



Interlaboratory diagnostic test evaluation using Bayesian latent class models

Knowing diagnostic test accuracy is essential when using test results to infer the presence, prevalence, or absence of a disease in a population

AIM

Proof of concept for cost-effective diagnostic test evaluation

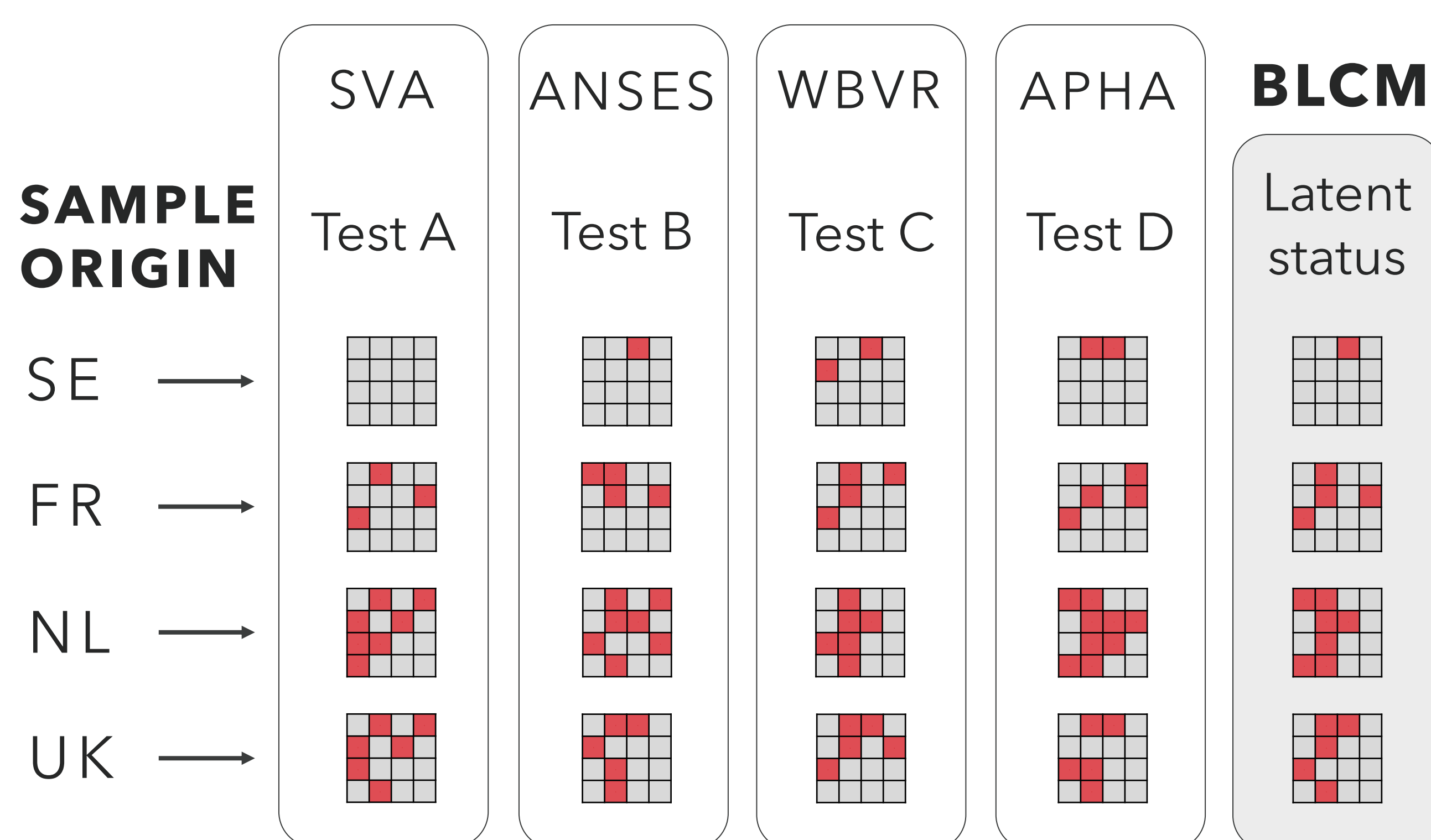
CHALLENGES

Lack of gold standard test
 Lack of positive samples
 Budget constraints

SOLUTIONS

Bayesian latent class models
 Samples from multiple countries
 Inter-laboratory evaluation

LAB ANALYSES



The Bayesian latent class model (BLCM) combines the test results in each population and infers the most likely *true* value for each sample, i.e. the *latent status*.

CASE STUDIES

Serological detection of **BVD & IBR**

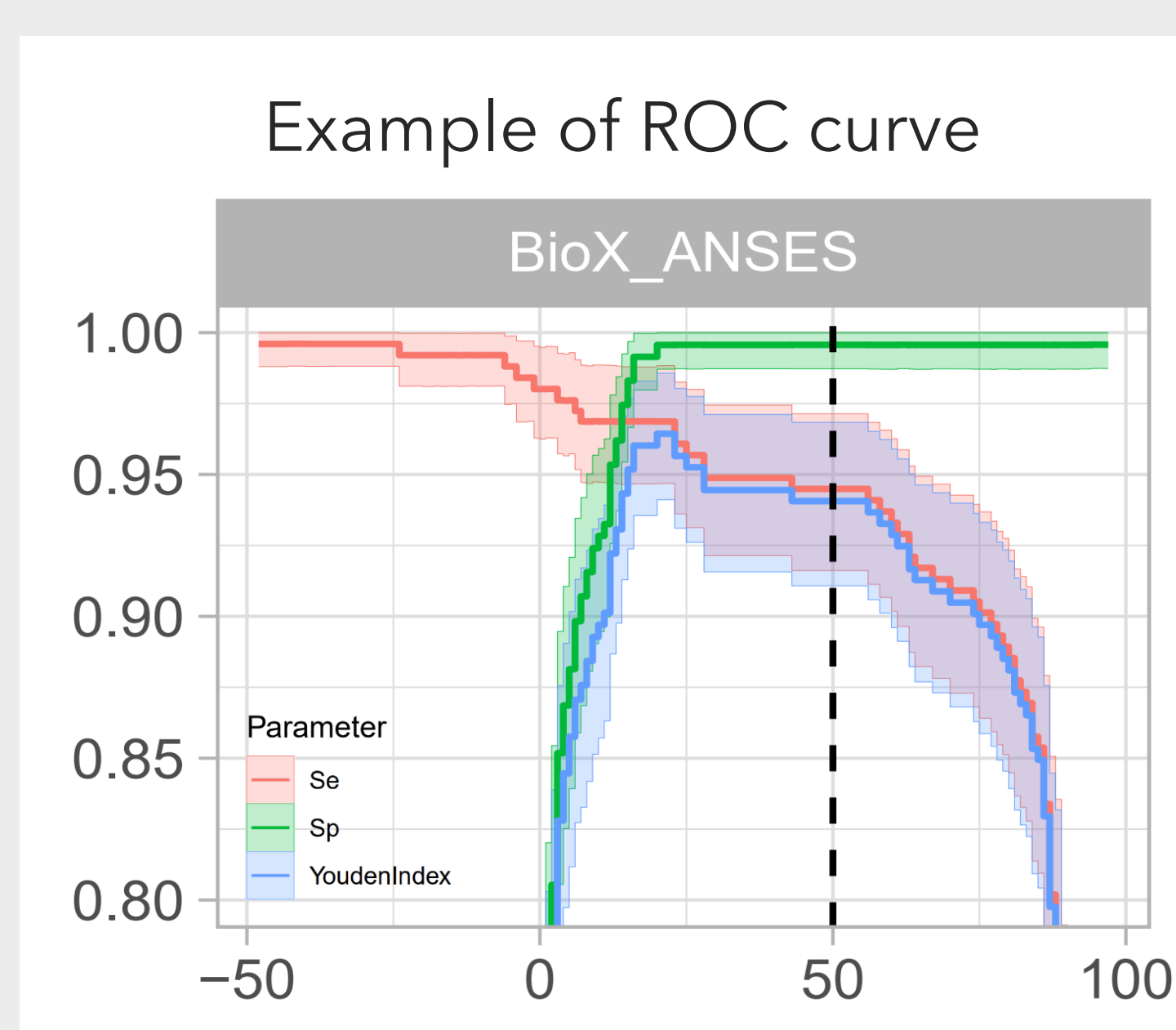
- 2 diseases
- 4 countries
- 4 laboratories
- 6 epidemiologists
- 6 laboratory experts
- 7 serological tests for IBR
- 8 serological tests for BVD
- 1000 samples analysed in total

STUDY DESIGN

- Sample sharing between labs
- Each lab applied their own routine diagnostic test(s)
- Joint data analysis using BLCM

CONCLUSIONS

- Cost-effective approach to diagnostic test evaluation → especially valuable for routine diagnostics
- Useful insights for the labs and tools for test optimization
- Applying several tests entails:
 - 👉 correlations that increase model complexity
 - 👍 possibility to remove tests and get post hoc estimates
- Requires deep understanding of tests, populations and underlying latent status



Example of population-specific estimates (Svanovir_SVA)

Population	Median specificity	Credible interval
SE	0.995	[0.977 - 1.000]
NL	0.345	[0.198 - 0.509]
UK	0.916	[0.780 - 0.997]
FR	0.988	[0.948 - 1.000]
Combined	0.903	[0.863 - 0.938]

OUTCOMES

- Diagnostic sensitivity and specificity of ELISA tests for detection of Bovine Viral Diarrhoea (BVD) and Infectious Bovine Rhinotracheitis (IBR)
- Population-specific accuracy and ROC curves for cut-off optimization
- R code for inter-laboratory diagnostic test evaluation using BLCM:
 - algorithm for **optimal sample allocation** among populations
 - methods for **assessing the empirical fit** of Hui-Walter models
 - **post hoc accuracy estimates** for tests that were excluded from the model