

# Introduction to diagnostic test accuracy network meta-analysis

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# Outline

- 1. Introduce Diagnostic Test Accuracy (DTA) Studies
- 2. Discuss about process of conducting a systematic review with DTA meta-analysis
- 3. Present how to build the network geometry of DTA studies
- 4. Extend DTA meta-analysis methods to DTA network meta-analysis methods (DTA-NMA)
- 5. Identify potential implications in DTA-NMA







#### Which of the following best describes your role?

- Editor of systematic reviews
- User of systematic reviews
- Systematic reviewer
- Statistician
- Methodologist
- Other

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# Poll Question 2

What is your familiarity with Meta-Analysis of Diagnostic Test Accuracy studies?

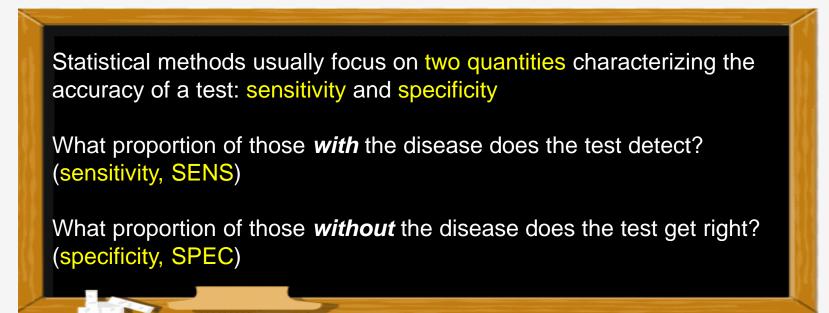
- I know about it and have used it.
- I am aware of it, but have not applied it before.
- I have no idea what it is.

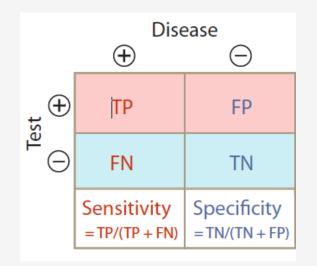
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# Diagnostic Test Accuracy studies

- Diagnostic Tests are used to ascertain whether an individual has or not a disease
- Most tests are imperfect, errors will occur not always accurate
- 'Reference standard' is a test that can be used to estimate the accuracy of the imperfect tests
- Binary outcome: positive / negative test result

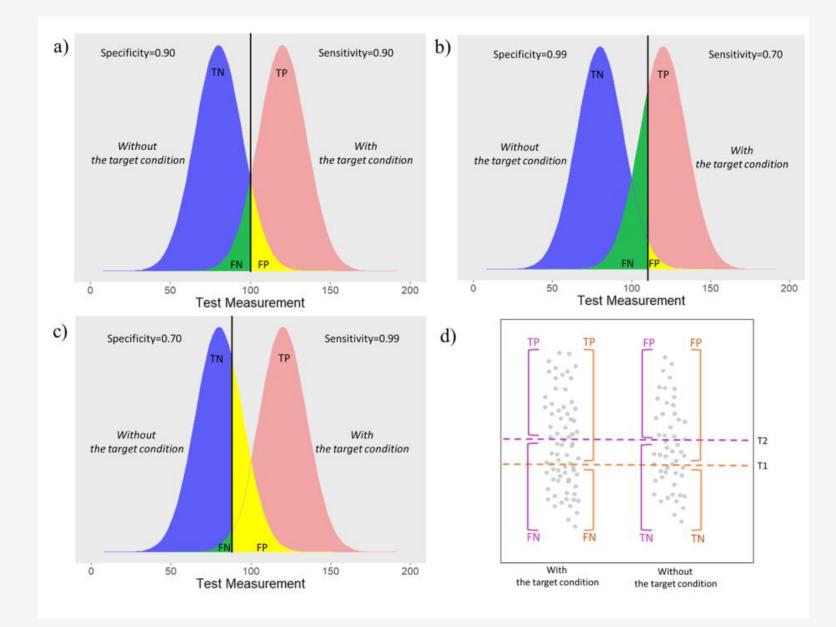




# Thresholds

- Binary markers (X-rays)
- Continuous markers (blood tests)
  - Require setting cut-off values (thresholds)
  - Trade-off between sensitivity and specificity

There is a **trade-off** between sensitivity and specificity as the threshold is set in **different points**!

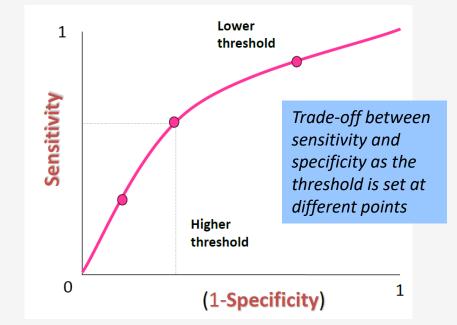


# **Threshold effect**

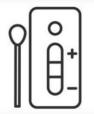
- The same threshold can imply different SENS and SPEC in different groups
- A solution can be to perform Meta-Analysis at each threshold separately or a subset of thresholds

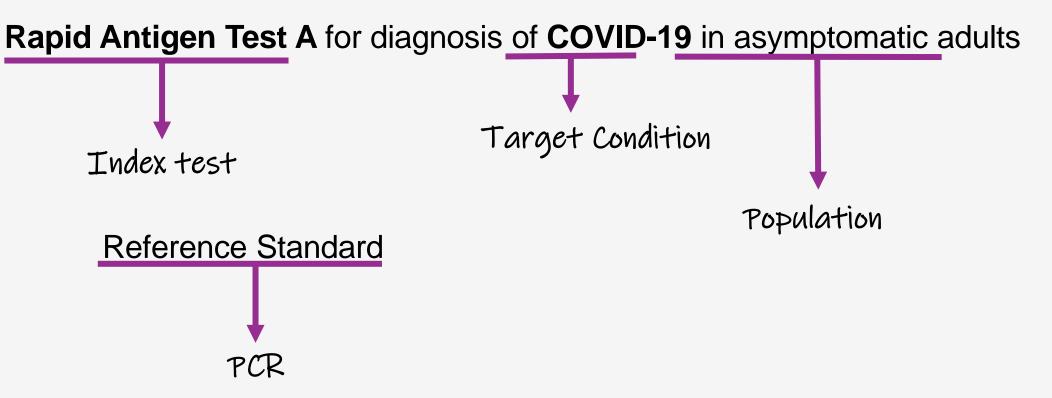
#### **BUT...**

- Restricting to a common threshold reduces data
- The common threshold may not be the threshold a reader wants to know about



# Example: The anatomy of a DTA research question







# Example: 2x2 table

Index test: Rapid Antigen test A for COVID-19 Reference Standard: RT-PCR

|                      |               | Reference standar           |                     |                                       |
|----------------------|---------------|-----------------------------|---------------------|---------------------------------------|
|                      |               | Positive (D+) Negative (D-) |                     | Total                                 |
|                      | Positive (T+) | TP= <b>27</b>               | FP= <b>2</b>        | Positive Test Results = <b>29</b>     |
| Index Test<br>Result | Negative (T-) | FN= <b>3</b>                | TN= <mark>98</mark> | Negative Test Results =<br><b>101</b> |
| Result               | Total         | Diseased= 30                | Non-Diseased= 100   | Sample size =<br><b>130</b>           |

- Sensitivity, Specificity (90%, 98%)
- Test identified 90% of COVID-19 diseased and 98% of non-diseased individuals

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# Steps of a Systematic Review of DTA studies

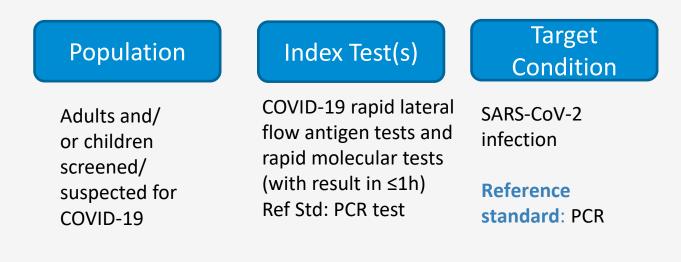


#### 1. Define the question

- 2. Define objectives and eligibility criteria
- 3. Develop protocol
- 4. Search for studies
- 5. Study selection and Data collection
- 6. Assess bias and applicability
- 7. Analyze and present results
- 8. Interpret results and draw conclusions

#### **Review Question**

What is the diagnostic accuracy of rapid antigen and rapid molecular tests for the diagnosis of the SARS-CoV-2 infection in adults and children according to the reference standard PCR test?





# Intervention vs DTA reviews

#### **Components of Intervention review research question (PICO)**

- **P** opulation
- Interventions
- **C** omparators
- O utcomes
- **S** tudy design



#### **Components of Intervention review research question (PIT)**

- **P** opulation

#### Diagnostic Test Accuracy (DTA) Reviews

**Intervention Reviews** 

- I ndex Test(s)
- **T** arget Condition
  - Reference Standard
- **S** tudy design





# Steps of a Systematic Review of DTA studies



#### 1. Define the question

- 2. Define objectives and eligibility criteria
- 3. Develop protocol
- 4. Search for studies
- 5. Study selection and Data collection
- 6. Assess bias and applicability
- 7. Analyze and present results
- 8. Interpret results and draw conclusions

Primary objective To assess the diagnostic accuracy of rapid antigen and rapid molecular tests for the diagnosis of the SARS-CoV-2 infection in adults and children



To assess the accuracy of clinical assessment in SARS-CoV-2 infection :

**Objectives of the review** 

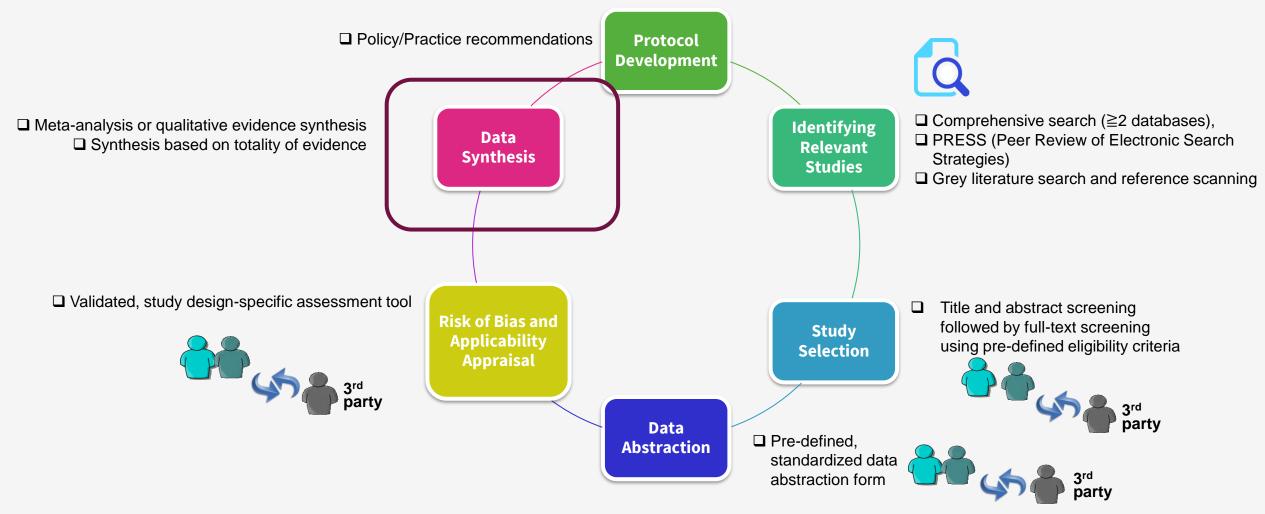
- according to sample type (e.g., saliva, nasal swab)
- In symptomatic and asymptomatic participants



# Steps of a Systematic Review of DTA studies

https://training.cochrane.org/handbook

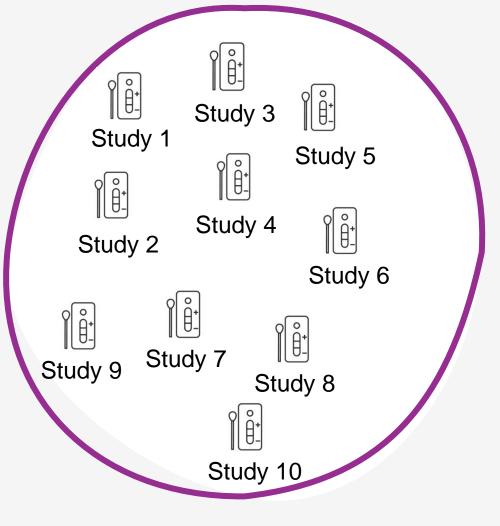
PICOS(T) framework, developed using PRISMA-P
Register with PROSPERO (and publish in open access journal)



- Deeks JJ et al. Cochrane Handbook for Systematic Reviews of Diagnostic Test Accuracy. Version 2.0. Cochrane. 2023
- McInnes MDF et al. Preferred Reporting Items for a Systematic Review and Meta-analysis of Diagnostic Test Accuracy Studies: The PRISMA-DTA Statement. JAMA. 2018
- Whiting PF et al. QUADAS-2: A Revised Tool for the Quality Assessment of Diagnostic Accuracy Studies. Ann Intern, 2011
- Yang B et al. QUADAS-C: A Tool for Assessing Risk of Bias in Comparative Diagnostic Accuracy Studies. Ann Intern Med. 2021



#### Meta-analysis 10 studies exploring accuracy of Test A for Covid-19



- Summarize information
- Synthesis of information from individual studies, addressing the same research question
- Statistically combine study-results to obtain summary estimates



# The generic meta-analysis process

- 1. Calculation of an overall summary (average) of high precision, coherent with all observed data
- 2. Typically a "weighted average" is used where more informative (larger) studies have more say
- 3. Assess the degree to which the study results deviate from the overall summary
- 4. Investigate possible explanations for the deviations

What is **SO critical** that we have to consider in meta-analyses? **Test threshold!!!** 

- Accuracy varies with index test threshold
- Can we average over test thresholds?
- How would we interpret the result?
- Thresholds can be important for both index and reference tests





# The generic meta-analysis process

#### **Challenges for DTA reviews**

- There are **two summary statistics** for each study: **SENS** and **SPEC**
- Threshold effects induce correlations between SENS and SPEC
  - Often thresholds vary between studies
- Heterogeneity is the norm substantial variation in sensitivity and specificity
  - Different groups can have different sensitivities and specificities at the same threshold

#### Pooling sensitivity and specificity *separately*?

- Ignores threshold as source of heterogeneity
- Is biased towards studies with high sensitivity or specificity



 Pooled estimates of sensitivity and specificity may be biased towards 1 or 0, depending on study results

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# Multiple studies – Single index test

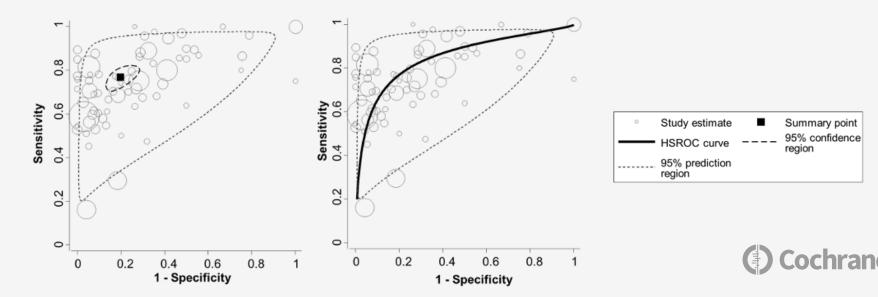
- Systematic review evaluating a single index test:
  - $\circ$   $\,$  Aims to evaluate a diagnostic test vs. a reference standard  $\,$
- How does test accuracy vary with clinical & methodological characteristics?
- The outcome is to model the test results (binary outcome: positive / negative test result) assess the diagnostic accuracy of a single test

#### **Bivariate model**

- Single threshold
- Summary point

#### HSROC model

- Multiple thresholds
- Summary curve



Reitsma J et al. Journal of Clinical Epidemiology. 2005; Rutter C, Gatsonis C. Stat Med. 2001

# Multiple Diagnostic Tests vs. Multiple Interventions

• Diagnostic tests are usually compared in the same subjects within a study

Correlated observations – the NMA methods should account for this correlation structure
Should estimate sensitivity & specificity: bivariate model

- Interventions are compared between independent groups (different groups of patients)
  - Use effect measures (OR, RR, RD) to compare effectiveness among treatments

|               |                 | Interventions                                      | Diagnostic tests  |
|---------------|-----------------|--|---|
|               | Aim             | Compare two treatments                             | Discriminate two groups   |
| Pairwise      | Groups          | 2 interventions                                    | With/without target condition   |
| meta-analysis | Outcome         | Event yes/no                                       | Test positive/negative  |
|               | Proportions     | $r_1, r_0$   | Sens, 1 – Spec  |
|               | Effect measures | $RD = r_1 - r_0$                                   | J = Sens + Spec - 1   |
|               |                 | $OR = \frac{r_1(1-r_0)}{r_0(1-r_1)}$               | $DOR = \frac{Sens*Spec}{(1-Sens)(1-Spec)}$                            |
|               | Modeling        | Univariate model, contrast-based                   | Bivariate model, arm-based  |
| Multivariate  | Groups          | 2 interventions                                    | With/without target condition   |
| pairwise      | Outcome         | $K \ge 2$ outcomes                                 | $K \ge 2$ tests   |
| meta-analysis | Measures        | Pairs of proportions                               | Pairs of accuracy measures  |
|               |                 | $(r_{1k}, r_{0k}), k = 1, \dots, K$                | $(\operatorname{Sens}_k, 1 - \operatorname{Spec}_k), k = 1, \dots, K$ |
|               | Effect measures | $RD_k, k = 1, \dots, K$<br>$OR_k, k = 1, \dots, K$ | $J_k, k = 1, \dots, K$ $DOR_k, k = 1, \dots, K$                       |
|               | Modeling        | Multi( <i>K</i> )variate model                     | Multi $(2K)$ variate model  |

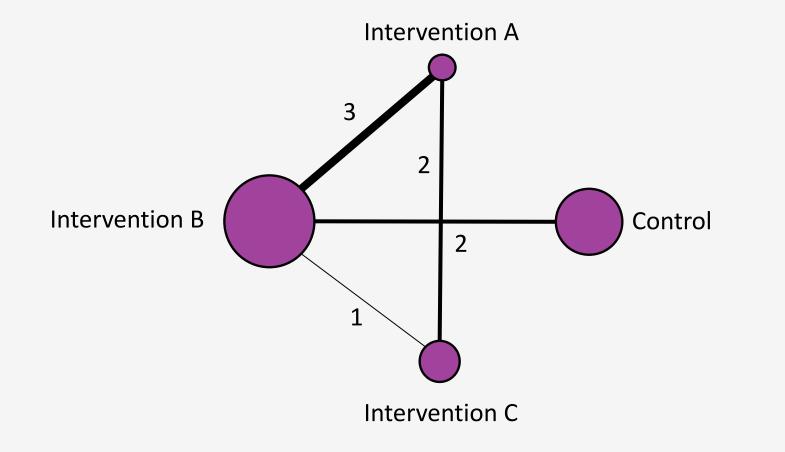
RD = risk difference; OR = odds ratio; DOR = diagnostic odds ratio; J = Youden index.

Rücker G. Springer, Cham. 2018

# Network of interventions

All interventions and the control group are depicted in the network plot

Studies compare at least 2 interventions (2-arm, 3-arm, etc.)

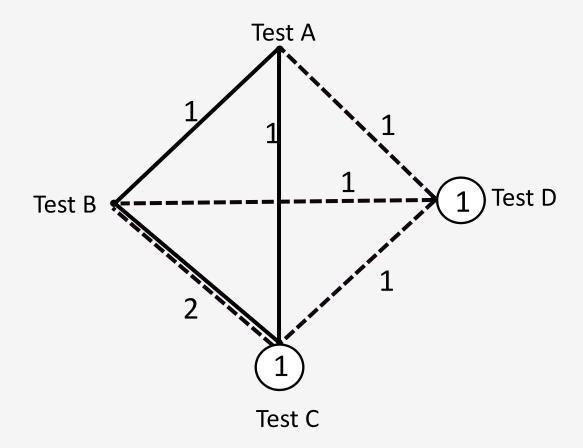


| Study ID | Type of<br>study | Intervention comparisons |
|----------|------------------|--------------------------|
| 1        | 2-arm            | B vs C                   |
| 2        | 3-arm            | A vs B vs C              |
| 3        | 2-arm            | A vs C                   |
| 4        | 2-arm            | B vs Control             |
| 5        | 2-arm            | A vs B                   |
| 6        | 2-arm            | A vs B                   |
| 7        | 2-arm            | B vs Control             |

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#### Network of diagnostic tests

Reference standard (RS) is not considered in the network but as a bridge for comparing index tests. Index test vs RS: single-test study



| Study<br>ID | Type of<br>study | Data   | Test<br>comparisons   | Edges/Circles in the<br>network                                    |
|-------------|------------------|--|---|--|
| 1           | Single-<br>test  | Test D vs RS                                 | Test D vs. RS   | Circle for test D  |
| 2           | Paired-<br>test  | Test B vs RS<br>Test C vs RS                 | Test B vs. Test C   | Dashed line connecting<br>tests B and C                            |
| 3           | Triple-<br>test  | Test A vs RS<br>Test B vs RS<br>Test C vs RS | Test A vs. Test B<br>Test A vs. Test C<br>Test B vs. Test C | Closed triangle with<br>solid line connecting<br>tests A, B, and C |
| 4           | Paired-<br>test  | Test B vs RS<br>Test D vs RS                 | Test B vs. Test D   | Dashed line connecting<br>tests B and D                            |
| 5           | Single-<br>test  | Test C vs RS                                 | Test C vs.<br>Reference                                     | Circle for test C  |
| 6           | Paired-<br>test  | Test A vs RS<br>Test D vs RS                 | Test A vs. Test D   | Dashed line connecting<br>tests A and D                            |
| 7           | Paired-<br>test  | Test C vs RS<br>Test D vs RS                 | Test C vs. Test D   | Dashed line connecting<br>tests C and D                            |



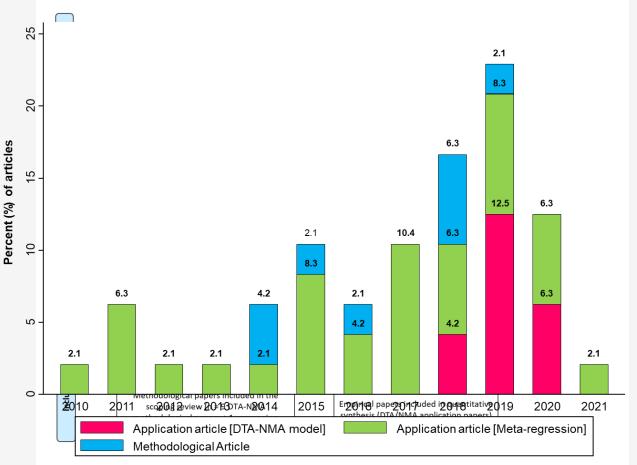
# Scoping Review of DTA-NMA methods





# **Scoping Review**

- Search of PubMed, Web of Science, Scopus databases up until the 3rd March 2021
- Methodological and application papers comparing the accuracy of at least three index tests using:
  - hierarchical meta-regression models
  - models developed specifically for DTA-NMA



() Cochrane

# **DTA-NMA** in the literature



Abbreviations: DOR, diagnostic odds ratio; SE, standard error; DTA, diagnostic test accuracy; NMA, network meta-analysis; HSROC, hierarchical summary receiver operating characteristic a 2 × 2 data includes the number of true positives, true negatives, false positives and false negatives.

 Properties of DTA-NMA models differ and may influence interpretation and decisionmaking

#### DTA-NMAs:

- 'Borrow strength' across studies by simultaneously analysing multiple DTA studies
- Account for between-study correlations between sensitivity and specificity induced through threshold effects



Popula



# Joint classification tables

Index test: Rapid Antigen test A, Rapid Antigen test B for COVID-19 Reference Standard: RT-PCR

|        |                  | Reference stand           |                      |                                |
|--------|------------------|---------------------------|----------------------|--------------------------------|
|        |                  | Positive (D+)             | Negative (D-)        | Total                          |
| Index  | Positive<br>(T+) | TP= 27                    | FP= 2                | Positive Test<br>Results = 29  |
| Test A | Negative<br>(T-) | FN= <mark>3</mark>        | TN= <mark>98</mark>  | Negative Test<br>Results = 101 |
| Result | Total            | Diseased= <mark>30</mark> | Non-Diseased=<br>100 | Sample size =<br>130           |

|          |          | Reference stand | Reference standard Result |                           |  |
|----------|----------|-----------------|---------------------------|---------------------------|--|
|          |          | Positive (D+)   | Negative (D-)             | Total                     |  |
| Positive |          | TP= 17          | TP= 17 FP= 9              |                           |  |
| Index    | (T+)     | IP-1/           | FP- 3                     | Results = <mark>26</mark> |  |
| Test B   | Negative | FN= 13          | TN= <mark>91</mark>       | Negative Test             |  |
|          | (T-)     |                 |                           | <b>Results = 104</b>      |  |
| Result   | Total    | Diseased= 30    | Non-Diseased=<br>100      | Sample size =<br>130      |  |

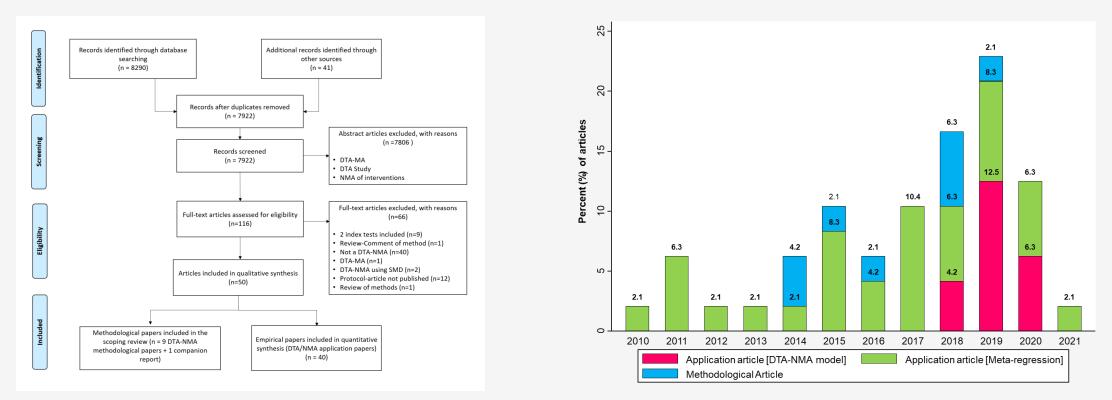
|        |                          | Index Test    | Index Test A Result |                           |  |  |
|--------|--------------------------|---------------|---------------------|---------------------------|--|--|
|        |                          | Positive (D+) | Negative (D-)       | Total                     |  |  |
|        | Positive                 | TP= 20        | FP= <b>10</b>       | Positive Test             |  |  |
| Index  | (T+)<br>Negative<br>(T-) | IP= 20        | LL= TO              | Results = <mark>30</mark> |  |  |
| IIIUEA |                          | FN= 10        |                     | Negative                  |  |  |
| Test B |                          |               | TN= <mark>90</mark> | <b>Test Results</b>       |  |  |
| Result |                          |               |                     | = 100                     |  |  |
| Result |                          |               | Non-                | Sample size               |  |  |
|        | Total                    | Diseased= 30  | Diseased=           | =                         |  |  |
|        |                          |               | 100                 | 130                       |  |  |

Individual Participant Data required





# **Application Papers**



- Majority employed bivariate/HSROC meta-regression models
- 2x2 tables were available for 32 networks
  - 8 of these reported data at multiple thresholds per study





### **DTA-NMA** in the literature

|                                       | Format of data<br>tables required <sup>a</sup> | Arm-based<br>model | Can model<br>imperfect<br>reference<br>standards | Can model<br>multiple<br>thresholds | Type of<br>studies that<br>can be<br>modelled | Bayesian<br>setting | Accounts for<br>correlation<br>between tests | Models more<br>than two index<br>tests | Software  |
|---------------------------------------|--|--------------------|--|-------------------------------------|---|---------------------|--|--|---|
| Bivariate<br>meta-regression [21]     | 2 × 2  | Yes                | No   | No                                  | Any   | No                  | No   | Yes                                    | R (CopulaDTA [24],Ime4 [25],<br>mada [26],meta4diag<br>[27],Metatron [28],Mvmeta [29]<br>Stata (meqrlogit [30]) |
| HSROC<br>meta-regression [22]         | 2 × 2  | Yes                | No   | Yes <sup>d</sup>                    | Any   | No                  | No   | Yes                                    | OpenBUGS/ WinBUGS<br>[31]R( <i>NMADiagT</i> [32])   |
| Trikalinos 2014 [5]                   | Joint<br>classification                        | Yes                | No   | No                                  | Single- /<br>Paired-test                      | Yes                 | Yes  | No <sup>b</sup>                        | R ( <i>rjags</i> [33])  |
| Menten-Lesaffre<br>2015 [4]           | 2 × 2  | No                 | Yes <sup>c</sup>                                 | No                                  | Paired- /<br>Multiple-test                    | Yes                 | No   | Yes                                    | OpenBUGS/ WinBUGS [31]  |
| Dimou 2016 [3]                        | Joint<br>classification                        | Yes                | No   | No                                  | Single- /<br>Paired-test                      | No                  | Yes  | No <sup>b</sup>                        | Stata ( <i>mvmeta</i> [34])   |
| Cheng 2016 [Model<br>A] [8]           | Joint<br>classification                        | Yes                | No   | No                                  | Any   | Yes                 | No   | Yes                                    | R (R2 <i>jags</i> [35])   |
| Cheng 2016 [Model<br>B] [8]           | Joint<br>classification                        | Yes                | No   | Yes <sup>d</sup>                    | Any   | Yes                 | No   | Yes                                    | R (R2 <i>jags</i> [35])   |
| Cheng 2016 [Model<br>C] [8]           | Joint<br>classification                        | Yes                | No   | No                                  | Any   | Yes                 | Yes  | Yes                                    | R (R2 <i>jags</i> [35])   |
| Nyaga (ANOVA)<br>2018 [2]             | 2 × 2  | Yes                | No   | No                                  | Any   | Yes                 | Yes  | Yes                                    | Stan ( <i>rstan</i> [36],[37] in R)   |
| Nyaga<br>(beta-binomial) 2018<br>[38] | 2 × 2  | Yes                | No   | No                                  | Any   | Yes                 | Yes  | Yes                                    | Stan ( <i>rstan</i> [36],[37] in R)   |
| Ma 2018 [9] <sup>e</sup>              | Joint<br>classification                        | Yes                | Yes  | No                                  | Any   | Yes                 | Yes  | Yes                                    | OpenBUGS/ WinBUGS [31], R<br>(NMADiagT [45])  |
| Owen 2018 [39]                        | 2 × 2  | Yes                | No   | Yes                                 | Any   | Yes                 | Yes  | Yes                                    | OpenBUGS/ WinBUGS [31]  |
| Lian 2019 [40]                        | Joint<br>classification                        | Yes                | Yes  | Yes <sup>u</sup>                    | Any   | Yes                 | Yes  | Yes                                    | Stan ( <i>rstan</i> [36],[37] in R), R<br>(NMADiagT [45])   |

<sup>a</sup> 2 × 2 data includes the number of true positives, true negatives, false positives and false negatives.



# **DTA-NMA** in the literature

**Bivariate meta-regression model** *Reitsma et al. (2005)* 

- A covariate for test type is used to explore sensitivity and specificity between tests
- Assumes that participants undergoing different tests are independent subgroups within each study
- Does not account for the within-study correlation between tests within study

ANOVA model Nyaga et al. (2018)

- A two-stage hierarchical model based on a two-way ANOVA model
- Allow for correlations between tests within study

#### **Beta-binomial model**

Nyaga et al. (2018)

- Sensitivity & specificity are directly modelled using a betabinomial defined in [0,1]
- Allow for correlations between tests within study

#### **Hierarchical Latent Class model**

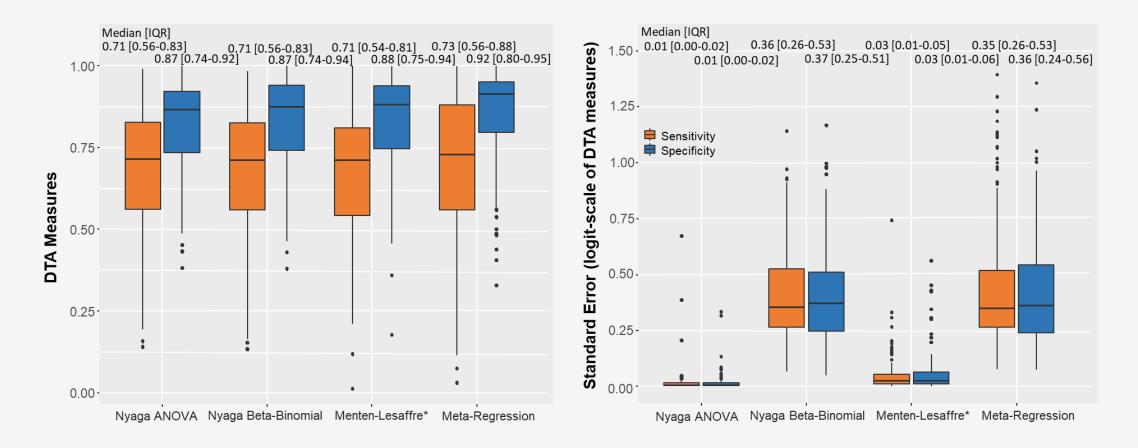
Menten and Lesaffre (2015)

- Based on differences (contrasts) between the different tests in the network
- Allows for imperfect reference standards
- Correlations between tests from the same study are ignored

#### Variance component model Owen et al. (2018)

- Allows for considering multiple thresholds
- Incorporates constraints on threshold effects

## Empirical assessment of the DTA-NMA methods



- Nyaga beta-binomial model estimated lower between study heterogeneity for both sensitivity and specificity
- Owen *et al.* model showed that different test thresholds included, may cause differences in results

#### In summary...

- Bivariate/HSROC meta-regression model:
  - It has been widely used over the years
  - Conservative approach and accessible to many review authors
  - But, it ignores the within-study correlation between tests assumes observations are independent
- More advanced methods and models have been developed
  - Most account for correlations between tests within a study
- NMA methodology of intervention studies is not applicable to DTA studies
  - Correlated observations tests are given to the same participants
  - Two effect sizes should be modelled (sensitivity & specificity) pairs of accuracy measures should be modelled in multivariate models (2K-variate, with K tests).
  - Network geometry differs single-test studies are presented (reference standard is not a node in the network)

#### In summary...

- Software and Model Complexity
  - most of the detected models use Bayesian setting
  - programming challenges code availability problems (including convergence issues)
  - time-consuming models (e.g., dataset with antigen COVID-19 tests required >48 hours to run the Nyaga ANOVA model)
- Datasets
  - within the same study different number of participants may receive the index tests of interest (i.e., missing participant data problem)
  - correlations between tests are frequently not available in the original DTA studies (i.e. the joint classification table is rarely provided in publications)



#### In summary...

- There is not a single valid method for DTA-NMA analysis
  - multiple factors influence the choice of model (data availability, test thresholds, study designs, software familiarity)
  - meta-regression models ignore the within-study correlation between tests
  - selection between the methods may impact on the NMA results, especially for specificity

- Some models require joint classification tables
  - individual participant data would make this information available
  - rarely reported in DTA studies
  - difficulties in their availability-data sharing

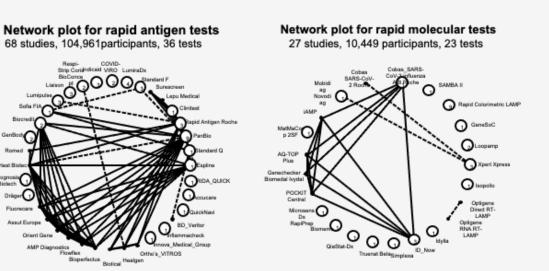


# **DTA-NMA Example**

More than a year ago Health Canada and the Public Health Agency of Canada commissioned the team to conduct a review to determine the most sensitive and/or specific rapid test for the diagnosis of COVID-19

| Veroniki et al. BMC Medicine (2023) 21:110<br>https://doi.org/10.1186/s12916-023-02810-0   | BMC Medicine   |
|--|--|
| REVIEW   | Open Access  |
| Rapid antigen-based and rapi<br>tests for the detection of SARS<br>review with network meta-an<br>test accuracy studies  | S-CoV-2: a rapid   |
| Areti Angeliki Veroniki <sup>1,2*</sup> , Andrea C. Tricco <sup>1,3,4</sup> , Jennifer Watt <sup>1</sup> , Sofia T.<br>Ahmed Negm <sup>6</sup> , Amanda Doherty-Kirby <sup>7</sup> , Paul Taylor <sup>7</sup> , Carole Lunny <sup>1</sup><br>Patrick Mallon <sup>9</sup> , David Moher <sup>10</sup> , Sabrina Wong <sup>11</sup> , Jacqueline Dinnes <sup>1</sup><br>Adrienne Chan <sup>13</sup> , Wanrudee Isaranuwatchai <sup>14</sup> , Bryn Lander <sup>15</sup> , Adrier | <sup>1</sup> , Jessie McGowan <sup>8</sup> , Julian Little <sup>8</sup> ,<br><sup>12</sup> , Yemisi Takwoingi <sup>12</sup> , Lynora Saxinger <sup>6</sup> , |





We set up our team considering to include the policy-makers who requested the evidence, at least one clinician/content expert, two patient partners, content experts, research methodologists, and statisticians.

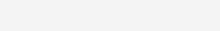
Sharon E. Straus<sup>1,2,17</sup>

# **Research Question**

Research question and eligibility criteria

- **Population**: Adults and/or children screened/suspected for COVID-19
- Index tests: We included studies evaluating one or more commercially available COVID-19 rapid lateral flow antigen test or rapid molecular test (providing a result in ≤1 hour) used for screening of asymptomatic individuals or the diagnosis of COVID-19 infection in symptomatic individuals
- *Target condition*: COVID-19 infection
  - **Reference Standard**: polymerase chain reaction (PCR) test
- **Study design**: We included RCTs and observational studies, providing the 2x2 table data
- **Outcome**: Sensitivity and specificity of rapid antigen and molecular tests suitable for screening and diagnosing COVID-19

Registered protocol with PROSPERO: CRD42021289712





#### Data analysis

- Limited to basic descriptive summary of studies
  - Country of conduct and type of rapid test
- Kept the analysis high-level:
  - Random-effects DTA meta-analysis (bivariate model)
  - Random-effects DTA-NMA (Nyaga ANOVA model)
- Estimated sensitivity and specificity for each test along with their 95% credible intervals
- Investigated potential sources of heterogeneity that may influence diagnostic accuracy using:
  - Subgroup analysis: symptom status (asymptomatic vs symptomatic), sample type (e.g., saliva, nasal swab), participant type (e.g., general public, healthcare worker), and rapid molecular test category (i.e., rRT-PCR, PT-Isothermal, RT-Lamp)
  - Meta-regression: age
- Assessed transitivity based on the distribution of the above potential effect modifiers across test comparisons

### **Report Findings**

Used reporting guidelines to ensure transparent and complete lacksquarereporting of our research approach and findings (e.g., PRISMA-DTA and PRISMA-NMA Checklist)

Cobas\_SARS-CoV-2 influenza A/B Roche

OigStat-Dv

Truenat Beta

SAMBA I

(9)

Rapid Colorimetric LAMP

GeneSoC

2 Loopamp

1 Isopollo

Optigene RNA

RT-I AMP

Optigene Direct

RT-LAME

Xpert Xpress

(1)

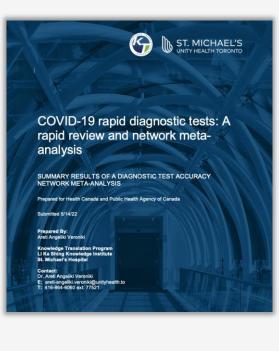
#### Network plot for rapid antigen tests Network plot for rapid molecular tests 68 studies, 104,961participants, 36 tests 27 studies, 10,449 participants, 23 tests (a) (b) Cobas SARS-LumiraD CoV-2 Roche Mobidia Lumipul \_epu Medical Sofia FIA Biocred Rapid Antigen Roche MatMaCorp 2SF GenBody Romed AQ-TOP Plus Certest Biotec Genechecker Bion lvydal Prognosis Biotech RIDA\_QUICK POCKIT Dräger Central Fluorecare MicrosensDx RapiPrep OuickNa (1)Assut Europe (1)Biomeme Orient Ge $\begin{pmatrix} 1 \end{pmatrix}$

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Ortho's VITROS

Healgen

Biotical





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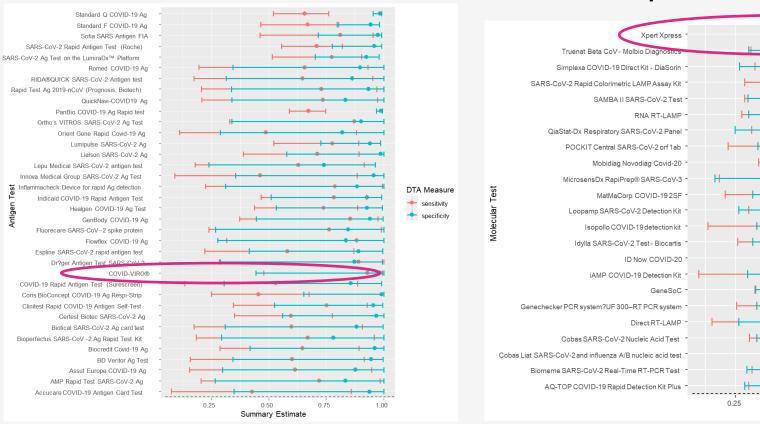
AMP Diagnostic

Flowflex

Bioperfectus

#### Summarized results DTA-NMA results

#### Rapid antigen tests



DTA Measure

🔶 sensitivity

+ specificity



0.50

Summary Estimate

0.75

1.00

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### **Report Findings**



 Used reporting guidelines to ensure transparent and complete reporting of our research approach and findings

(e.g., PRISMA-DTA and PRISMA-NMA Checklist)

#### Summarized results from the bivariate DTA meta-analysis model

|                      |  |             | Summary estimates    |                      | Heterogeneity standard deviation |             |
|----------------------|--|-------------|----------------------|----------------------|----------------------------------|-------------|
| Туре                 | Test # Studies (# patients)            |             | Sensitivity (95% CI) | Specificity (95% CI) | Sensitivity                      | Specificity |
| Rapid molecular test | Xpert Xpress                           | 5 (763)     | 0.98 (0.94, 1.00)    | 0.98 (0.94, 0.99)    | 0.79                             | 0.53        |
| Rapid antigen test   | Standard Q COVID-19 Ag                 | 13 (8740)   | 0.72 (0.53, 0.86)    | 0.99 (0.98, 1.00)    | 1.49                             | 1.82        |
|                      | PanBio COVID-19 Ag Rapid test (Abbott) | 16 (32,151) | 0.72 (0.61, 0.81)    | 0.99 (0.99, 1.00)    | 0.98                             | 1.72        |
|                      | SARS-CoV-2 Rapid Antigen Test (Roche)  | 7 (6065)    | 0.77 (0.55, 0.90)    | 0.99 (0.96, 1.00)    | 1.33                             | 1.52        |
|                      | Standard F COVID-19 Ag                 | 5 (6428)    | 0.65 (0.50, 0.78)    | 0.98 (0.97, 0.99)    | 0.67                             | 0.41        |



# There is still a lot to explore!

- Explore which factors impact on the performance of the DTA-NMA methods
- Extend the ranking metrics for multiple outcomes to DTA-NMA methods
- **DTA-NMA assumptions**: Appropriate methods are needed to explore the consistency assumption in DTA-NMA accounting for both sensitivity and specificity
- New methods are necessary to deal with and account for different study designs in a DTA-NMA



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Ridhi Agarwald · Eirini Pagkalidou · Gerta Rücker · Dimitris Mavridis · Yemisi Takwoingi

Diagnostic test accuracy network meta-analysis methods: A scoping review and empirical assessment

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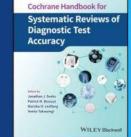
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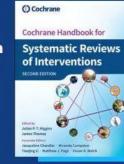
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