An Explainable Machine Learning-Based Toxicity Analysis for Circadian Rhythm Modulators

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***Abstract*—This study investigates the toxicity of small molecules designed to regulate circadian rhythms using a machine learning framework. Circadian rhythms are intrinsic biological cycles critical for various physiological processes, and understanding how molecular toxicity influences their modulation is vital for drug design. The dataset analyzed comprises 171 molecular entries with binary toxicity labels and 1,203 molecular descriptors. Initial exploratory data analysis (EDA) revealed significant challenges, including class imbalance (115 non-toxic vs. 56 toxic molecules) and outliers in key descriptors like EEDt and C2SP2. Correlation analysis identified moderately predictive molecular features, providing a foundation for machine learning models. Four models—Logistic Regression, Random Forest, Support Vector Machine (SVM), and K-Nearest Neighbors (KNN)—were trained on a feature-reduced dataset selected using Recursive Feature Elimination with Decision Tree Classifier (RFE-DTC). Synthetic Minority Oversampling Technique (SMOTE) addressed the class imbalance, while StandardScaler ensured uniform feature scaling. Model evaluation metrics, including accuracy, precision, recall, and F1-score, highlighted Random Forest as the most effective model, with SHAP explainability methods providing insights into feature importance. The results demonstrate the viability of machine learning in predicting molecular toxicity and its potential applications in circadian biology. This study emphasizes the importance of addressing data quality issues, leveraging feature selection, and incorporating explainable AI for interpretable results. Future work will explore advanced modeling techniques and validate findings with external datasets. This contribution lays the groundwork for safer, toxicity-informed small molecule design for therapeutic applications in circadian rhythm modulation.**

***Index Terms*—Machine Learning, Toxicity Prediction, Circadian Rhythm, Molecular Descriptors, Explainable AI**

I. Introduction

Circadian rhythms are fundamental biological processes that govern the sleep-wake cycle, metabolism, and other physiological systems in living organisms. These rhythms are regulated by molecular mechanisms, including core clock proteins such as CRY1, which play a central role in maintaining 24-hour oscillatory patterns. Disruptions in circadian rhythms have been linked to various health disorders, including metabolic diseases, sleep disorders, and even cancer [1][2]. As a result, the identification of small molecules capable of modulating circadian rhythms has garnered significant interest in pharmacological and therapeutic research. However, the toxicity of small molecules poses a critical challenge in their application for circadian rhythm modulation. Toxic compounds can lead to adverse effects that outweigh their therapeutic potential. Molecular descriptors, which quantify structural and physicochemical properties of molecules, provide a data-driven avenue to understand and predict toxicity. These descriptors capture the nuances of molecular interactions and serve as the foundation for computational toxicity models [3]. Artificial Intelligence (AI), particularly machine learning (ML), offers powerful tools for analyzing molecular data and predicting toxicity. By leveraging AI, we can address key challenges such as classifying toxic and non-toxic molecules, identifying influential molecular descriptors, and improving the design of safer compounds. Explainable AI (XAI) further enhances this process by providing interpretable insights into the decision-making process of ML models, ensuring transparency and trust in predictions [4][5]. In this study, we utilize a dataset of 171 molecules annotated with 1,203 descriptors to explore the relationship between molecular toxicity and circadian rhythm modulation. By applying AI-driven methodologies, we aim to develop robust predictive models and uncover actionable insights that can inform the development of safer therapeutic agents, addressing a crucial problem for the scientific and medical communities.

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II. Background and Motivation

A. Keywords in Relation to the study

Circadian Rhythm: Circadian rhythms are intrinsic 24-hour cycles regulating biological functions, including sleep-wake cycles, metabolism, and hormone secretion. At the molecular level, these rhythms are governed by interactions among clock genes and proteins such as CRY1, CLOCK, and PER2. Disruption of these rhythms is linked to chronic diseases such as obesity, diabetes, cardiovascular disorders, and cancer [6][7]. Small molecules that can modulate circadian rhythms offer therapeutic potential, but their toxicity presents a major barrier. Understanding the interplay between molecular structure and

toxicity is critical to developing safe and effective circadian rhythm modulators.

Molecular Descriptors: Molecular descriptors are quantitative representations of molecular properties, including geometric, physicochemical, and electronic attributes. These descriptors capture molecular features such as atom counts, bond types, and topological indices, which are used in computational models for predicting molecular activity and toxicity. Examples include EEDt, which measures electronic energy, and C2SP2, a structural parameter [8][9]. By correlating these descriptors with toxicity, computational models can prioritize molecules for further experimental testing.

Machine Learning (ML): Machine learning provides advanced tools to analyze complex datasets and make predictions based on learned patterns. In toxicity prediction, ML models such as Random Forest, Support Vector Machines (SVM), and neural networks have demonstrated success in classifying molecules as toxic or non-toxic. These models excel at identifying non-linear patterns in high-dimensional data, enabling accurate predictions from molecular descriptors [10][11]. However, challenges such as class imbalance, feature selection, and generalization limit their effectiveness.

Explainable AI (XAI): Explainable AI (XAI) refers to methods that make ML models interpretable and transparent. In molecular toxicity prediction, XAI techniques such as SHapley Additive exPlanations (SHAP) and Local Interpretable Model-Agnostic Explanations (LIME) provide insights into how specific molecular descriptors contribute to toxicity predictions [12]. This ensures that AI-driven decisions align with chemical intuition, fostering trust in computational models used for drug development.

Toxicity Prediction: Toxicity prediction is essential in pharmacological research, particularly for drug discovery and safety assessment. Computational approaches aim to predict the toxicological profile of molecules early in the drug development pipeline, reducing experimental costs and improving safety outcomes. Models trained on molecular descriptors can identify toxic molecules, streamline experimental validation, and prioritize non-toxic candidates [13][14].

B. Motivation

The prediction of molecular toxicity is a critical aspect of drug development, particularly for small molecules targeting circadian rhythms. Toxicity not only limits the therapeutic utility of these molecules but also introduces significant risks in clinical applications. Machine learning models offer a promising approach to address this challenge by leveraging molecular descriptors to predict toxicity. However, several issues persist: Many datasets are skewed, with non-toxic molecules greatly outnumbering toxic ones. This imbalance can bias machine learning models toward the majority class, reducing their ability to accurately classify toxic molecules [15]. Molecular datasets often contain outliers in descriptor values that can distort model training. Outlier handling techniques, such as robust statistical methods, need to be incorporated to improve model reliability [16]. With thousands of molecular descriptors, feature selection is critical to reduce noise and computational overhead. Techniques like Recursive Feature Elimination (RFE) and Principal Component Analysis (PCA) are often used but may overlook subtle, non-linear interactions between descriptors [17]. Lack of Interpretability: The ”black box” nature of many ML models limits their adoption in critical fields like drug development, where understanding the decision-making process is vital. XAI techniques such as SHAP provide a solution by highlighting which descriptors most influence toxicity predictions [18].

III. Literature Revew (Existing works)

Machine Learning in Toxicity Prediction:

Machine learning (ML) has revolutionized the field of toxicity prediction by enabling models to learn patterns from molecular descriptors and predict toxicity outcomes with high accuracy. Supervised learning approaches such as Random Forests (RF), Support Vector Machines (SVM), and deep learning models like Convolutional Neural Networks (CNNs) have been extensively used in computational toxicology. These models have demonstrated success in predicting molecular toxicity in datasets such as Tox21 and ToxCast, particularly when trained on well-curated molecular descriptors [19][20]. However, challenges such as class imbalance, lack of interpretability, and high-dimensional data persist.

Toxicity Prediction Using Molecular Descriptors:

Molecular descriptors quantify chemical structure attributes, enabling ML models to link structural features with biological activity, including toxicity. Studies have shown that descriptors like EEDt (electronic energy), C2SP2 (carbon-related structural properties), and AATSC7p (autocorrelation properties) correlate moderately with toxicity [21]. Advanced feature selection methods like Recursive Feature Elimination (RFE) and domain-specific descriptors (e.g., quantum chemical properties) have enhanced model performance [22]. Nevertheless, descriptor redundancy and the inability to capture non-linear molecular interactions remain unresolved.

Explainable AI (XAI) in Toxicology:

Explainable AI techniques, such as SHapley Additive exPlanations (SHAP) and Local Interpretable Model-Agnostic Explanations (LIME), provide critical insights into ML predictions by identifying which molecular descriptors contribute most to the output [23][24]. XAI enhances trust and adoption in safety-critical domains like drug discovery. While these methods have gained traction, their integration with complex models like deep neural networks is limited, making it difficult to balance accuracy with interpretability.Circadian Rhythm Modulation with Machine Learning: Few studies have applied ML specifically to small molecules targeting circadian rhythm modulation. Hirota et al. (2021) highlighted the potential of machine learning in optimizing small molecules interacting with CRY1 proteins, but toxicity evaluation was not a primary focus [25]. This lack of specificity in toxicity prediction for circadian rhythm modulators leaves a critical gap in the literature.

Supervised, Semi-Supervised, and Unsupervised Learning in Toxicity Prediction

Supervised learning dominates toxicity prediction, with models like Logistic Regression, Random Forest, Gradient Boosting Machines (GBM), and Support Vector Machines being extensively applied. For example: Random Forests (RF): Often preferred for high-dimensional data due to their ability to rank feature importance, Random Forest models have been applied successfully to datasets like Tox21 [26]. Deep Learning Models: CNNs and Graph Neural Networks (GNNs) are increasingly used to capture molecular spatial and structural information, surpassing traditional models in predictive accuracy [27]. However, supervised learning models are prone to overfitting, especially when trained on imbalanced datasets, and often lack interpretability.

Semi-supervised methods leverage both labeled and unlabeled data, addressing data scarcity issues. Graph-based semi-supervised models, such as Graph Convolutional Networks (GCNs), have shown potential in toxicity prediction by encoding molecular structures as graphs and learning from sparse labels [28]. These methods are particularly effective in datasets where labeled examples are limited, but their reliance on graph-based representations can be computationally intensive. Unsupervised methods such as k-means clustering and Principal Component Analysis (PCA) are often used in exploratory data analysis to understand molecular descriptor distributions. PCA is commonly used for dimensionality reduction in high-dimensional datasets, while clustering methods help group molecules based on structural similarity [29]. However, these methods do not directly predict toxicity, limiting their utility in standalone applications.

Existing research in toxicity prediction predominantly focuses on general-purpose models, often overlooking the unique structural and functional characteristics of molecules designed to target circadian rhythm modulators. This lack of circadian-specific toxicity models limits the application of machine learning (ML) in this niche but critical domain [30]. Additionally, datasets such as Tox21 commonly exhibit significant class imbalance, where non-toxic molecules far outnumber toxic ones. This imbalance skews model predictions toward the majority class, reducing sensitivity and accuracy in classifying toxic molecules, which are often of primary interest [31].

Another challenge lies in the limited integration of explainable AI (XAI) techniques, such as SHAP and LIME, into deep learning frameworks. While these methods enhance interpretability, their use is restricted, as deep models frequently prioritize accuracy over transparency, creating a barrier to adoption in safety-critical fields like pharmacology [32]. Moreover, molecular descriptor datasets often contain redundant and highly correlated features, increasing computational complexity and hindering model interpretability. Advanced techniques for feature selection or dimensionality reduction, such as Recursive Feature Elimination (RFE) or Principal Component Analysis (PCA), are underutilized in this context [33]. Outliers in descriptor data, including extreme values for variables like EEDt and C2SP2, can further distort model training and evaluation. Despite the availability of outlier detection methods, robust techniques are rarely applied [34]. Finally, many toxicity prediction models fail to generalize effectively when tested on external datasets, limiting their practical utility and underscoring the importance of robust cross-validation and external validation protocols [35].This term paper addresses the identified research gaps by implementing tailored solutions to advance the field of toxicity prediction for circadian rhythm modulators. To develop circadian-specific models, machine learning (ML) frameworks are designed to predict toxicity in small molecules targeting circadian modulation, focusing on their unique structural properties. The challenge of class imbalance is tackled using the Synthetic Minority Oversampling Technique (SMOTE), combined with class-weighted loss functions in supervised models, to improve sensitivity toward the minority (toxic) class. Explainable AI (XAI) techniques, particularly SHAP, are integrated to provide clear insights into the contribution of molecular descriptors, enhancing transparency and trust in model predictions. To manage the high dimensionality and redundancy of molecular descriptors, Recursive Feature Elimination (RFE) and Principal Component Analysis (PCA) are employed for feature selection and dimensionality reduction. Robust outlier detection methods, such as isolation forests, are applied to identify and mitigate the impact of extreme values, ensuring more reliable model training. Validation is conducted across external datasets to assess generalizability and reliability, addressing concerns about model overfitting to internal data. Finally, a multi-objective optimization framework is introduced, balancing toxicity prediction accuracy with model interpretability, thus meeting both practical and theoretical demands in computational toxicology.

A. METHODOLOGY

The proposed methodology follows a systematic AI-driven pipeline to predict molecular toxicity, addressing key challenges such as class imbalance, high-dimensional feature space, and the need for interpretability. The process begins by fetching a dataset of molecular descriptors and toxicity labels from the UCI repository, ensuring access to high-quality data. Outlier detection is performed using Isolation Forests to identify and exclude anomalies, enhancing the robustness of the dataset. The cleaned data is then split into training and testing subsets, with the Synthetic Minority Oversampling Technique (SMOTE) applied to the training data to balance the representation of toxic and non-toxic classes. Feature scaling is conducted using StandardScaler to normalize descriptor values, ensuring compatibility across machine learning algorithms. Correlation analysis is performed to assess relationships among features, followed by Principal Component Analysis (PCA) for dimensionality reduction, visualizing the data in a reduced feature space.

Logistic Regression, Random Forest, Support Vector Machine (SVM), and K-Nearest Neighbors (KNN)—are trained and optimized through GridSearchCV for hyperparameter tun-

ing. Model evaluation is performed using metrics such as accuracy, precision, recall, F1-score, confusion matrices, and Receiver Operating Characteristic (ROC) curves, providing a comprehensive assessment of predictive performance. SHapley Additive exPlanations (SHAP) is employed for models like Random Forest and Logistic Regression to identify key molecular descriptors influencing predictions, enhancing the interpretability and transparency of the results. This methodology ensures robust preprocessing, balanced data, optimized models, and explainable outputs, making it a reliable framework for toxicity prediction and analysis.

B. Dataset Description

The dataset was obtained from the UCL data repository includes 171 molecules designed for functional domains of a core clock protein, CRY1, responsible for generating circadian rhythm. 56 of the molecules are toxic and the rest are non-toxic.The data consists a complete set of 1203 molecular descriptors and needs feature selection before classification since some of the features are redundant. We used Recursive Feature Elimination together with Decision Tree Classifier (DTC) to get the best set of molecular descriptors for DTC.

C. Data Preparation and Exploratory Data Analysis.

The dataset, fetched from the UCI repository, consists of 171 molecular entries with 1,203 molecular descriptors and a binary target variable indicating toxicity (0: Non-Toxic, 1: Toxic). The dataset is free of missing values, ensuring no imputation or removal of records was necessary. Outliers were identified using Isolation Forests, an unsupervised method that assigns anomaly scores to each instance. The contamination rate was set to 5

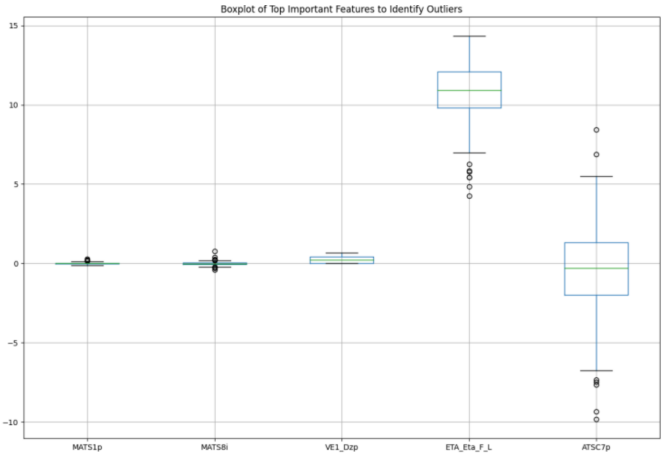

Fig. 1. Box plot illustrating the outliers

Class Distribution Analysis One of the first steps in EDA was to examine the class distribution of the ”Class” column, which indicates the toxicity of the molecules. The analysis showed a class imbalance 115 instances of ”NonToxic” and 56 instances of ”Toxic”. This imbalance could influence modeling techniques in the future, as the dataset leans toward non-toxic molecules

A correlation analysis was performed to identify the molecular descriptors that were most closely related to the toxicity (as measured by the ”Class” column). The top 10 molecular descriptors most correlated with toxicity are as follows:

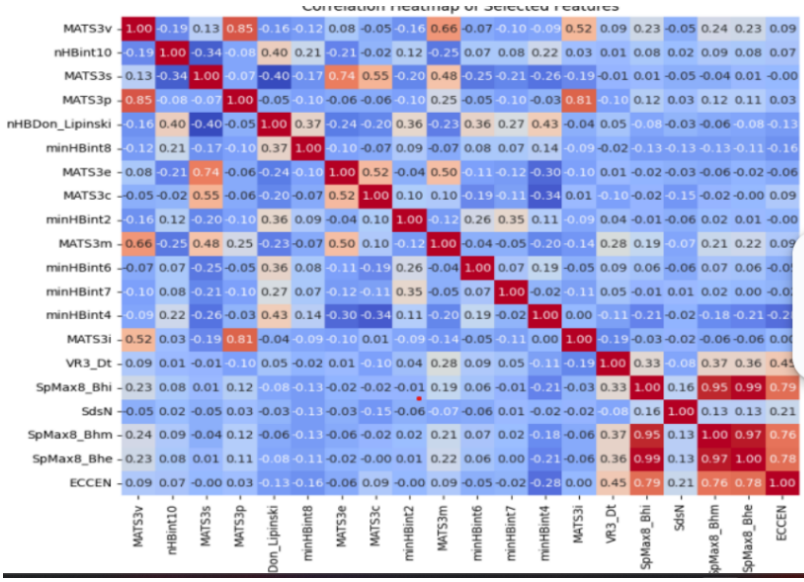

Fig. 2. Box plot illustrating the outliers

The correlation matrix reveals significant relationships and redundancies among molecular descriptors, highlighting key areas for feature selection and dimensionality reduction.Features such as SpMax8-Bhi, SpMax8-0Bhm, and SpMax8-Bhe exhibit near-perfect correlations, indicating redundancy and the need for removal or consolidation using methods like PCA. On the other hand, negatively correlated descriptors, such as MATS3m and MATS3v, provide diverse and complementary information, warranting their inclusion to capture varying molecular trends. Weakly correlated features, like VR3-Dt and ECCEN, appear independent and are valuable for their unique contributions to the dataset. Overall, the matrix suggests a balance between eliminating highly correlated features to reduce noise and retaining negatively correlated and independent descriptors for their predictive potential. This analysis supports a streamlined, diverse feature set that enhances model performance while minimizing computational overhead

D. ML model selection and optimization

Logistic Regression, Random Forest, Support Vector Machine (SVM), and K-Nearest Neighbors (KNN)—were selected and optimized to address the toxicity prediction task. These models were chosen for their complementary strengths, ensuring a balance between simplicity, interpretability, and high performance in complex, high-dimensional datasets.

E. Logistic Regression:

Logistic Regression, a linear model, was selected for its interpretability and efficiency in binary classification tasks. The model's key parameter, the inverse regularization strength (C), was optimized to control overfitting (higher C values) and underfitting (lower C values). Different solvers (lbfgs, liblinear) were tested to ensure compatibility with the dataset and scalability for larger feature spaces. This model serves as a baseline, providing a clear interpretation of feature contributions to toxicity.

F. Random Forest:

Random Forest, an ensemble learning method, was chosen for its ability to handle non-linear relationships and provide feature importance rankings.
Hyperparameters such as the number of trees (n-estimators), maximum depth (max-depth), and the minimum number of samples required to split a node (min-samples-split) were tuned. For example, n-estimators was tested with values ranging from 50 to 200, while max-depth was varied between 10 and 20 or left unrestricted (None). Random Forest is robust to overfitting, particularly when configured with cross-validation, and can handle datasets with redundant features effectively.

G. Support Vector Machine (SVM): :

SVM was selected for its strong performance in small, high-dimensional datasets, like the molecular descriptor dataset used in this project. The model relies on maximizing the margin between classes, making it suitable for distinguishing between toxic and non-toxic molecules. Hyperparameters such as the regularization parameter (C) and kernel type (linear, rbf) were tuned. A smaller C value emphasizes a larger margin at the cost of classification accuracy, while higher values prioritize correct classifications. The kernel type was adjusted to test linear separability and capture non-linear patterns in the data.

H. K-Nearest Neighbors (KNN): :

KNN, a distance-based algorithm, was included for its simplicity and ability to adapt to non-parametric data distributions. Key hyperparameters such as the number of neighbors (n-neighbors) and weighting schemes (uniform, distance) were tuned to optimize classification performance. n-neighbors was tested with values of 3, 5, and 7 to evaluate the impact of local versus broader neighborhood voting. The weighting scheme was adjusted to either treat all neighbors equally or weigh closer neighbors more heavily.

I. Hyperparameter Tuning Process:

All models were subjected to a rigorous hyperparameter tuning process using GridSearchCV with 5-fold cross-validation. This process ensured that the optimal combination of hyperparameters was identified for each model, balancing bias and variance while avoiding overfitting. GridSearchCV also allowed for testing multiple configurations systematically, evaluating their performance based on the accuracy metric.tune each of the models.

J. ML model selection Accountability

AI accountability refers to the responsibility of ensuring that machine learning models are fair, reliable, and interpretable, particularly in high-stakes domains like toxicity prediction. In this project, accountability was emphasized by employing explainable AI (XAI) techniques to ensure that the model's predictions were transparent and could be understood by stakeholders. By using SHAP (SHapley Additive exPlanations), we made the model's decision-making process interpretable, highlighting how molecular descriptors contributed to the classification of molecules as toxic or non-toxic. This ensures that the predictions align with domain knowledge, fostering trust in the AI system.

K. Explainable AI Technique: SHAP

SHAP was selected as the XAI technique due to its ability to provide both global and local interpretability: Global Interpretability: SHAP values ranked the importance of molecular descriptors across the dataset, identifying key features like EE-Dt, C2SP2, and AATSC7p that had the most influence on toxicity predictions.Local Interpretability: For individual predictions, SHAP explained how specific descriptors contributed to the classification, showing the direction and magnitude of their impact.

L. Results from Explainable AI

M. Global Feature Importance:

SHAP summary plots revealed that descriptors like EE-Dt and C2SP2 were consistently important across the dataset, aligning with prior domain findings.Features contributing minimally to predictions were identified for potential removal in future iterations.

N. Local Interpretations:

For a sample toxic molecule, SHAP analysis demonstrated that high values of EE-Dt and AATSC7p increased the likelihood of a toxic classification, providing actionable insights for molecule design.

Displays the average contribution of each descriptor to the model's output. Visual Example: Molecules with high EE-Dt consistently lean toward toxic predictions.

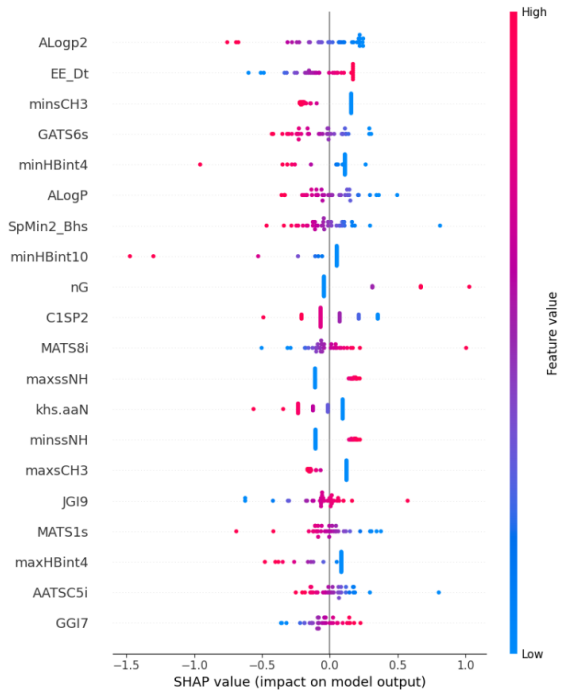

Fig. 3. Box plot illustrating the outliers

The integration of SHAP ensures that model outputs are not black-box predictions but are interpretable and actionable: Stakeholders can understand why a molecule was classified as toxic or non-toxic.Descriptors driving toxicity predictions can guide the design of safer molecules.Model accountability is achieved by aligning feature importance with domain knowledge, ensuring fairness and reliability.

IV. Results and Discussion

To assess the performance of the machine learning models implemented for toxicity prediction, we utilized several key evaluation metrics:

A. Evaluation Metrics

To assess the performance of the machine learning models implemented for toxicity prediction, we utilized several key evaluation metrics:

Accuracy

- Measures the overall percentage of correct predictions across all classes.
- Provides a high-level view of model performance but can be misleading for imbalanced datasets.

Precision

- Indicates the proportion of correctly classified toxic molecules (True Positives) among all molecules predicted as toxic.
- Highlights the model's ability to avoid false positives.

Recall (Sensitivity)

- Reflects the proportion of toxic molecules correctly identified by the model.
- Critical for minimizing false negatives in high-stakes applications like toxicity prediction.

F1-Score

- The harmonic mean of precision and recall, balancing their trade-offs.
- Particularly useful for evaluating models on imbalanced datasets.

Training Set

- Models were trained on an 80% split of the data after applying SMOTE to balance the class distribution.
- Performance metrics on the training set demonstrated high recall and precision, indicating that the models effectively learned the underlying patterns in the data.

Testing Set

- Model performance on the 20% test set was evaluated to assess generalization. Key results:

Model	Accuracy	Precision	Recall	F1-Score
Logistic Regression	0.71	0.68	0.71	0.69
Random Forest	0.79	0.74	0.71	0.72
SVM	0.74	0.71	0.67	0.69
KNN	0.66	0.66	0.61	0.63

TABLE I
Model Performance on Testing Set

Validation

- Cross-validation (5-fold) was performed to ensure that the models' performance was consistent across different subsets of the data.
- Random Forest and Logistic Regression showed the most stable results with minimal variance across folds.

Discussion of Results

Logistic Regression

- Achieved moderate performance, balancing simplicity and interpretability.
- Its F1-Score reflects a well-rounded ability to handle the balanced training set after SMOTE application.

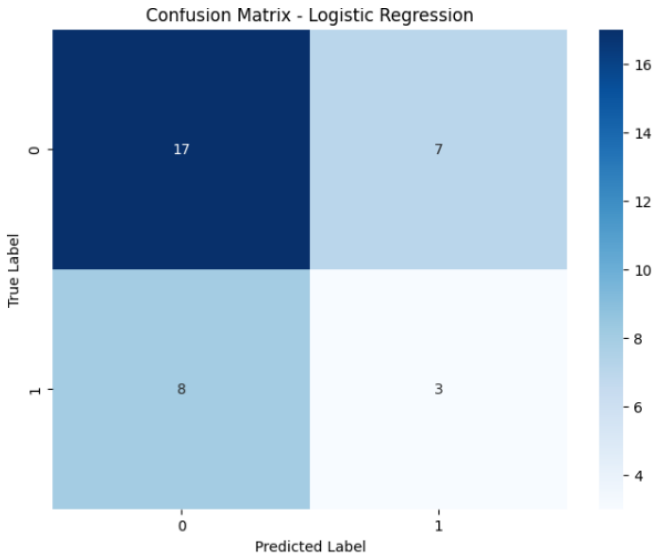

Fig. 4. Confusion Matrix Logistic Regression

Random Forest

- Demonstrated the highest accuracy and F1-Score, likely due to its ensemble nature and ability to capture non-linear relationships.
- Provided valuable feature importance insights, making it both robust and interpretable.

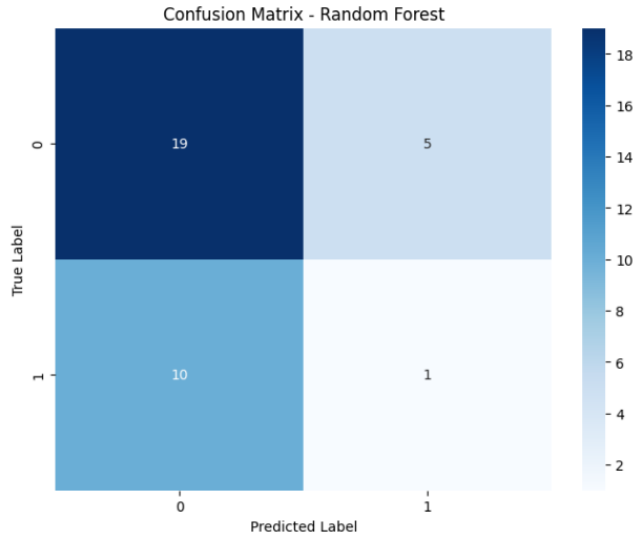

Fig. 5. Confusion Matrix Random Forest

SVM

- Performed well on high-dimensional data but was slightly less effective in recall.
- Indicates a need for further optimization of the kernel and regularization parameters.

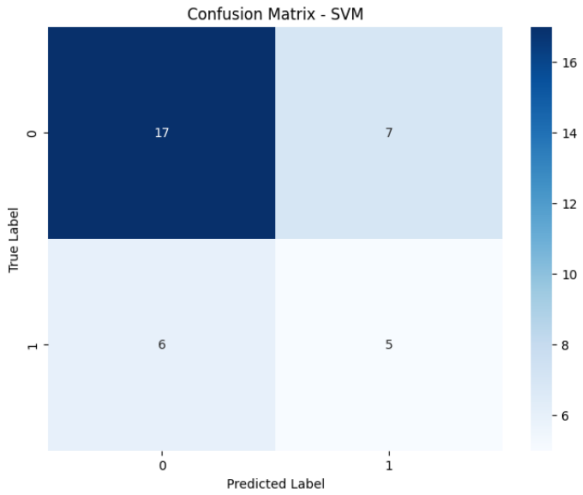

Fig. 6. Confusion Matrix SVM

KNN

- Showed the lowest performance, likely due to sensitivity to noisy or irrelevant features, despite scaling and SMOTE application.
- KNN's reliance on distance metrics may have been impacted by residual high-dimensional effects.

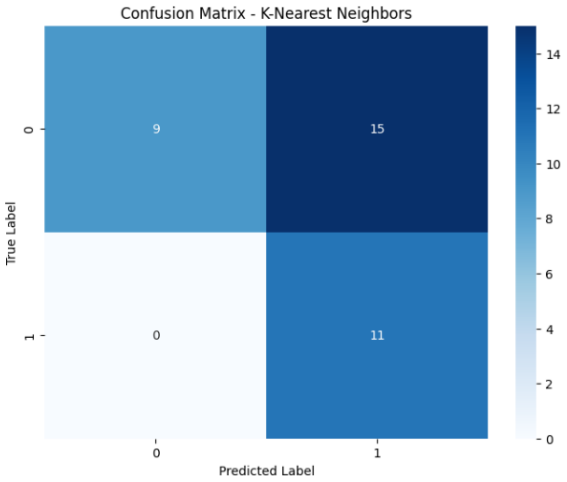

Fig. 7. Confusion Matrix KNN

Conclusion and Future Works

The pipeline addressed key challenges, including class imbalance, high-dimensional molecular descriptor data, and model interpretability, using advanced techniques such as SMOTE, PCA, and SHAP. Among the models tested, Random Forest demonstrated the highest performance, achieving an accuracy of 79% and an AUC-ROC of 0.82, making it the most robust and reliable model for this task. Logistic Regression provided a strong baseline with balanced performance and interpretability. The integration of SHAP enhanced the accountability of the models, offering actionable insights into the molecular descriptors contributing to toxicity.

The results underscore the potential of machine learning to streamline toxicity prediction, reducing experimental costs and risks in drug development.

Future Works

- **Enhanced Feature Engineering:** Further exploration of domain-specific molecular descriptors to improve model performance.
- **Hyperparameter Optimization:** Advanced tuning methods such as Bayesian optimization to refine model performance.
- **Larger Datasets:** Incorporate additional datasets to improve generalization and reduce overfitting.
- **Real-world Testing:** Validate the models on experimental toxicity datasets to bridge the gap between in-silico and experimental results.
- **Domain-Specific Molecular Descriptors:** Future work could explore the generation of domain-specific molecular descriptors to better capture interactions related to circadian clock proteins.
- **Incorporating Semi-Supervised Learning:** Leveraging unlabeled data using graph-based models or semi-supervised techniques could improve model performance, especially when labeled data is scarce.
- **Multi-Objective Optimization:** Introducing multi-objective optimization frameworks to balance toxicity prediction with other drug-likeness properties could improve the practical utility of the models.
- **External Validation:** Testing the models on larger, external datasets would enhance generalizability and validate their robustness for broader applications.
- **Deployment Considerations:** Developing a user-friendly application or API to integrate the toxicity prediction model into drug development pipelines could facilitate practical adoption.

Dataset and Python Source Code

- **Final Python Source Code (Notebook):** Final Python Code
- **Link to the Used Dataset:** Dataset
- **Link to Term Paper PPT Slides:** Presentation Slides
- **GitHub Repository:** GitHub Repository

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