Diagnostic meta-analysis with the R-package mada

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Abstract

Diagnostic meta-analysis aims to pool the endpoints of diagnostic primary studies. The diagnostic procedure at hand can be a biomarker, an imaging technology or even a questionnaire. Central for the method is, that data on the sensitivity and specificity of the procedure are available. In contrast to many other meta-analytic techniques, two endpoints are to be pooled. In general these two are not independent. Hence a bivariate model with random effects (Reitsma et al., 2005), or equivalently the HSROC (Rutter & Gatsonis, 2001), has become the standard model for the analysis of such data.

Since diagnostic meta-analysis poses these additional challenges, only little software is available for this purpose. The R-package "mada: Meta-analysis of diagnostic accuracy" (Doebler, 2012) is an open source package providing several modern approaches to diagnostic meta-analysis. The package's output can then be used in the Cochrane Review Manager for a diagnostic meta-analysis. I will present the package and how to use it. Apart from the bivariate approach, mada also provides functions for meta-regression and an extension of the bivariate model of Doebler, Holling und Böhning (2012).

In addition to pooling sensitivities and specificities, diagnostic meta-analysis also integrates the receiver operating characteristic curves (ROC curves) of the primary studies. The result is called a summary ROC (SROC) curve. SROC curves implied by the bivariate model of Reitsma et al. (2005) can be contraintuitve, if not false (Rücker & Schuhmacher, 2010), and so the literature contains various other approaches to calculate SROC curves in a different fashion. Certain univariate measures of diagnostic accuracy prove to be useful in this context. Inspired by work of Holling et al. (2012), I present an application of (covariate adjusted) mixtures, which does not yield one underlying SROC curve, but a mixture of such curves.

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