ROC and MTMM

```r
# Define a function for formatting numbers
comma <- function(x, d = 2) format(x, digits = d, big.mark = ",")
```

```r
library(readxl)  # for reading excel data
library(haven)  # for reading SPSS data
library(ROCit)  # for ROC analysis
library(psych)
library(tidyverse)
library(modelsummary)  # for summarizing data
```

```
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```

Classification Accuracy

Data analyzed in this paper: https://journals.sagepub.com/doi/10.1177/07342829211067128

```r
tmp_path <- tempfile(fileext = "xlsx")  # temporary file
download.file("https://osf.io/download/tsm7x/", destfile = tmp_path)
dat1 <- readxl::read_xlsx(tmp_path, na = "NA")
dat1$asd <- recode(
    dat1$`Diagnosis(1=Non-typically developing; 2=ASD; 3=Neurotypical)`,
    `1` = "Non-TD",
    `2` = "ASD",
    `3` = "TD"
)
# Filter out Neurotypical
dat1_sub <- filter(dat1, asd != "TD")
```

First, sum the 16 items. Note that the sum is missing if any one item is missing

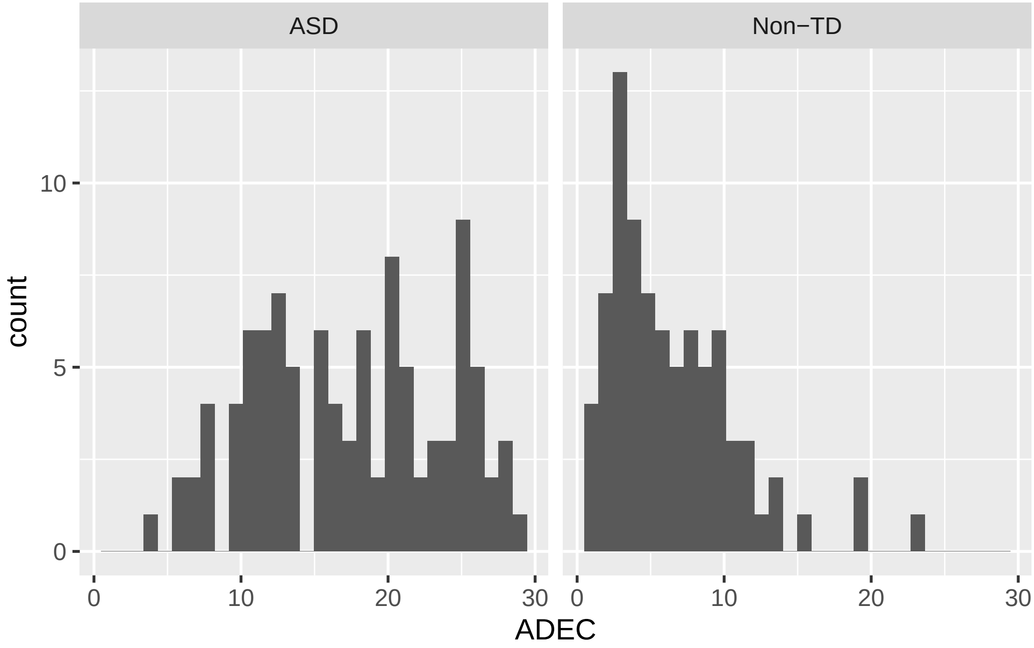
```r
dat1_sub$ADEC <- rowSums(select(dat1_sub, ADEC_I01:ADEC_I16))  # NA if any item is NA
# Or treat missing as 0
dat1_sub$ADEC_rm_na <- rowSums(select(dat1_sub, ADEC_I01:ADEC_I16), na.rm = TRUE)
```

Now, we can look at the distribution of ADEC sum score by diagnosis:

```r
ggplot(dat1_sub, aes(x = ADEC)) +
    geom_histogram() +
    facet_wrap(~ asd)
```

```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

```
Warning: Removed 12 rows containing non-finite values (`stat_bin()`).
```



Classification Table

Let's first use ADEC = 11 as cutoff. We then get the following contingency table

```
with(dat1_sub,
    table(ADEC >= 11, asd))
```

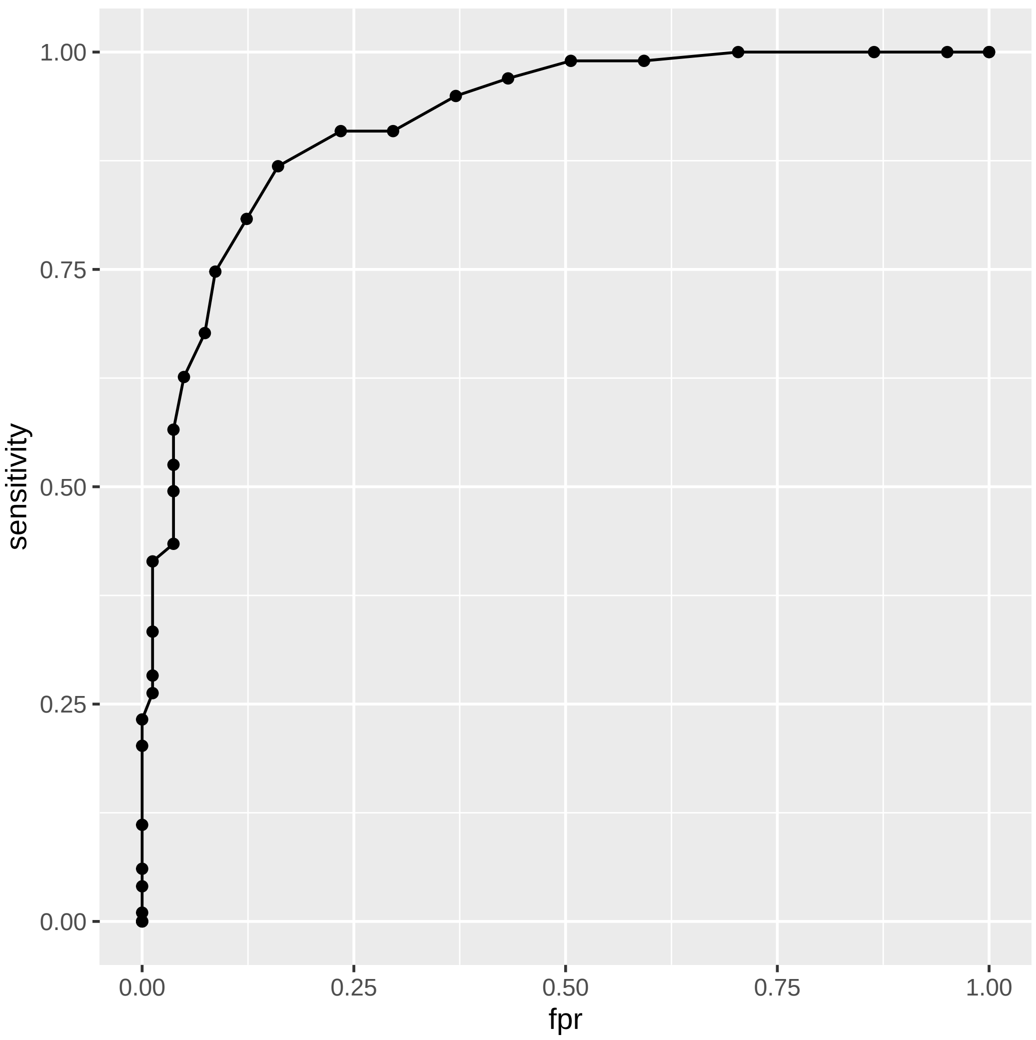
```
       asd
        ASD Non-TD
  FALSE  13     68
  TRUE   86     13
```

So the accuracy with this cutoff is (86 + 68) / 180 = 0.86. The sensitivity is 86 / (86 + 13) = 0.87, and the specificity is 68 / (68 + 13) = 0.84.

ROC

We can plot an ROC curve

```
compute_sens <- function(
    cut, x = dat1_sub$ADEC,
    crit = dat1_sub$asd == "ASD") {
    tp <- sum(x >= cut & crit, na.rm = TRUE)
    fn <- sum(x < cut & crit, na.rm = TRUE)
    tp / (tp + fn)
}
compute_spec <- function(
    cut, x = dat1_sub$ADEC,
    crit = dat1_sub$asd == "ASD") {
    tn <- sum(x < cut & !crit, na.rm = TRUE)
    fp <- sum(x >= cut & !crit, na.rm = TRUE)
    tn / (tn + fp)
}
sensitivity <- lapply(32:0, compute_sens) |>
    unlist()
specificity <- lapply(32:0, compute_spec) |>
    unlist()
data.frame(sensitivity, fpr = 1 - specificity) |>
    ggplot(aes(x = fpr, y = sensitivity)) +
    geom_point() +
    geom_line()
```



```
# AUC
dfpr <- c(diff(1 - specificity), 0)
dsens <- c(diff(sensitivity), 0)
sum(sensitivity * dfpr) + sum(dsens * dfpr) / 2
```

```
[1] 0.920626
```

Questions

Q1

Which cutoff gives the smallest difference between sensitivity and specificity? Please show your code.

```
# Your code and answer here
```

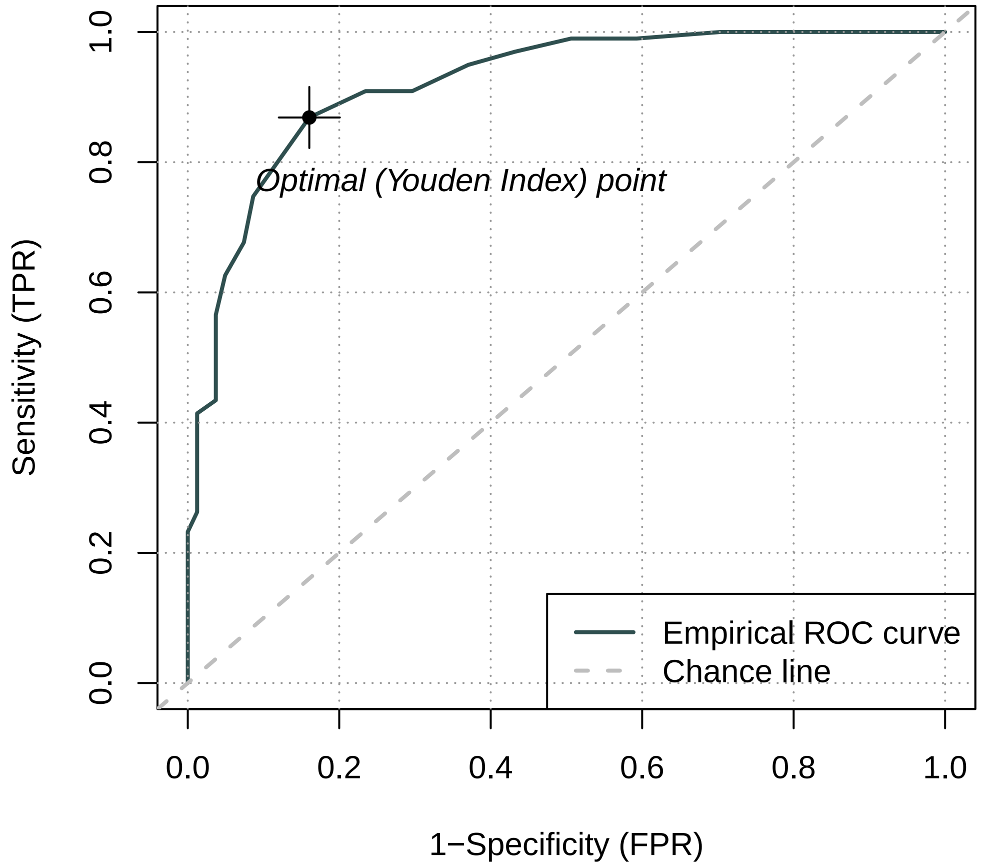
Q2
If one wants at least 90% sensitivity, what is the maximum specificity one can get?
Answer:

You can also use the ROCit package

```
roc_adec <- rocit(dat1_sub$ADEC, class = dat1_sub$asd == "ASD")
```

```
Warning in rocit(dat1_sub$ADEC, class = dat1_sub$asd == "ASD"): NA(s) in score
and/or class, removed from the data.
```

```
plot(roc_adec)
```



```
summary(roc_adec)
```

```
Method used: empirical
Number of positive(s): 99
Number of negative(s): 81
Area under curve: 0.9206
```

```
ciAUC(roc_adec)
```

```
estimated AUC : 0.920626013218606
AUC estimation method : empirical

CI of AUC
confidence level = 95%
lower = 0.880257283328194     upper = 0.960994743109017
```

Questions

The following shows the item discrimination values for the 16 items:

```r
compute_discrimination <- function(i, data = dat1_sub[, 4:19]) {
    # Exclude Item i
    person_mean_noi <- rowMeans(data[, -i], na.rm = TRUE)
    # Correlation
    cor(data[[i]], person_mean_noi, use = "complete")
}
# Apply to all items
sapply(1:16, FUN = compute_discrimination) |> round(2)
```

```
 [1] 0.70 0.50 0.20 0.67 0.55 0.64 0.54 0.57 0.36 0.71 0.65 0.51 0.30 0.28 0.62
[16] 0.53
```

Q3
Repeat the ROC and AUC analysis, but using only the five items with the highest discrimination values.

```r
# Your code and answer here
```

MTMM

Data from this paper: https://drive.google.com/file/d/1O4_MVWchC5kyCaf5p7GH4AjRIrY8zHJ8/

```r
dat <- haven::read_sav("https://osf.io/download/5ayjb/")
dat_red <- haven::read_sav("https://osf.io/download/3uecq/")
```

The data set contains scale scores for Neuroticism (N), Extraversion (E), Openness (O), Agreeableness (A), and Conscientiousness (C) with four methods of assessment: Self-reports (SR), from a close-other who is a female (RF), from a close-other who is a male (RM), implicit association tests (IAT), and behavioral assessment (BIH). You can see the labels in the SPSS data set using

```r
# Loop over each column, and call `attr(which = "label")` for each column
# to obtain the label stored as an attribute
dat_labels <- lapply(dat_red, FUN = attr, which = "label")
# Put things into a table (tibble format)
tibble(variable = names(dat_red), label = unlist(dat_labels))
```

```
# A tibble: 43 x 2
   variable label
   <chr>    <chr>
 1 age      age of respondent
 2 sex      sex
 3 NSR      Neoroticism-self report total
 4 ESR      Extraversion-self report total
 5 OSR      Openness-self report total
 6 ASR      Agreeableness-self report total
 7 CSR      Conscientiousness-self report total
 8 NRF      Neoroticism total-female rating
 9 ERF      Extraversion total-female rating
10 ORF      Openness total-female rating
# i 33 more rows
```

To make the size of the matrix a bit more manageable, we will select only E, A, and C for illustration, and with the SR, RF, and IAT methods.

Descriptive Statistics

Here are the descriptives:

```r
var_names <- c("ESR", "ASR", "CSR", "ERF", "ARF", "CRF", "EIAT", "AIAT", "CIAT")
datasummary_skim(dat_red[var_names])
```

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```

	Unique (#)	Missing (%)	Mean	SD	Min	Median	Max	
ESR	73	0	111.5	23.1	41.0	112.0	163.0	
ASR	79	0	114.9	24.3	35.0	116.5	163.0	
CSR	73	0	126.7	24.2	60.0	131.5	175.0	
ERF	63	0	111.7	21.0	47.0	112.0	159.0	
ARF	69	0	122.1	20.6	57.0	124.0	162.0	
CRF	67	0	140.7	22.5	75.0	141.0	182.0	
EIAT	146	0	0.2	0.4	−1.1	0.2	1.1	
AIAT	146	0	0.5	0.4	−0.5	0.5	1.3	
CIAT	146	0	0.5	0.4	−1.0	0.5	1.6	

```
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```

MTMM Matrix

```r
datasummary_correlation(dat_red[var_names])
```

```
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	ESR	ASR	CSR	ERF	ARF	CRF	EIAT	AIAT	CIAT
ESR	1	.	.	.	.	.	.	.	.
ASR	0.19	1	.	.	.	.	.	.	.
CSR	0.20	0.31	1	.	.	.	.	.	.
ERF	0.60	0.26	0.08	1	.	.	.	.	.
ARF	0.08	0.57	0.09	0.24	1	.	.	.	.
CRF	0.06	0.17	0.46	0.28	0.30	1	.	.	.
EIAT	0.07	−0.06	0.10	0.01	−0.03	−0.01	1	.	.
AIAT	−0.03	−0.12	−0.05	−0.19	−0.03	0.02	0.11	1	.
CIAT	0.01	0.03	0.08	−0.12	0.01	0.06	0.05	0.28	1

```
See help("Deprecated")
```

Questions

Q4
Do the IAT measures show convergent validity with other measures? Report the relevant coefficients.
Answer: