Solutions:

1a. Create a 2x2 table based on a CMMS score _ 20 being used to identify people with dementia.

CMMS Score	Non-Demented	Demented	Total
0-5	0	2	2
6-10	0	1	1
11-15	3	4	7
16-20	9	5	14
Total	12	12	24

	A	B	Total
A	12	12	24
B	4	34	38
Total	16	46	62

1b

$$\text{Sensitivity} = P(T|D) = \frac{P(T \cap D)}{P(D)} = \frac{P(+\text{treadmill test} \cap \text{CHD})}{P(\text{CHD})} = \frac{a}{a+c}$$

1 - Sensitivity = 1 - TPR = **False Negative Rate (FNR)**

Test	Gold Standard/ Disease Status		Total
	Positive (D)	**Negative** $(\bar{D})$	
Positive (T)	a (true positives)	b (false positives)	a+b
Negative $(\bar{T})$	c (false negatives)	d (true negatives)	c+d
Total	a+c	b+d	N (a+b+c+d)

N = 62, a+b = 24, c+d = 38, a+c = 16, b+d = 46

Sensitivity = 12/16 = 0.75

$$\text{Specificity} = P(\bar{T}|\bar{D}) = \frac{P(\bar{T} \cap \bar{D})}{P(\bar{D})} = \frac{P(\text{-treadmill test} \cap \text{no CHD})}{P(\text{no CHD})} = \frac{d}{b+d}$$

1 - Specificity = 1 - TNR = **False Positive Rate (FPR)**

Specificity = 34/46 = 0.74

```
1 epi.tests(cmms_t1)
```

```
          Outcome +    Outcome -      Total
Test +           12           12         24
Test -            4           34         38
Total            16           46         62

Point estimates and 95 % CIs:
-------------------------------------------------------------
Apparent prevalence                    0.39 (0.27, 0.52)
True prevalence                        0.26 (0.16, 0.38)
Sensitivity                            0.75 (0.48, 0.93)
Specificity                            0.74 (0.59, 0.86)
Positive predictive value              0.50 (0.29, 0.71)
Negative predictive value              0.89 (0.75, 0.97)
Positive likelihood ratio              2.87 (1.64, 5.05)
Negative likelihood ratio              0.34 (0.14, 0.80)
-------------------------------------------------------------
```

```
1 epi.2by2(cmms_t1)
```

```
            Outcome +    Outcome -      Total        Inc risk *        Odds
Exposed +          12           12         24              50.0       1.000
Exposed -           4           34         38              10.5       0.118
Total              16           46         62              25.8       0.348

Point estimates and 95% CIs:
-------------------------------------------------------------------
Inc risk ratio                                4.75 (1.73, 13.04)
Odds ratio                                    8.50 (2.30, 31.47)
Attrib risk *                                 39.47 (17.22, 61.73)
Attrib risk in population *                   15.28 (0.66, 29.90)
Attrib fraction in exposed (%)                78.95 (42.22, 92.33)
Attrib fraction in population (%)             59.21 (11.05, 81.29)
-------------------------------------------------------------------
 Test that OR = 1: chi2(1) = 11.971 Pr>chi2 = <0.001
 Wald confidence limits
 CI: confidence interval
 * Outcomes per 100 population units
```

By seeing the result we can tell that both calculation and R package is giving same result.

1c.

Positive Predictive Value: A/(A+B) × 100 = 12/(12+12) * 100 = 50%

It is the probability that subjects with a positive test truly have the disease. That means in our case 50% people are demented. 50% patients have positive test who are correctly diagnosed

Negative Predictive Value: D/(D+C) × 100 = 34/(34+4)* 100 = 89.47%

It is the probability that subjects with a negative test truly don't have the disease. Here 89.47% people are Non- demented. In our data 89.47% patients have negative test results who are correctly diagnosed (as negative).

1d.

Both False positive and false negative can be problematic.

A **false positive** can lead to unnecessary treatment. These numbers can lead to give extra medications even if the person is not affected by any disease. This will lead to consume unnecessary tests and medicines.

A **false negative** can lead to a false diagnostic, which is very serious since a disease has been ignored and might increase in near future. For example- a person is diagnosed as not having tumour where as in real, the person is already suffering. So forget about medication, the person might die if the disease is life threatening.

1e.

TPR =1- 0.75

FPR = 1- 0.74

```
dat1 <- read.csv('D:/3rd_Semester/6611_biostatisticalmethod/hw5/d.csv')
```

```
head(dat1)
```

cmms_score	dementia
5	1
5	1
10	1
15	0
15	0
15	0

```
roc_binormal <- rocit(score = dat1$cmms_score,
                      class = dat1$dementia,
                      method = "bin")
```

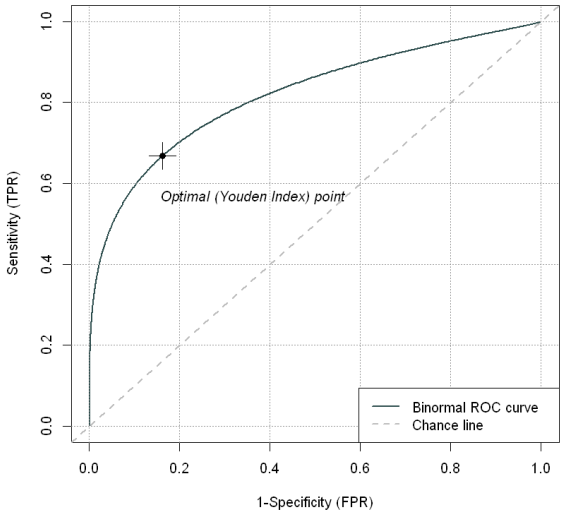
```
summary(roc_binormal)
```

```
Method used: binormal
Number of positive(s): 16
Number of negative(s): 46
Area under curve: 0.8191
```

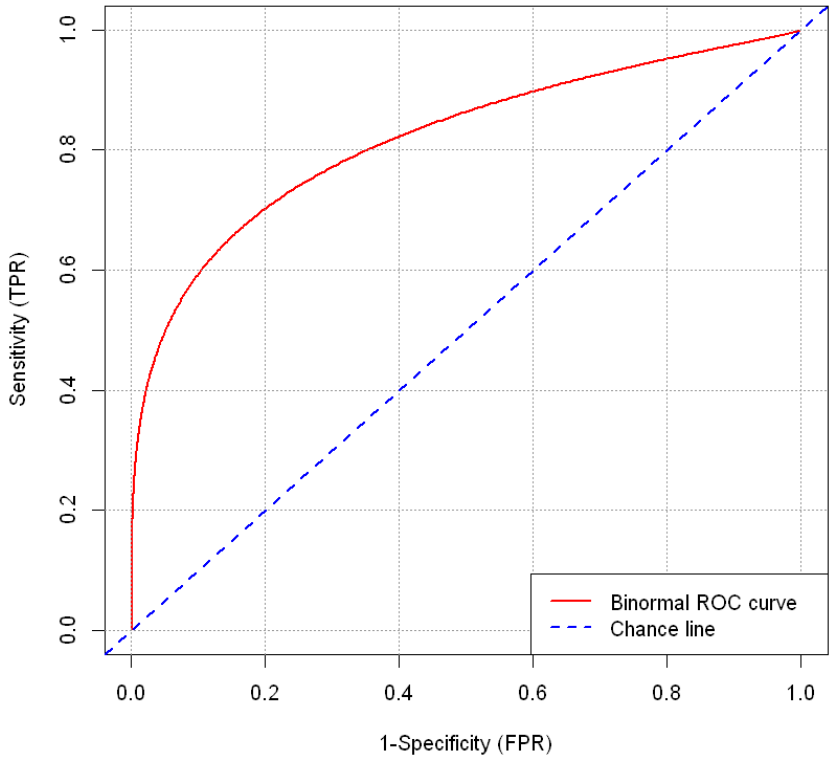
AUC is towards to 1

A test with an AUC of 1 has perfect accuracy. But in our case its 0.8191 which is nearly prefect.

plot(roc_binormal, values = T)



plot(roc_binormal, YIndex = F, values = F, col = c(2,4))



AUC is as the probability that our model ranks more positive example than a negative results.

AUC is 0.81, it means there is 81% chance that model will be able to distinguish between positive class and negative class. In our scenario the classification as well as false and true positives are also distinguished with 81% correctly.

Exercise 2: Effect Estimates and Analysis of 2x2 Tables

Test	Gold Standard/ Disease Status		Total
	Positive (D)	**Negative** ($\bar{D}$)	
Positive (T)	a (true positives)	b (false positives)	a+b
Negative ($\bar{T}$)	c (false negatives)	d (true negatives)	c+d
Total	a+c	b+d	N (a+b+c+d)

	Nausea		
Anaesthetic	Yes	No	Total
A	65	15	80
B	72	48	120
Total	137	63	200

2a

Risk difference =

P1-p2 = 65/ 80 - 72/120**= 0.812 – 0.6 = 0.212**

P = 65+48 / 200 = 0.565

SE(p1−p2)= √p(1−p)(1/n1+1/n2)

= root over all (**0.565(1 - 0.565)(1/80 + 1/120))**

= root over all (**0.565(0.435)(0.020))**

= 0.07

95% CI: $(p_1 - p_2) \pm Z_{1-\frac{\alpha}{2}} SE(p_1 - p_2)$ **=**

0.212 ±Z0.975 (0.07) = 0.212 ± 0.137 = **(1.1310 ,1.6213**)

The estimated risk difference is .7% (95% CI: 1.13% to 1.62%). Therefore the anaesthetic rate for group A is .7% lower compared to those who has received anaesthetic"B", however this is not significant since our 95% CI includes the null risk difference of 0%.

Risk ratio:

RR=p1/p2 = 0.812/ 0.6 = 1.353
The estimated risk ratio is **1.353**
As *RR* > 1 indicates a risk factor

$$SE[\log(RR)] = \sqrt{\frac{b}{an_1} + \frac{d}{cn_2}} =$$ **root(15 / 65*80 + 48/ 72*120)**
= root (18.46 + 80 = 98.46) = 9.92

95% CI:
$$\exp\{\log(RR) \pm Z_{0.975} SE[\log(RR)]\}$$
exp{log(**1.353**)±1.96×**9.92**} = exp(0.131±19.44)

Those who received anaesthetic A are 1.35 times more likely than those who received anaesthetic B to have nausea

Here the group Anaesthetic "A" has 1.35 times (CI = 1.13to 19.79) the risk of Nausea the CI contains >1, so significant result

P1 = 65/80 = 0.812
P2 = 72/120 = 0.6

OR= p1/ 1-p1)/(p2/1-p2) = (0.812/ 1- 0.812)/(0.6/1-0.6)
= (0.812/0.188)/1.5 **= 2.89**

$$SE[\log(OR)] = \sqrt{\frac{1}{a} + \frac{1}{b} + \frac{1}{c} + \frac{1}{d}}$$ = Root(1/65 + 1/15 + 1/72 +1/48)

= 0.34

95% CI:
$$\exp\{\log(OR) \pm Z_{0.975} SE[\log(OR)]\}$$
= exp{log(2.89)±1.96×0.34}

= (0.937, 5.98)

The estimated odds ratio is 2.89 (95% CI: 0. 937to 5.98).

Anaesthesia in group A is 2.89 (CI: (0.937, 5.98)times the odds in group B who has Nausea." Again, CI contains nearly 1 (marginally), so results are not significant

```
lc <-as.table(matrix(c(65,15,72,48) ,ncol=2,byrow=T))
dimnames(lc)<-list(groups=c("A","B"),
x=c("Yes","No"))
```

```
epi.2by2(lc)
```

```
             Outcome +    Outcome -      Total        Inc risk *        Odds
Exposed +           65           15         80              81.2        4.33
Exposed -           72           48        120              60.0        1.50
Total              137           63        200              68.5        2.17

Point estimates and 95% CIs:
-------------------------------------------------------------------
Inc risk ratio                                 1.35 (1.13, 1.62)
Odds ratio                                     2.89 (1.48, 5.64)
Attrib risk *                                  21.25 (9.00, 33.50)
Attrib risk in population *                    8.50 (-2.38, 19.38)
Attrib fraction in exposed (%)                 26.15 (11.58, 38.32)
Attrib fraction in population (%)              12.41 (4.35, 19.79)
-------------------------------------------------------------------
 Test that OR = 1: chi2(1) = 10.045 Pr>chi2 = 0.00
 Wald confidence limits
 CI: confidence interval
 * Outcomes per 100 population units
```

```
epi.tests(lc)
```

```
          Outcome +    Outcome -      Total
 Test +           65           15         80
 Test -           72           48        120
 Total           137           63        200

 Point estimates and 95 % CIs:
 ---------------------------------------------------------
 Apparent prevalence                   0.40 (0.33, 0.47)
 True prevalence                       0.68 (0.62, 0.75)
 Sensitivity                           0.47 (0.39, 0.56)
 Specificity                           0.76 (0.64, 0.86)
 Positive predictive value             0.81 (0.71, 0.89)
 Negative predictive value             0.40 (0.31, 0.49)
 Positive likelihood ratio             1.99 (1.24, 3.21)
 Negative likelihood ratio             0.69 (0.56, 0.85)
 ---------------------------------------------------------
```

2b. Conduct the following tests of association in R or by hand based on the 2x2 table:
1. chi-squared test without continuity correction

X^2 Test of Independence

```
chisq.test(lc, correct=F)
```

```
        Pearson's Chi-squared test

data:  lc
X-squared = 10.045, df = 1, p-value = 0.001527
```

2. chi-squared test with continuity correction

```
chisq.test(lc, correct=T)
```

```
        Pearson's Chi-squared test with Yates' continuity correction

data:  lc
X-squared = 9.0845, df = 1, p-value = 0.002578
```

3. Fisher's exact test

```
fisher.test(lc)
```

```
        Fisher's Exact Test for Count Data

data:  lc
p-value = 0.001799
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 1.420827 6.074658
sample estimates:
odds ratio
   2.87396
```

4. McNemar's test with continuity correction.

McNemar's Chi-squared test with no correction

```
lc <-as.table(matrix(c(65,15,72,48) ,ncol=2,byrow=T))
dimnames(lc)<-list(groups=c("A","B"), x=c("Yes","No"))

mcnemar.test(lc, correct=F) # no correction
```

```
        McNemar's Chi-squared test

data:  lc
McNemar's chi-squared = 37.345, df = 1, p-value = 9.898e-10
```

McNemar's Chi-squared test with w/continuity correction

```
lc <-as.table(matrix(c(65,15,72,48) ,ncol=2,byrow=T))
dimnames(lc)<-list(groups=c("A","B"), x=c("Yes","No"))

mcnemar.test(lc, correct=T) # w/continuity correction
```

```
        McNemar's Chi-squared test with continuity correction

data:  lc
McNemar's chi-squared = 36.046, df = 1, p-value = 1.927e-09
```

Chi-squared test without continuity correction	*X*2= 10.045	P = 0.0015
Chi-squared test with continuity correction	*X*2= 9.0845	P = 0.0025
Fisher's exact test	NA =	P = 0.0017
McNemar's test with continuity correction	*X*2= 36.046	P = 1.927

2c. R (or your own hand) won't necessarily stop you from conducting an inappropriate test. Given our context, are any of these tests inappropriate in 2b? Why?

Our problem statement is all about if anesthetic "A" has less risk of nausea in patients undergoing tonsillectomy compared to anesthetic "B".

In statement itself the number of observation between both the groups are less and with variation of 40.

All the above tests which includes Chi-squared(with/without continuity correction) and Fisher's exact test, these 2 tests are significant on the basis of sample analog and both majors give similar result as well.

McNemar's test with continuity correction might be not relevant. As we don't know if there exists of any concordant pairs. This test also includes chi-square test then there is no point to calculate again with McNemar's test. The P value is also high compared to other tests.

- It is a test for checking if the disagreements between two cases match
- Less Direct Comparison from Chi squared
- As we have a low sample size that's why it is not appropriately approximating the null distribution of the test statistic by a chi-squared distribution

2d. Select the most appropriate of the tests conducted. Interpret its p-value in the context of our problem for the association of nausea after procedure A or B.

From both the test **Chi-squared test without continuity correction and** Fisher's exact test

Here we got 2 similar p-value of 0.0015 and P = 0.0017 means that a sample as extreme as that observed would occur 1 time in 1000 if the null hypothesis was true.
But
X^2 of 9.0845 and a p value of .0025. so We reject the null hypothesis, type of anaesthetic and nausea are related.
Both the procedures are somehow related.
As there is a significant relationship between nausea after procedure A or B. Therefore, knowing the value of A variable helps to predict the value of the B.