Swab

Abdelaziz A. Awad

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```r
library(readxl)
library(mada)
```

```
## Loading required package: mvtnorm

## Loading required package: ellipse

##
## Attaching package: 'ellipse'

## The following object is masked from 'package:graphics':
##
##     pairs

## Loading required package: mvmeta

## This is mvmeta 1.0.3. For an overview type: help('mvmeta-package').

## Loading required package: metafor

## Loading required package: Matrix

## Loading required package: metadat

## Loading required package: numDeriv

##
## Loading the 'metafor' package (version 4.8-0). For an
## introduction to the package please type: help(metafor)

##
## Attaching package: 'metafor'

## The following object is masked from 'package:mvmeta':
##
##     blup
```

```
##
## Attaching package: 'mada'

## The following object is masked from 'package:metafor':
##
##     forest
```
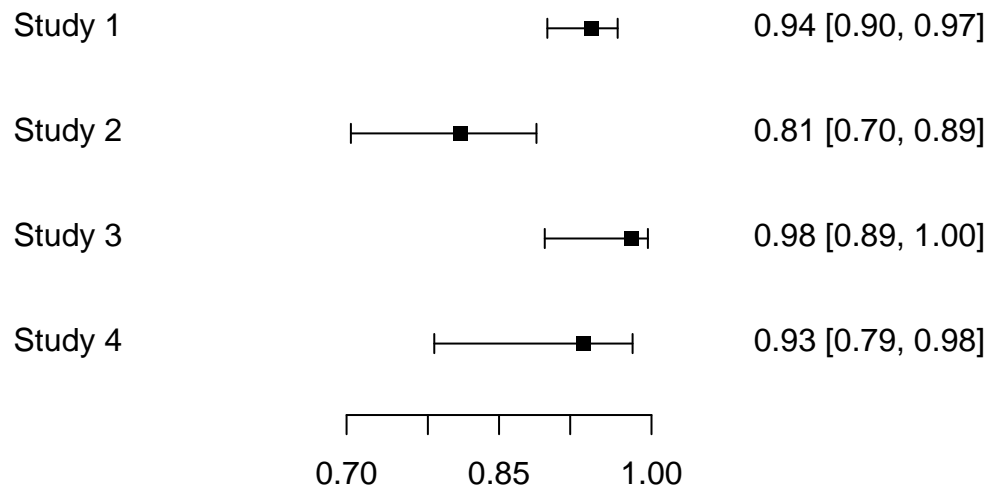
```r
### load your data and create the madad object with 95% CI
setwd("~/Desktop/swab")
df <- read_excel("Outcome.xlsx")
meta <- madad(df, level = 0.95)
```

```
## Warning in checkdata(origdata): Some of the values of TP,FN,FP or TN do have
## non zero decimal places. Did you forget to round?

## Warning in checkdata(origdata): There are very few primary studies!
```
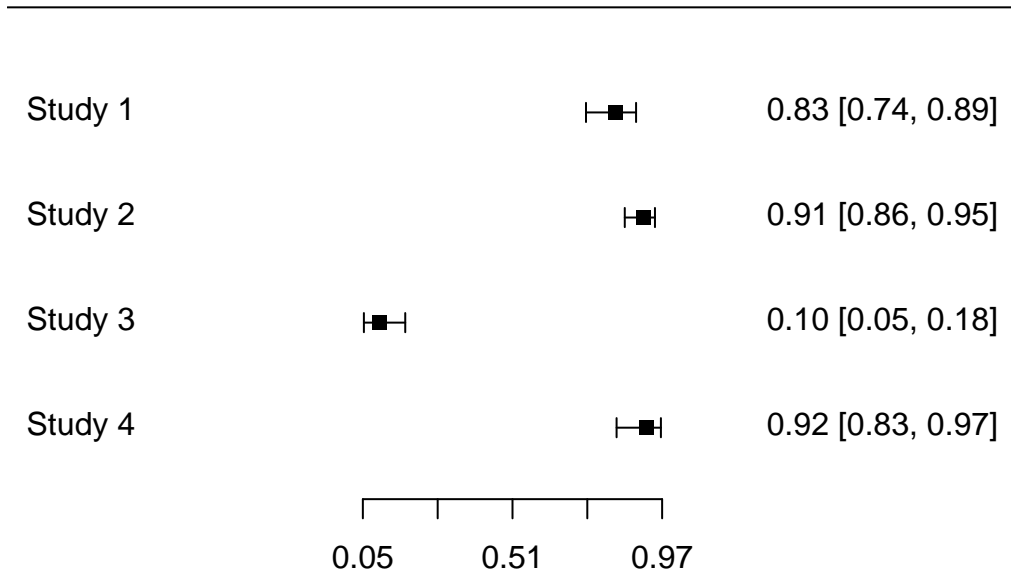
```r
mada:::forest.madad(meta, type = "sens")
```
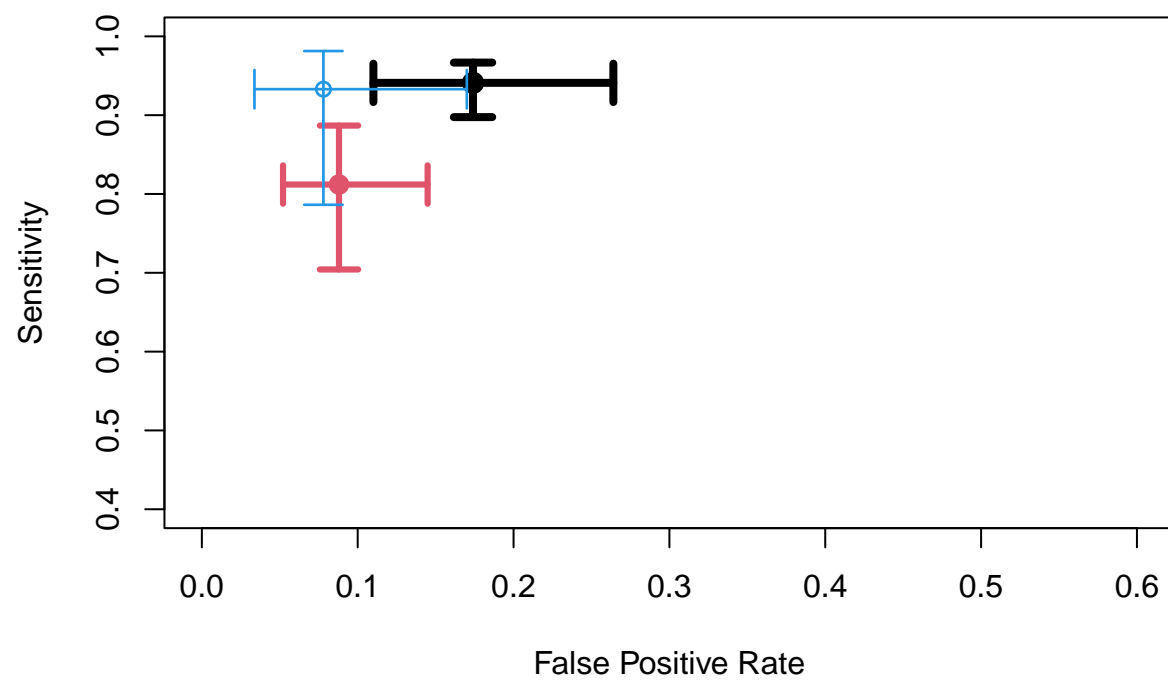
Forest plot


```r
mada:::forest.madad(meta, type = "spec")
```

Forest plot

Study 1		0.83 [0.74, 0.89]
Study 2		0.91 [0.86, 0.95]
Study 3		0.10 [0.05, 0.18]
Study 4		0.92 [0.83, 0.97]

```
      0.05        0.51       0.97
```
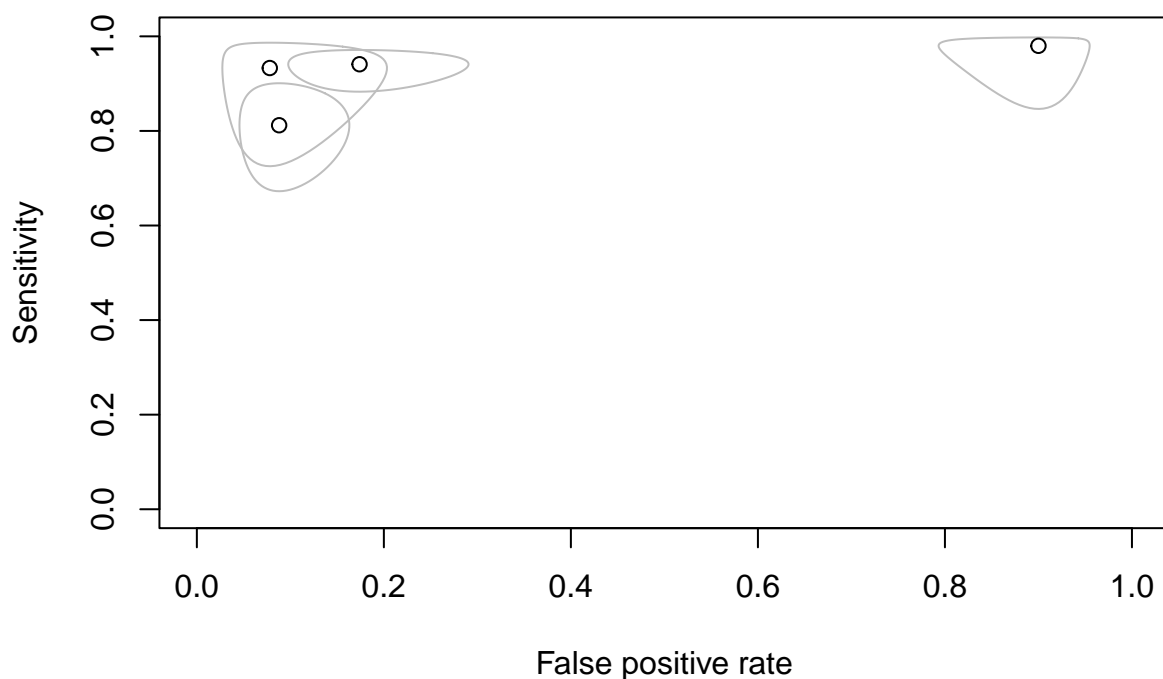
```
rs <- rowSums(df[,c(2,3,4,5)])
weights <- 4 * rs / max(rs)
crosshair(df, xlim = c(0,0.6), ylim = c(0.4,1),
          col = 1:14, lwd = weights)
```

```
ROCellipse(df, pch = "")
points(fpr(df), sens(df))
```

```
### Diagnostic odds ratio approach with DerSimonian and Laird (random effects)
(fit.DOR.DSL <- madauni(df, method = "DSL"))
```

```
## Call:
## madauni(x = df, method = "DSL")
##
##     DOR   tau^2
## 50.877  0.474
```

```
summary(fit.DOR.DSL)
```

```
## Call:
## madauni(x = df, method = "DSL")
##
## Estimates:
##        DSL estimate   2.5 %   97.5 %
## DOR         50.877  20.217  128.033
## lnDOR        3.929   3.007    4.852
## tau^2        0.474   0.000   28.830
## tau          0.689   0.000    5.369
##
## Cochran's Q: 4.475 (3 df, p = 0.215)
## Higgins' I^2: 32.963%
```

```
# For DSL method
mada:::forest.madauni(fit.DOR.DSL)
```

Forest plot

Noh 2020	⊢■⊣	4.33 [3.51, 5.14]
Noh 2024	⊢■⊣	3.80 [2.97, 4.63]
Soh 2023	⊢■⊣	1.69 [−0.40, 3.79]
Yoshikawa 2024	⊢■⊣	5.10 [3.41, 6.80]
Summary (DSL)	◇	3.93 [3.01, 4.85]

−0.4   3.2 5.0 6.8

log diagnostic odds ratio

```
### Diagnostic odds ratio approach with Mantel-Haenszel (fixed effects)
(fit.DOR.MH <- madauni(df, method = "MH"))
```
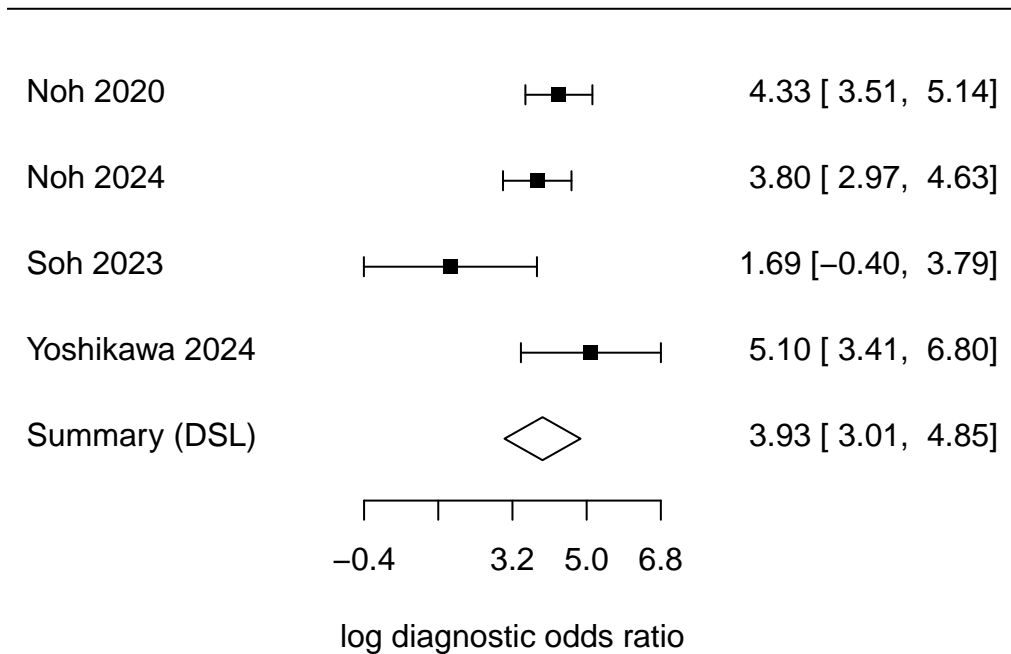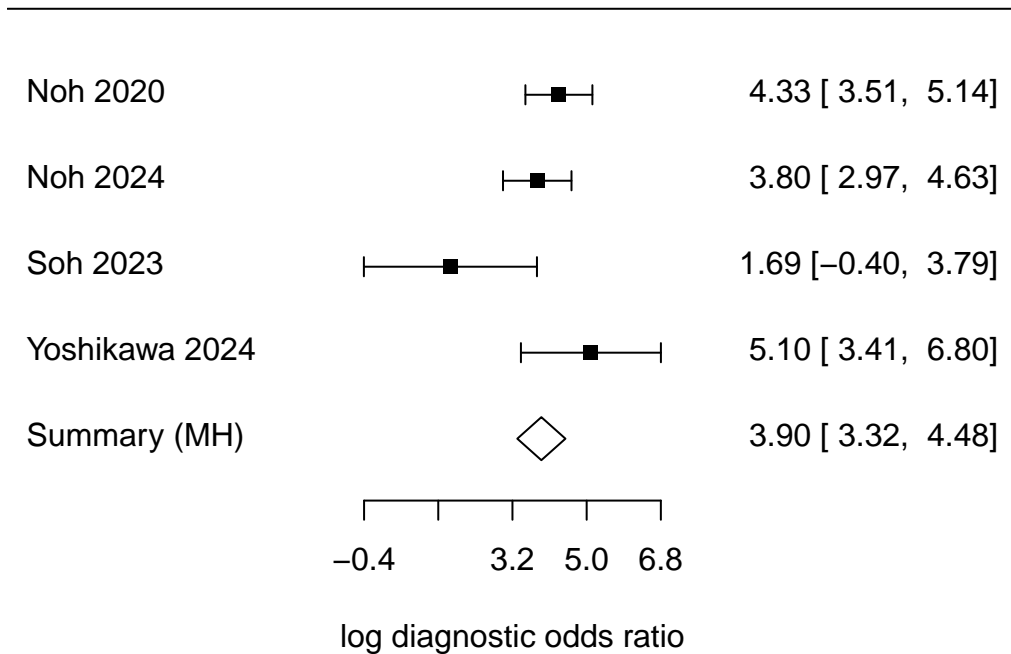
```
## Call:
## madauni(x = df, method = "MH")
##
##       DOR
## 49.46703
```

```
summary(fit.DOR.MH)
```

```
## Call:
## madauni(x = df, method = "MH")
##
## Estimates:
##        MH estimate  2.5 % 97.5 %
## DOR        49.467 27.595 88.674
## lnDOR       3.901  3.318  4.485
##
## Cochran's Q: 2979.947 (3 df, p = 0)
```

```
# For MH method
mada:::forest.madauni(fit.DOR.MH)
```

Forest plot

Noh 2020	⊢■⊣	4.33 [3.51, 5.14]
Noh 2024	⊢■⊣	3.80 [2.97, 4.63]
Soh 2023	⊢■⊣	1.69 [−0.40, 3.79]
Yoshikawa 2024	⊢■⊣	5.10 [3.41, 6.80]
Summary (MH)	◇	3.90 [3.32, 4.48]

−0.4　　3.2　5.0　6.8

log diagnostic odds ratio

```
### Proportional hazards model approach
(fit.phm.homo <- phm(df, hetero = FALSE))
```

```
## Warning in checkdata(freqdata): Some of the values of TP,FN,FP or TN do have
## non zero decimal places. Did you forget to round?

## Warning in checkdata(freqdata): There are very few primary studies!

## Call:
## phm.default(data = df, hetero = FALSE)
##
## Coefficients:
##      theta
## 0.04085144
```

```
(fit.phm.het <- phm(df))
```

```
## Warning in checkdata(freqdata): Some of the values of TP,FN,FP or TN do have
## non zero decimal places. Did you forget to round?
## Warning in checkdata(freqdata): There are very few primary studies!
```

```
## Warning in phm.default(df): Reached maximum number of iterations!
```

```
## Call:
## phm.default(data = df)
##
## Coefficients:
##      theta    taus_sq
## 0.03401997 0.00000000
```

summary(fit.phm.homo)

```
## Call:
## phm.default(data = df, hetero = FALSE)
##
##         Estimate     2.5 %     97.5 %
## theta 0.04085144 0.02083656 0.06086632
##
## Log-likelihood: 11.198 on 1 degrees of freedom
## AIC:  -20.4
## BIC:  -21
##
##  Chi-square goodness of fit test (Adjusted Profile Maximum Likelihood
##  under homogeneity)
##
## data:  x
## Chi-square = 4.7474, df = 1, p-value = 0.1913
##
##
##    AUC  2.5 % 97.5 %   pAUC  2.5 % 97.5 %
##  0.961  0.980  0.943  0.965  0.982  0.949
```

summary(fit.phm.het)

```
## Call:
## phm.default(data = df)
##
##           Estimate          2.5 %        97.5 %
## theta    0.03401997   0.0070177764 0.0610221695
## taus_sq 0.00000000 -0.0004986968 0.0004986968
##
## Log-likelihood: 11.073 on 2 degrees of freedom
## AIC:  -18.1
## BIC:  -19.4
##
##  Chi-square goodness of fit test (Adjusted Profile Maximum Likelihood
##  under heterogeneity)
##
## data:  x
## Chi-square = 5.3762, df = 2, p-value = 0.06801
##
##
##    AUC  2.5 % 97.5 %   pAUC  2.5 % 97.5 %
##  0.967  0.993  0.942  0.971  0.994  0.949
```

```r
plot(fit.phm.het, xlim = c(0,0.6), ylim = c(0.4,1))
ROCellipse(df, add = TRUE)
```