

# Hands-on training session 6

Meta-analyses with imperfect reference test

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# Introduction

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Date/time:

- 20th February 2020
- 14.00 - 15.30

Teachers:

- Paolo Eusebi (presenter)
- Giles Innocent

# Recap

- Important points from previous sessions

# **Session 6a: Meta-Analysis of Diagnostic Test Accuracy Studies**

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## DTA-MA: perfect reference test

- There is an increasing interest in meta-analyzing data from diagnostic accuracy studies
- The data from the primary studies are summarized in a 2-by-2 cross-tabulation of the dichotomized test result against the true disease status

	D+	D-
T+	TP	FP
T-	FN	TN

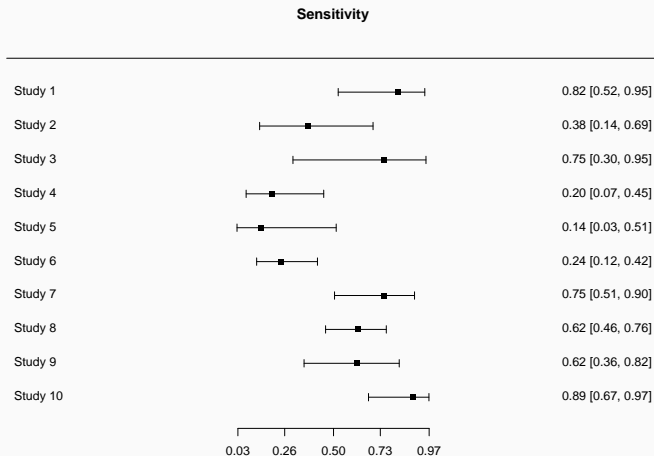
## DTA-MA: perfect reference test

- Data on magnetic resonance (MR) imaging from 10 studies on evaluation of lymph node metastases in patients with cervical cancer (Scheidler et al 1997).

StudyID	TP	FP	FN	TN
Study 1	9	2	2	44
Study 2	3	6	5	32
Study 3	3	2	1	16
Study 4	3	1	12	44
Study 5	1	1	6	16
Study 6	7	2	22	167
Study 7	12	4	4	29
Study 8	23	5	14	230
Study 9	8	5	5	53
Study 10	16	2	2	22

# DTA-MA: perfect reference test

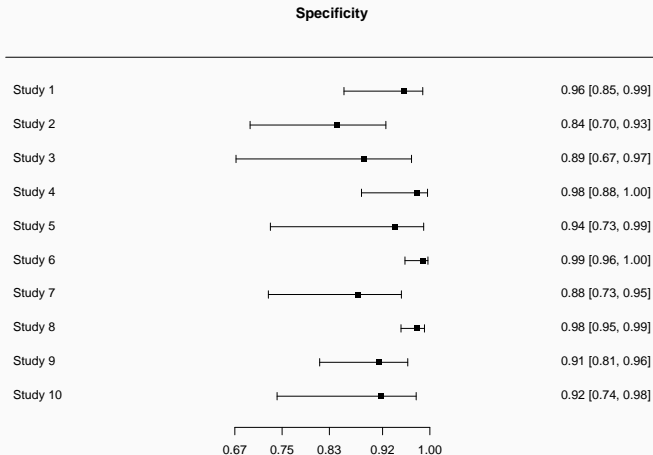
- Forest plot of sensitivity





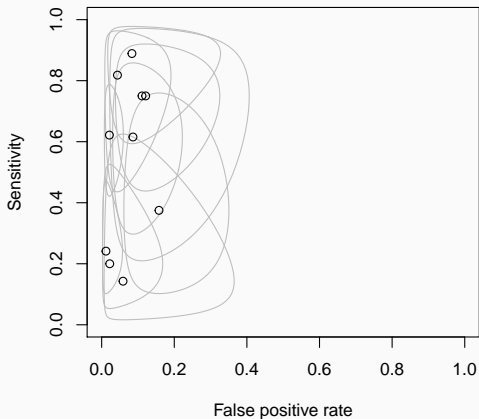
# DTA-MA: perfect reference test

- Forest plot of specificity



## DTA-MA: perfect reference test

- Data points with confidence ellipses on a ROC space



Two main framework:

- Hierarchical Summary ROC (Rutter and Gatsonis 2001)
- Bivariate analysis of sensitivity and specificity (Reitsma et al. 2005)

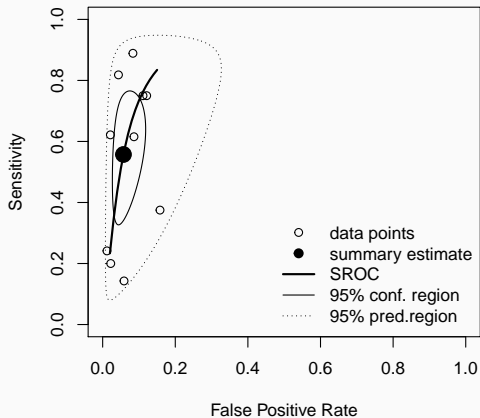
## DTA-MA: bivariate analysis of sensitivity and specificity

```
1  fit.reitsma <- reitsma(MRI2)
2  print(summary(fit.reitsma)[1], digits = 2)
```

```
1  ## $coefficients
2  ##               Estimate Std. Error      z Pr(>|z|)
3  ## tsens.(Intercept)   0.230      0.39  0.59    0.55
4  ## tfpr.(Intercept)  -2.801      0.32 -8.64    0.00
5  ## sensitivity         0.557        NA    NA     NA
6  ## false pos. rate    0.057        NA    NA     NA
7  ##               95%ci.lb 95%ci.ub
8  ## tsens.(Intercept)  -0.534      0.99
9  ## tfpr.(Intercept)  -3.437     -2.17
10 ## sensitivity        0.370      0.73
11 ## false pos. rate    0.031      0.10
```

# DTA-MA: bivariate analysis of sensitivity and specificity



## DTA-MA: bivariate analysis of sensitivity and specificity

The function returns also HSROC parameters

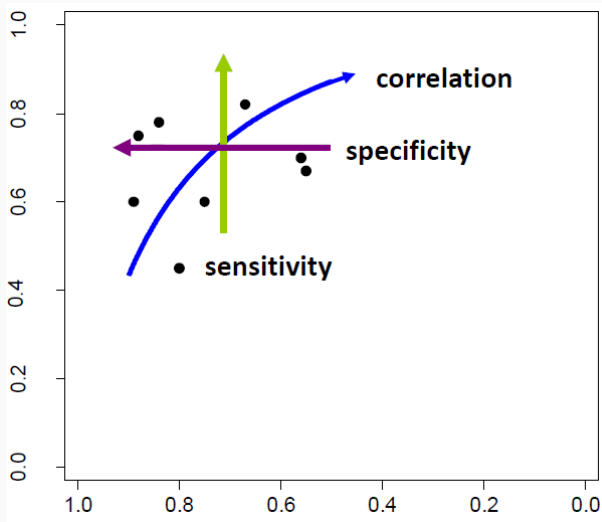
```
1  print(summary(fit.reitsma)[20], digits = 2)

1  ## $coef_hsroc
2  ## $coef_hsroc$Theta
3  ## [1] -1.5
4  ##
5  ## $coef_hsroc$Lambda
6  ## [1] 3.4
7  ##
8  ## $coef_hsroc$beta
9  ## [1] -0.26
10 ##
11 ## $coef_hsroc$sigma2theta
12 ## [1] 0.62
13 ##
14 ## $coef_hsroc$sigma2alpha
15 ## [1] 0.72
```

This is because Bivariate and HSROC approaches are equivalent when covariates are not included (Harbord et al. 2007)

- Parameter estimates from either model can be used to produce a summary operating point, an SROC curve, confidence regions, or prediction regions.
- The choice between these parameterizations depends partly on the degrees of and reasons for between-study heterogeneity and the threshold effect.

## DTA-MA: bivariate analysis of sensitivity and specificity



**Figure 1:** Alt text



## DTA-MA: hierarchical summary ROC (HSROC)

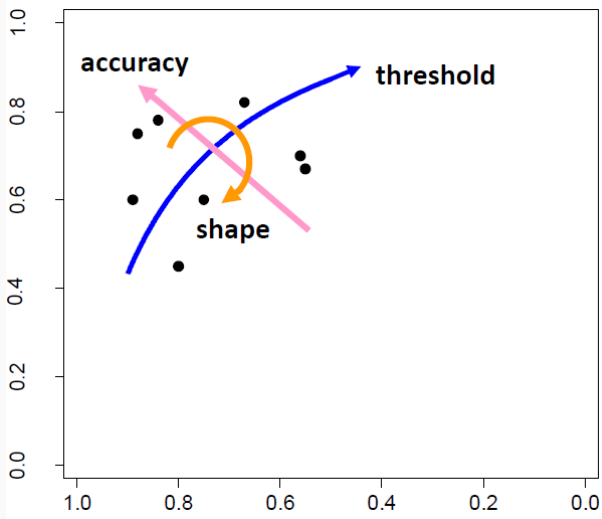


Figure 2: Alt text

# DTA-MA: hierarchical summary ROC (HSROC)

## Use of HSROC package

```
1  HSROC(data = MRI,  
2        iter.num = 5000,  
3        init = init)  
4  
5  HSROCSummary(data = MRI,  
6               burn_in = 1000,  
7               Thin = 2,  
8               print_plot = T)
```

## DTA-MA: hierarchical summary ROC (HSROC)

- The HSROC package allows to run multiple chains

```
1 HSROCSummary(data = MRI,  
2               burn_in = 1000,  
3               Thin = 2,  
4               print_plot = T,  
5               chain = list(dir.chain1, dir.chain2, dir.chain3))
```

A single call to the function HSROCSummary will summarize all chains (3 in our example).

## Exercise

Fit a HSROC model assuming imperfect reference for the data on Tibsit

Use rjags and HSROC