Chapter 1

Introduction

1.1 Background

Colorectal cancer remains a leading cause of cancer-related morbidity and mortality worldwide, presenting a significant public health challenge (Xi et al., 2021). Early and accurate diagnosis is crucial for improving survival outcomes, as prompt clinical intervention significantly enhances the likelihood of successful treatment. Diagnostic imaging techniques—such as colonoscopy, computed tomography (CT), magnetic resonance imaging (MRI), and positron emission tomography (PET)—are central to the early detection and staging of colorectal cancer. However, despite technological advancements, imaging interpretation continues to suffer from notable limitations including operator dependency, interobserver variability, and the persistent risk of missed lesions (Patharia et al., 2024).

In recent years, machine learning (ML) has emerged as a transformative tool in medical imaging, offering automated methods capable of processing vast amounts of data, identifying complex visual patterns, and enhancing diagnostic accuracy (Debellotte et al., 2025). Algorithms such as convolutional neural networks (CNNs), support vector machines (SVMs), and ensemble models like random forests have been widely adopted in clinical imaging research. Multiple studies have shown that ML-based systems can improve performance metrics such as sensitivity, specificity, and adenoma detection rate (ADR). However, these improvements are not universally consistent across studies. Differences in dataset composition, imaging protocols, algorithm design, and evaluation criteria often produce highly heterogeneous diagnostic outcomes, complicating efforts to generalize ML's effectiveness in clinical practice (Tharwat et al., 2022).

Meta-analysis is a well-established methodology for synthesizing quantitative evidence across studies, offering a means to estimate pooled diagnostic performance and explore sources of heterogeneity. Traditional meta-regression (MR) extends this by examining how study-level covariates influence effect sizes. While effective in many contexts, MR assumes linearity and often lacks the flexibility to capture the nonlinear interactions and multicollinearity typical of ML-based imaging studies. This limitation becomes more pronounced when dealing with highly variable data sources and outcome measures, as is frequently encountered in the diagnostic ML literature.

Surprisingly, while ML is commonly the subject of meta-analysis, it has rarely been used as a tool within meta-analytic modeling itself. To date, there is a clear absence of studies exploring how ML could be applied to synthesize heterogeneous outcomes by learning from study-level predictors. This gap presents a unique methodological opportunity: can machine learning offer a more robust, adaptable alternative to traditional MR in the context of diagnostic accuracy meta-analysis?

This study addresses that gap by proposing a benchmarking framework that evaluates ML not only as a diagnostic enhancer but also as a meta-analytic modeling strategy. Specifically, we compare the performance of multiple ML algorithms (including Random Forest, XGBoost, SVM, KNN, and ANN) against classical and regularized MR approaches (OLS, Ridge, Lasso, ElasticNet) in synthesizing standardized diagnostic outcomes extracted from colorectal cancer imaging studies. In doing so, this study offers a novel contribution to the field, demonstrating how ML can serve not just as an object of inquiry but as a statistical tool to improve the flexibility and accuracy of evidence synthesis in highly heterogeneous clinical research domains.

1.2 Objective

This study aims to investigate the effectiveness of machine learning-based diagnostic imaging techniques for colorectal cancer by conducting a meta-analysis across published studies. Furthermore, it benchmarks the performance of traditional meta-regression models against machine learning algorithms to assess which method more effectively handles heterogeneity and synthesizes diverse diagnostic performance outcomes. The proposed framework may also serve as a scalable methodology for evidence synthesis in other fields where complex and heterogeneous data challenge traditional meta-analytical approaches.

1.3 Hypothesis

It is hypothesized that integrating machine learning into the meta-analytic process will result in superior performance for modeling heterogeneous diagnostic accuracy outcomes compared to traditional meta-regression methods. The null hypothesis (H_0) states that there is no significant difference in predictive performance between ML models and meta-regression. The alternative hypothesis (H_1) posits that ML models provide a more accurate and adaptable framework for synthesizing diagnostic performance metrics due to their capacity to capture nonlinear interactions and complex patterns within study-level variables that conventional statistical models may overlook.