Bayesian Additive Regression Trees for Predicting Colon Cancer: Methodological Study (Validity Study).

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- **Abstract:** Objective: The occurrence of colon cancer starts in the inner wall of the large intestine. The survival of colon cancer patients strongly relies on early detection. Diagnosing colon cancer using clinical approaches often takes longer, especially in most developing countries with limited facilities. The recent use of microarray technology has presented a new approach for the oncologist to diagnose cancer cells using non-clinical machine learning methods. In this paper, the aim is to predict the status of colon cancer tissues using the Bayesian Additive Regression Trees (BART) and 2 other machine learning methods. Material and Methods: The development and comparative analysis of BART alongside 2 other competing methods (Random Forest: RF and Gradient Boosting Machine: GBM) were implemented. The dataset used for the analysis is the microarray colon cancer data which consists of 2,000 gene expression measurements for 62 tissue samples. Results: The methods are compared based on overall metrics (accuracy, balance accuracy, detection rate, F-measure and AUC) and class-specific metrics (sensitivity, specificity, positive predictive value and negative predictive value). The overall metrics results showed that the best method is RF. The class-specific metrics results showed that BART is better than RF. Conclusion: On average, BART is more sensitive in detecting the presence of colon cancer cells, while RF is more accurate and specific in detecting the presence or absence of colon cancer cells.

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