APPENDIX 1 (as submitted by the authors): Data Synthesis and Analysis

For the bivariate model for diagnostic and prognostic meta-analysis, we used a between-studies model based on the bivariate normal distribution of the pairs of the logits of sensitivity and 1-specificity and a within-study model based on the binomial distribution of the number of subjects with a positive test given the disease of interest (sensitivity model) and the number of patients with a negative test given the freedom of disease of interest (specificity model).\textsuperscript{1-3}

All analyses were conducted with the free, open-source statistic software R. In particular, we used the GLMM framework implemented with the lmer-function of the contributed R-package lme4. The bivariate model was set-up as a model without intercept. In this model the pooled estimates for sensitivity and 1-specificity correspond to the anti-logit of the fixed effects.\textsuperscript{2}

In a secondary approach we fitted the same models in a Bayesian framework using Markov chain Monte Carlo (MCMC) methods implemented in the contributed R package MCMCglmm.\textsuperscript{4}

The rational to extend the analyses was to provide easily interpretable posterior distributions of the pooled sensitivity, 1-specificity and the pooled positive predictive values (PPV) and negative predictive values (NPV). For the Bayesian approach, we used a non-informative inverse Wishart prior for the (co)variances and a normal prior for the fixed effects.

References


