



UMC Utrecht  
Julius Center

# Individual Participant Data (IPD) Meta-analysis of prediction modelling studies

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*for the Cochrane IPD Meta-analysis Methods Group*

*(Co-convenors: Jayne Tierney, Mike Clarke, Lesley Stewart,  
Maroeska Rovers)*

# Conflict of interest

**We have developed and validated several multivariable prediction models.**

**We performed several individual patient data meta-analyses, in addition to methodological work**

**We have no actual or potential conflict of interest in relation to this presentation**



# Prediction models: dynamic world

- Waves of new biomarkers and prediction models
- Increasing pressure for their evaluation
- Recognition of the importance of external validation
- Performance of models is likely to be variable
- Individual patient data: insight why models vary in performance or to build more robust models
- Improvements in methodology



# Illustration

[https://www.youtube.com/watch?v=OM\\_X\\_Czujrs&feature=player\\_detailpage](https://www.youtube.com/watch?v=OM_X_Czujrs&feature=player_detailpage)



# Workshop objectives

Provide guidance to conduct individual participant data (IPD) meta-analysis in prediction research

- To explain key concepts in prediction research
- To describe potential benefits of IPD
- To identify challenges for IPD reviews
- To provide examples of IPD meta-analyses
- To illustrate basic and novel methods



# Prediction

- Risk prediction = foreseeing / foretelling  
... (probability) of something that is yet unknown
- Turn available information (predictors) into a statement about the probability:
  - ... of having a particular disease -> diagnosis
  - ... of developing a particular event -> prognosis

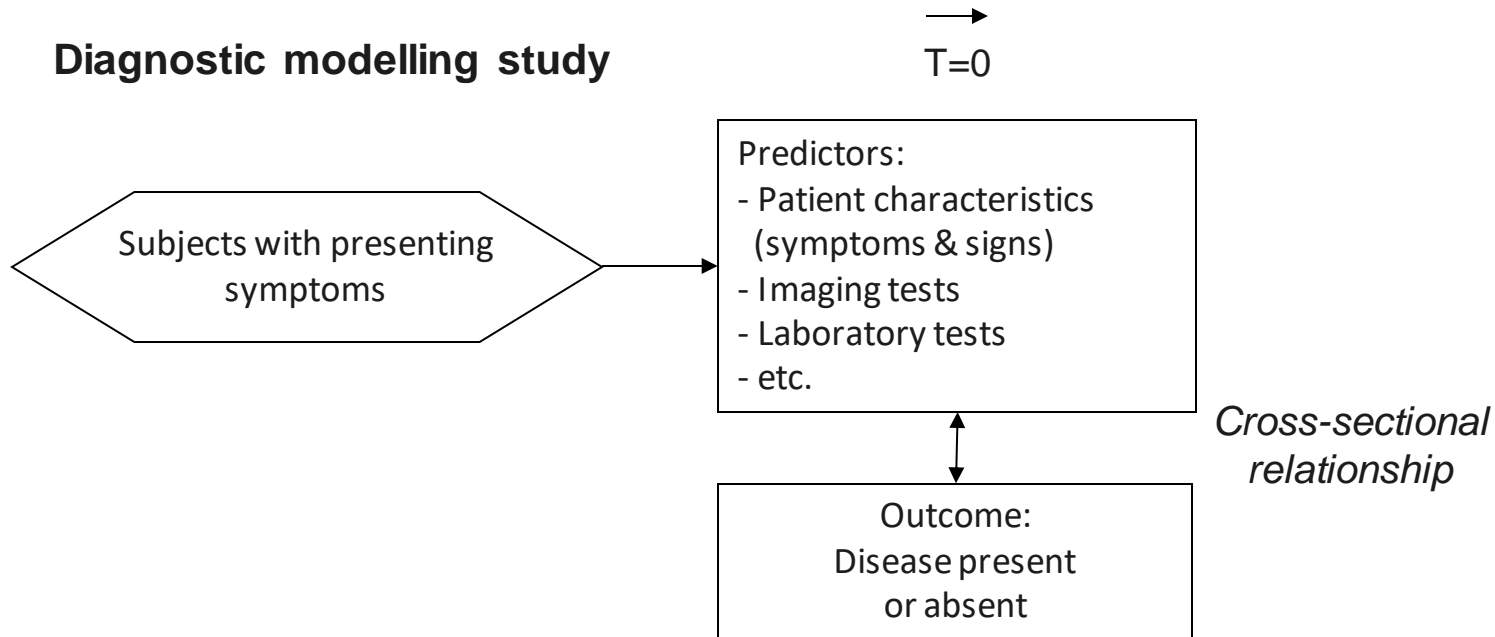


# Multivariable prediction models

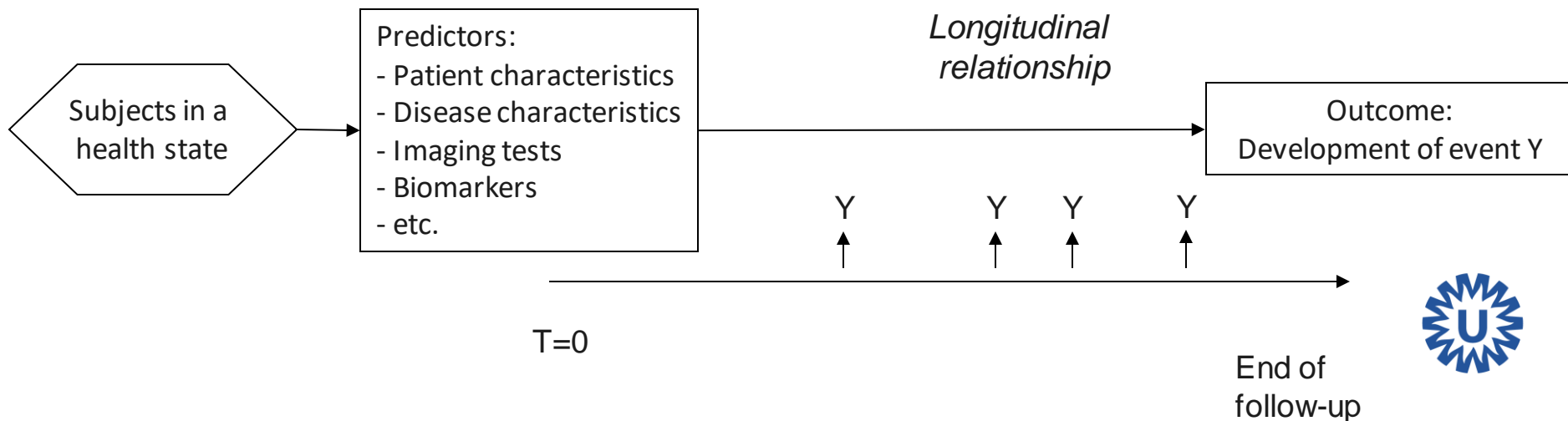
- To calculate absolute risk based on individual profile
- Predict outcome from demographic, patient and disease characteristics (predictors, covariates, risk factors, X variables)
- Use of regression models, two main types:
  - Logistic regression
  - Time-to-event analysis (Kaplan-Meier, Cox)
- Statistical modelling: (1) overlap in information from different predictors; (2) acknowledge strength of each predictor



## Diagnostic modelling study



## Prognostic modelling study





# Prediction models

Predictors (in both diagnostic & prognostic models) are from:

- history taking
- physical examination
- tests (imaging, ECG, biomarkers, genetic 'markers')
- disease severity
- therapies received



# Prediction models

Presented as:

- Mathematical formula requiring computer
- Simple scoring rules
- Score charts / Nomograms



## Women

## Men

Non-smoker      Smoker

Age

Non-smoker      Smoker

180	7	8	9	11	14
160	5	6	7	8	10
140	3	4	5	6	7
120	2	3	3	4	5

65

180	12	14	17	22	27
160	8	10	13	16	20
140	6	7	9	11	14
120	4	5	6	8	10

180	4	4	5	6	8
160	3	3	4	5	6
140	2	2	3	3	4
120	1	2	2	2	3

60

180	8	9	12	15	18
160	5	7	8	11	13
140	4	5	6	8	10
120	3	3	4	5	7

180	2	2	3	3	4
160	1	2	2	2	3
140	1	1	1	2	2
120	1	1	1	1	2

55

180	5	6	7	9	12
160	3	4	5	7	9
140	2	3	4	5	6
120	2	2	3	3	4

180	1	1	1	2	2
160	1	1	1	1	1
140	0	1	1	1	1
120	0	0	0	1	1

50

180	3	4	4	6	7
160	2	3	3	4	5
140	1	2	2	3	4
120	1	1	2	2	3

180	0	0	0	0	0
160	0	0	0	0	0
140	0	0	0	0	0
120	0	0	0	0	0

40

180	1	1	1	2	2
160	1	1	1	1	2
140	0	1	1	1	1
120	0	0	0	1	1

Systolic blood pressure (mmHg)

3 4 5 6 7

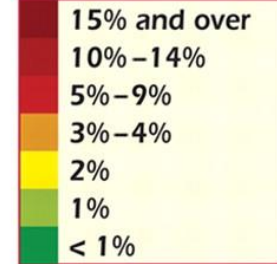
3 4 5 6 7

3 4 5 6 7

3 4 5 6 7

Total cholesterol: HDL  
Cholesterol ratio

# SCORE



10-year risk of fatal CVD in populations at high CVD risk

© ESC 2007



# Predicting bacterial cause in conjunctivitis

**Table 3** Results of logistic regression analysis. Independent indicators of positive bacterial culture and their clinical score

Indicator	Odds ratio (95% CI)	Regression coefficient	Clinical score*
Two glued eyes	14.99 (4.36 to 51.53)	2.707	5
One glued eye	2.96 (1.03 to 8.51)	1.086	2
Itching	0.54 (0.26 to 1.12)	-0.61	-1
History of conjunctivitis	0.31 (0.10 to 0.96)	-1.161	-2
Area under ROC curve (95% CI)	0.74 (0.65 to 0.82)	-	-

ROC=receiver operating characteristics.

\*Clinical scores of every symptom present are added up. For example, a patient with two glued eyes, itch, and no history of conjunctivitis has a clinical score of:  $5 + -1 = 4$ .



# Predicting bacterial cause in conjunctivitis

Clinical score	Percentage (95% CI) predicted positive cultures†
+5	77 (57 to 90)
+4	65 (47 to 79)
+3	51 (23 to 79)
+2¶	40 (26 to 55)
+1	27 (17 to 39)
0	18 (7 to 38)
-1	11 (4 to 26)
-2	7 (2 to 28)
-3	4 (1 to 15)



# Pitfalls of prediction research

- The **quality** of much prognosis research is poor (incomplete reporting, poor data sharing, incomplete registrations, absent study protocols)
- Development dataset often **too small or too local**
- Most prediction models are never validated in independent data (**external validation**)
- **Heterogeneity** across studies and settings, requiring local adjustments
- Many prediction models **generalize poorly** across different but related study populations, and tend to perform more poorly than anticipated when applied in routine care



# Meta-analysis of individual participant data

## Opportunities

- Increase total sample size
  - Reduce risk of overfitting
  - Ability to investigate more complex associations
- Increase available case-mix variability -> enhances the model's potential generalisability
- Ability to standardize analysis methods across IPD sets
- Ability to evaluate generalisability and usability of prediction models across different situations



# Meta-analysis of individual participant data

## IPD – are we realistic?

- Researchers **protective** over their own data
- Worried about Data Protection Act (**ethics**) – however, no need to include patient ID numbers
- **Cost, time** – when does it become worthwhile?

To conduct better prognostic & diagnostic research we need:

- To be prepared to **collaborate** and share data to make IPD available – in paper, on Web, on request
- To be involved in **prospectively planned** pooled analyses





# Meta-analysis of individual participant data

## Why do we need specific guidance?

Evidence synthesis currently gold standard for summarizing relative treatment effects – many methods available!

However,

- Meta-analysis models cannot *mutate mutandis* be applied to prediction modeling studies
- Researchers often simply combine all IPD, and produce a prediction model averaged across all study populations
- There are major differences in the aims, design and analysis of primary studies between prediction modeling and intervention studies!



# What are the main differences between prediction and intervention research?

Intervention research	Prediction research
<b>Aim(s)</b> <ul style="list-style-type: none"><li>• Estimation of therapeutic effect of a specific treatment</li><li>• Study treatment effect in subgroups</li></ul>	<b>Aim(s)</b> <ul style="list-style-type: none"><li>• Estimation of absolute risk probabilities for distinct individuals across different populations or subgroups</li><li>• Evaluate accuracy of model predictions across subgroups</li></ul>
<b>Association measures:</b> relative risk estimates	<b>Association measures:</b> absolute probability of risk estimates
<b>Study design:</b> Randomized studies	<b>Study design:</b> observational research
<b>Evaluation:</b> bias and precision of estimated comparative treatment effects	<b>Evaluation:</b> model discrimination and calibration



# Types of IPD-MA of prediction modeling studies

1. Validation and comparison of existing model(s)
2. Improving upon existing model(s)
  - Updating
  - Added value of novel marker
3. Development of new model(s)



# Validation and comparison of existing model(s)

Apply meta-analysis to:

- Summarize estimates of model discrimination and calibration



Use IPD to:

- Investigate sources of heterogeneity in model performance
- Identify which models perform best in what (sub)population, setting or country



# Validation and comparison of existing model(s)

After a systematic review to identify which models existed, an IPD was initiated

Articles



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## Non-invasive risk scores for prediction of type 2 diabetes (EPIC-InterAct): a validation of existing models



*Andre Pascal Kengne, Joline W J Beulens, Linda M Peelen, Karel G M Moons, Yvonne T van der Schouw, Matthias B Schulze, Annemieke M W Spijkerman, Simon J Griffin, Diederick E Grobbee, Luigi Palla, Maria-Jose Tormo, Larraitz Arriola, Noël C Barengo, Aurdio Barricarte, Heiner Boeing, Catalina Bonet, Françoise Clavel-Chapelon, Laureen Dartois, Guy Fagherazzi, Paul W Franks, José María Huerta, Rudolf Kaaks, Timothy J Key, Kay Tee Khaw, Kuanrong Li, Kristin Mühlenbruch, Peter M Nilsson, Kim Overvad, Thure F Overvad, Domenico Palli, Salvatore Panico, J Ramón Quirós, Olov Rolandsson, Nina Roswall, Carlotta Sacerdote, María-José Sánchez, Nadia Slimani, Giovanna Tagliabue, Anne Tjønneland, Rosario Tumino, Daphne L van der A, Nita G Forouhi, Stephen J Sharp, Claudia Langenberg, Elio Riboli, Nicholas J Wareham*

The Lancet, Diabetes & Endocrinology (2014)



# Validation and comparison of existing model(s)

## IPD meta-analysis

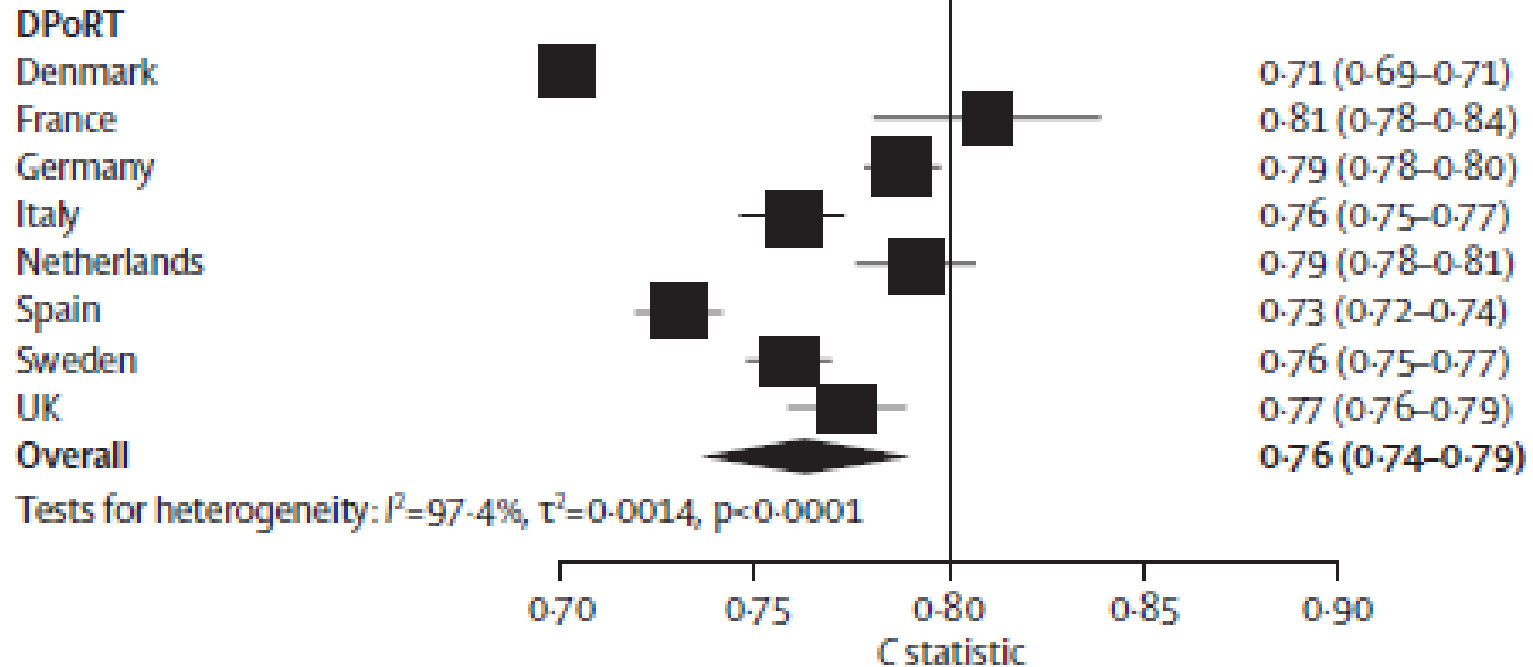
- EPIC-InterAct international study
  - 27,779 participants of whom 12,403 with incident diabetes
  - 8 countries
- External validation of 12 literature models (with non-laboratory based variables)
  - Discrimination: c-statistic
  - Calibration: calibration plot, ratio expected versus observed
  - Other performance measures: Yates slope, Brier score



# Validation and comparison of existing model(s)

## Discrimination of model "DPoRT"

(overall and by country)



Prediction of incident type 2 diabetes at 10 years of follow-up



# Improving upon existing model(s)

Different types of improvements

- Adjusting baseline risk (e.g. intercept term)
- Adjusting common slope
- Updating individual predictor effects
- Adding new predictors or (bio)markers
- Removing exiting predictors

Aim: Tailor the model(s) to specific (sub)populations, settings or countries





# Improving upon existing model(s)

**Example:** Majed and colleagues evaluated whether the calibration of the Framingham risk equation for coronary heart disease and stroke improved by applying local adjustments.

	E:O ratio			C statistic		
	O	R	L	O	R	L
PRIME-total	1.94	0.98	1.00	0.68	0.68	0.68
PRIME-France	2.23	0.99	1.00	0.67	0.67	0.68
PRIME-Ireland	1.42	0.99	1.00	0.67	0.67	0.67

Ref: Majed *et al. Preventive Medicine* 2008 **57**.



# Improving upon existing model(s)

Apply meta-analysis to:

- Summarize estimates of added value
  - Adjusted predictor effects
  - Improvement in model calibration
  - Improvement in model discrimination
  - Improvement in model reclassification

Use IPD to:

- Investigate sources of heterogeneity in added value
- Identify relevant subgroups that yield different added value



# Improving upon existing model(s)

**Example:** The clinical usefulness of carotid intima-media thickness measurements (CIMT) in cardiovascular risk prediction

**Background:** problems with Framingham risk score in predicting CVD risk

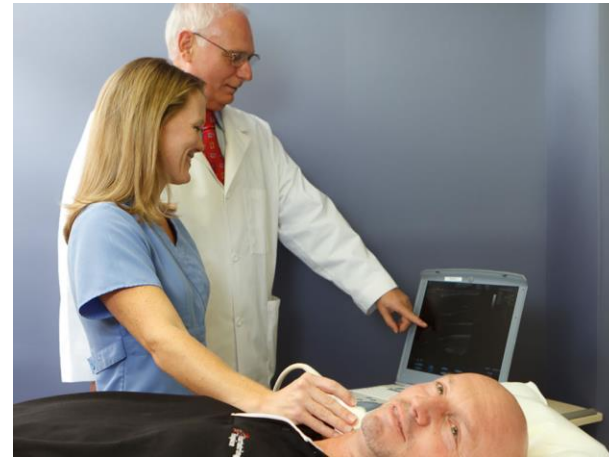
- No events despite high risk
- Many events in low risk categories

(Hester den Ruijter, Department of experimental cardiology, Julius Center for Health Sciences and Primary Care)



# Improving upon existing model(s)

B-mode ultrasound measurement of the Carotid Intima Media Thickness (CIMT)



[https://www.youtube.com/watch?v=OM\\_X\\_Czujrs&feature=player\\_detailpage](https://www.youtube.com/watch?v=OM_X_Czujrs&feature=player_detailpage)



# Improving upon existing model(s)

Improvement in CVD risk prediction: incorporation of non-invasive measurement of **atherosclerosis** by means of CIMT measurements

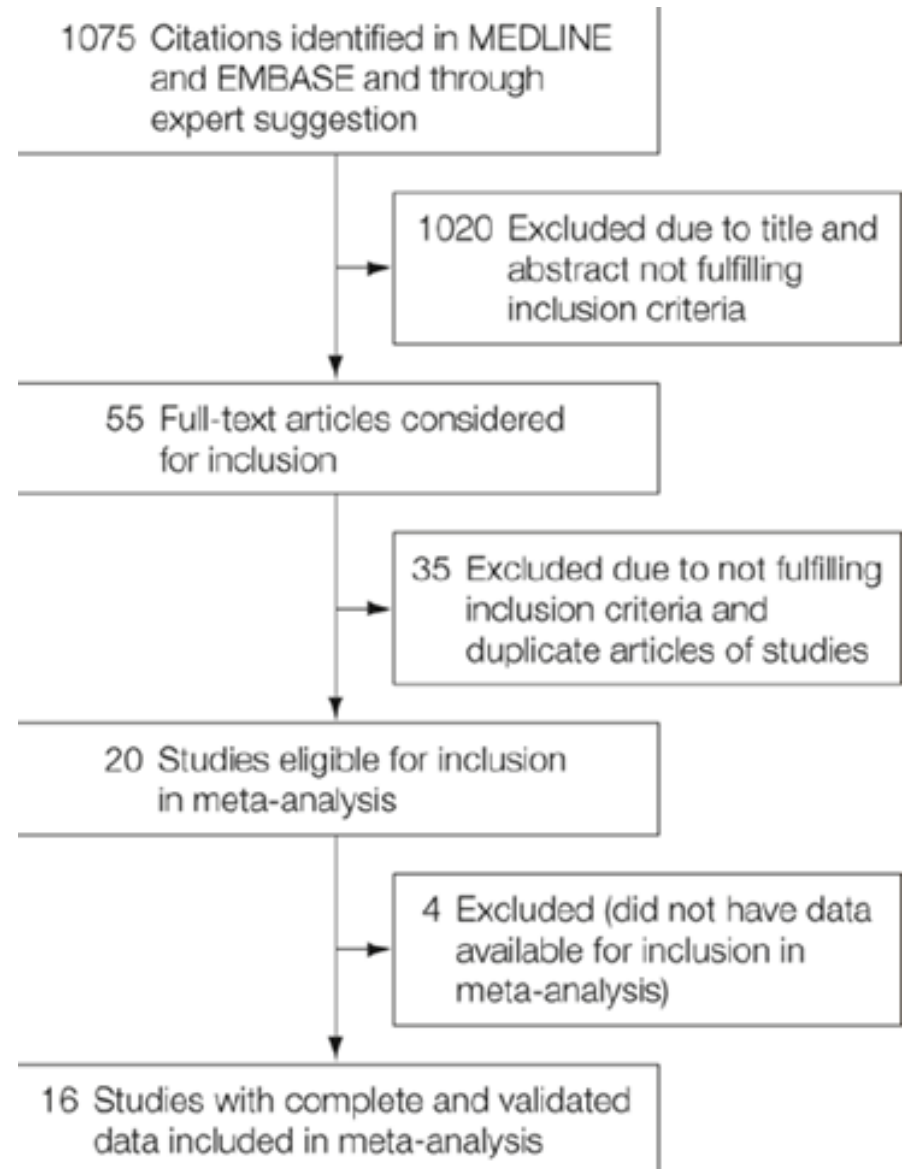
- Reflects long-term exposure to risk factor levels
- Predicts future cardiovascular events
- Modifiable by treatment
- Intermediate between risk factors and events



# Improving upon existing model(s)

## USE-IMT collaboration

- Ongoing individual participant data meta-analysis of general population
- Studies were invited to participate when they had data on Framingham risk score, CIMT measurements and follow-up to CVD



# Improving upon existing model(s)

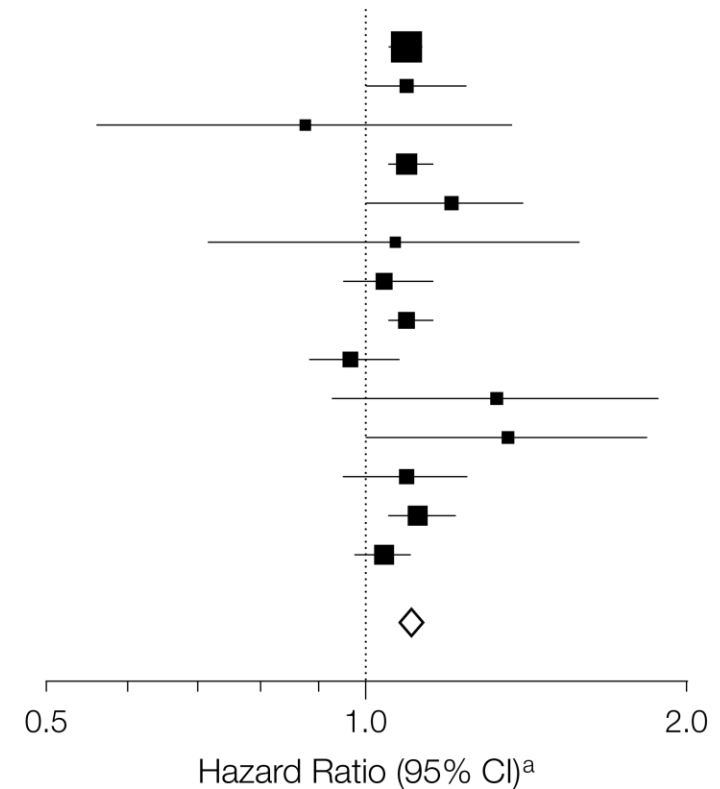
- Two Cox proportional hazards models with stroke and MI
  - FRS (refit age, gender, cholesterol, blood pressure, smoking, blood pressure medication)
  - FRS (refit age, gender, cholesterol, blood pressure, smoking, blood pressure medication) + **CIMT**
- Do these two models reclassify patients differently?

FRS = Framingham Risk Score



# Improving upon existing model(s)

Source	Contribution to Total USE-IMT Population, % of Total	Hazard Ratio (95% CI) <sup>a</sup>
ARIC, <sup>25</sup> 1994	31	1.11 (1.08-1.14)
CAPS, <sup>26</sup> 2006	8	1.10 (0.99-1.23)
Charlottesville, <sup>27</sup> 2006	1	0.88 (0.56-1.36)
CHS, <sup>28</sup> 2007	7	1.11 (1.06-1.16)
FATE, <sup>8</sup> 2011	3	1.20 (1.01-1.42)
Hoorn Study, <sup>29</sup> 2003	1	1.07 (0.72-1.59)
KIHD, <sup>30</sup> 1991	2	1.05 (0.96-1.16)
Malmö, <sup>31</sup> 2000	10	1.10 (1.04-1.17)
MESA, <sup>32</sup> 2007	13	0.98 (0.89-1.08)
Nijmegen Study, <sup>33</sup> 2009	3	1.34 (0.94-1.90)
NOMAS, <sup>34</sup> 2007	2	1.36 (0.99-1.85)
OSACA2 Study, <sup>35</sup> 2007	1	1.09 (0.96-1.24)
Rotterdam Study, <sup>36</sup> 1997	8	1.13 (1.06-1.20)
Tromsø Study, <sup>37</sup> 2000	9	1.04 (0.98-1.10)
<i>I</i> <sup>2</sup> = 12.30%; Q test for heterogeneity, <i>P</i> = .24		1.09 (1.07-1.12)





# Improving upon existing model(s)

**A** Distribution of 45 828 individuals without and with events in USE-IMT across risk categories

**Without events**

		Framingham Risk With CIMT		
		<5%	5%-20%	>20%
Framingham Risk	<5%	20271 →	867	-
	5-20%	1115	← 17280 →	362
	>20%		315	← 1611

**Total without events, No. (%)**

39 162 (93.6%)	No change
1229 (2.9%)	Up classification
1430 (3.4%)	Down classification

**With events**

		Framingham Risk With CIMT		
		<5%	5%-20%	>20%
Framingham Risk	<5%	537 →	67	-
	5-20%	69	← 2410 →	102
	>20%		85	← 737

**Total with events, No. (%)**

3684 (91.9%)	No change
169 (4.2%)	Up classification
154 (3.8%)	Down classification



# Improving upon existing model(s)

## Conclusion

The **added value of common CIMT** in 10-year risk prediction of cardiovascular events, in addition to the Framingham risk score, **is small and unlikely to be of clinical importance**

Den Ruijter et al. , JAMA 2012



# Developing a new prediction model

## Main opportunities

- Increase total sample size
  - Avoid overfitting
  - Investigate more complex associations
- Increase available case-mix variability
  - Improve generalizability of risk predictions
  - Assess model performance across different settings and populations



# Developing a new prediction model

## Prognosis of amyotrophic lateral disease

- IPD-MA
  - 14 cohort studies (specialized ALS centres)
- Sample size
  - 190 to 1,936 per study (total N = 11,475)
- Composite endpoint
  - Non-invasive ventilation for more than 23h/day, or death
  - Total number of events  $E = 8,819$
- Median follow-up: 97.5 months

Development of the NCALS model



# Developing a new prediction model



## THE LANCET Neurology

Volume 17, Issue 5, May 2018, Pages 423-433



### Articles

## Prognosis for patients with amyotrophic lateral sclerosis: development and validation of a personalised prediction model

Henk-Jan Westeneng MD <sup>a</sup>, Thomas P A Debray PhD <sup>b, c</sup>, Anne E Visser MD <sup>a</sup>, Ruben P A van Eijk MD <sup>a</sup>, James P K Rooney MSc <sup>d</sup>, Andrea Calvo MD <sup>e</sup>, Sarah Martin BSc <sup>f</sup>, Prof Christopher J McDermott PhD <sup>g</sup>, Alexander G Thompson BMBCh <sup>h</sup>, Susana Pinto PhD <sup>i</sup>, Xenia Kobeleva MD <sup>j</sup>, Angela Rosenbohm MD <sup>k</sup>, Beatrice Stubendorff PhD <sup>l</sup>, Helma Sommer <sup>m</sup>, Bas M Middelkoop <sup>a</sup>, Annelot M Dekker MD <sup>a</sup>, Joke J F A van Vugt PhD <sup>a</sup>, Wouter van Rheenen MD <sup>a</sup> ... Prof Leonard H van den Berg MD <sup>a</sup>  



# Developing a new prediction model

## Prognosis of amyotrophic lateral disease

- Royston-Parmer survival model with country-specific (but proportional) baseline hazard

Variable	Value
$\gamma_0$	-6.409
$\gamma_1$	2.643
$\gamma_2$	-0.546
$\gamma_3$	0.585
$\beta_1$ (ALSFERS-R slope)	-1.837
$\beta_2$ (Diagnostic delay)	-2.373
$\beta_3$ (Age at onset)	-0.267
$\beta_4$ (Forced vital capacity)	0.477
$\beta_5$ (Bulbar onset)	0.269
$\beta_6$ ('Definite' ALS*)	0.233
$\beta_7$ (Frontotemporal dementia)	0.388
$\beta_8$ (C9orf72 repeat expansion)	0.256

Supplementary Table S15. Parameters of the final prediction model. \*According to the El Escorial criteria.



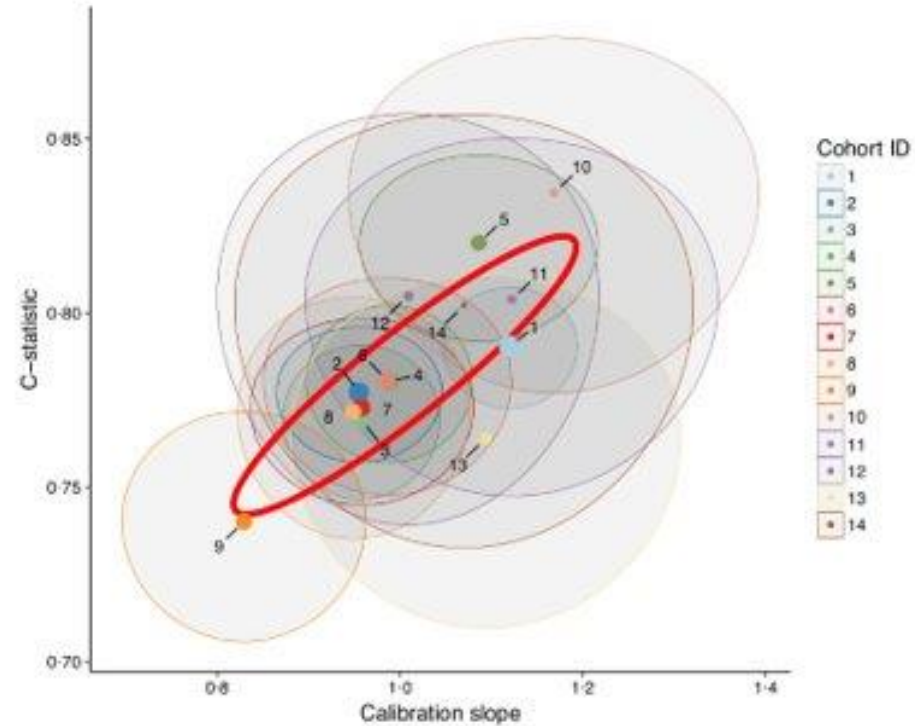
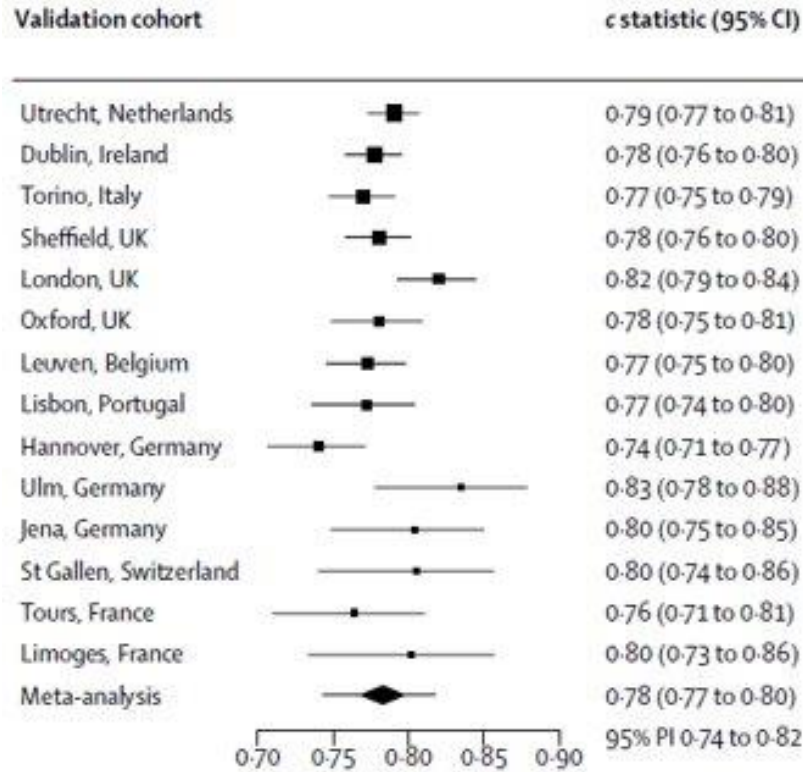
# Developing a new prediction model

Iteratively develop pre-defined model in 13 studies, and externally validate in remaining study (**Internal-external cross-validation**)

- Meta-analysis of concordance statistic
  - Summary estimate: **0.78** (0.77 to 0.80)
  - 95% PI: 0.74 to 0.82
- Meta-analysis of calibration-in-the-large
  - Summary: **-0.12** (-0.33 to 0.08)
  - 95% PI: -0.88 to 0.63
- Meta-analysis of calibration slope
  - Summary: **1.01** (0.95 to 1.07)
  - 95% PI: 0.83 to 1.18



# Developing a new prediction model





# Developing a new prediction model

Measure	Criteria	Prob. of “good” performance	Joint probability
Concordance statistic	$> 0.70$	100%	98.3%
Calibration slope	0.80 to 1.20	97.1%	
Calibration-in-the-large	-0.587 to 0.587	85.5%	




# Developing a new prediction model

THE LANCET  
Neurology

CORRESPONDENCE | [VOLUME 17, ISSUE 8, P662-663, AUGUST 01, 2018](#)

## The life expectancy of Stephen Hawking, according to the ENCALS model

[Henk-Jan Westeneng](#) • [Ammar Al-Chalabi](#) • [Orla Hardiman](#) • [Thomas PA Debray](#) • [Leonard H van den Berg](#) 

DOI: [https://doi.org/10.1016/S1474-4422\(18\)30241-2](https://doi.org/10.1016/S1474-4422(18)30241-2)

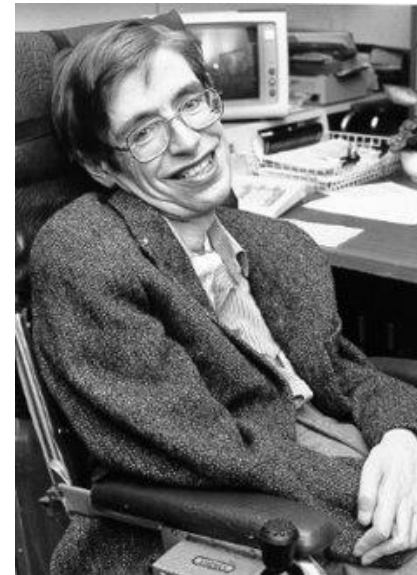


# Developing a new prediction model

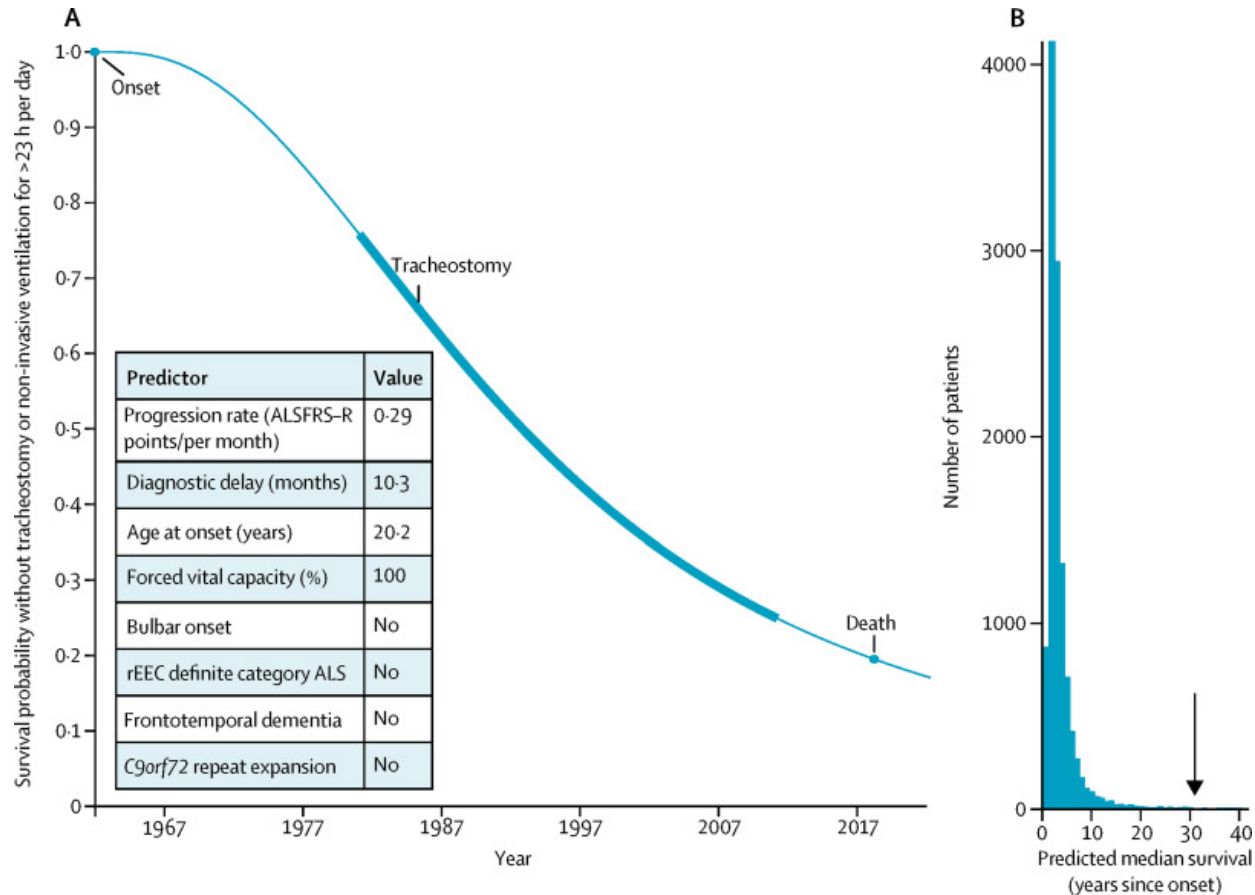
## The life expectancy of Stephen Hawking, according to the ENCALs model

*"Using publicly available data, we examined whether Professor Hawking's survival was as rare as his intellectual performance, or could be predicted solely based on his disease characteristics at diagnosis in 1963."*

- Predicted 10-year survival probability: 94%
- The IQR for his predicted survival lay between 1981 and 2011
- Young age of onset was the most important factor for his long survival



# Developing a new prediction model



Personalised survival curve for Stephen Hawking (A) and comparison with other patients with ALS (B)



GUIDELINES AND GUIDANCE

## Individual Participant Data (IPD) Meta-analyses of Diagnostic and Prognostic Modeling Studies: Guidance on Their Use

**Thomas P. A. Debray<sup>1,2\*</sup>, Richard D. Riley<sup>3</sup>, Maroeska M. Rovers<sup>4</sup>, Johannes B. Reitsma<sup>1,2</sup>, Karel G. M. Moons<sup>1,2</sup>, Cochrane IPD Meta-analysis Methods group<sup>¶</sup>**

**1** Julius Center for Health Sciences and Primary Care, University Medical Center Utrecht, Utrecht, The Netherlands, **2** The Dutch Cochrane Centre, Julius Center for Health Sciences and Primary Care, University Medical Center Utrecht, Utrecht, The Netherlands, **3** Research Institute for Primary Care and Health Sciences, Keele University, Staffordshire, The United Kingdom, **4** Radboud Institute for Health Sciences, Radboudumc Nijmegen, The Netherlands

<sup>¶</sup> Membership of the Cochrane IPD Meta-analysis Methods group is listed in the Acknowledgments.

\* [T.Debray@umcutrecht.nl](mailto:T.Debray@umcutrecht.nl)



# Take home messages

## Major advantages IPD-MA

- Better insight in performance of prediction model(s) within and across different settings and populations
  - Quantify heterogeneity
  - Notably calibration
- Improving the performance of prediction model(s)
  - Tailoring of model(s)
- Integrate development and external validation when developing a new model



# Take home messages

## Remaining challenges in IPD meta-analysis

- IPD-MA no panacea against poorly designed primary studies
  - Prospective multi-center studies remain important
- Addressing heterogeneity in prediction model performance
  - One model fits all?
  - Role of received intervention(s)
  - Updating continuous process?

**New methods are on their way!**



# Take home messages

## Reasons to be optimistic

### Cochrane Prognosis Methods Group

- Aims to facilitate evidence-based prognosis research
- Improve design, quality & reporting of primary studies
- Facilitate systematic reviews & meta-analysis in long-run
- Bring together prognosis researchers, and guide Cochrane reviewers facing prognostic information
- Developing guidance





# Take home messages

## Reasons to be optimistic



GUIDELINES AND GUIDANCE

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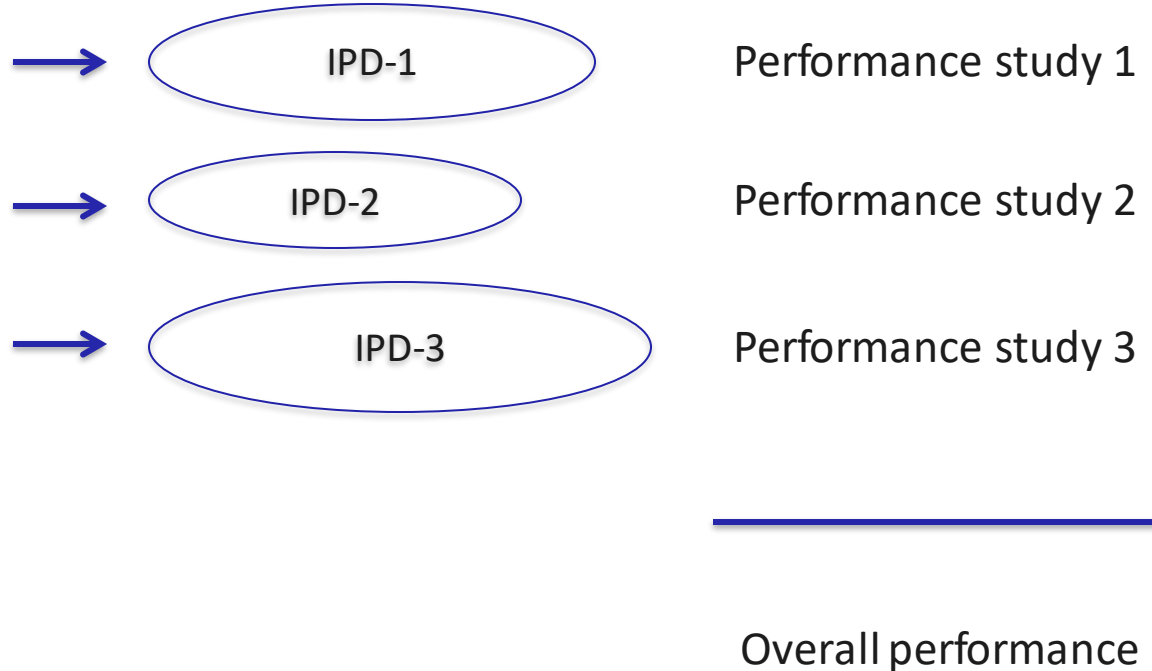


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# TYPE I: VALIDATION OF EXISTING MODEL(S)

Existing (published) model(s)  
 $y = \alpha + \beta_1 X_1 + \beta_2 X_2 + \dots + \beta_n X_n$



## Output:

What is the overall performance?

How large is the heterogeneity?

What are drivers of heterogeneity?

Competing models: difference in performance?



## TYPE II: TAILORING EXISTING MODEL

Existing (published) model(s)  
 $y = \alpha + \beta_1 X_1 + \beta_2 X_2 + \dots + \beta_n X_n$



+ updating 1  
+ refitting 1



+ updating 2  
+ refitting 2



+ updating 3  
+ refitting 3

---

Updating needed?  
Refitting needed?

### Output:

Updating needed?

For which setting / populations

Updated model(s)



# TYPE III: EXAMINING ADDED VALUE

Existing (published) model(s)  
 $y = \alpha + \beta_1 X_1 + \beta_2 X_2 + \dots + \beta_n X_n$



+ new factor  
increase in performance 1



+ new factor  
increase in performance 2



+ new factor  
increase in performance 3



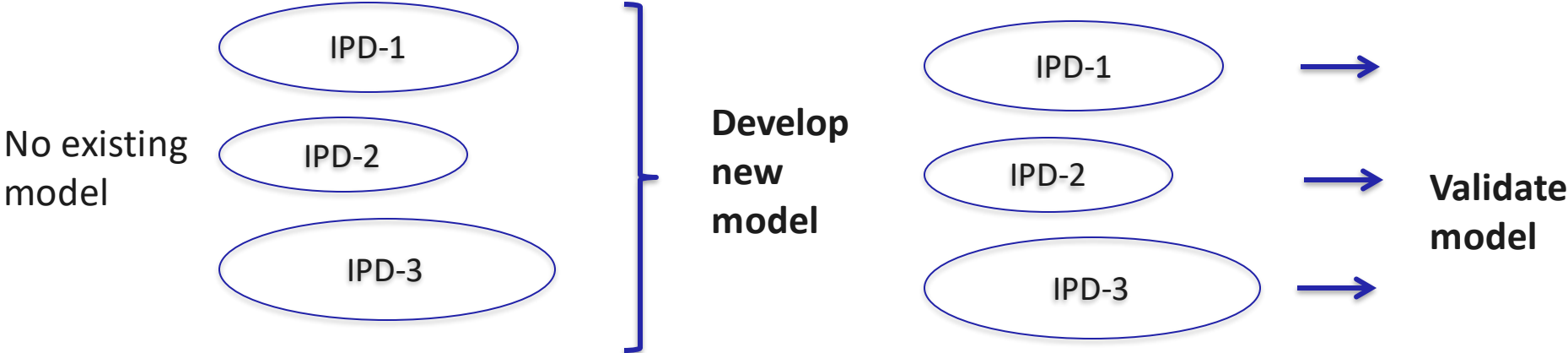
Overall increase in  
performance

**Output:**

- What is the overall added value?
- Heterogeneity in added value?
- Drivers of heterogeneity?
- What is the updated model?



# TYPE IV: DEVELOPMENT NEW MODEL AND VALIDATION



**Output:**  
New model / tailored models

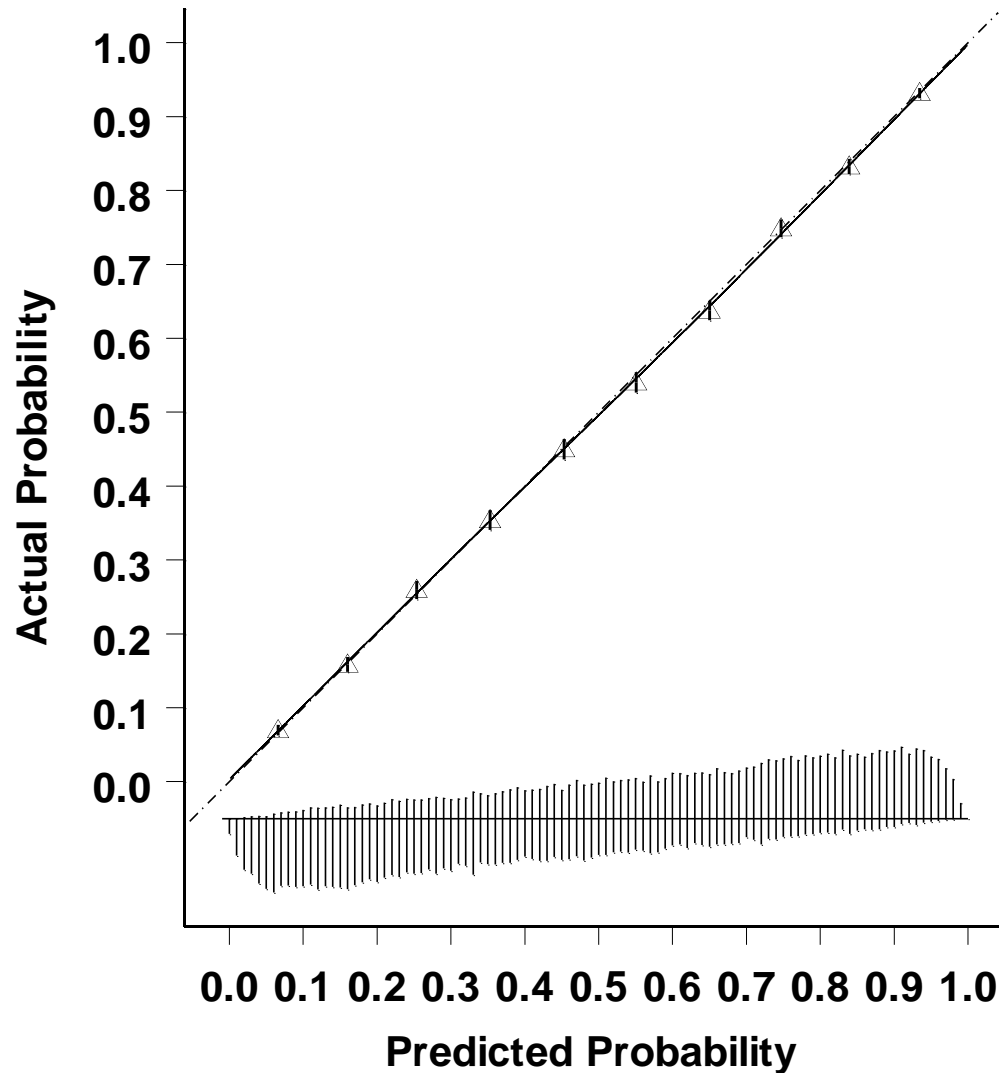


# Prediction model performance measures

- **Calibration** plot  
(for specific time point in case of survival models)
- **Discrimination**
  - C-statistic (ROC area for logistic regression)
- **(Re)classification** → requires probability thresholds
  - Assess the potential effect on patient-level outcomes
  - Comparative test accuracy studies
  - Examples: Net Reclassification Index, Net Benefit, ...



# Calibration plot

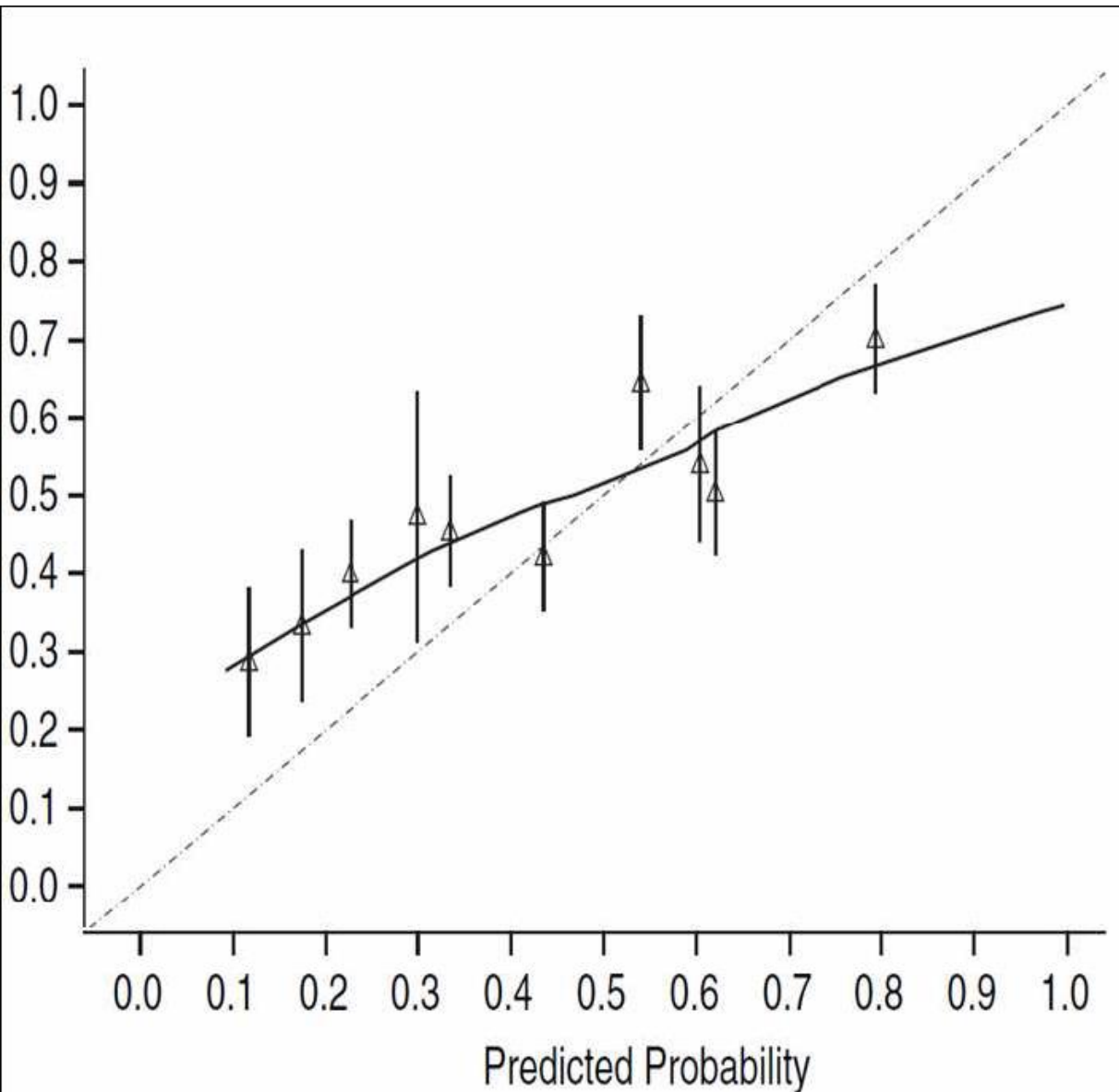


**Ideal calibration**  
Observed versus  
expected risk (O/E) = 1

Slope = 1



# External validation: typical result



- Slope plot  $< 1.0$ 
  - Low prob too low
  - High prob too high
    - Overfitted
- AUC = 0.63 (was 0.75)

