
1. Introduction

Medicines have become an important foundation for improving the quality of life and extending the human life expectancy. Although pharmaceuticals have provided great benefits, every drug has the potential to cause adverse effects on the biological system of the human body. This is referred to as adverse side effects or complex interactions between drugs and the human body's biological system that cause negative reactions [1]. A study found that between ten and one hundred side effects can appear in 69% of current drugs [2]. This suggests that a wide range of medicines kinds on the market have common negative effects. This fact demonstrates the intricacy of the interactions between medications and the human body's biological systems, as well as the significance of recognizing, comprehending, and successfully managing side effects in clinical practice.

In a traditional approach, before subjecting a drug to human clinical trials, a commonly used traditional method to evaluate the potential negative effects of drugs is animal research. As mentioned earlier, the biological differences between animal and human species are one of the major concerns of this method even though it gives important preliminary results [3]. Due to the fact that animals and humans differ in their physiology, metabolic rate, and mechanism of action of drugs, it is wrong to assume that the results of the experiments on animals will be the same as in humans [4]. Thus, it is impossible to translate all the findings from the animal studies to the human population. Therefore, it is difficult to determine the accuracy of the side effects of drugs on human beings through the experimental use of animals. However, there are weaknesses and this is where the *in silico* comes in. This is because *in silico* is one way of mitigating such shortcomings. The use of computer software and algorithms this method is a computer science methodology that involves the modeling, analysis, and prediction of physical, chemical, and biological processes. This method eliminates the necessity for direct animal testing and allows for the prediction of medication side effects. When compared to other traditional approaches, this approach can also reduce the time and expense needed for the research process. An effective and resource-efficient way to anticipate and treat medication side effects is through the use of *in silico* techniques [5].

Several studies have been conducted to predict the side effects of drugs using machine learning with different methods. In 2024, Dzaky Raihan Ahmad and his colleagues conducted a study to predict side effects, with a case study of metabolic and nutritional disorders. By implementing the Hybrid Bat Algorithm with Ensemble method, namely Random Forest, AdaBoost, and XGBoost, they found that XGBoost produces the most accurate and best the most accurate model and the best performance, with 74.3% accuracy and f1-score of 81.1% [6]. The next research was conducted in 2023, Pietro Bongini and his friends conducted research on DruGNN using the method of Composite Graph Neural Network (CGNN) method. This research resulted in a model with 86.13% accuracy in predicting the side effects of drugs [7]. At In 2017, Wei-Po Lee and his friends conducted a study comparing several methods, using three datasets to predict the side effects of drugs. The methods compared in Pauwels method, Liu method, Cheng method, RBMBM, INBM, and Ensemble. On the three datasets used, the Ensemble method managed to achieve the highest accuracy successively, namely 96.2%, 95.8%, and 96% [8]. In 2019, Kanurakan Velswamy and his friends carried out research on extreme rainfall prediction using the Support Vector Machine with Bees Algorithm as the algorithm for feature selection. Bees Algorithm was used to find the optimum feature subset and produced an accuracy of 89.18%. While those that do not use feature selection have an accuracy of 88.98% [9]. Based on the studies that have been carried out, it can be concluded that the widespread application of machine learning has proven its ability to improve the prediction of side effects of drugs. However, the paucity of studies that focus on the use of feature selection in this context suggests that the role of feature selection in the prediction of adverse effects of drugs is important. This context shows that the role of feature selection is important to obtain more optimized prediction results. Feature selection is an important process of selecting a subset of the most relevant or important features to improve model performance. One of the promising approaches in feature selection is using metaheuristic algorithms, such as the Bees Algorithm.

This research uses a Support Vector Machine (SVM) optimized with the Bees Algorithm to predict side effects in the context of reproductive system and breast disorders. These settings were chosen due to the high frequency and substantial influence of medication side effects on the reproductive system and breast conditions. For instance, a number of medications have the potential to induce breast cancer, infertility, or menstrual problems, all of which have detrimental effects on a patient's quality of life. It is anticipated that by optimizing SVMs using the Bees Algorithm, pharmacological side effects would be better understood and addressed, leading to the creation of safer and more efficient treatment plans.