Abstract

Meta-analysis plays a critical role in synthesizing diagnostic accuracy evidence; however, traditional statistical models such as meta-regression (MR) often fall short when dealing with high heterogeneity and nonlinear study-level patterns. This study introduces a novel application of machine learning (ML) as a modeling tool within the meta-analytic framework, focusing on diagnostic imaging studies in colorectal cancer. A systematic review was conducted following PRISMA 2020 guidelines and registered in PROSPERO. Twenty eligible studies were identified through PubMed, MDPI, IEEE Xplore, and Google Scholar, each reporting diagnostic performance metrics such as sensitivity, specificity, or AUC. Extracted outcomes were transformed into a standardized long-format dataset and analyzed using both ML algorithms (Random Forest, XGBoost, SVM, KNN, ANN) and MR techniques (OLS, Ridge, Lasso, ElasticNet). Heterogeneity was notably high (Cochran's Q = 17,408.60; I^2 = 99.98%), necessitating robust modeling approaches. Benchmark results showed that Random Forest achieved the best predictive performance with the lowest Root Mean Squared Error (RMSE) and highest R^2, followed closely by XGBoost. ML models also produced better residual distributions, with fewer outliers and more normally distributed error structures than MR models. Literature searches in PubMed and Elsevier found no existing studies using ML as a modeling tool for meta-analytic synthesis in diagnostic imaging, highlighting the originality of this work. These findings demonstrate that ML, especially ensemble-based methods, offers a powerful alternative to traditional meta-regression for synthesizing complex, heterogeneous diagnostic data and represents a promising advancement in evidence synthesis methodology.

Keywords: machine learning, meta-analysis, diagnostic imaging, colorectal cancer, meta-regression, heterogeneity, ensemble models, systematic review, study-level features, diagnostic accuracy