Bayesian meta-analysis

For each measure (i.e., sensitivity, specificity, accuracy as referred to true-positive, true-negative and overall accuracy rates, respectively) within each study, we computed, with a Bayesian approach, their 95% credibility intervals considering that the numerator of a generic rate within the study i (n_i) is a binomially distributed random number with the true study-specific rate (r_i) as probability parameter, for $i = \{1, \dots N\}$ studies.

Following Verde,[1] a bivariate random effects meta-analysis was used for jointly modeling sensitivity and specificity outcomes. For each study the number of true positives (false positive) is assumed to be binomially distributed with the true study-specific positive rate TPR_i (false positive rate FPR_i) as probability parameter. The N pairs of TPR_i and FPR_i probabilities were then transformed by the logit link function for easier computations and we specified two study accuracy effects: differences D_i and sums S_i of these rates in the link logit scale. The former is associated with diagnostic discriminatory power while the latter is associated with diagnostic threshold value. We modelled the variability between studies using D_i and S_i with *a scale mixture of bivariate normal distributions*:

$$(D_i, S_i) \sim N(\mu, w_i\Lambda) \qquad w_i \sim p(w_i) \qquad i = 1, \dots, N$$

where $\mu = (\mu_D, \mu_S)$, represent the vector of difference and sum of rates means, whereas $\Lambda = \Sigma^{-1}$ is the precision matrix, w_i are weights associated to each study that allow to identify the studies with unusual heterogeneity, and $p(w_i)$ is a scale mixing density. We considered a truncated double exponential distribution for $w_i \sim Exp(1)$, with lower truncation point to avoid computational problems. The following priors are considered for hyper-parameters: a $Norm(0, 0 \cdot 25)$ for μ_D and μ_S; a Wishart distribution with identity scale matrix and three degrees of freedom for the precision matrix. Finally, the meta-analytic summaries of sensitivity and specificity were obtained with appropriate back transformation.

In the same fashion, a univariate binomial random effects meta-analysis model was used to obtain a pooled estimation for accuracy rate. The sum of true positives and true negatives ($TRUE_i$) is assumed to be binomially distributed with the true study-specific accuracy (ACC_i) as probability parameter. It is assumed that the logit of the parameter ACC_i follows independent normal distributions $Norm(MA_{ACC}, tau_{ACC})$. MA_{ACC} is the pooled accuracy and we placed non-informative prior normal distribution for it. We considered weakly informative prior for the precision parameter tau_{ACC}: a truncated distribution $Gamma(10^{-2}, 10^{-3})$, with lower truncation point at 10^{-6}. The same approach was used to obtain a further pooled estimate for specific outcomes (i.e. sensitivity) in order to include also those studies for which it was possible to obtain only partial information. We ran 100000 iterations for each model. Results for each parameter were reported as median along with its 95% credible interval (CrI) derived from the Markov Chain Monte Carlo (MCMC) posterior distribution (discarding the first 20,000 burn-in updates). In order to check chain convergence we used the diagnostic procedures, and specifically trace plots and autocorrelation plots inspection. Forest plots were produced to display all pooled estimates. Analyses were performed using WinBUGS version 1.4.[2]

1. Verde PE. Meta-analysis of diagnostic test data: A bivariate Bayesian modeling approach. Statist Med 2010; 29: 3088–3102.
2. Spiegelhalter DJ, Thomas A, Best N. WinBUGS, Version 1.4, Upgraded to 1.4.1, User Manual. MRC Biostatistics Unit: Cambridge, 2004