

ROC analysis

2024-11-03

ROC analysis of S1P in our cohort

```
roc.s1p <- rocit(data$s1p.levels, data$cancer)
```

```
## Warning in rocit(data$s1p.levels, data$cancer): NA(s) in score and/or  
class,  
## removed from the data.
```

ROC plot of S1P sensitivity and 1-Specificity:

```
plot(roc.s1p)
```

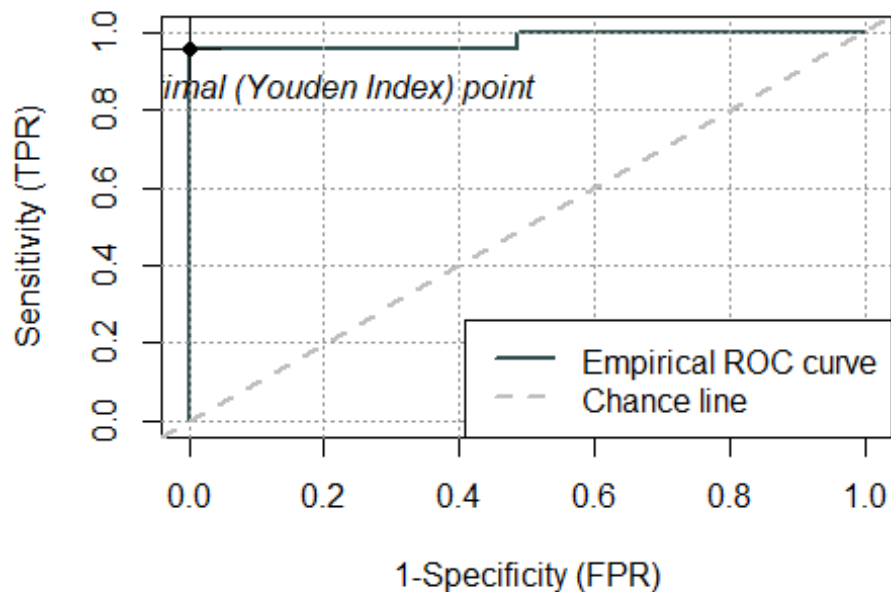


Table of TPR, FPR and cutoff values:

```
cbind(roc.s1p$TPR, roc.s1p$FPR, roc.s1p$Cutoff)
```

```
##      [,1]      [,2]      [,3]  
## [1,] 0.00 0.00000000      Inf  
## [2,] 0.04 0.00000000 4532.19  
## [3,] 0.08 0.00000000 4349.33  
## [4,] 0.12 0.00000000 4290.86  
## [5,] 0.16 0.00000000 4281.45
```

```
## [6,] 0.20 0.00000000 4190.45
## [7,] 0.24 0.00000000 4121.02
## [8,] 0.28 0.00000000 4063.96
## [9,] 0.32 0.00000000 4035.94
## [10,] 0.36 0.00000000 4028.30
## [11,] 0.40 0.00000000 3968.78
## [12,] 0.44 0.00000000 3955.81
## [13,] 0.48 0.00000000 3931.16
## [14,] 0.52 0.00000000 3925.62
## [15,] 0.56 0.00000000 3921.44
## [16,] 0.60 0.00000000 3754.43
## [17,] 0.64 0.00000000 3710.98
## [18,] 0.68 0.00000000 3702.57
## [19,] 0.72 0.00000000 3691.76
## [20,] 0.76 0.00000000 3688.27
## [21,] 0.80 0.00000000 3623.29
## [22,] 0.84 0.00000000 3605.63
## [23,] 0.88 0.00000000 3602.99
## [24,] 0.92 0.00000000 3526.30
## [25,] 0.96 0.00000000 3397.89
## [26,] 0.96 0.02564103 969.75
## [27,] 0.96 0.05128205 903.51
## [28,] 0.96 0.07692308 812.09
## [29,] 0.96 0.10256410 669.11
## [30,] 0.96 0.12820513 663.28
## [31,] 0.96 0.15384615 646.08
## [32,] 0.96 0.17948718 635.75
## [33,] 0.96 0.20512821 607.06
## [34,] 0.96 0.23076923 568.95
## [35,] 0.96 0.25641026 499.83
## [36,] 0.96 0.28205128 483.57
## [37,] 0.96 0.30769231 464.99
## [38,] 0.96 0.33333333 451.50
## [39,] 0.96 0.35897436 435.38
## [40,] 0.96 0.38461538 424.83
## [41,] 0.96 0.41025641 424.05
## [42,] 0.96 0.43589744 407.30
## [43,] 0.96 0.46153846 406.01
## [44,] 0.96 0.48717949 380.61
## [45,] 1.00 0.48717949 374.34
## [46,] 1.00 0.51282051 345.50
## [47,] 1.00 0.53846154 316.00
## [48,] 1.00 0.56410256 302.84
## [49,] 1.00 0.58974359 292.62
## [50,] 1.00 0.61538462 264.03
## [51,] 1.00 0.64102564 257.98
## [52,] 1.00 0.66666667 239.03
## [53,] 1.00 0.69230769 236.33
## [54,] 1.00 0.71794872 223.64
## [55,] 1.00 0.74358974 223.63
```

```
## [56,] 1.00 0.76923077 218.43
## [57,] 1.00 0.79487179 149.37
## [58,] 1.00 0.82051282 148.04
## [59,] 1.00 0.84615385 101.65
## [60,] 1.00 0.87179487 75.64
## [61,] 1.00 0.89743590 46.54
## [62,] 1.00 1.00000000 0.00
```

```
summary(optimal.cutpoints(s1p.levels~cancer, tag.healthy = 0, methods =
"ValueDLR.Negative", data = data))
```

```
## Warning: There is no cutpoint that yields the exact Diagnostic Negative
## Likelihood Ratio designated. The cutpoint having the closest value to the
## designated Diagnostic Negative Likelihood Ratio has therefore been
selected.
```

```
##
## Call:
## optimal.cutpoints.formula(X = s1p.levels ~ cancer, tag.healthy = 0,
## methods = "ValueDLR.Negative", data = data)
##
```

```
## Area under the ROC curve (AUC): 0.981 (0.942, 1.019)
```

```
##
## CRITERION: ValueDLR.Negative
## Number of optimal cutoffs: 2
```

```
##
## Estimate
## cutoff 3925.620000
## Se 0.5200000
## Sp 1.0000000
## PPV 1.0000000
## NPV 0.7647059
## DLR.Positive Inf
## DLR.Negative 0.4800000
## FP 0.0000000
## FN 12.0000000
```

```
##
## Estimate
## cutoff 3931.16
## Se 0.48
## Sp 1.00
## PPV 1.00
## NPV 0.75
## DLR.Positive Inf
## DLR.Negative 0.52
## FP 0.00
## FN 13.00
```

ROC analysis of anti-ceramide antibody levels in our cohort

```
roc.cerab <- rocit(data$cerab, data$cancer)
```

ROC plot of anti-ceramide antibody sensitivity and 1-Specificity:

```
plot(roc.cerab)
```

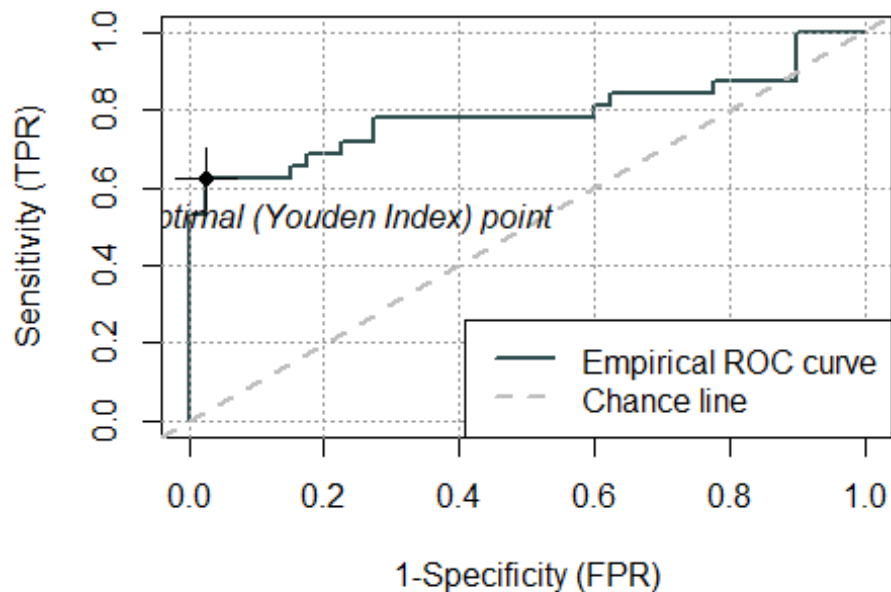


Table of TPR, FPR and cutoff values:

```
cut.values <- as.data.frame(cbind(roc.cerab$TPR, roc.cerab$FPR,
roc.cerab$Cutoff))
names(cut.values) <- c("TPR", "FPR", "Cutoff")
cut.values
```

##	TPR	FPR	Cutoff
## 1	0.00000	0.000	Inf
## 2	0.03125	0.000	496.20710
## 3	0.06250	0.000	483.14269
## 4	0.09375	0.000	477.30283
## 5	0.12500	0.000	432.02890
## 6	0.15625	0.000	418.90427
## 7	0.18750	0.000	403.01023
## 8	0.21875	0.000	392.71523
## 9	0.25000	0.000	378.74774
## 10	0.28125	0.000	364.35882
## 11	0.31250	0.000	357.61589
## 12	0.34375	0.000	355.80975
## 13	0.37500	0.000	342.20349
## 14	0.40625	0.000	304.63576
## 15	0.43750	0.000	296.02649
## 16	0.46875	0.000	276.88140

##	17	0.50000	0.000	270.25880
##	18	0.53125	0.000	267.54967
##	19	0.53125	0.025	258.82353
##	20	0.56250	0.025	256.05057
##	21	0.59375	0.025	255.26791
##	22	0.62500	0.025	246.05659
##	23	0.62500	0.050	245.58824
##	24	0.62500	0.075	244.11765
##	25	0.62500	0.100	239.70588
##	26	0.62500	0.125	238.23529
##	27	0.62500	0.150	237.50000
##	28	0.65625	0.150	237.02589
##	29	0.65625	0.175	231.61765
##	30	0.68750	0.175	230.64419
##	31	0.68750	0.200	230.14706
##	32	0.68750	0.225	228.67647
##	33	0.71875	0.225	226.61048
##	34	0.71875	0.275	224.26471
##	35	0.75000	0.275	223.35942
##	36	0.78125	0.275	221.37267
##	37	0.78125	0.300	219.85294
##	38	0.78125	0.325	218.38235
##	39	0.78125	0.350	213.23529
##	40	0.78125	0.375	210.29412
##	41	0.78125	0.400	209.55882
##	42	0.78125	0.425	208.08824
##	43	0.78125	0.450	207.35294
##	44	0.78125	0.475	206.61765
##	45	0.78125	0.500	205.88235
##	46	0.78125	0.525	204.41176
##	47	0.78125	0.550	200.73529
##	48	0.78125	0.575	200.00000
##	49	0.78125	0.600	194.85294
##	50	0.81250	0.600	188.32029
##	51	0.81250	0.625	184.55882
##	52	0.84375	0.625	180.79470
##	53	0.84375	0.650	177.20588
##	54	0.84375	0.675	172.05882
##	55	0.84375	0.700	166.91176
##	56	0.84375	0.725	156.61765
##	57	0.84375	0.750	143.38235
##	58	0.84375	0.775	140.44118
##	59	0.87500	0.775	121.67369
##	60	0.87500	0.800	119.11765
##	61	0.87500	0.825	111.02941
##	62	0.87500	0.850	105.88235
##	63	0.87500	0.875	102.94118
##	64	0.87500	0.900	100.73529
##	65	0.90625	0.900	83.80494
##	66	0.93750	0.900	76.52017

```
## 67 0.96875 0.900 71.40277
## 68 1.00000 0.900 68.81397
## 69 1.00000 0.925 47.79412
## 70 1.00000 0.950 44.85294
## 71 1.00000 0.975 36.02941
## 72 1.00000 1.000 32.35294
```

Optimal cutoff using the best negative likelihood ratio:

```
summary(optimal.cutpoints(cerab~cancer, tag.healthy = 0, methods =
"ValueDLR.Negative", data = data))
```

```
##
## Call:
## optimal.cutpoints.formula(X = cerab ~ cancer, tag.healthy = 0,
##   methods = "ValueDLR.Negative", data = data)
##
## Area under the ROC curve (AUC): 0.788 (0.668, 0.908)
##
## CRITERION: ValueDLR.Negative
## Number of optimal cutoffs: 2
##
##               Estimate
## cutoff      184.5588235
## Se          0.8125000
## Sp          0.3750000
## PPV         0.5098039
## NPV         0.7142857
## DLR.Positive 1.3000000
## DLR.Negative 0.5000000
## FP         25.0000000
## FN          6.0000000
##
##               Estimate
## cutoff      270.2588020
## Se          0.5000000
## Sp          1.0000000
## PPV         1.0000000
## NPV         0.7142857
## DLR.Positive      Inf
## DLR.Negative 0.5000000
## FP          0.0000000
## FN         16.0000000
```

Based on the above analysis patients who were true positives were considered to have high levels of anti-ceramide antibody, and false negatives were considered low level patients.