROC analysis of skin assessments in the diagnosis of scleroderma

Variables	AUC (95% CI)	P	Optimal cutoff	Sensitivity, %	Specificity, %	Accuracy, %	PPV, %	NPV, %
Skin scores ^a	0.712 (0.658, 0.763)	<0.001	>0	42.47	100.00	64.33	100.00	51.58
Strain ratio	0.522 (0.464, 0.580)	0.510	≤0.88	21.51	92.11	48.33	81.63	41.83
Thickness	0.585 (0.527, 0.642)	0.009	>1.31	38.17	82.46	55.00	78.02	44.98
SAM	0.812 (0.763, 0.854)	<0.001	>0.025	61.83	84.21	70.33	86.47	57.49

FIG. 3 Comparisons of scleroderma diagnostic accuracy among tests



Rheumatology 59.11 (2020): 3201-3210.

ROC SPSS dataset

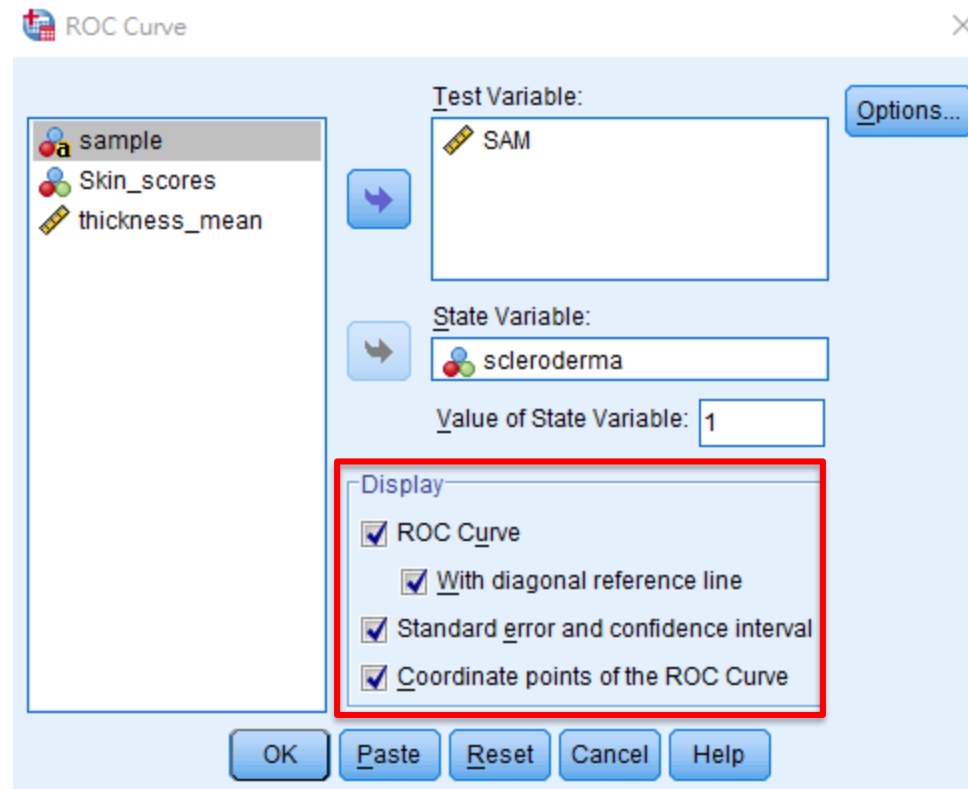
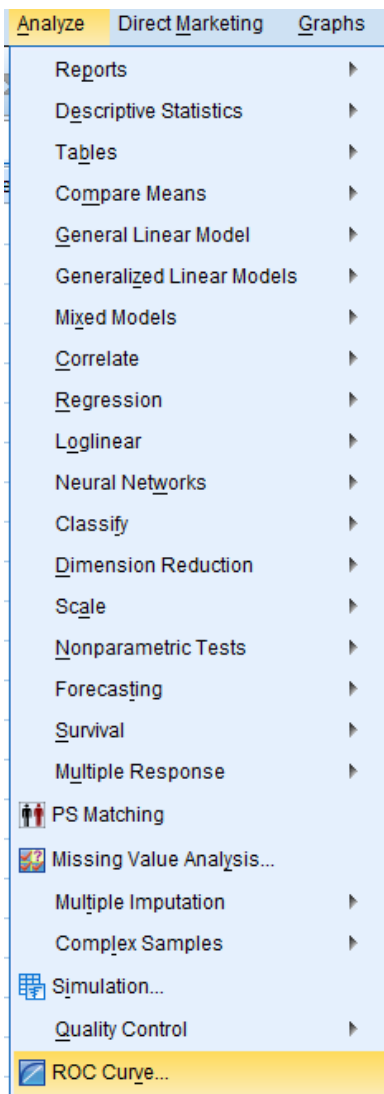


	caseno	scleroderma	Skin_scores	thickness_mean	SAM	Strainratio
1	1	1.00	.00	.175	.016	1.02
2	2	1.00	.00	.129	.014	5.07
3	3	1.00	.00	.142	.022	4.53
4	4	1.00	.00	.127	.011	1.12
5	5	1.00	.00	.131	.015	1.45
6	6	1.00	.00	.148	.014	7.93
7	7	1.00	2.00	.255	.041	.19
8	8	1.00	2.00	.253	.038	3.16
9	9	1.00	2.00	.216	.038	6.15
10	10	1.00	2.00	.216	.044	1.91
11	11	1.00	2.00	.203	.040	6.77
12	12	1.00	2.00	.161	.012	5.81

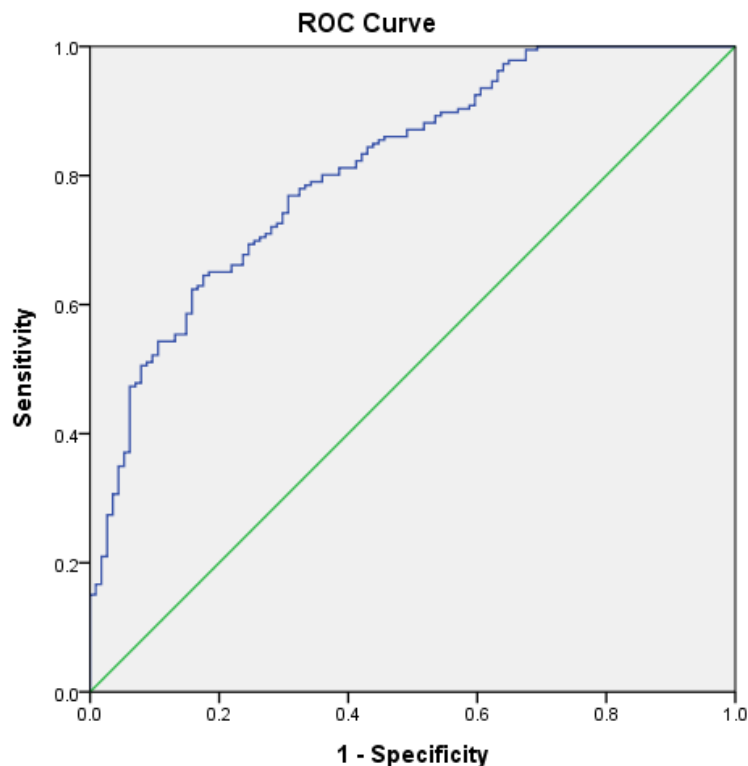
ROC SPSS analysis



分析>ROC曲線



ROC SPSS output



AUC

Area Under the Curve

Test Result Variable(s): SAM

Area	Std. Error ^a	Asymptotic Sig. ^b	Asymptotic 95% Confidence Interval	
			Lower Bound	Upper Bound
.812	.025	.000	.764	.861

a. Under the nonparametric assumption

b. Null hypothesis: true area = 0.5

Coordinates of the Curve

Test Result Variable(s): SAM

Positive if Greater Than or Equal To ^a	Sensitivity	1 - Specificity
.0000	1.000	1.000
.0045	1.000	.991
.0055	1.000	.974
.0065	1.000	.930
.0075	1.000	.886
.0085	1.000	.833
.0095	1.000	.789
.0105	1.000	.711
.0115	.989	.675
.0125	.973	.640
.0135	.935	.614
.0145	.903	.579
.0155	.892	.544
.0165	.860	.491
.0175	.833	.421
.0185	.823	.412
.0195	.769	.316
.0205	.726	.289
.0215	.715	.281

Youden Index

- Youden Index = sen + spe - 1
- 新增spe欄位, 公式為1 - (1-specificity)
- 將 sen + spe - 1 欄 由大至小排序

Coordinates of the Curve				
Test Result \ SAM				
Positive if Greater Than or Equal To ^a	Sensitivity	1 - Specificity	spe	sen+spe-1
.0255	.618	.158	0.842	0.460
.0195	.769	.316	0.684	0.453
.0245	.651	.202	0.798	0.449
.0235	.661	.219	0.781	0.442
.0205	.726	.289	0.711	0.436
.0225	.672	.237	0.763	0.435
.0215	.715	.281	0.719	0.434
.0265	.575	.149	0.851	0.426
.0285	.516	.096	0.904	0.420
.0275	.548	.132	0.868	0.417
.0175	.833	.421	0.579	0.412
.0305	.473	.061	0.939	0.412
.0185	.823	.412	0.588	0.410
.0295	.484	.079	0.921	0.405
.0315	.435	.061	0.939	0.374
.0165	.860	.491	0.509	0.369
.0325	.419	.061	0.939	0.358

Medcalc ROC-1



分析 > ROC curves > ROC curve analysis

<https://www.medcalc.org/download/>

The screenshot shows the MedCalc software interface. The 'Statistics' menu is open, and 'ROC curves' is selected. A sub-menu is displayed with the following options:

- ROC curve analysis...
- Interactive dot diagram...
- Plot versus criterion values...
- Predictive values...
- Interval likelihood ratios...
- Comparison of ROC curves...

In the background, a data table is visible with columns D, E, and F. The data rows are as follows:

	D	E	F
ores kness_mean	0.175	0.016	1.
	0.129	0.014	5.
	0.142	0.022	4.
	0.127	0.011	1.
	0.131	0.015	1.
	0.148	0.014	7.
	0.255	0.041	0.
	0.253	0.038	3.
	0.216	0.038	6.
	0.216	0.044	1.
	0.203	0.040	6.
	0.161	0.012	5.

Medcalc ROC-2



ROC curve analysis

Variable: SAM

Classification variable: scleroderma

Filter:

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 negative groups reflects the prevalence of the disease.
- Other value (%): 62

Options

- List criterion values with test characteristics
 - Include all observed criterion values
- 95% Confidence Interval for:
 - Sensitivity/Specificity
 - Likelihood ratios
 - Predictive Values
- Calculate optimal criterion value taking into account costs:
FPC: 1 FNC: 1 TPC: 0 TNC: 0

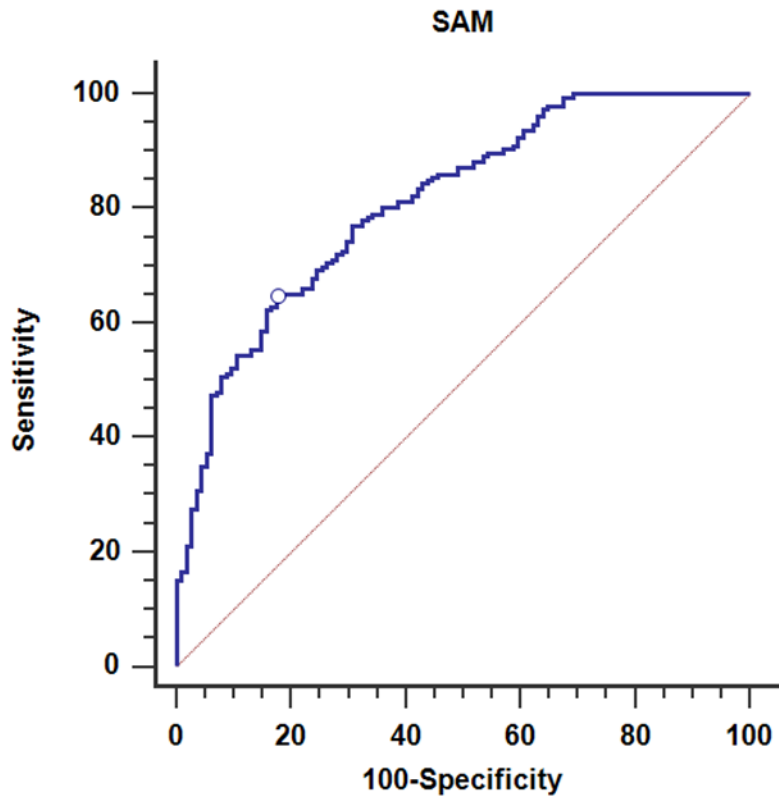
Advanced...

Graphs

- Display ROC curve window
 - Mark points corresponding to criterion values
 - Include 95% Confidence Bounds

OK Cancel

Medcalc ROC-2



Variable	SAM
Classification variable	scleroderma

Sample size	300
Positive group : scleroderma = 1	186
Negative group : scleroderma = 0	114

Disease prevalence (%)	62
------------------------	----

Area under the ROC curve (AUC)

Area under the ROC curve (AUC)	0.812
Standard Error ^a	0.0248
95% Confidence interval ^b	0.763 to 0.854
z statistic	12.560
Significance level P (Area=0.5)	<0.0001

^a DeLong et al., 1988

^b Binomial exact

Youden index

Youden index J	0.4604
Associated criterion	>0.025
Sensitivity	61.83
Specificity	84.21

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
>0.025	61.83	54.4 - 68.8	84.21	76.2 - 90.4	3.92	2.5 - 6.1	0.45	0.4 - 0.6	86.5	79.5 - 91.8	57.5	49.6 - 65.1
>0.026	57.53	50.1 - 64.7	85.09	77.2 - 91.1	3.86	2.4 - 6.1	0.50	0.4 - 0.6	86.3	79.0 - 91.8	55.1	47.4 - 62.6
>0.027	54.84	47.4 - 62.1	86.84	79.2 - 92.4	4.17	2.6 - 6.8	0.52	0.4 - 0.6	87.2	79.7 - 92.6	54.1	46.6 - 61.5
>0.028	51.61	44.2 - 59.0	90.35	83.4 - 95.1	5.35	3.0 - 9.5	0.54	0.5 - 0.6	89.7	82.3 - 94.8	53.4	46.1 - 60.6
>0.029	48.39	41.0 - 55.8	92.11	85.5 - 96.3	6.13	3.2 - 11.7	0.56	0.5 - 0.7	90.9	83.4 - 95.8	52.2	45.1 - 59.3
>0.03	47.31	40.0 - 54.7	93.86	87.8 - 97.5	7.71	3.7 - 16.0	0.56	0.5 - 0.6	92.6	85.4 - 97.0	52.2	45.1 - 59.2
>0.031	43.55	36.3 - 51.0	93.86	87.8 - 97.5	7.09	3.4 - 14.8	0.60	0.5 - 0.7	92.0	84.3 - 96.7	50.5	43.5 - 57.4
>0.032	41.94	34.8 - 49.4	93.86	87.8 - 97.5	6.83	3.3 - 14.3	0.62	0.5 - 0.7	91.8	83.8 - 96.6	49.8	42.9 - 56.6
>0.033	38.17	31.2 - 45.6	93.86	87.8 - 97.5	6.22	3.0 - 13.0	0.66	0.6 - 0.7	91.0	82.4 - 96.3	48.2	41.5 - 55.0
>0.034	36.02	29.1 - 43.4	94.74	88.9 - 98.0	6.84	3.1 - 15.3	0.68	0.6 - 0.8	91.8	83.0 - 96.9	47.6	40.9 - 54.3
>0.035	33.33	26.6 - 40.6	95.61	90.1 - 98.6	7.60	3.1 - 18.3	0.70	0.6 - 0.8	92.5	83.4 - 97.5	46.8	40.2 - 53.4
>0.036	29.03	22.6 - 36.1	96.49	91.3 - 99.0	8.27	3.1 - 22.2	0.74	0.7 - 0.8	93.1	83.3 - 98.1	45.5	39.1 - 52.0
>0.037	25.27	19.2 - 32.1	97.37	92.5 - 99.5	9.60	3.1 - 30.1	0.77	0.7 - 0.8	94.0	83.5 - 98.7	44.4	38.1 - 50.8
>0.038	22.58	16.8 - 29.3	97.37	92.5 - 99.5	8.58	2.7 - 27.0	0.80	0.7 - 0.9	93.3	81.7 - 98.6	43.5	37.4 - 49.9
>0.039	20.43	14.9 - 26.9	98.25	93.8 - 99.8	11.65	2.9 - 47.4	0.81	0.8 - 0.9	95.0	83.1 - 99.4	43.1	37.0 - 49.3
>0.04	17.74	12.5 - 24.0	98.25	93.8 - 99.8	10.11	2.5 - 41.3	0.84	0.8 - 0.9	94.3	80.8 - 99.3	42.3	36.2 - 48.5

Medcalc ROC-3



分析 > ROC curves > Comparison of ROC curves

The screenshot shows the MedCalc software interface. The 'Statistics' menu is open, and the path 'ROC curves > Comparison of ROC curves...' is highlighted. The background data table is as follows:

	C	D	E
in_scores	thickness_mean	SAM	
	0.00	0.175	0.016
	0.00	0.129	0.014
	0.00	0.142	0.022
	0.00	0.127	0.011
	0.00	0.131	0.015
	0.00	0.148	0.014
	2.00	0.255	0.041
	2.00	0.253	0.038
	2.00	0.216	0.038
	2.00	0.216	0.044
	2.00	0.203	0.040
	2.00	0.161	0.012

16	SSC004-I1	1.00
17	SSC004-I2	1.00
18	SSC004-I3	1.00
19	SSC006-r1	1.00
20	SSC006-r2	1.00
21	SSC006-r3	1.00

Medcalc ROC-4



Comparison of ROC curves

The screenshot shows the 'Comparison of ROC curves' dialog box in MedCalc. It is divided into two main sections: 'Variables' and 'Methodology'.
Variables: This section contains five dropdown menus. The first four are labeled 'Skin_scores', 'Strainratio', 'thickness_mean', and 'SAM'. The fifth dropdown menu is empty. Below these is the 'Classification variable:' section with a dropdown menu containing 'scleroderma'. At the bottom of this section is a 'Filter:' dropdown menu, which is also empty.
Methodology: This section contains three options:

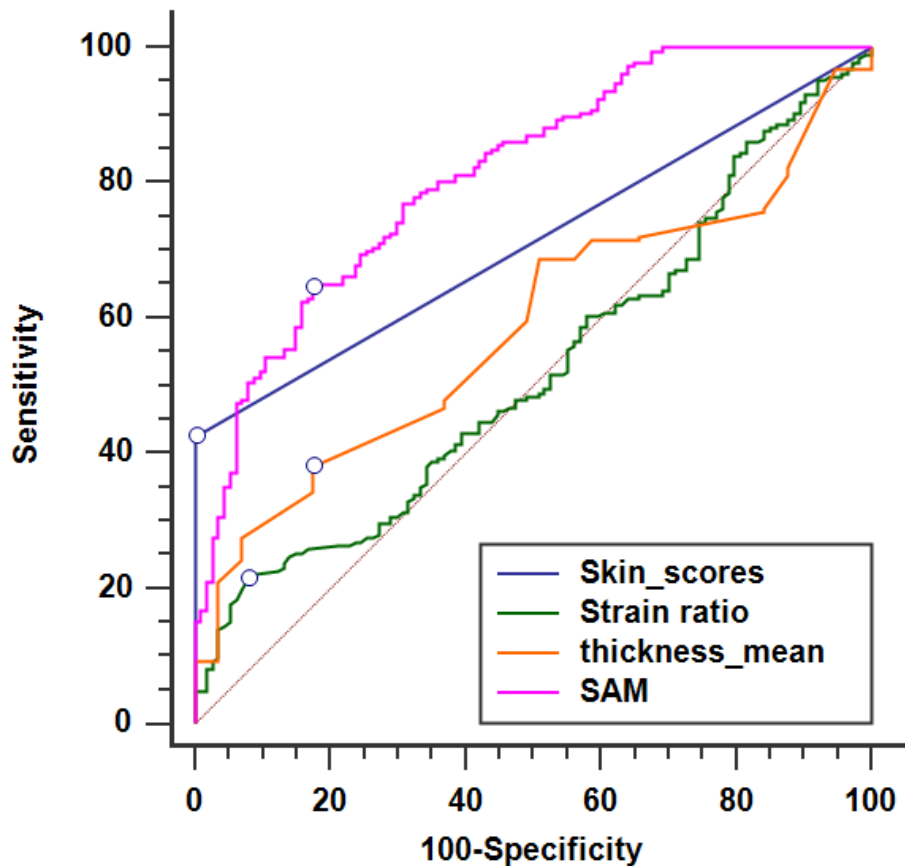
- DeLong et al.
- Hanley & McNeil
- Binomial exact Confidence Interval for the AUC

Graph: This section contains two options:

- Display ROC curves window
- Mark points corresponding to criterion values

At the bottom right of the dialog box are 'OK' and 'Cancel' buttons. A help icon (?) is located in the bottom left corner of the dialog box.

Medcalc ROC-5



Pairwise comparison of ROC curves

Skin_scores ~ Strainratio	
Difference between areas	0.190
Standard Error ^o	0.0371
95% Confidence Interval	0.117 to 0.263
z statistic	5.126
Significance level	P < 0.0001
Skin_scores ~ thickness_mean	
Difference between areas	0.127
Standard Error ^o	0.0318
95% Confidence Interval	0.0647 to 0.189
z statistic	3.996
Significance level	P = 0.0001
Skin_scores ~ SAM	
Difference between areas	0.0997
Standard Error ^o	0.0283
95% Confidence Interval	0.0443 to 0.155
z statistic	3.527
Significance level	P = 0.0004
Strainratio ~ thickness_mean	
Difference between areas	0.0631
Standard Error ^o	0.0523
95% Confidence Interval	-0.0394 to 0.165
z statistic	1.207
Significance level	P = 0.2276
Strainratio ~ SAM	
Difference between areas	0.290
Standard Error ^o	0.0427
95% Confidence Interval	0.206 to 0.374
z statistic	6.785
Significance level	P < 0.0001
thickness_mean ~ SAM	
Difference between areas	0.227
Standard Error ^o	0.0399
95% Confidence Interval	0.149 to 0.305
z statistic	5.681
Significance level	P < 0.0001

^o DeLong et al., 1988



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Thank you !

