Chapter 24

Augmenting Chronic Kidney Disease Diagnosis With Support Vector Machines for Improved Classifier Accuracy

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ABSTRACT

Mitigating chronic kidney disease poses a substantial challenge to the healthcare community. This study assesses diverse classification algorithms, encompassing NaiveBayes, multi-layer perceptron, and support vector machine. The analysis involves scrutinizing the chronic kidney disease dataset from the UCI machine learning repository. Techniques like replacing missing values, unsupervised discretization, and normalization are employed for precision enhancement. The empirical results of the classification models are evaluated for accuracy and computational time. The conclusive observation indicates that the support vector machine performs notably better than all other classification methods, with a 76% classifier accuracy which is better than classifiers such as MLP and NB. The lack of application of those feature selection methods to the dataset is a drawback of this study.

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INTRODUCTION

Global healthcare systems face a basic issue in delivering accessible and accurate diagnoses. Artificial intelligence and machine learning have developed into potent tools in recent years for resolving complicated issues in various fields (Tomašev et al., 2019; Veronin et al., 2020). In particular, machine learning-assisted diagnosis promises to change healthcare by using vast patient data to give exact and personalized diagnoses (Liang et al., 2019; Topol, 2019; Yu et al., 2018). Diagnostic algorithms have struggled to match the accuracy of clinicians in differential diagnosis (Litjens et al., 2016; Semigran et al., 2016; Zhang et al., 2019; Rahimzade et al., 2021) when there are several potential causes of a patient's symptoms, despite major academic efforts and increasing commercial interest (Ravi et al., 2023).

In recent years, data mining has emerged as one of the most effective and powerful methods for extracting patterns from data, manipulating data, and establishing data that can be used for decision-making (Dayekh & Al-Nayili, 2022; Schumaker et al., 2021a). Data mining is used in a variety of fields, including sales and marketing, production, customer relationship management (CRM), manufacturing, the medical industry, Internet domains, AI, and mobile applications (Dodvad et al., 2012; Rafi & Farhan, 2016; Schumaker et al., 2021b).

Instead of relying on interpreting information hidden in the data store, clinical diagnostic and surgical decisions are made based on the doctors' expertise and intuition (Dodwad et al., 2010; Rafi et al., 2019; Veronin et al., 2020). It frequently leads to unnecessary preferences, errors, and comparatively expensive medical costs that can impact the standard of care provided to ailing patients (Farhan et al., 2018). A variety of technologies can support data mining operations. Waikato Environment for Knowledge Analysis (WEKA) is one of these tools (Ghulam et al., 2021). The most popular tool for data mining, which aids several data mining methods for classifier prediction, is WEKA (Goudarzi et al., 2021; Kukreja et al., 2011; Neisan et al., 2023). This chapter's main objective is to increase the predictive classification accuracy and forecast the presence or absence of patients' illness disease using dataset values (Kadhem & Alshamsi, 2023; Veena & Gowrishankar, 2022b).

The study examines a disease dataset from the University of California (UCI) 's ML repository. The illness dataset is pre-processed using unsupervised discretization, missing value replacement, and normalization. Various classification methods have been developed to diagnose diseases, including SVM, NB, and MLP (Veena & Gowrishankar, 2022b). The experimental result of the categorization models is regarded to be accurate.

LITERATURE REVIEW

Jongbo et al. (2020) introduced a model using data scaling for diagnosing CKD employing three base learners: DT, NB, KNN, and two ensemble approaches such as bagging and random subspace methods. Two major steps followed in this work are pre-processing and classification. (i) Data pre-processing is done before classification to deal with missing values and data scaling in a manner that normalizes the range of distinct variables. (ii) The two ensemble approaches improve the model's classification performance. Sensitivity, specificity, accuracy, kappa statistics, and ROC criteria were employed to measure the model's effectiveness. The dataset contains 400 CKD patients' instances with various symptoms, each with its own set of 24 features, with 11 numeric and 13 nominal values. Empirical results on the CKD dataset from the UCI ML repository demonstrate that ensemble approaches outperform individual

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