## Prognosis of infectious diseases

A plea for meta-analysis of individual participant data

#### **Thomas Debray**



#### About me

### Background in biostatistics, epidemiology & machine learning

- Assistant Professor
- Founder
- Affiliated Researcher
- Honorary Senior Research Associate
- Honorary Departmental Senior Research Fellow







Estimate something that is yet unknown

- Presence of a certain disease (diagnosis)
- Future occurrence of a particular event (prognosis)







Calculate the absolute risk (probability) for distinct individuals

Example: What is my risk of having a coronavirus-19 infection?

Equally



Impossible	Unlikely	Likely	Likely	Certain
0	1	1/2	34	1
0	0.25	0.5	0.75	1
0%	25%	50%	75%	100%
$\bigcirc$	$\bigcirc$			$\bigcirc$







What is my risk of being diseased with coronavirus-19?

#### **COVID-19 Early Warning Score (COVID-19 EWS)**

Parameters	Assessment	Score		
Signs of pneumonia on CT	Yes	5		
History of close contact with COVID-19 confirmed patient	Yes	5		
Fever	Yes	3		
Age	≥ 44 years old	1		
Sex	Male	1		
Tmax <sup>a</sup>	≥ 37.8 °C (100 °F )	1		
Meaningful respiratory symptoms (including cough, expectoration, and dyspnea)	≥ 1 sympotom	1		
NLR <sup>b</sup>	≥ 5.8	1		
Highly suspected patient				
*SARS-CoV-2 nucleicacid detection positive is the independent diagnostic indicator.				

a Tmax: the highest body temperature from illness onset to first hospital admission bNLR: neutrophil-to-lymphocyte ratio



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#### What is my risk of being diseased with coronavirus-19? Quite low!

#### **COVID-19 Early Warning Score (COVID-19 EWS)**



## Why do we predict?

To support clinical decision-making for individual patients

- Inform patients and their families
- Decide upon further testing (e.g. magnetic resonance imaging)
- Decide upon patient referral (e.g. to secondary care)
- Targeting prevention strategies (e.g. vaccination)
- Guide treatment decisions (e.g. chemotherapy)







#### How to develop a prediction model?

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#### Adopt regression modeling and/or machine learning methods





## The reality of (most) prediction models

Many prediction models perform more poorly than anticipated, do not affect clinical practice, or are implemented for the wrong reasons

- Small & poor quality studies
- Limited variation in studied patients, settings or populations
- Lack of validity and effectiveness assessments







## Prediction models for COVID-19

#### RESEARCH

the**bm** 

# OPEN ACCESS Prediction models for diagnosis and prognosis of covid-19: Systematic review and critical appraisal

Laure Wynants,<sup>1,2</sup> Ben Van Calster,<sup>2,3</sup> Gary S Collins,<sup>4,5</sup> Richard D Riley,<sup>6</sup> Georg Heinze,<sup>7</sup> Ewoud Schuit,<sup>8,9</sup> Marc M J Bonten,<sup>8,10</sup> Johanna A A Damen,<sup>8,9</sup> Thomas P A Debray,<sup>8,9</sup> Maarten De Vos,<sup>2,11</sup> Paula Dhiman,<sup>4,5</sup> Maria C Haller,<sup>7,12</sup> Michael O Harhay,<sup>13,14</sup> Liesbet Henckaerts,<sup>15,16</sup> Nina Kreuzberger,<sup>17</sup> Anna Lohmann,<sup>18</sup> Kim Luijken,<sup>18</sup> Jie Ma,<sup>5</sup> Constanza L Andaur Navarro,<sup>8,9</sup> Johannes B Reitsma,<sup>8,9</sup> Jamie C Sergeant,<sup>19,20</sup> Chunhu Shi,<sup>21</sup> Nicole Skoetz,<sup>17</sup> Luc J M Smits,<sup>1</sup> Kym I E Snell,<sup>6</sup> Matthew Sperrin,<sup>22</sup> René Spijker,<sup>8,9</sup> Ewout W Steyerberg,<sup>3</sup> Toshihiko Takada,<sup>4</sup> Sander M J van Kuijk,<sup>23</sup> Florien S van Royen,<sup>8</sup> Christine Wallisch,<sup>7,24,25</sup> Lotty Hooft,<sup>8,9</sup> Karel G M Moons,<sup>8,9</sup> Maarten van Smeden<sup>8</sup>

**Results**: 4909 titles were screened, and 51 studies describing 66 prediction models were included (31 march 2020)



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**FAST TRACK** 

## Prediction models for COVID-19

Status quo: 66 prediction models

- 3 models for predicting hospital admission from pneumonia
- 47 diagnosis models for COVID-19 or COVID-19 pneumonia
  - 34 based on medical images (deep learning)
- **16 prognosis models** for predicting mortality risk, progression to severe disease, or length of stay





## Prediction models for COVID-19

Critical appraisal using PROBAST

Assess risk of bias on **four domains** using "signaling questions"

- Participants (2 questions)
- Predictors (3 questions)
- Outcome (6 questions)
- Analysis (9 questions)

If risk of bias was high in at least one domain, overall risk of bias was judged to be high





## Prediction models for COVID-19: critical appraisal

- Participants domain: 24/51 at high risk of bias
  - Non-representative of the target population (e.g., non-consecutive patients)
- Predictors domain: 6/51 at high risk of bias
  - Predictors not available at time of intended model use
- Outcome domain: 18/51 at high risk of bias
  - Subjective or proxy outcomes
- Analysis domain: 50/51 at high risk of bias
  - Small sample size (->overfitting & no adjustment), incomplete reporting of model performance (e.g., no calibration)

All studies at high risk of bias

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## Prediction models for COVID-19: what is the problem?

- Available data sources
  - Are often small
  - Entail a particular setting or population (e.g. single hospital)
- Prediction model studies
  - Are hastily conducted
  - Adopt inappropriate statistical methods
  - Do not adequately report methods & results

The majority of developed prediction models are unreliable and unsuitable for use in routine care.





### How to move forward?

Collaborative research is urgently needed

- To defragment ongoing research activities
- To improve the overall quality and validity of COVID-19 related prediction models

3 strategies:

- Formation of international consortia
- Development of data sharing platforms
- Meta-analysis of individual participant data







## Improving collaborative research

# Re CoD ID

#### **Reconciliation of Cohort Data for Infectious Diseases**



Intellectual Property

 Public platform

 where cohort meta 

 data can be uploaded.

 Potential users can

 contact the owners, to

 get access to the data

 (or the data is freely

 available).

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#### Technology

"Cohort Cloud,, Hosting the data Supported by the Danish Computerome and EMBL

"PEARL, solutions - politial, ethical, administrative, regulatory, legal

www.recodid.eu



#### Improving collaborative research

Re CoDID



• "... we will [...] bridge infectious disease cohorts and the open science community to ensure that populations in **the global south** are not left behind by the **personalized medicine revolution**".







### Improving collaborative research: Zika Virus



#### Zika Virus Individual Participant Data Consortium

- Global collaboration to streamline an international response to ZIKV
  - Studies and surveillance systems
  - Data from Brazil, Colombia, Ecuador, Cuba , St Martin, Martinique, Mexico, Guadaloupe, French Guyana, Honduras, Haiti, Jamaica, Panama, El Salvador, Spain, Suriname, and Venezuela
- Sharing of deidentified participant level data
  - To perform a pooled cohort analysis
  - To investigate the relation between Zika virus infection during pregnancy and adverse fetal, infant and child outcomes





#### Improving collaborative research: Zika Virus

#### Zika Virus Individual Participant Data Consortium

Epidemiology Protocol

Understanding the relation between Zika virus infection during pregnancy and adverse fetal, infant and child outcomes: a protocol for a systematic review and individual participant data meta-analysis of longitudinal studies of pregnant women and their infants and children











## Improving collaborative research: COVID-19



Large consortium to validate existing models for COVID-19

- Lead by UMC Utrecht (the Netherlands)
- Summarize performance and explore sources of heterogeneity

Partners from

- Europe (the Netherlands, Switzerland, Sweden, UK)
- America (USA)
- Asia (China, Singapore)

We are looking for more partners







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#### Slides

Prediction models for COVID-19 – Maarten van Smeden

#### Images

<u>Deep Learning</u> - <u>https://ai.googleblog.com/2018/05/deep-learning-for-electronic-health.html</u> <u>Probabilities</u> - <u>http://mathfor7thgrade.weebly.com/probability.html</u> <u>COVID-19 score</u> - <u>https://www.medrxiv.org/content/10.1101/2020.03.05.20031906v1</u> <u>Collaboration</u> - <u>https://www.nature.com/articles/d41586-018-06037-5</u>



