Harnessing uncertainty in clinical prediction models using Stata

Dr. Joie Ensor

Associate Professor in Biostatistics University of Birmingham

elinical prediction models

models

Why?

• Clinical prediction models aim to inform individual patient care

model × you = your probability of outcome

• Unreliable models can lead to critical mistakes in clinical decision-making



Most published models are not fit for purpose

- Models are products of their development data
- Predictions become unreliable when:
 - Development samples are too small
 - Model complexity is large relative to outcome events
 - No adjustment for overfitting

Riley RD, Collins GS. Stability of clinical prediction models developed using statistical or machine learning methods. Biometrical Journal. 2023

Sample size is a fundamental issue

- 73% of published models use inadequate sample sizes
- Median deficit of 387 patients, IQR (-1207 to +49) (Dhiman et al.)

• Mann et al. found only 10% of studies reported a sample size calculation

Dhiman P, Ma J, Qi C, Bullock G, Sergeant JC, Riley RD, Collins GS. Sample size requirements are not being considered in studies developing prediction models for binary outcomes: a systematic review. BMC Medical Research Methodology. 2023

Mann M, Collins G, Riley R, Ensor J. (2024) How are published clinical prediction model studies assessing and reporting calibration performance at external validation? doi: 10.17605/OSF.IO/74R9U

models

THE MULTIVERSE OF MODELS

- Model instability: different samples → markedly different models
- Any single model = merely one example from a multiverse of possible models



Riley RD, Pate A, Dhiman P, Archer L, Martin GP, Collins GS. Clinical prediction models and the multiverse of madness. BMC medicine. 2023

Visualising Model Instability

Predictors	Large sample	Development samples of N=100									
i i odiotorio		1	2	3	4	5	6	7	8	9	10
Age	1.15	1.63	X	1.65	Х	X	X	Х	Х	X	X
Sex	X	X	Х	X	Х	X	X	Х	Х	0.22	X
Systolic BP	0.99	X	X	X	Х	X	0.96	Х	Х	X	0.96
Bicarbonate	0.95	X	X	X	0.79	X	X	Х	Х	X	X
Creatinine	3.28	X	X	53.45	Х	X	39.77	Х	Х	30.25	10.03
Hemoglobin	0.88	X	Х	X	Х	X	X	Х	Х	X	X
Platelets	1.00	X	0.99	X	0.99	X	X	Х	Х	X	Х
Potassium	1.66	Х	6.68	Х	Х	3.09	Х	3.86	5.24	2.74	X
Blood oxygen	X	X	Х	Х	Х	X	X	Х	Х	X	X

Riley RD, Ensor J et al. The importance of sample size on the quality and utility of AI-based prediction models for healthcare. Forthcoming – The Lancet Digital Health 2025.

Visualising Model Instability

- Same modelling approach on different samples produces variation in models → instability in predicted probabilities
- Stability checks should become standard practice

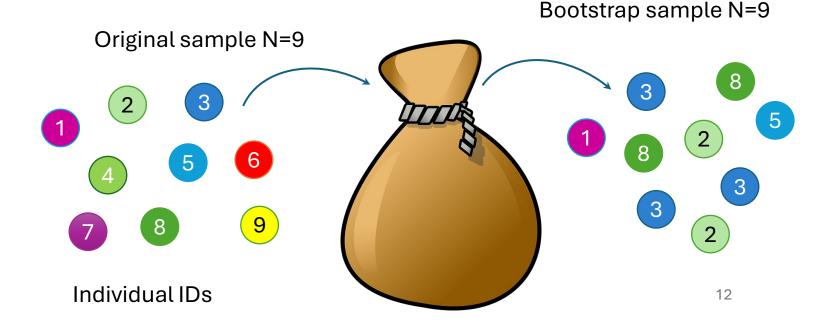
Predictors	Large sample	Development samples of N=100									
Treaterors	Eurge sumpte	1	2	3	4	5	6	7	8	9	10
Age	1.15	1.63	Х	1.65	Х	Х	Х	Х	Х	Х	X
Sex	X	X	Х	X	Х	X	Х	Х	Х	0.22	X
Systolic BP	0.99	X	Х	X	Х	Х	0.96	Х	Х	Х	0.96
Bicarbonate	0.95	X	Х	X	0.79	X	Х	Х	Х	X	X
Creatinine	3.28	Х	Х	53.45	Х	X	39.77	Х	Х	30.25	10.03
Hemoglobin	0.88	X	Х	Х	Х	X	Х	Х	Х	Х	X
Platelets	1.00	X	0.99	Х	0.99	X	Х	Х	Х	X	X
Potassium	1.66	Х	6.68	Х	Х	3.09	Х	3.86	5.24	2.74	X
Blood oxygen	X	Х	Х	Х	Х	Х	Х	Х	Х	X	X

Today's roadmap

- Internal validation for uncertainty visualisation
- Using uncertainty metrics in study design
- By the end of this talk:
 - Practical workflow for your next model study
 - Tools to assess and address model instability

Internal validation concept

- Bootstrap resampling examines impact of sampling variability
- Must match:
 - Original sample size (N)
 - Exact modelling approach



Clinical example

- **Prediction target**: Acute kidney injury in intensive care patients (48hr window)
- Data source: MIMIC-III database
- **Approach**: Fixed set of predictors based on evidence and clinical consensus

Logistic regression				LR Pro		286 12.06 0.1485 0.0422
AKI	Coefficient	Std. err.	z	P> z	[95% conf.	interval]
gender	.2078414	.3450336	0.60	0.547	4684121	.8840949
<pre>bicarbonate_mean</pre>	0574709	.0439213	-1.31	0.191	1435552	.0286133
creatinine_mean	1.125994	.7757663	1.45	0.147	39448	2.646468
hemoglobin_mean	0822802	.0815089	-1.01	0.313	2420346	.0774743
bun_mean	01488	.0184731	-0.81	0.421	0510866	.0213266
potassium_mean	. 5765495	.3599629	1.60	0.109	1289649	1.282064
sysbp_mean	0121554	.0107667	-1.13	0.259	0332578	.008947
spo2_mean	0270447	.0894051	-0.30	0.762	2022755	.1481861
_cons	1.82889	9.397801	0.19	0.846	-16.59046	20.24824

Clinical example

- **Prediction target**: Acute kidney injury in intensive care patients (48hr window)
- Data source: MIMIC-III database
- Approach: Fixed set of predictors based on evidence and clinical consensus

Discrimination statistics ...

	Estimate	SE	Lower_CI	Upper_CI
C-Statistic	0.647	0.039	0.570	0.725
Somers D	0.295	0.079	0.140	0.449

Calibration statistics ...

	Estimate	Lower_CI	Upper_CI
E/0	1.000	0.788	1.335
E-0	-0.000	-0.054	0.050
CITL	0.000	-0.297	0.297
C-Slope		0.416	1.584
C-310pe	1.000	0.410	1.564

Overall performance statistics ...

	Estimate	Lower_CI	Upper_CI
Cox-Snell R2	0.041	0.005	0.092
R2 Nagelke~e	0.065	0.008	0.143
R2 McFadde~s	0.042	0.005	0.095
Briers Score	0.153	0.125	0.184

Additional summary statistics ...

	Mean	SD	Median	LQ	UQ	
LP Dist	-1.473	0.535	-1.463	-1.831	-1.109	
Sample size	286.000	•		•	•	

pmintval overview

- New Stata package for internal validation and uncertainty visualisation
- Returns dataset with predictions from original and bootstrap models
- Examines prediction stability across the model multiverse

Fit development model, predict probabilities for original sample

Bootstrap sample of size N

Build multiverse model

Predict probabilities for original sample using multiverse model

Visualise model stability

pmintval syntax

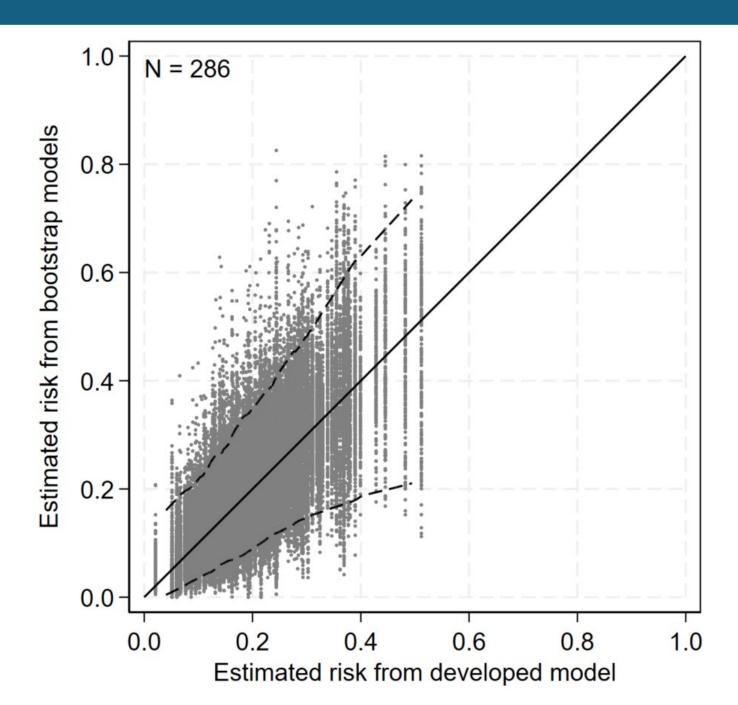
Command line

pmintval AKI gender bicarbonate_mean creatinine_mean hemoglobin_mean bun_mean potassium_mean sysbp_mean spo2_mean, boot(200)

	pr1	pr2	pr3	pr4	pr5	pr6	pr7	pr8	pr9	pr10	pr11	pr12
1	.1452606	.1554341	.1804096	.1664165	.1692847	.1834505	.1475054	.1826395	.1633522	.1548582	.152133	.1794005
2	.0457026	.057397	.0640362	.0417281	.052992	.0525907	.0436598	.043273	.0508877	.0476608	.0467994	.048035
3	.072901	.0884458	.0906838	.074332	.0881848	.079837	.0749723	.066966	.0797636	.0780905	.0743829	.0765029
4	.2357282	.2097052	.2216702	.2302375	.2448104	.2270528	.2043875	.2396001	.2448246	.2210204	.237456	.2033944
5	.1562723	.1653154	.1907796	.166422	.1511118	.1824354	.1745607	.1847174	.1878714	.1736683	.1590132	.189984
6	.2063501	.224724	.2450891	.2315639	.2354372	.247393	.223059	.2513075	.2371853	.2253135	.2178639	.2448219
7	.091362	.1113398	.1182475	.0828711	.1048185	.1035374	.084993	.0891667	.0981059	.0963472	.0909408	.0883589
8	.2109131	.2312233	.2497026	.2680111	.2438476	.251814	.2452061	.2496253	.2565619	.2428534	.2275574	.2689827

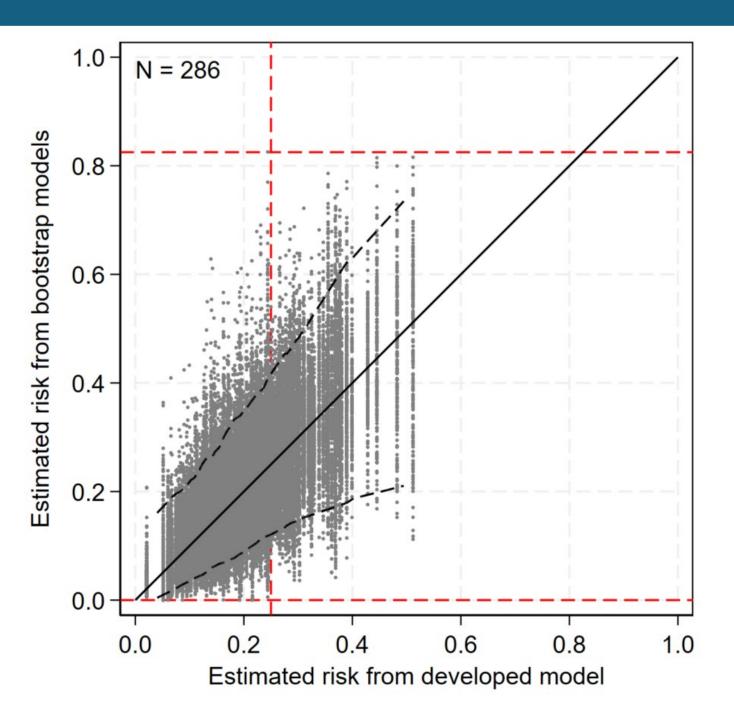
Prediction Instability Visualisation

• Illustration of potential prediction variability for individual patients



Prediction Instability Visualisation

- Illustration of potential prediction variability for individual patients
- For a patient with 25% predicted risk, true risk could range from 0% to 82.5%



Clinical Implications of Instability

- Wide prediction intervals → misleading risk communication
- Unreliable for clinical decision support
- Undermines clinician trust in the model



19

Option A



Option B



Certainty by design

- Traditional approaches target "average" model performance
 - pmsampsize package
 - Minimises overfitting & precisely estimates overall risk
- Our approach: target prediction stability for individual risk estimation

Riley, R. D., Collins, G. S., Whittle, R., Archer, L., Snell, K. I., Dhiman, P., ... & Ensor, J. (2024). A decomposition of Fisher's information to inform sample size for developing fair and precise clinical prediction models - part 1: binary outcomes. arXiv preprint arXiv:2407.09293.

pmstabilityss Package - Overview

- Uses information from development sample and internal validation
- Calculates required sample size for specified prediction stability
- Uses a decomposition of Fisher's information
 - Computationally quick

Riley, R. D., Collins, G. S., Whittle, R., Archer, L., Snell, K. I., Dhiman, P., ... & Ensor, J. (2024). A decomposition of Fisher's information to inform sample size for developing fair and precise clinical prediction models - part 1: binary outcomes. arXiv preprint arXiv:2407.09293.

pmstabilityss Package - syntax

Command line

pmstabilityss gender bicarbonate_mean creatinine_mean hemoglobin_mean bun_mean potassium_mean sysbp_mean spo2_mean, prev(.1993) cstat(0.65) pmss lp(lin_pred)

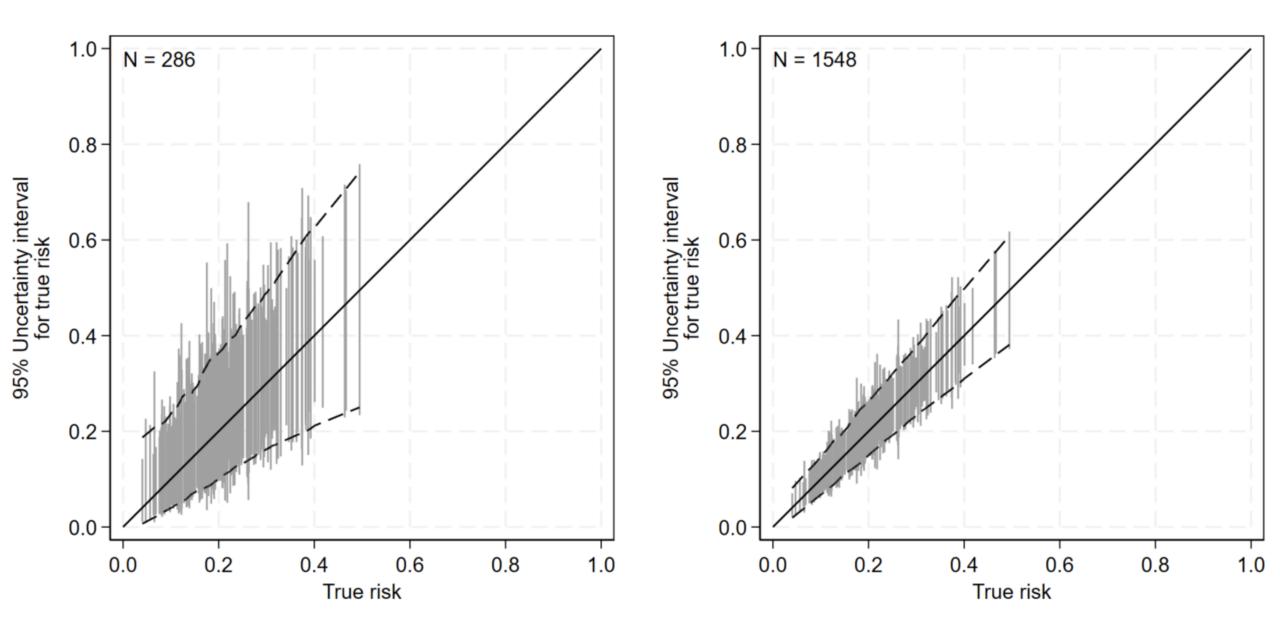
Fixed SS of input dataset = 286

Minimum SS required by pmsampsize = 1548

Overall summary UI widths

Max	Median	Min	Mean	N
.62	.25	.13	. 26	286
. 29	.1	.048	.11	1548

Visualising Stability at Different Sample Sizes



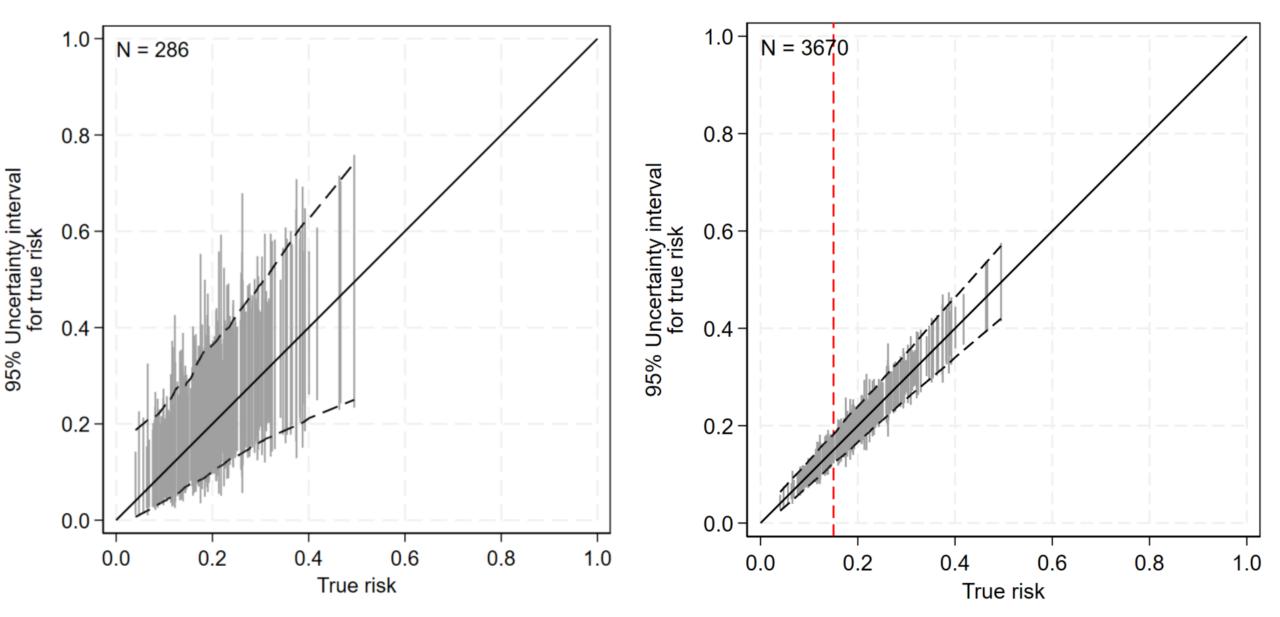
Options to customise stability targets

- pciwidth():target acceptable prediction interval widths
- pcutpoints(): cutpoints in the interval [0,1] corresponding
 with target widths specified

Command line

pmstabilityss gender bicarbonate_mean creatinine_mean hemoglobin_mean bun_mean potassium_mean sysbp_mean spo2_mean, prev(.1993) cstat(0.65) lp(lin_pred) pcut(.15 1) pci(.1 .25)

Specifying Stability Requirements



Specifying Stability Requirements

Fixed SS of input dataset = 286

Minimum SS required to meet target UI widths = 3670

Overall summary UI widths

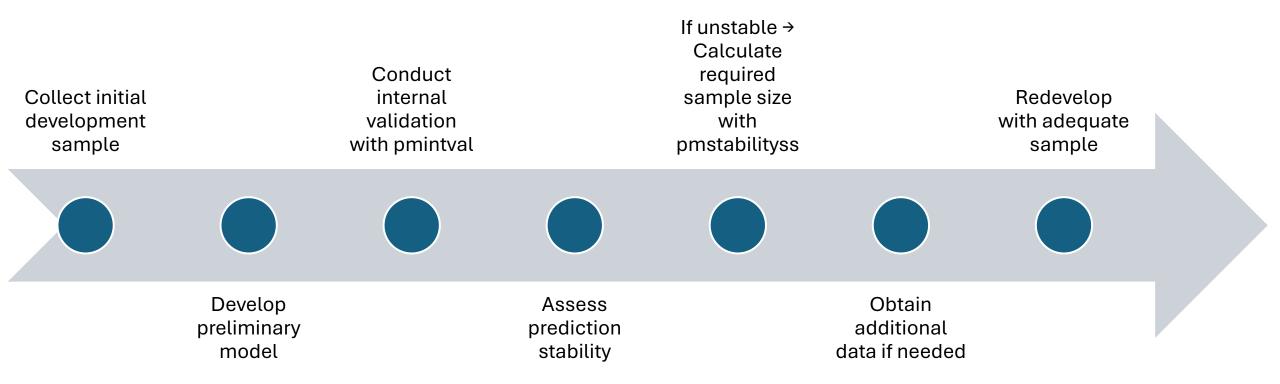
	Ν	Mean	Min	Median	Мах
2	86	. 26	.13	.25	.62
36	70	.073	.03	.067	.19

Summary UI widths by probability categories

N	P category	Target width	Mean	Min	Median	Мах	Prop target width met
286	.15	.1	.2	.13	.19	.4	.26
286	1	.25	. 29	.15	.27	.62	.26
3670	.15	.1	.054	.03	.049	.1	1
3670	1	.25	.083	.041	.075	.19	1

27

Complete workflow



Key takeaways

- Quantifying model uncertainty is essential for clinical models
- Balance needed between stability requirements and feasibility
- If a model cannot be developed with reasonable stability → reconsider its use

Future developments

- Upcoming features:
 - Time-to-event and continuous outcome support
 - Prospective study design with minimal inputs
- Tutorial and documentation available soon

Questions?



- Email: j.ensor@bham.ac.uk
- BlueSky: @joieensor.bsky.social
- X: @joie_ensor
- GitHub: https://github.com/JoieEnsor/pm-suite