

Introduction to Meta-analysis of Accuracy Data

Hans Reitsma MD, PhD

Dept. of Clinical Epidemiology, Biostatistics & Bioinformatics

Academic Medical Center - Amsterdam

Continental European Support Unit - Cochrane Collaboration

Copenhagen

February, 2009

Outline

- Nature of the outcome measures
- Descriptive analysis: plots and figures
- Statistical models
- REVMAN

Diagnostic Accuracy Data

- Agreement between results of the index test and reference standard
- Many measures of agreement
- Focus on pairs of sensitivity & specificity

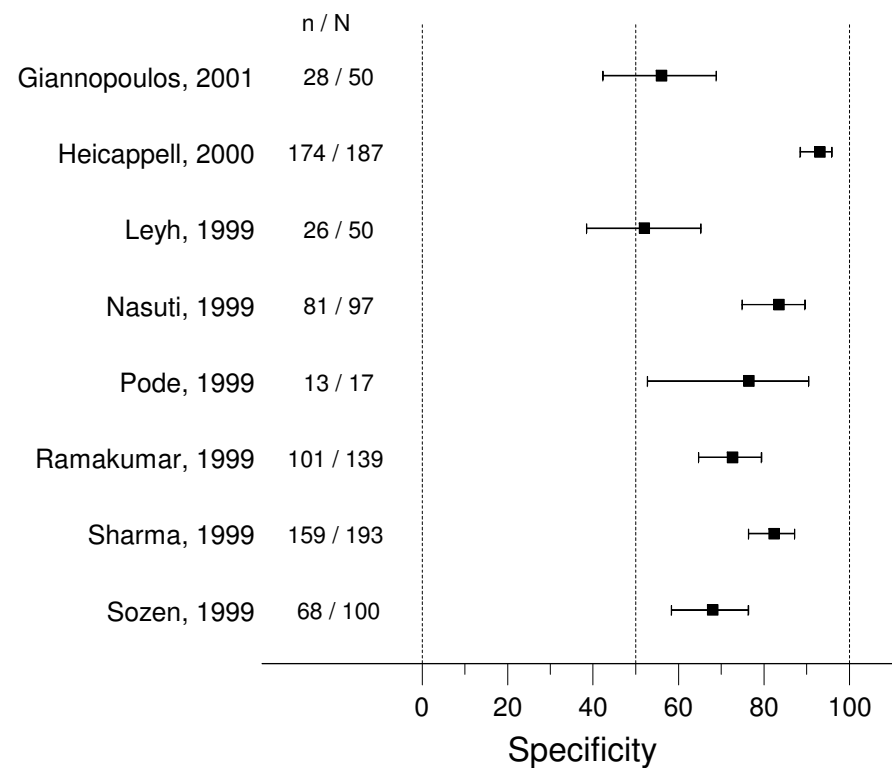
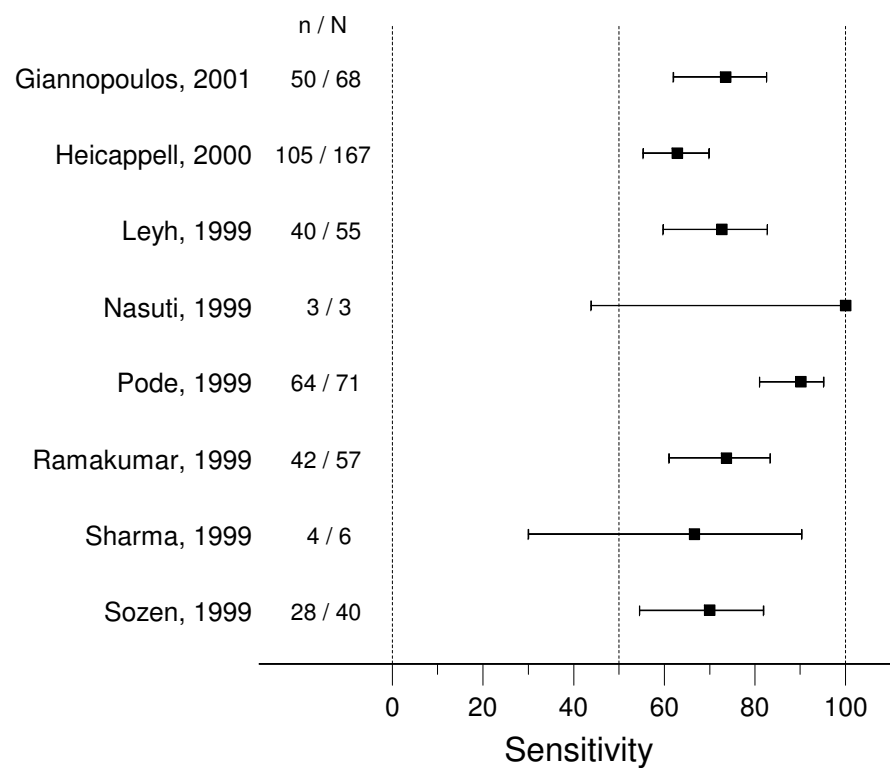
Clinical Example

- Tumor markers for the detection of bladder cancer
- Measurement in urine rather than invasive cystoscopy
- Several markers: focus on bladder tumor antigen (BTA stat)
- N=8 studies

Descriptive Analysis

- Forest plots
 - point estimate with 95% CI
 - paired: sensitivity and specificity side-by-side

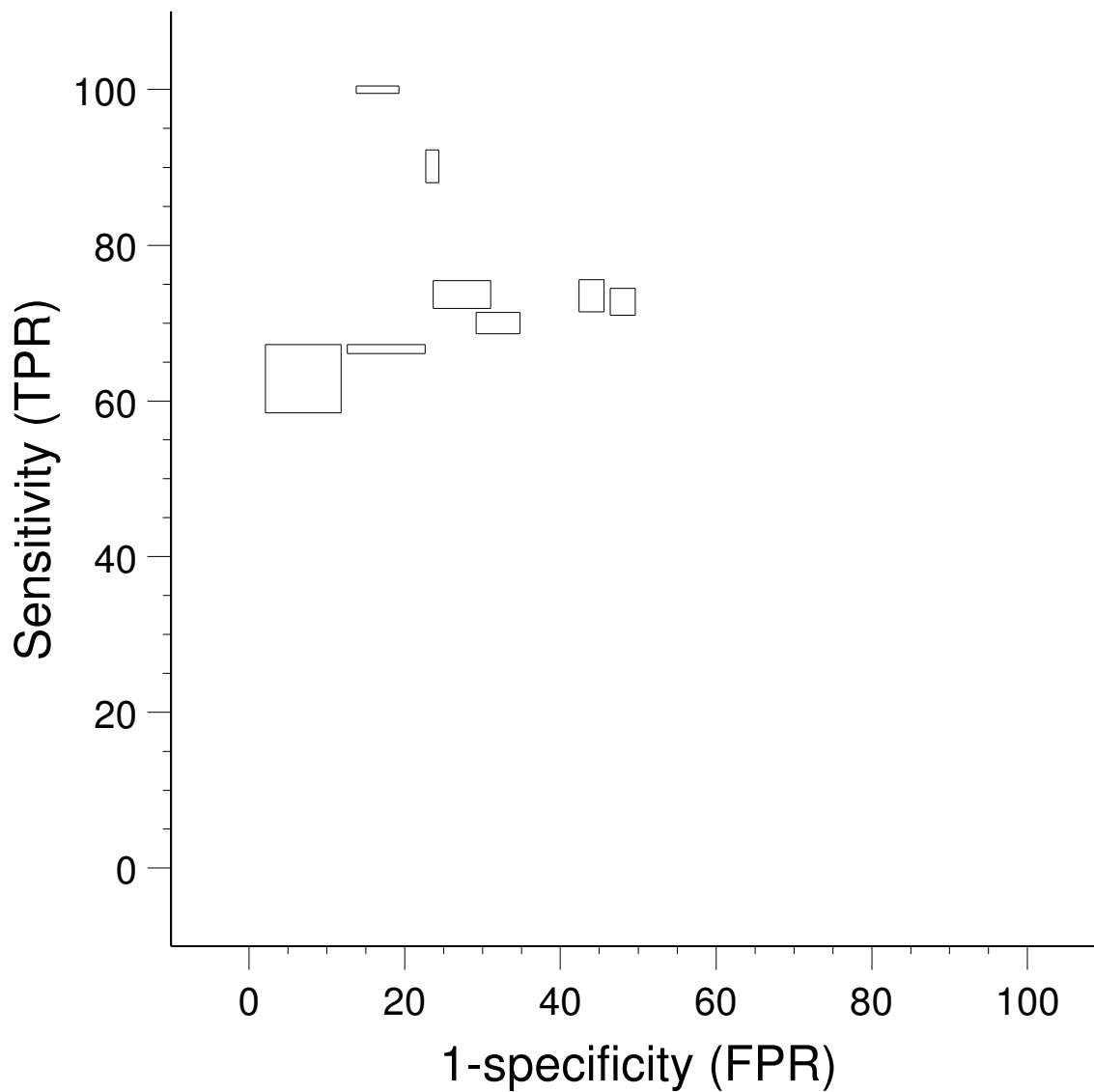
Forest Plot



Descriptive Analysis

- Forest plots
 - point estimate with 95% CI
 - paired: sensitivity and specificity side-by-side
- ROC plot
 - pairs of sensitivity & specificity in ROC space
 - bubble plot to show differences in precision

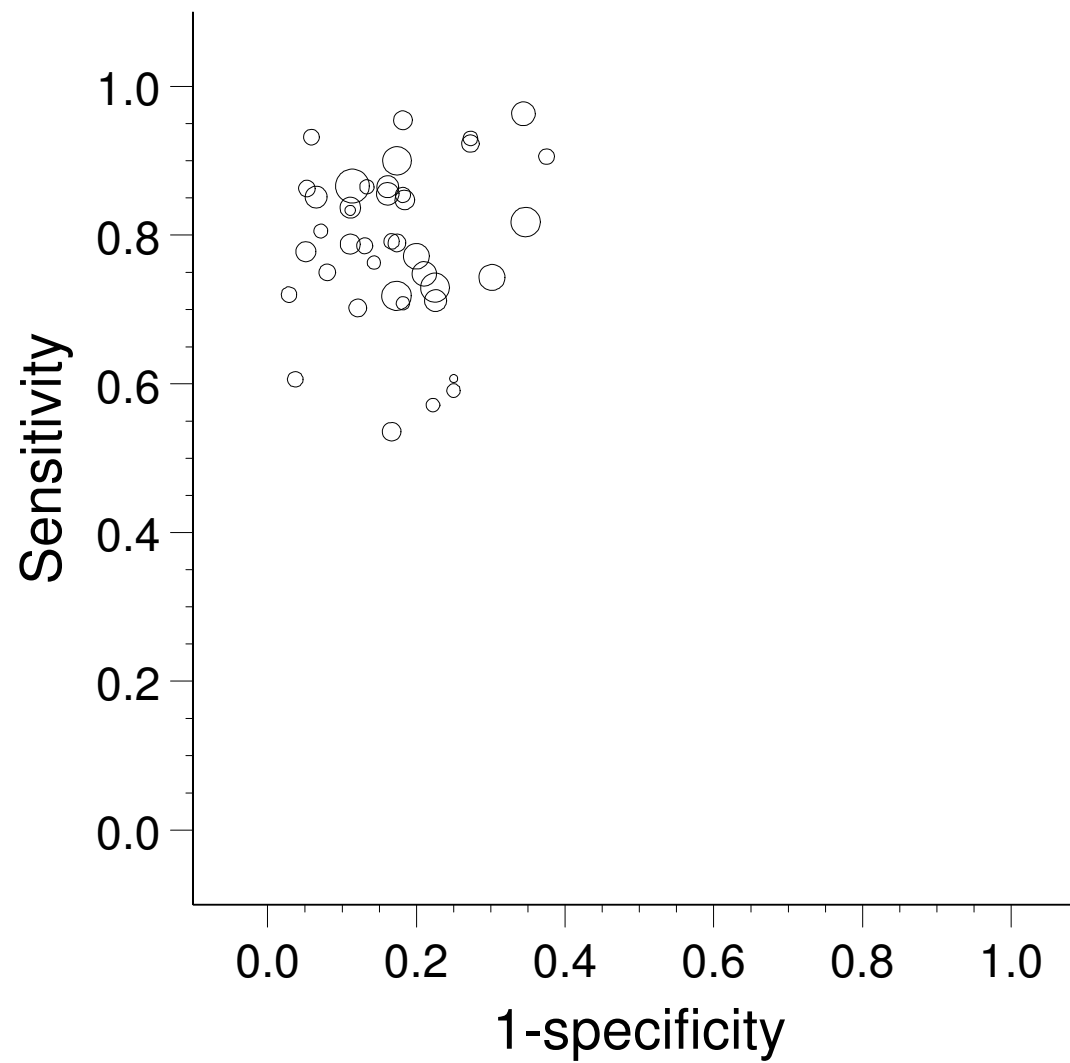
Plot in ROC Space



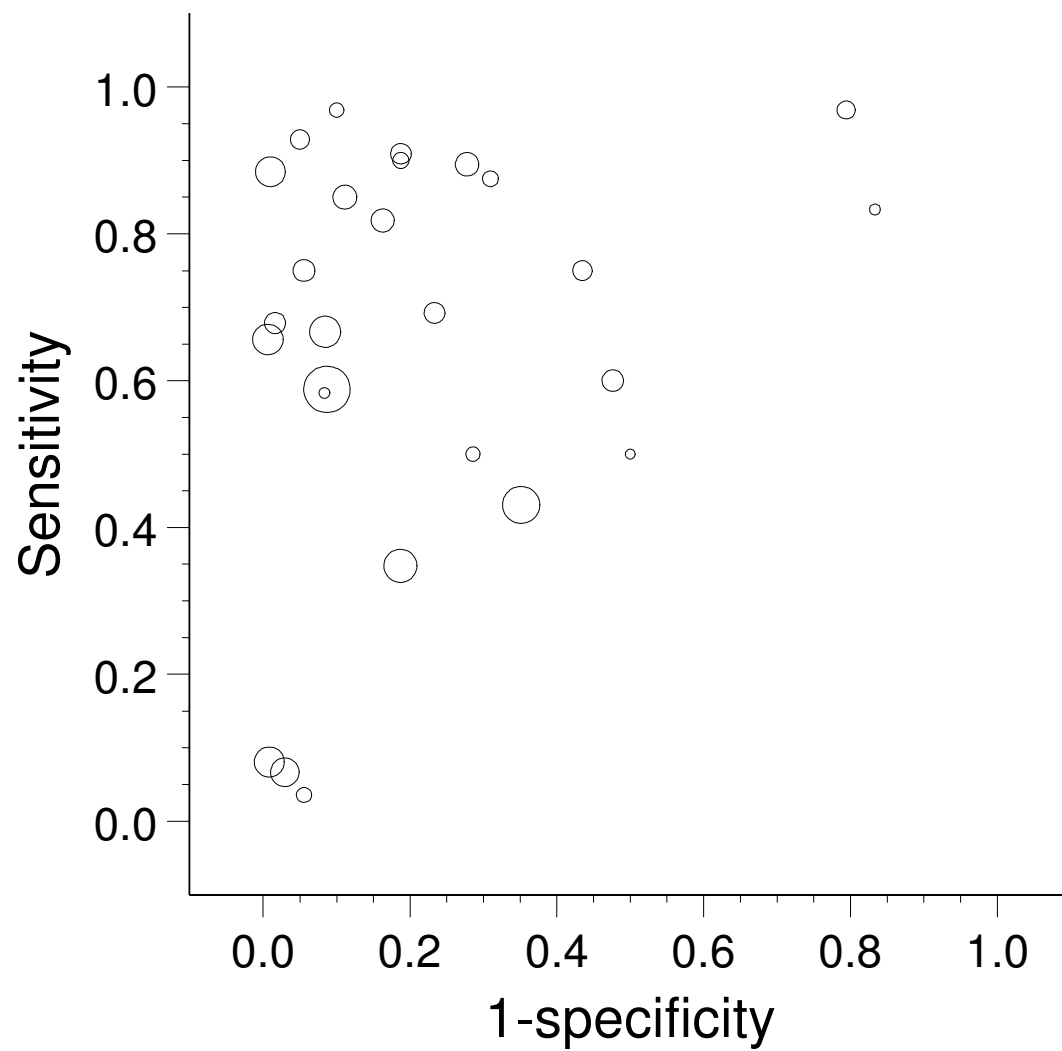
Challenge

- Understanding sources of variation, as results often vary between studies
- Providing informative summary measures of the data
- Drawing robust conclusions with respect to the research question

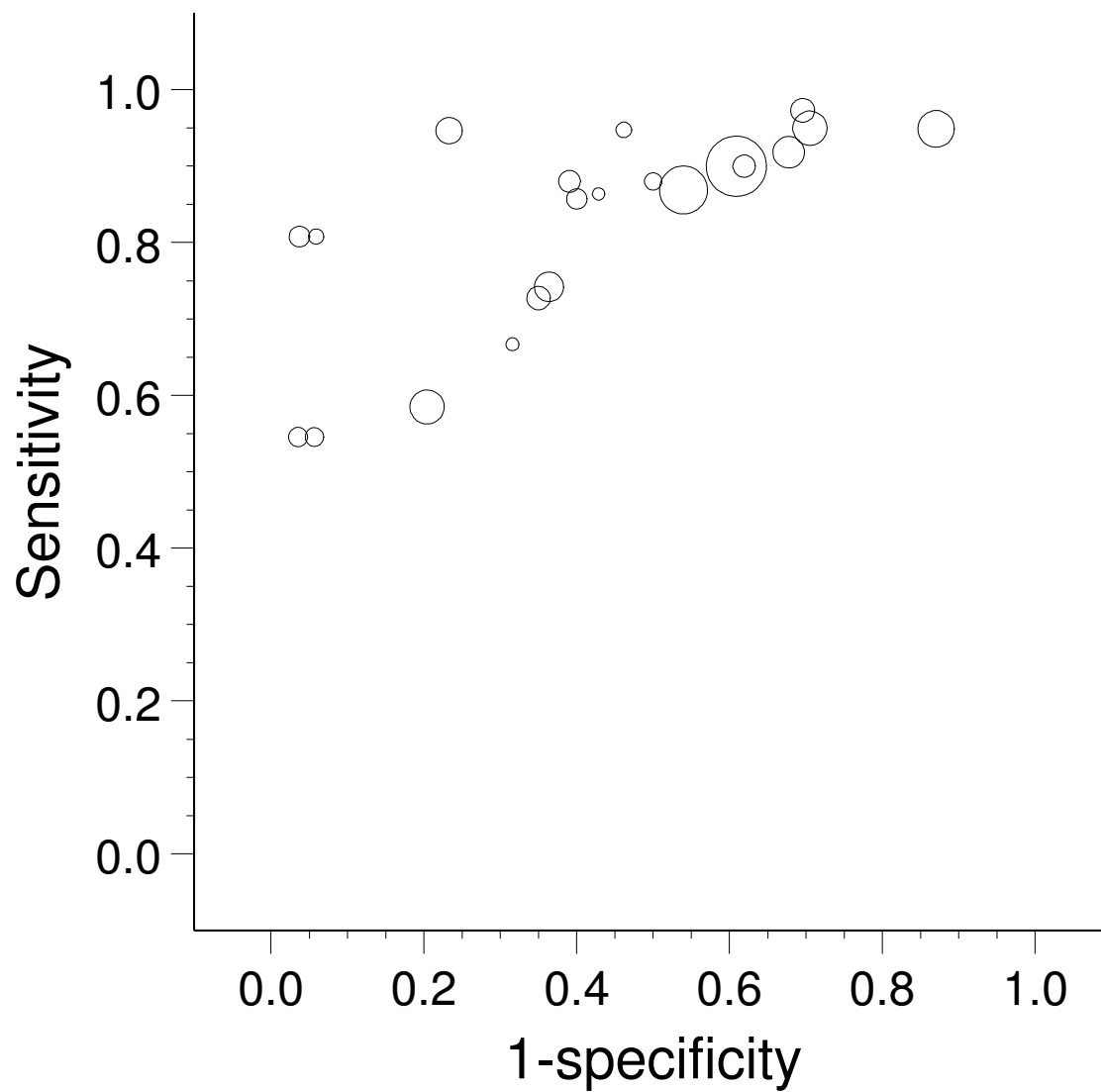
Echocardiography in Coronary Heart Disease



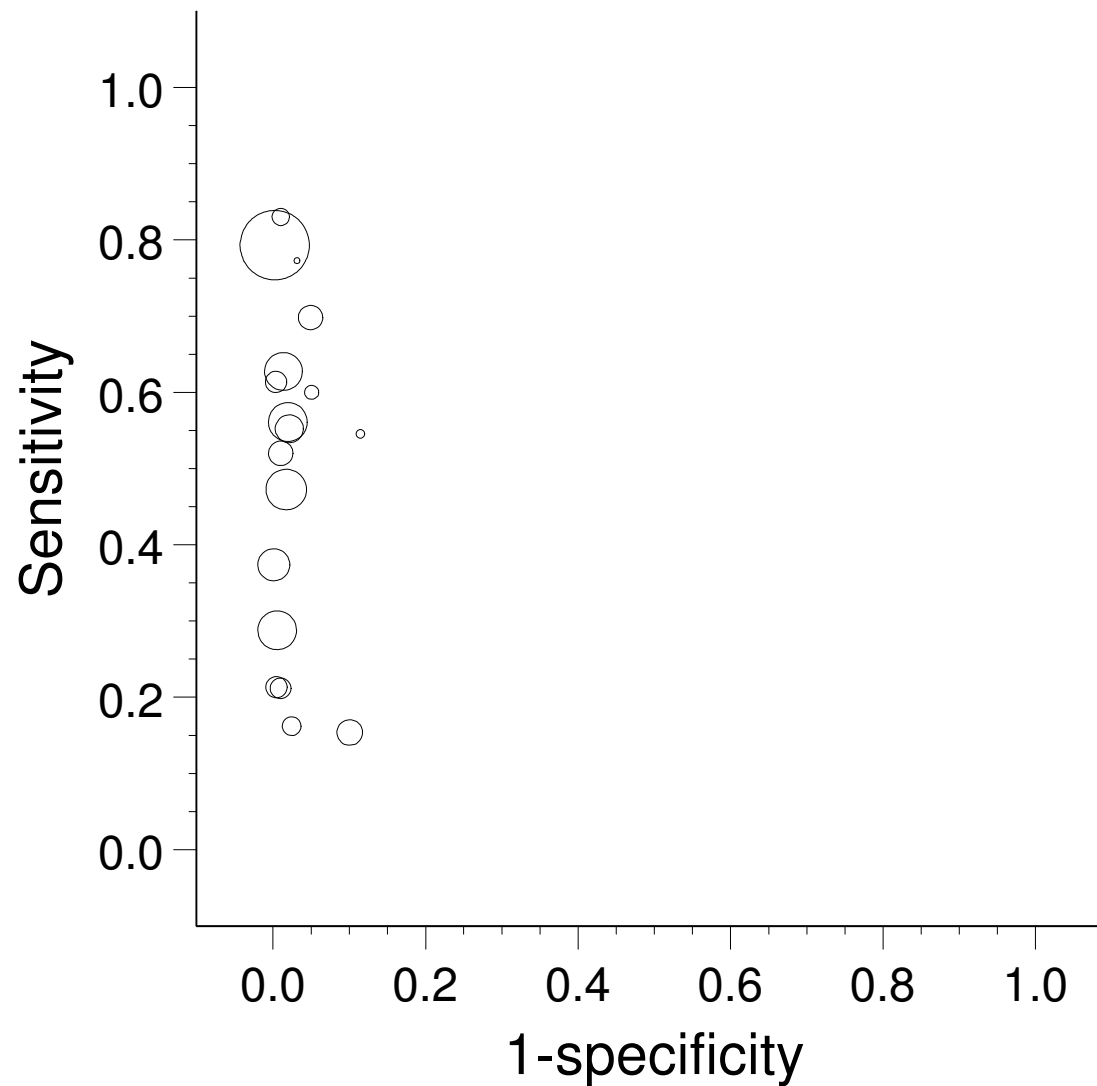
GLAL in Gram Negative Sepsis



F/T PSA in the Detection of Prostate cancer



Dip-stick Testing for Urinary Tract Infection



Sources of Variation

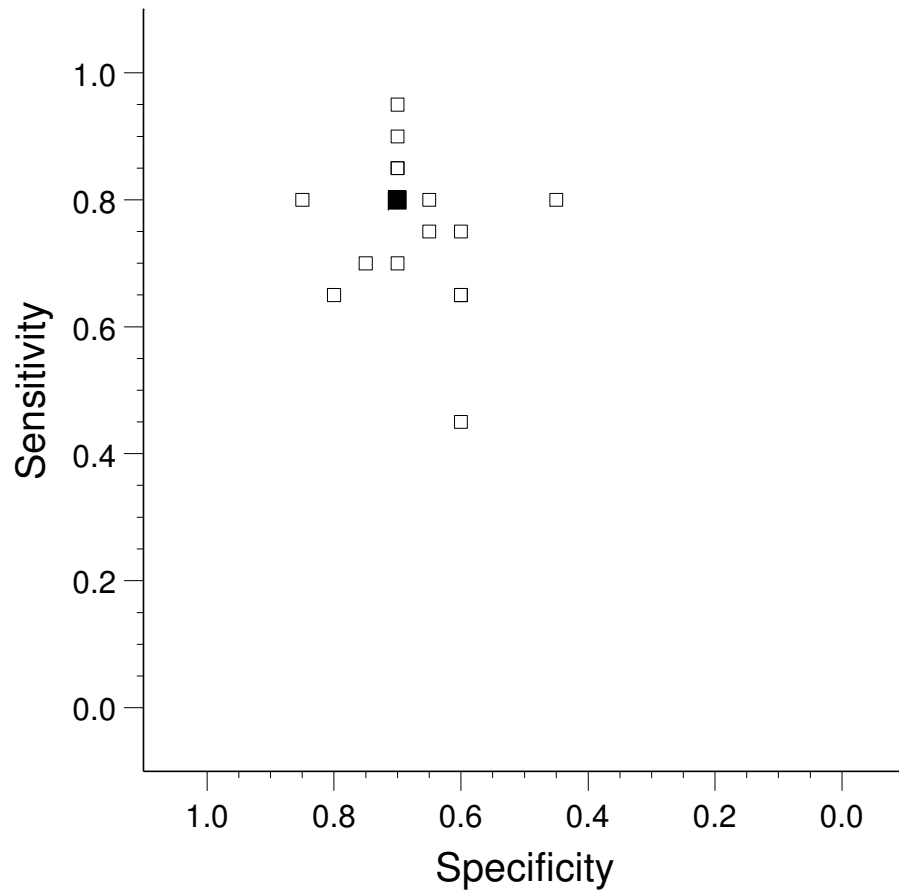
- Why do results differ between studies?

Sources of Variation

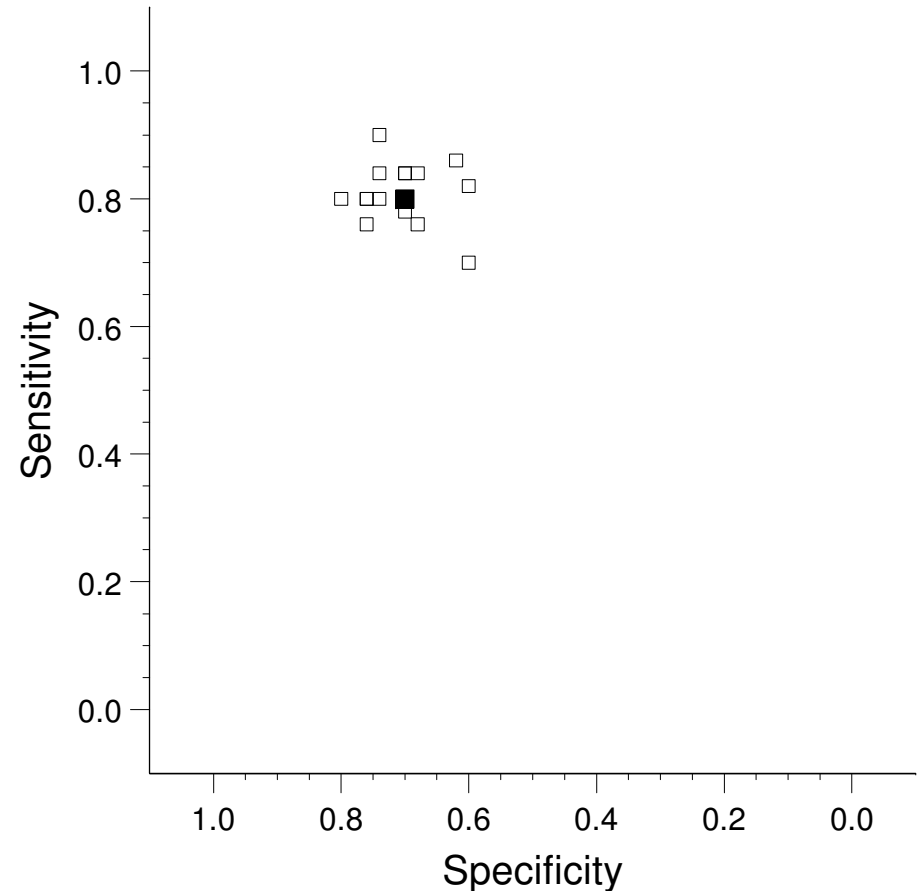
- I. Chance variation
- II. Differences in threshold
- III. Bias
- IV. Subgroups
- V. Unexplained variation

Sources of Variation: Chance

Chance variability:
sample size=40



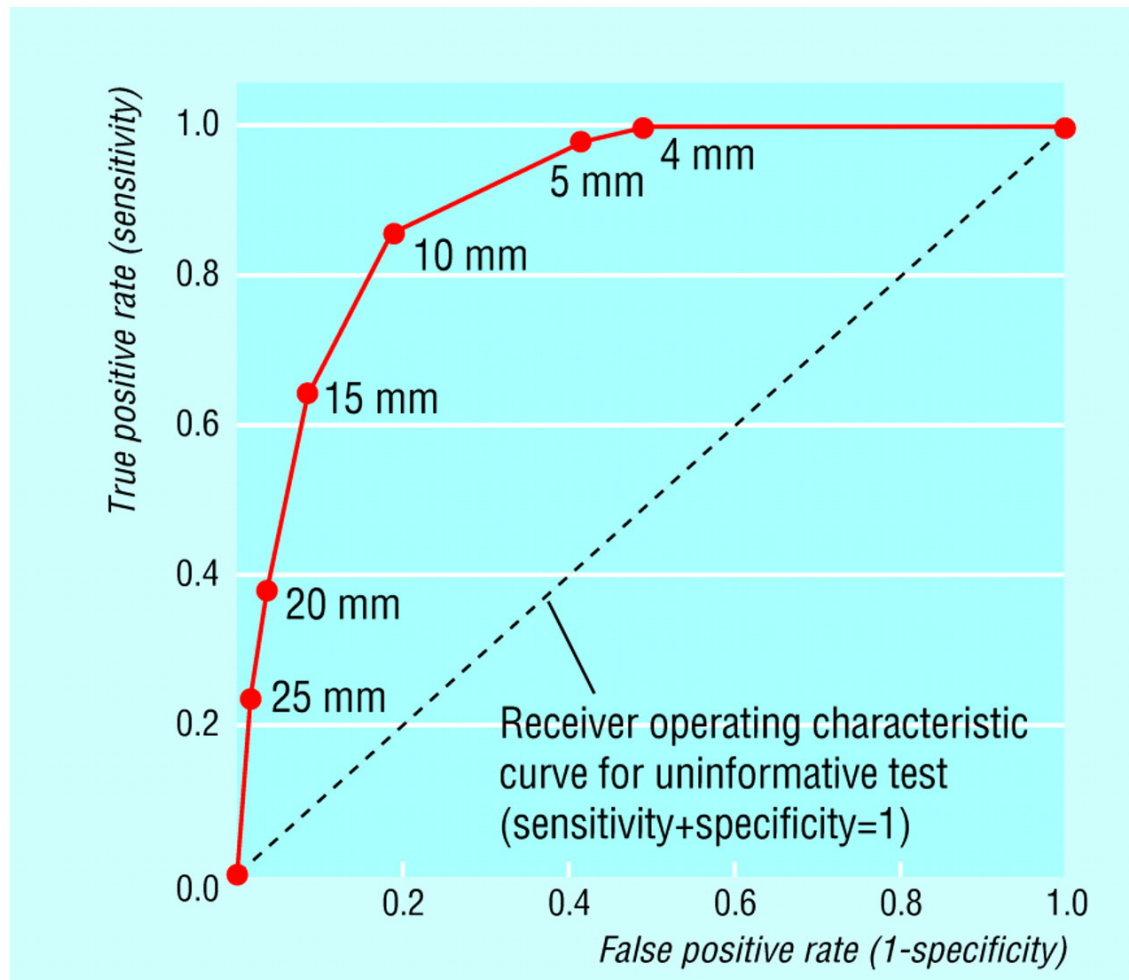
Chance variability:
sample size=100



Variation due to Threshold Differences

- Explicit differences
 - studies have used different cut-off values to define positive test results

Receiver characteristic operating (ROC) curve



The ROC curve represents the relationship between sensitivity and specificity of the test at various thresholds

Variation due to Threshold Differences

- Explicit threshold differences
 - studies have used different cut-off values to define positive test results
- Implicit threshold differences
 - differences in observers
 - differences in equipment
- Consequence: negative correlation arises between sensitivity and specificity

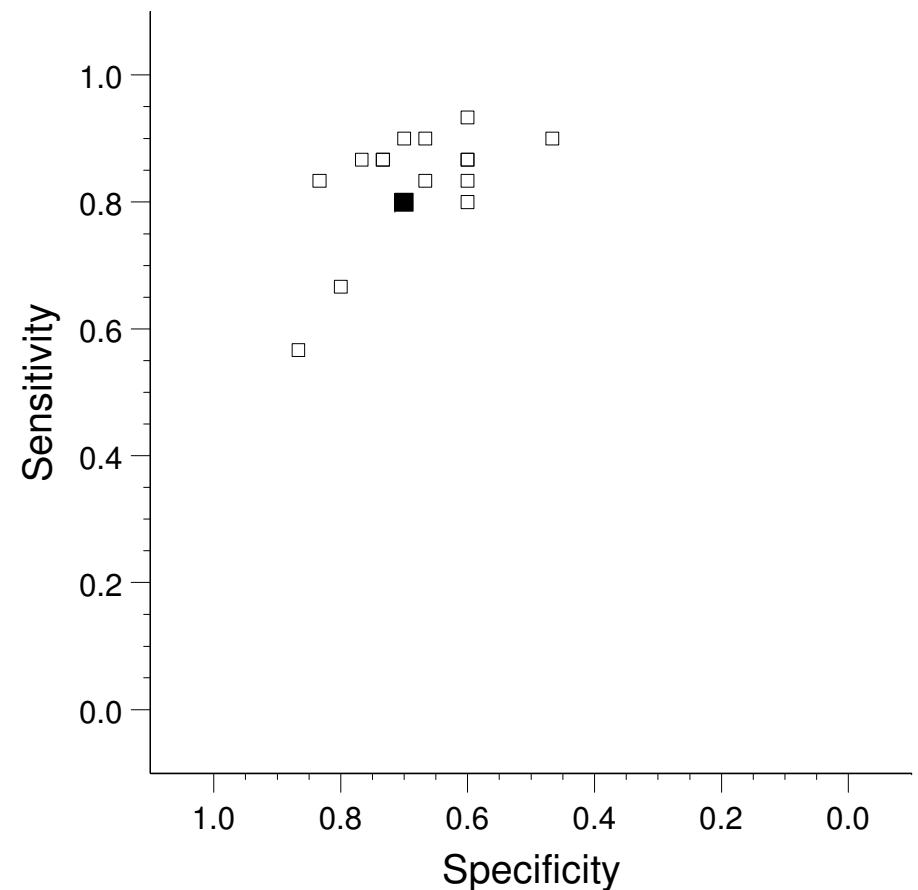
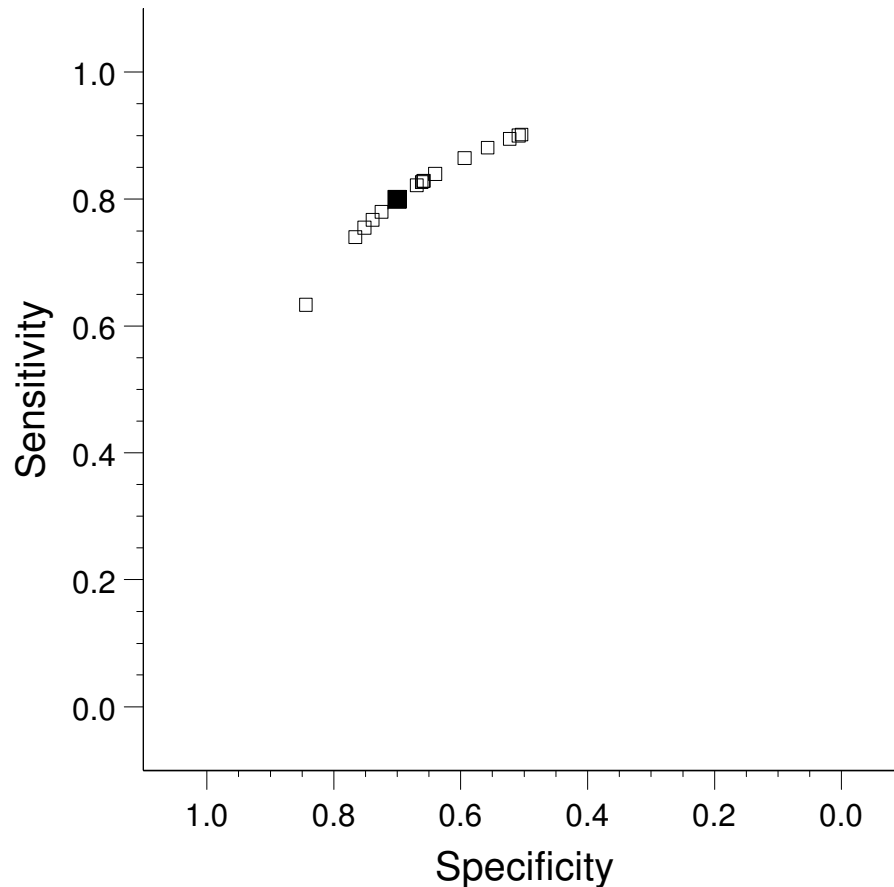
Sources of Variation: Threshold

Threshold:

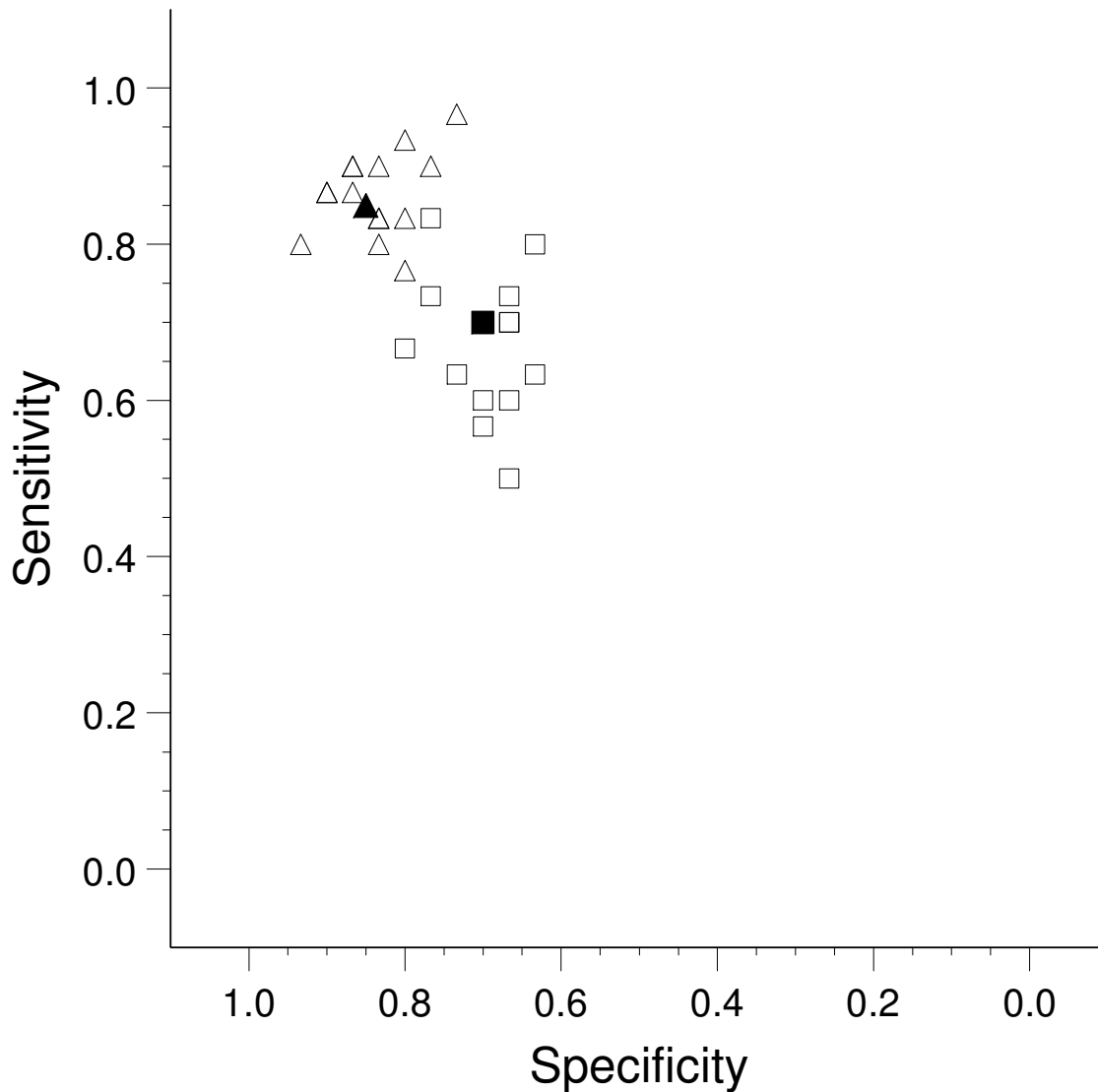
- perfect negative correlation
- no chance variability

Threshold:

- perfect negative correlation
- + chance variability: $ss=60$



Sources of Variation: Bias & Subgroup

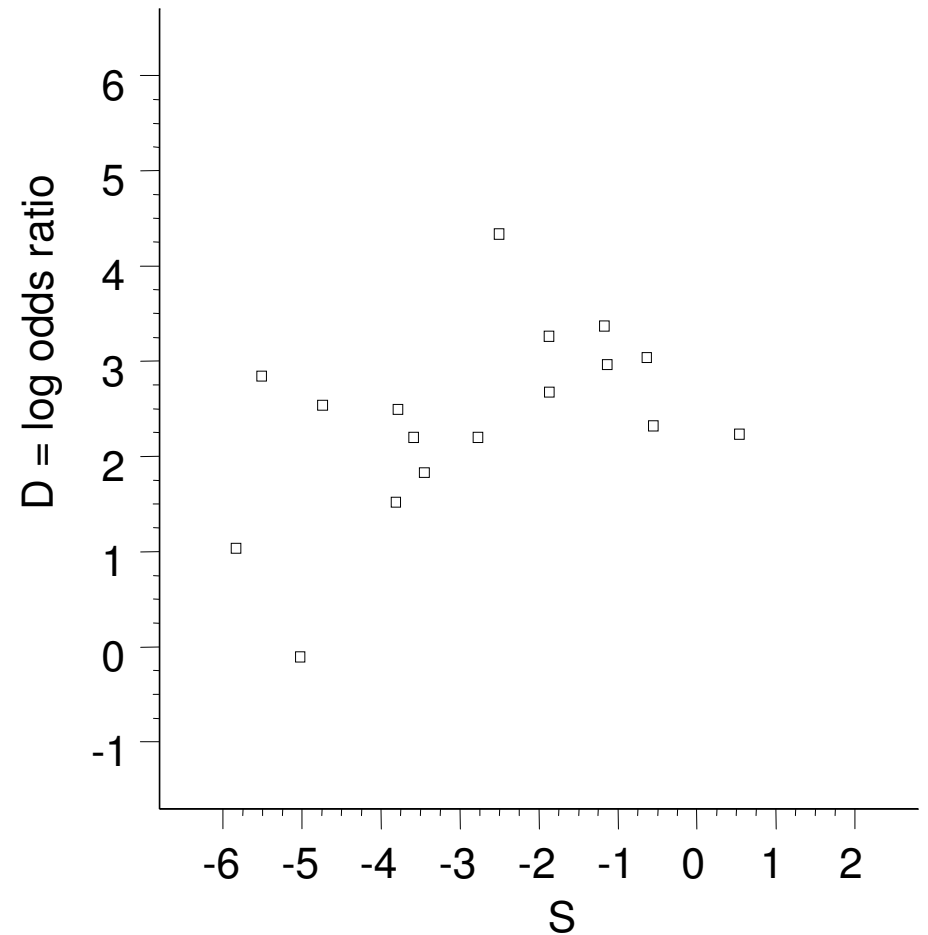
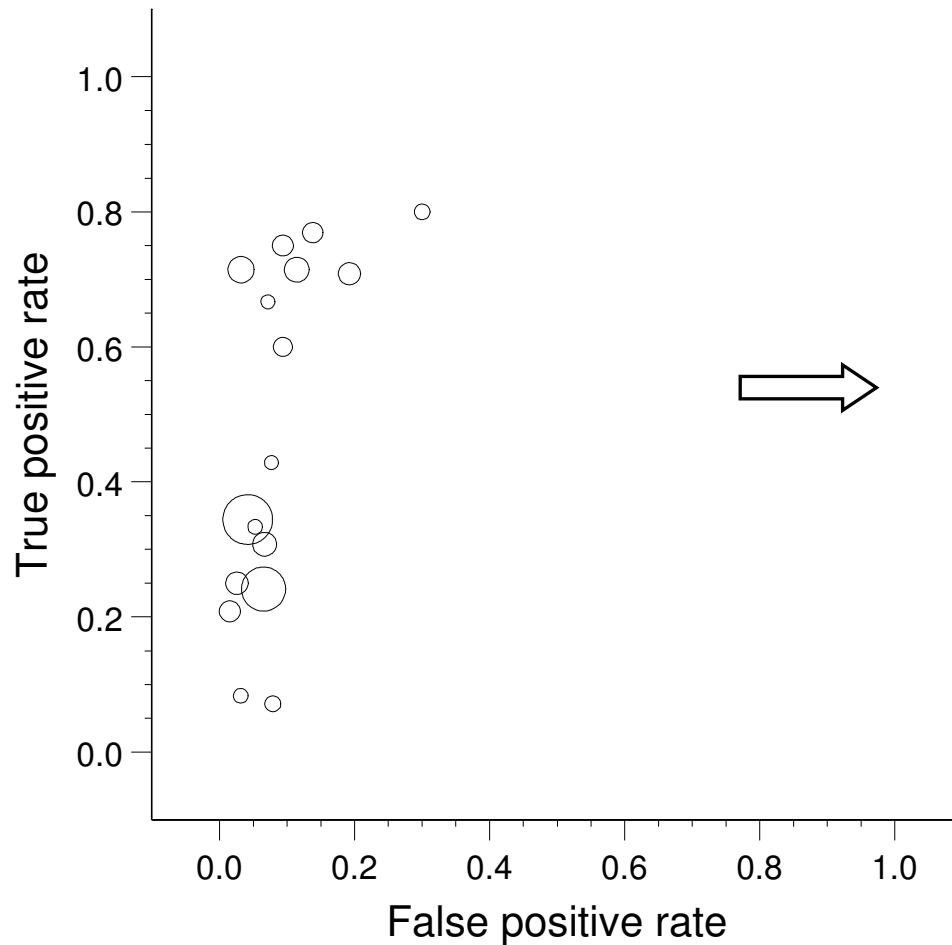


- Bias & Subgroup:
- sens & spec higher
 - ss=60
 - no threshold

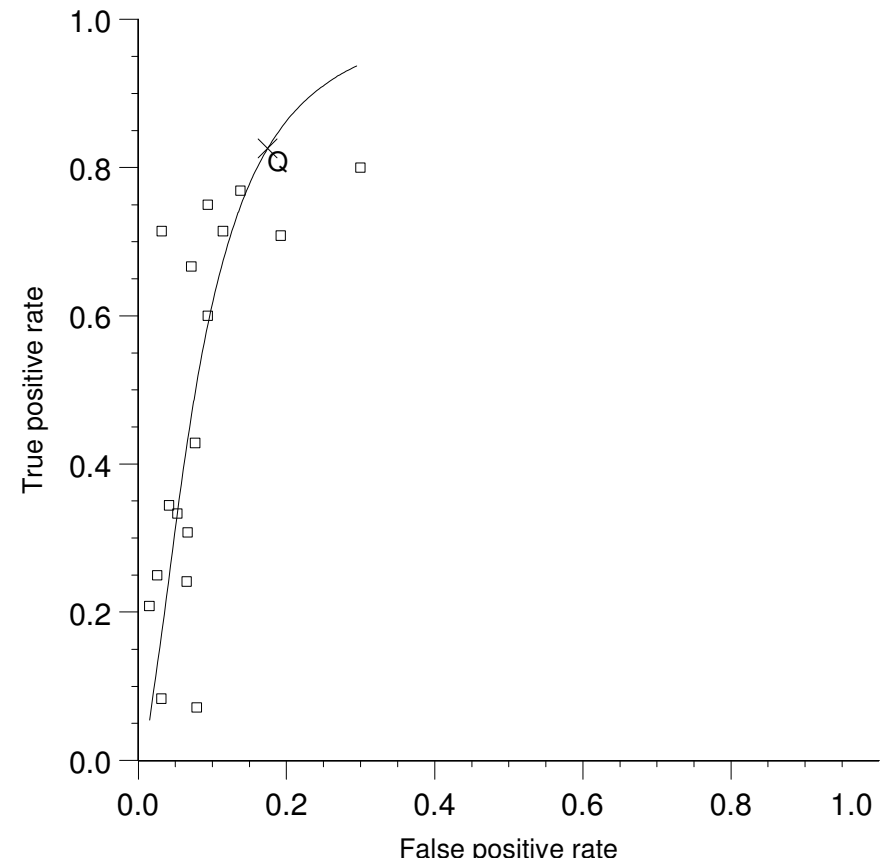
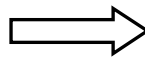
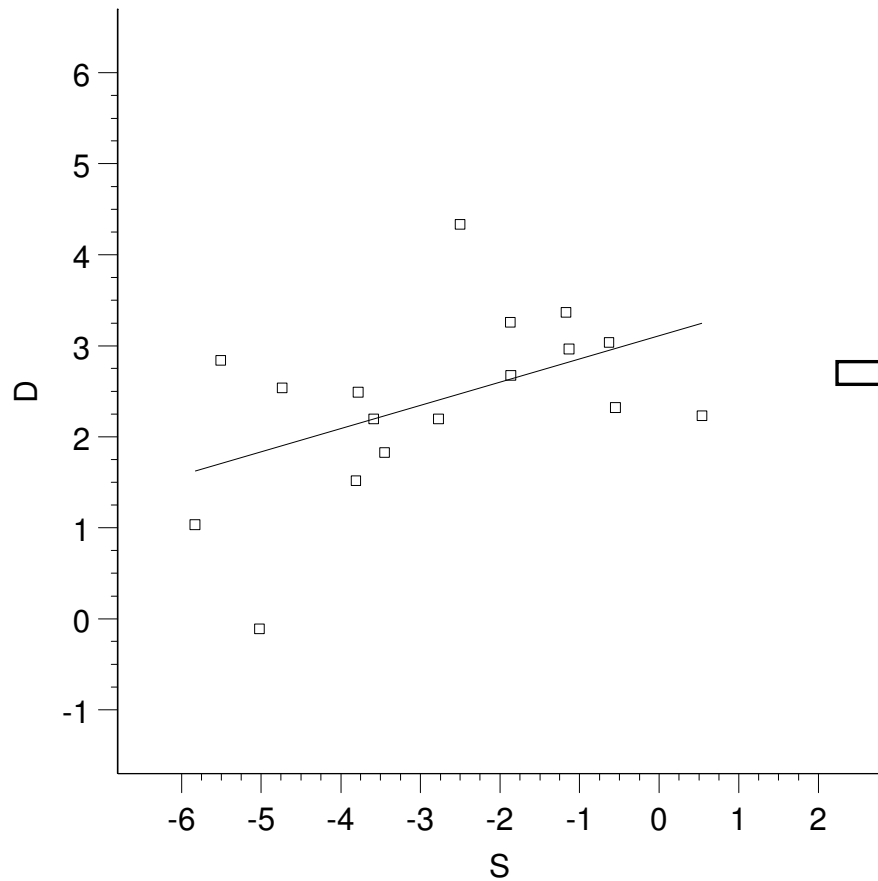
Overview of Statistical Approaches

- Summary ROC model / Moses-Littenberg (ML)
 - Traditional approach, straightforward
- More complex models
 - Bivariate random approach
 - Hierarchical summary ROC approach

ML approach: Finding Smooth Curve in ROC



Linear Regression & Back Transformation



Drawbacks Moses-Littenberg Approach

- Validity of significance tests
 - Sampling variability in individual studies not properly taken into account
 - P-values and confidence intervals erroneous
- Summary points
 - Average sensitivity/specificity cannot be obtained
 - Sensitivity for a given specificity can be estimated

Advanced Models - HSROC and Bivariate methods

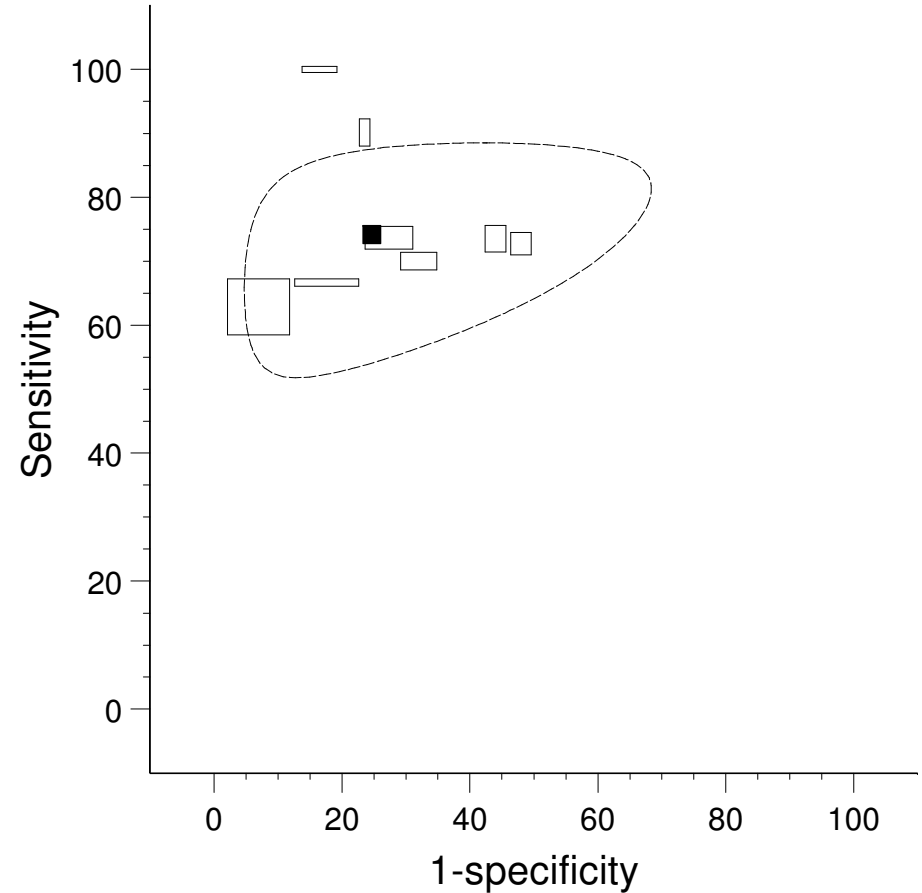
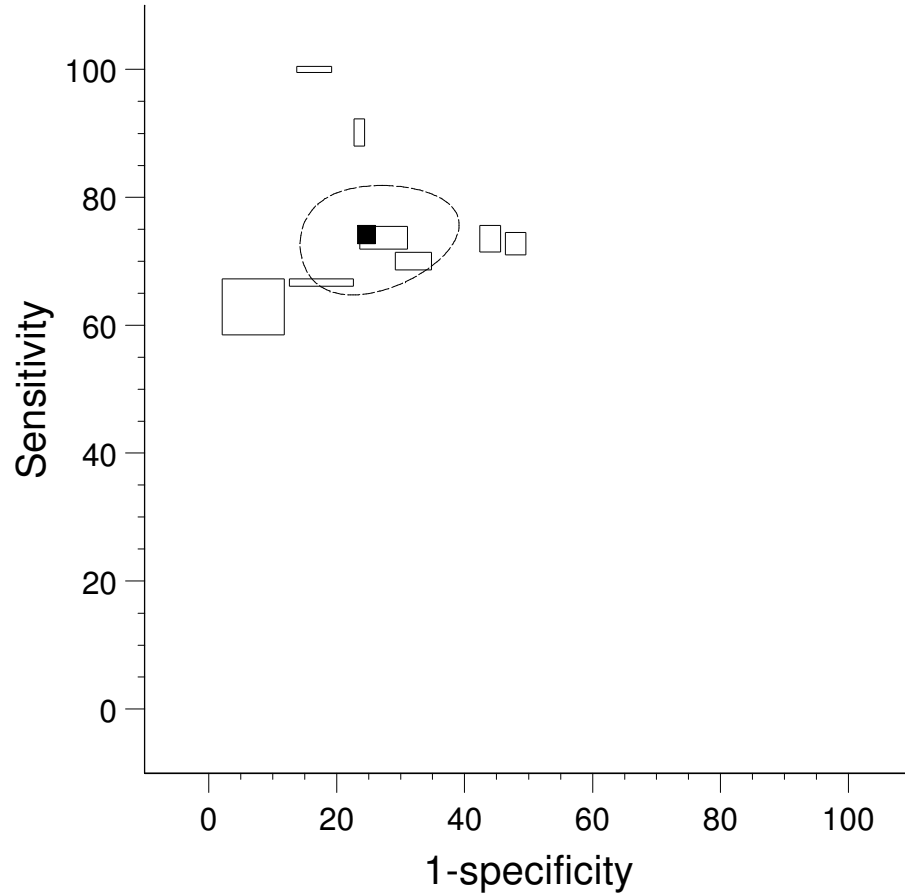
- Hierarchical / multi-level random effects
 - allows for both within and between study variability
- Binomial distribution
 - correctly models sampling uncertainty in both sensitivity and specificity
 - no zero cell adjustments needed
- Regression models
 - flexible in examining sources of heterogeneity

Presentation of Results

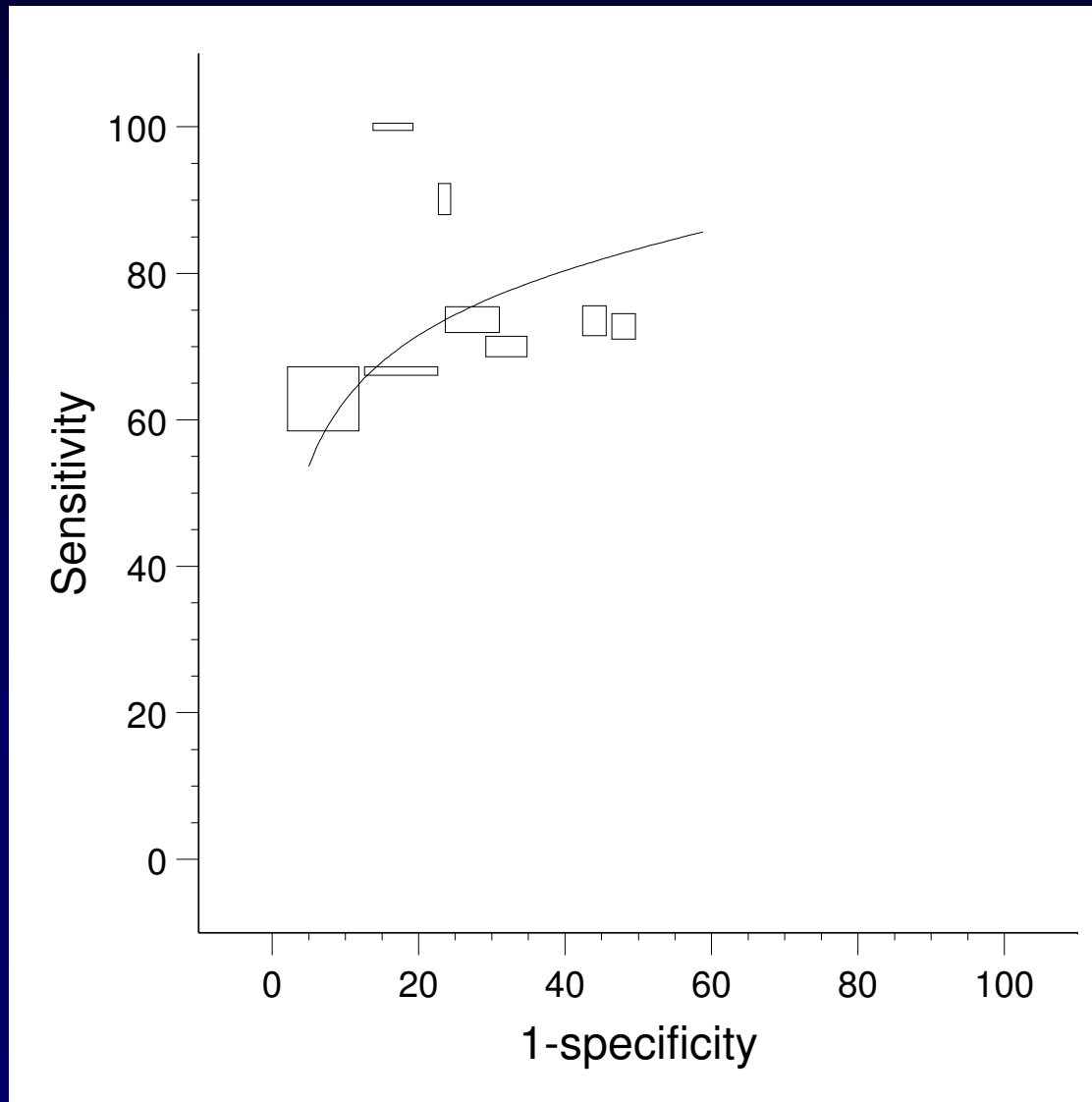
Summary Values with Ellipses

Ellipse around mean value

Prediction ellipse



Curves, Summary Points, Ellipses



Bad News

- Straightforward and most-frequently used method (Moses-Littenberg model) is statistically flawed
- Advanced models needed to make inferences (e.g. P-values) and to calculate appropriate confidence intervals
- Fitting and checking advanced models require statistical expertise
- Advanced methods not available in RevMan 5

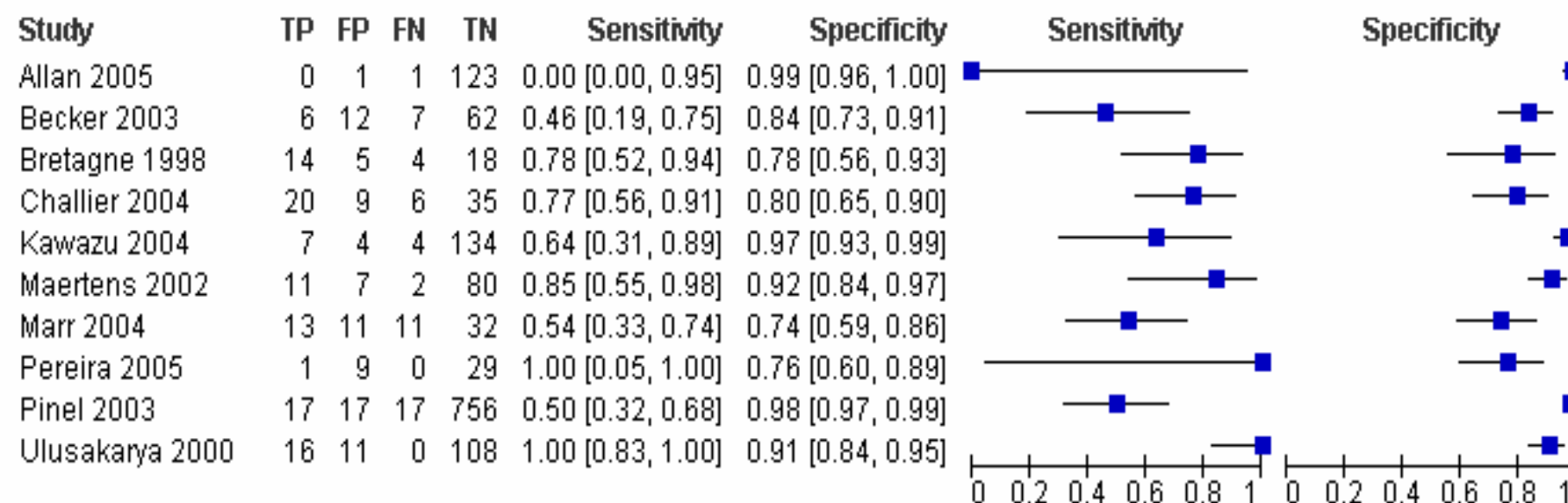
Good News

- Syntax to run more complex models in SAS, STATA, WINBUGS, S-PLUS, and R are available
- Results from these packages can be entered into RevMan 5 to make graphs

RevMan 5

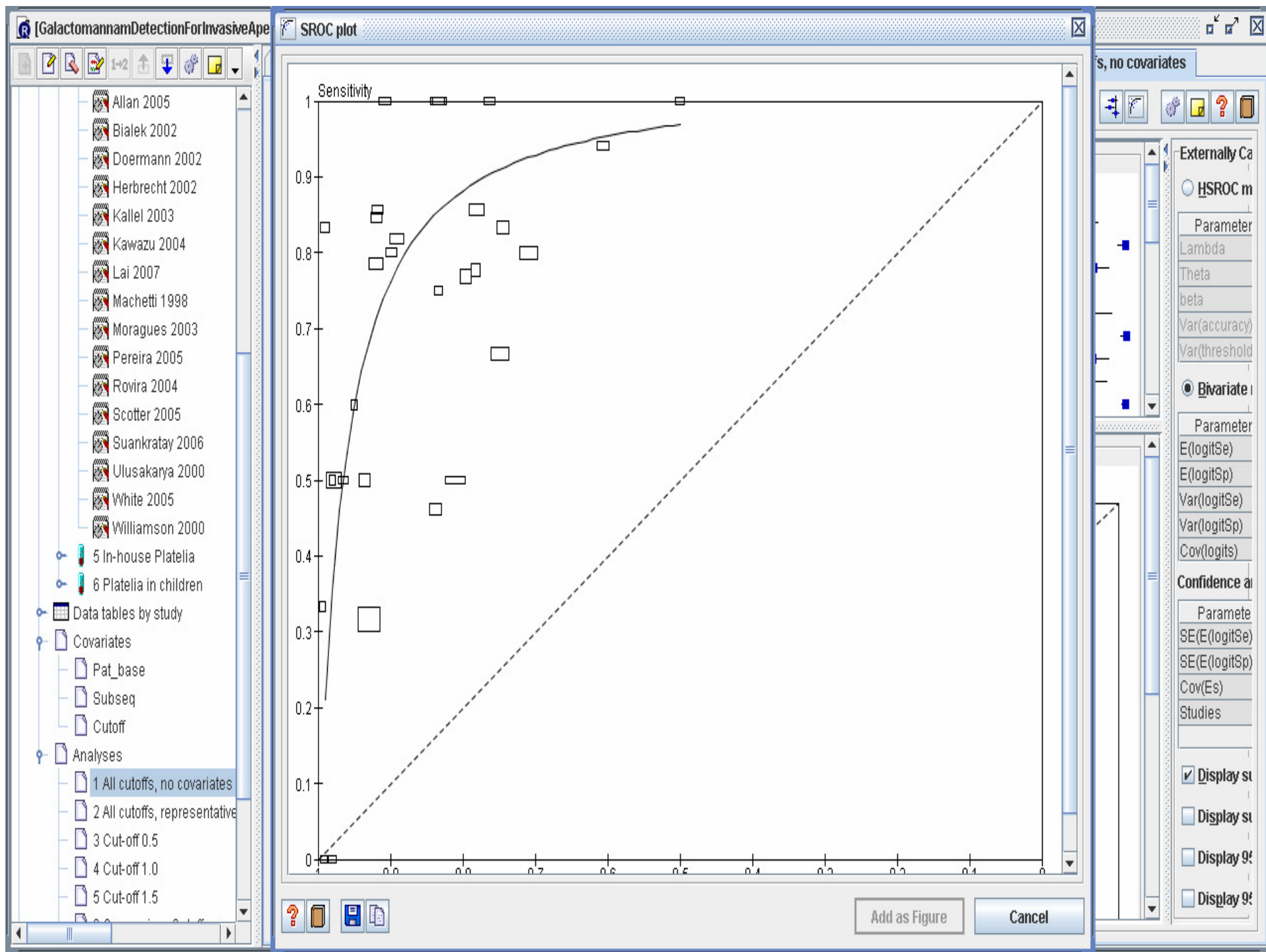
- Perform descriptive analyses
- Estimates from hierarchical SROC or bivariate model can be imported into REVMAN to:
 - plot fitted SROC curve
 - display summary points
 - draw confidence or prediction ellipses

Forest plot



Add as Figure

Cancel





[GalactomannanDetectionForInvasiveAspergillosis_Leeflang_200803201.rm5] Galactomannan detection for invasive aspergillosis in immunocompromized patients.



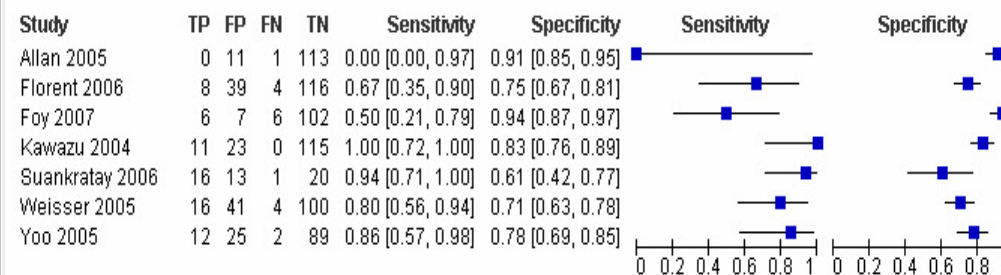
Diagnostic test accuracy review

- Title
- Review information
- Main text
- Tables
- Studies and references
- Data and analyses
 - Data tables by test
 - Data tables by study
 - Covariates
 - Analyses
 - 1 All cutoffs, no covariates
 - 2 All cutoffs, representative spectrum
 - 3 Cut-off 0.5 (subgroup analysis)
 - 4 Cut-off 1.0 (subgroup analysis)
 - 5 Cut-off 1.5 (subgroup analysis)
 - 6 ComparisonCutoffs (acc to subgroup)
 - 7 PairedComparison 1.0-1.5
 - 8 All cutoffs, representative or not
- Figures
- Sources of support
- Feedback
- Appendices

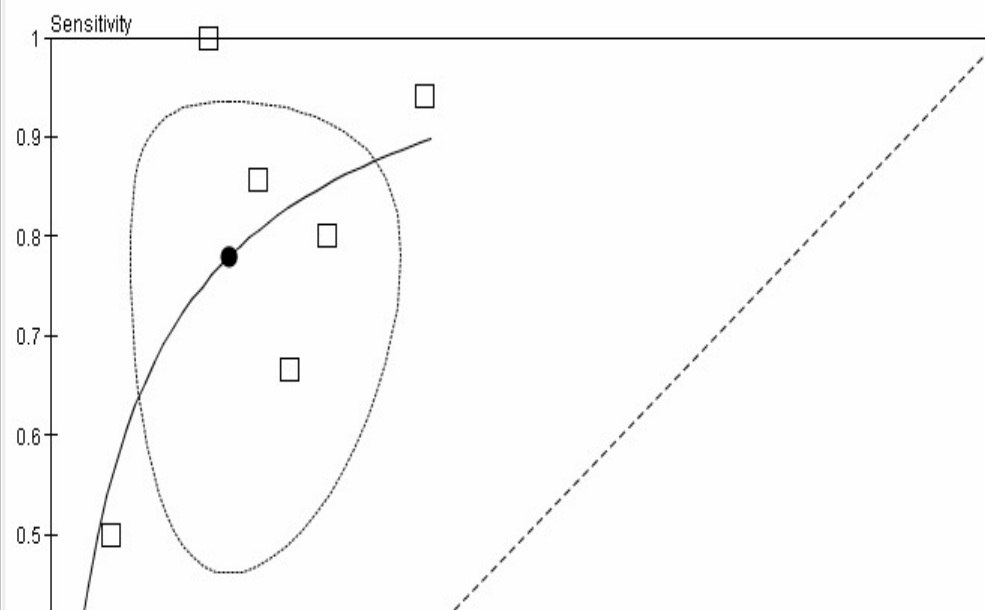
Text of Review ☒ 2 All cutoffs, representative... ☒ 3 Cut-off 0.5 (subgroup...)

Analysis: 3 Cut-off 0.5 (subgroup analysis)

Forest plot



SROC plot



Externally Calculated Parameters

☐ HSROC model parameters

| Parameter | Estimate |
|----------------|----------|
| Lambda | |
| Theta | |
| beta | |
| Var(accuracy) | |
| Var(threshold) | |

☒ Bivariate model parameters

| Parameter | Estimate |
|--------------|----------|
| E(logitSe) | 1.2618 |
| E(logitSp) | 1.4617 |
| Var(logitSe) | 0.4459 |
| Var(logitSp) | 0.6083 |
| Cov(logits) | -0.4839 |

Confidence and prediction regions

| Parameter | Estimate |
|----------------|----------|
| SE(E(logitSe)) | 0.4172 |
| SE(E(logitSp)) | 0.2721 |
| Cov(Es) | 0 |
| Studies | 7 |


- ☒ Display summary curve
- ☒ Display summary point
- ☒ Display 95% confidence region
- ☐ Display 95% prediction region

Support

- Cochrane support:
 - CESU and UKSU
 - explanatory papers
 - pilot reviews
 - editorial process with specific attention to meta-analysis
 - workshops at Cochrane Colloquia
- Courses
- Overview on website Diagnostic Test Accuracy Working Group (<http://srdta.cochrane.org>)

Diagnostic Test Accuracy Working Group - Statist...

Home RSS Print Pagina Extra



Welcome

DTA Editorial Team

Regional Support Units

Contact us

Statistical analysis

Handbook for DTA Reviews

Workshops and events

Frequently Asked Questions

Editorial Process of Diagnostic Test Accuracy reviews

More about us

Presentations

Cochrane entities >

Diagnostic Test Accuracy Working Group

Statistical analysis

Statistical models are used in meta-analyses of data in systematic reviews of diagnostic test accuracy.

Models can be run in a variety of different software programmes but this facility is not available in RevMan. Specific statistical parameters from the models run can be input into RevMan in order to draw appropriate graphical displays of the data.

Researchers have prepared macros for statistical models for meta-analysis of data from diagnostic test accuracy studies for several statistical analysis software programs. As these become available we will add them to this page.

Macro 1

METADAS: A SAS macro for meta-analysis of diagnostic accuracy studies. User guide version 1.0 beta. December 2008. [METADAS](#) (PDF 898KB)

Macro 2

METANDI: Stata module to perform meta-analysis of diagnostic accuracy. Harbord 2008

A user-written model for Stata for metaanalysis of DTA studies without covariates with results in both bivariate and HSROC parameterisations, and on a graph.


Search

This website

Search

Advanced

Tips



Take Home Messages

- Two potentially correlated outcome measures require more complex statistical models
- Moses-Littenberg model is not appropriate for formal testing
- Bivariate and hierarchical summary ROC model are sound, powerful and flexible models
- These models can not be fitted in RevMan, but results can be incorporated
- Statistical expertise required in review team



Meta-analysis of Accuracy Studies

- Results often highly heterogeneous
 - differences in design and conduct
 - differences in verification
 - differences in spectrum
 - differences in technology of tests or test execution
 - differences in threshold
 - chance variation

Powerful and Flexible Models

- Examples of multivariate meta-analysis:
all advantages apply
- Extension with study-level covariates to explain heterogeneity in results or differences in accuracy between test in accuracy
- Separate effects on sensitivity and specificity
- Testing of joint parameters
- Software: need for non-linear mixed models in SAS, STATA, R, S, WinBugs

Other View

