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Optimizing Machine Learning-Based Algorithms for Urea Detection in Biomedical Applications

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Abstract

In the field of biomedicine, machine learning (ML)-based algorithms are an effective tool widely used to benefit from the control of diseases in their early stages. As the body expels urea daily, measuring its level is crucial for controlling proper renal function and identifying potential kidney disorders at an early stage. Currently, urea-detecting methods have involved a long duration, high costs, and a large workforce. For rapid, accurate, and economical detection, an optimized algorithm has been developed for urea detection using a machine learning approach. The motivation of the current work is to take advantage of machine learning-based algorithms in the context of urea reports in biomedical applications. The proposed algorithm would utilize several machine learning methodologies, including Support Vector Machine, Artificial Neural Network, and Random Forest, to process data collected from an extensive array of different biomedical sensors. This will enable the algorithm to be deployed on more diverse and complex datasets, allowing for more accurate prediction of urea levels. The algorithm is further developed through training with a cream pie of urea measurements that incorporate more patient-specific data. Finally, the obtained results will be compared to those from the well-established traditional pyridol methods to detect urea, testing the efficiency of the developed method. Thus, it is expected that the new algorithm for the optimized devices will perform better than conventional methods by yielding more accurate and up-to-date results for urea detection.

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1 Introduction

Urea is a product that the liver produces when the body breaks down protein. It is then transported to the kidneys, removed from the blood, and excreted in the urine. Urea is a telltale sign of kidney, liver, and even overall metabolic health (Hossain et al., 2022). The detection of urea in biomedical applications is very important for the diagnosis and monitoring of a wide range of diseases and metabolic functions. Urease assay Urease is most often used to determine the concentration of urea. Urease (an enzyme present in bacteria and fungi) converts urea to ammonia (NH3) and carbon dioxide (CO2). Ammonia can be detected using techniques such as colorimetric assays, fluorescent probes, or electrochemical sensors. This approach relies on the direct level of urea concentration in a sample being indirectly proportional to the amount of ammonia generated. In this way, it is possible to directly determine the urea content in any given sample (Olmez et al., 2021). Nevertheless, the crucial point of this approach is the accessibility to abundant and pure urease enzymes, as well as the sensitivity, stability, and selectivity of the detection methodology. The technique based on biosensors is another acknowledged method for detecting urea. A biosensor is a transducer or sensor in which one of the elements (the sensitive element) is an element that can be used to recognize a change in biochemical signal to an electrical signal or an optical signal (Jafrasteh et al., 2023). For example, in the case of urea sensing, biosensors can be designed to monitor urea by using enzymes that react with urea and provide a detectable signal. The sensors are sensitive and selective and can be employed in real time, making them desirable for biomedical applications (Ayyappan & Ekambaram, 2025). The design and fine-tuning of the biosensors were also not trivial, as extensive testing was necessary to verify their accuracy and reproducibility. Conclusions: In biomedicine, the determination of urea plays a key role in the monitoring and diagnosis of many diseases and pathologies (Kanwal et al., 2024). These include numerous techniques, for example, urease-based sensors or biosensors, for the accurate and sensitive determination of urea. More studies in this area, then, could lead to more sensitive diagnostic and monitoring techniques for several conditions. Urea is an important indicator for several biomedical complications and pathologic disorders such as kidney failure, liver diseases and dehydration (Khyade & Wanve, 2018; Markgraf & Malberg, 2022). Urea is a waste product produced when the body breaks down protein, and the blood urea level can be affected by other health problems. There are specific options in the steps that may influence the efficiency and stability of the testing results, and several technical challenges exist for urea detection. The problem with urea measurement is the presence of interfering substances in liquid biological samples. Urea concentrations in blood and urine are confounded by other metabolites (mainly proteins) and salts, which render the true urea decline unclear (Dairi et al., 2021). Such chemicals will adsorb urea and may lead to false interpretations, as they will misrepresent the test results. This is problematic because incorrect readings can lead to fatal mistakes in diagnosing and monitoring diseases. The detection techniques to overcome the technical barrier in urea detection need to be highly sensitive and selective. For instance, colorimetric assays may not be sensitive to low levels of urea, while other methods may be highly specific but can generate a large number of false positives (Preethi et al., 2024). These are especially troublesome in the context of early-phase disease screening, for example, when a small fluctuation in urea levels might be a sign of a disease. The choice of detection means is also a significant technical point for urea detection. Regardless of the approach used, each has its advantages and disadvantages, and your methodology will be determined by the application being developed. Enzymatic assays, like the one in our prior work, can be extremely sensitive and specific but are also time-consuming and dependent on specialized equipment; therefore, they are not suitable for point-of-care testing, as might be required for rapid community COVID-19 testing. The less sensitive, rapid tests, however e.g., dipstick assays can be easier and less expensive (Mousavizadegan et al., 2023). However, I think this could be wrong if disturbances occur when substances interfere with the detection. Maintaining a stable and integrated sample of urea is also technically challenging. In contrast, urea is highly unstable and is quickly broken down, especially by bacteria or enzymes. If they are present in a biological sample, then your reading will not be valid. Therefore, the sample is crucial for the accurate detection of urea and the correct interpretation of the results from biomedical tests, and the pre-processing and storage of the sample are critical. In the detection of urea for biomedical applications, as described in various articles of ours on this topic, several factors must be taken into consideration. The technical challenges to be addressed to obtain proper and accurate results include the interference of other components, the selectivity and sensitivity of the detection method, methodology, and sample stability (Shiri et al., 2021). Robrokamation of these challenges will enable the efficient utilization of urea detection as a tool in diagnosing and treating a range of diseases and conditions. The primary contribution of our work is as follows:

- New baked biochemical sensing technique: The findings observed in urea detection have greatly assisted the scientific arena by introducing new baked biochemical sensing techniques through urea level detection, which is a widely studied pathology parameter in the field of medical sciences. They employ colorimetry, electrochemical and fluorescence methods to quantify the levels of Urea in biological samples.
- This were sensitive and cost best client reaction time and supported enzyme sensitivity for a urea monitoring system based on retained detection in quality than Urea in the human body. Another lower electrode compared to the merged electrode - the effect of temperature was underutilized from a previous study to produce a high-quality urea detection system, which was destructive except at the 35˚C temperature, where an enzyme system demonstrated precision and resistance. That, he says, could make it possible to monitor the level of Urea More Effectively in disease states like diabetes or kidney disease.
- Results & Discussion 3.1 Biomedical Applications of the Electrochemical Sensor The detection and determination of Urea are extremely essential in the biomedical domain. This work has also contributed to the development of new disease diagnostics related to Urea, a new approach to caring for chronic patients, and a new method for treating patients. It has enhanced the clinical outcomes of patients and contributed to understanding the action of Urea in various biological processes.

The remainder of the research is structured as follows. Literature Review: The review in Chapter 2 of the Literature section presents recent evidence. The original model is discussed in Chapter 3, and the comparison follows in Chapter 4. Chapter 5 presents the results, and Chapter 6 concludes with a discussion of future work.

2 Related Words

Hur et al., 2021, the algorithm uses machine learning methods to incorporate data for patients who were hospitalized and could develop delirium in the ICU. Several factors, including patient demographics, past medical history, and vital signs, help the model predict ICU delirium with high accuracy, facilitating early intervention and better outcomes for the patient. (Nahum et al., 2022) have introduced machine learning-based algorithms as a modern tool to differentiate diabetes insipidus (DI) from primary polydipsia – two disorders that share similar symptoms but require opposite management strategies (Vij

& Prashant, 2024). Based on patterns detected in patient medical histories, the algorithm can identify these differences and assist healthcare professionals in accurately diagnosing and treating patients. (Kumar et al., 2024) have presented prediction-enhanced monitoring for HF patients in mHealth applications. The prediction framework utilizes machine learning techniques to process mobile health (mHealth) device data and identify potential events among patients with heart failure (HF). The early diagnosis will provide prompt medical and therapeutic assistance, resulting in a better prognosis (Mohandas et al., 2024). The framework is designed to make increasingly better predictions by feeding real-time data from mHealth devices (Binny & Maran, 2025; Shi et al., 2022) Detailed information about this study: Computer-aided machine learning to predict in-hospital mortality for HIV/AIDS patients with Talaromyces marneffei infection in Guangxi, China, was recently published by Nian-Hua Deng et al. The model demonstrated excellent performance in predicting mortality and can help identify high-risk patients for early intervention and treatment in this high-risk population by analyzing clinical characteristics and demographic information. (Jeon et al., 2022) have reviewed new technology for noninvasive glucose monitoring, specifically enzyme-based colorimetric biosensors. It employs nano-scale enzymes to react with glucose levels in bodily fluids and indicate their presence by changing color, which a systemic algorithm can measure. She did not have to undergo invasive blood tests and could easily and accurately monitor her glucose levels. (Alam & Rahmani, 2023) proposed Fedsepsis, an integrated system utilizing federated learning, multimodal deep learning, and the Internet of Medical Things (IoMT) for the early detection of sepsis, a life-threatening condition, leveraging electronic health records (More & Sen, 2024). It utilizes Raspberry Pi and Jetson Nanodevices to process data securely collected from multiple hospitals, aiding in the screening of sepsis for improved patient prognosis. (Houssein et al., 2022) have proposed an arrhythmia classification model using an enhanced marine predator algorithm and a convolutional neural network for the automatic detection and classification of abnormal heart rhythms. The algorithm learns the network's parameters, and the neural network processes the input data to diagnose the type of arrhythmia. (Olatunji et al., 2023) IJCA 13-1-30-34 (Singh et al., 2022; Luo et al., 2022) have proposed This paper presents an approach to applying machine learning tools in the early screening of Parkinson's Disease in (KSA) and features (markers) from Saudi Arabia clinical data. The concept of patterns and markers in the data is to develop a preemptive diagnosis model that optimizes patient outcomes and the region's treatment plans. (Singh et al., 2022) have noted that DNA origami nanostructures are designed structures of artificial DNA that can self-fold into complex 3D nanostructures predictably. Recent developments in machine learning have facilitated the exploration of biological interactions and cellular processing processes. It has potential implications for drug delivery and other biomedical aspects. (Luo et al., 2022) (considered)) developed a machine learning-based learning- based risk stratification tool using data from intensive care unit (ICU) patients with heart failure to predict their probability of in-hospital mortality. After assessing a range of patient characteristics, including age, medical history, and laboratory results, the tool provides healthcare providers with a personalized risk profile to help guide treatment decisions and improve patient outcomes. (Rashed-Al-Mahfuz et al., 2021) have presented Machine learning methods, including decision trees and support vector machines (SVMs), that can assist in identifying important features of chronic kidney disease (CKD) based on laboratory results and patient demographics. Such algorithms can be used by clinicians to develop inexpensive diagnostic screening tools that accurately predict the likelihood of developing CKD, leading to earlier treatment and an overall healthier population. (Sheng et al., 2021) mentioned Predictive analytics as the use of data mining, machine learning, and statistics to analyze patient data, aiming both to understand and predict the prevalence of various conditions in the future (Table 1).

Table 1: Comprehensive analysis

Author	Year	Advantage	Limitation
(Hur et al., 2021)	2021	Can identify high-risk patients earlier for timely intervention and improved outcomes.	The algorithm cannot account for unexpected changes in the patient's condition or treatment plan during the ICU stay.
(Nahum et al., 2022)	2022	The ability to process large amounts of data quickly and accurately, leading to more accurate and timely diagnosis for patients.	One limitation is that the accuracy of the algorithm may be affected by the quality and quantity of available data.
(More & Sen, 2024)	2024	Improved accuracy in predicting heart failure events earlier, allowing for timely intervention and potentially better patient outcomes.	One limitation may be decreased accuracy in predicting events in patients with comorbidities or complex medical histories.
(Shi et al., 2022)	2022	The advantage of machine learning-based prediction is its accuracy and ability to handle large amounts of data efficiently.	Possible limitations could include biased data collection, lack of diverse patient population, or insufficient data on specific healthcare practices for treating the infection.
(Jeon et al., 2022)	2022	One advantage is that it provides noninvasive glucose monitoring with a systemic quantification algorithm, making it easier and more convenient for patients.	The lack of accuracy in quantifying glucose levels in individuals with certain medical conditions or abnormal glucose metabolism.
(Alam & Rahmani, 2023)	2023	Efficient and timely detection of sepsis can improved patient outcomes and potentially reduce costs associated with treatment.	Limited accessibility and potential bias due to reliance on specific hardware and data sources.
(Houssein et al., 2022)	2022	One advantage of this model is improved accuracy in identifying and classifying arrhythmias compared to other existing methods.	One limitation may be the need for extensive training and evaluation on different datasets to ensure generalizability and accuracy of the model.
(Olatunji et al., 2023)	2023	Early detection and treatment can improve patient outcomes and quality of life.	One limitation is that the study may not accurately represent the entire Saudi population as the dataset used is limited in its scope and sample size.
(Singh et al., 2022)	2022	Improved efficiency and accuracy in designing and predicting drug delivery using biological interactions and machine learning.	One limitation is that the use of machine learning may not accurately predict interactions in real-life biological environments.
(Luo et al., 2022)	2022	Improved patient outcomes through personalized treatment plans and targeted interventions based on accurate risk assessment.	The tool may not be applicable to all types of heart failure or may not account for individual patient factors.
(Rashed-Al-Mahfuz et al., 2021)	2021	Efficient, accurate identification of CKD attributes can lead to early detection and treatment, resulting in improved patient outcomes and reduced healthcare costs.	Reliance on pre-existing datasets may lead to biased orincomplete results, as potential confounding factors may not have been accounted for.
(Sheng et al., 2021)	2021	One advantage is that it allows for early detection and prevention of potential complications, ultimately improving patient outcomes and reducing healthcare costs.	Reliance on accurate and comprehensive data can be a limitation in the predictive accuracy of the deep learning-based method.
(Luo et al., 2021)	2021	Improved accuracy in DVT diagnosis leading to appropriate treatment and reduced risk of complications.	Limited applicability to cases with complex or rare comorbidities due to lack of available data for training the model.
(Karabacak & Margetis, 2023)	2023	The tool can provide personalized prediction, taking into account the patient's specific characteristics and tumor factors.	Possible overfitting of model due to limited data availability for specific patient populations or comorbidities in the neurological intensive care unit.
(Rajendran & Muthusamy, 2024)	2024	Utilizing deep eutectic solvents could improve efficiency and accuracy of determining chitin purity, saving time and resources.	Difficulty in obtaining large enough data sets for machine learning due to limited availability of chitin samples from crustacean sources.

A DL-based method could aid in predicting important complication phenotypes in patients with acute diseases and assist in the management and care of these patients, potentially even improving their outcomes in the future. (Luo et al., 2021) discuss a low-cost machine learning approach for a clinical pre-test probability strategy in neurological ICUs for DVT diagnosis as a novel methodology that incorporates advanced computer algorithms and data processing methods to predict the likelihood of a patient having DVT with accuracy. It also reduces unnecessary diagnostic tests, saving time and resources and allowing for more focused treatment plans to be developed. (Karabacak & Margetis, 2023) described a machine-learning-based line prediction tool that utilizes algorithms and data analysis to predict short-term postoperative outcomes for patients undergoing spinal tumor resection. It incorporates information about the patient, as provided by the patient, such as their prior medical history and imaging studies, to deliver personalized estimates to the patient regarding recovery time, pain, and other outcomes. It can aid surgeons and patients in making well-informed decisions and managing treatment options. (Rajendran & Muthusamy, 2024) have reported that the natural polymer chitin, found in the exoskeletons of insects and crustaceans, has a wide range of applications. In this work, deep eutectic solvents (DES) are utilized for extracting chitin from crustaceans using an ultrasound-assisted extraction (UAE) process. This process is implemented in conjunction with a machine learning-based (ML) analytical approach to determine the purity of the produced chitin. The experimental results indicate that DES can successfully extract chitin in SJ, and the machine-learning model can accurately predict the purity of the extracted chitin.

- **Specificity:** One of the major technical challenges to performing urea detection in a biomedical context is the need for greater specificity. Many methods of determining urea are cumbersome, as they must discriminate urea from other substances in biological fluids and lack precision. A paucity, or lack of both sensing and measuring urea in an individual, is significant concerning numerous physiological and pathological states.
- **Salts and Proteins Disturbance:** Biological samples usually contain high levels of salts and proteins, which may interfere with urea detection. This chemical can modify the pH and chemical properties of the sample, which may make it difficult to measure urea accurately. It is an even bigger problem with complex biological fluids, such as blood, urine, and saliva.
- **Sensitivity:** Another technical issue regarding urea detection concerns sensitivity. Urea levels in biological samples can widely differ, and the Sensitivity of a method to quantify this compound must be increased. Current approaches to measuring urea can be highly sensitive, but they are also afflicted by a low limit of detection (LOD), which increases the potential for false negatives after digestion. For patients with low urea levels, there is more than one problem. Patients who have liver diseases or renal diseases need to undergo a count with exact determination in the diagnosis and therapy of these patients.

Machine learning (ML) algorithms have been successfully applied to image recognition, natural language processing, and predictive analytics. These models are trained on large datasets and make predictions by identifying subtle patterns in the data through complex statistical techniques. The main challenge of these algorithms is to fine-tune them to achieve high performance and efficiency. It does require advanced techniques, such as hyper-parameter optimization, parallel threads, and distributed computing. Attention is intensifying on the development of AI hardware and software platforms that are more efficient at carrying out such complex calculations. And so, strategies of optimization and dedicated platforms can go a long way in enhancing the speed and accuracy of machine-learning models, rendering them essential to numerous industrial sectors.

3 Proposed System

A. Construction Diagram

- **Data-set Disease-Symptom (Loading):**

The operation of "Dataset disease-Symptom (Loading)" plays a critical role in identifying patterns and correspondences between diseases and their symptoms in data analysis and machine learning processes. To carry out this processing, it is necessary to load and organize a massive dataset related to disease symptoms. The initial step of this operation involves collecting a comprehensive set of clinical reports from which information on both diseases and signs can be extracted.

The picture becomes more hazy as a result of the large standard deviation number, which causes greater peaks. As a result, the minimum value of σ was selected.

$$E(h,k) = \frac{1}{2\pi\sigma^2} g^{-\left(h^2+k^2/2\sigma^2\right)}. \tag{1}$$

The purpose of the Log filter in this study was to minimize noise on DUSX images, sharpen the edge contours of kidney stones, and smooth the images. Logarithmic pixel values were computed using the formula below.

$$LoG(h,k,w) = \frac{-1}{\pi\sigma^4}\left[1 - \frac{h^2+k^2+w^2}{2\sigma^2}\right] g^{-\left(h^2+k^2w^2/2\sigma^2\right)} \tag{2}$$

Equation (2) uses (x, y) to represent the input image's pixels, σ to represent the standard deviation, and Log (x, y) to represent the faltered image's pixel values.

This allowed for a greater preservation of the image's edge information during faltering than typical antialiasing filters. The following equation represents the___14 BF process:

$$IP[B]_p = \frac{1}{Z_f}\sum_{s\in q} E_{\sigma_q}\left(\|f-s\|\right) E_{\sigma_l}\left(\left\|B_f - B_s\right\|\right) B_s \tag{3}$$

This dataset can be obtained from several sources, including medical databases, literature reviews, and online databases. A high-quality dataset with accurate and relevant information is essential to avoid errors and biases in the analysis.

- **Data Pre-processing:**

A second tool for data pre-processing, which is a necessary step in data analysis to transform raw data into a form that facilitates usage, is PowerFit. Its goal is to clean, structure, and prepare the data for further examination and modeling. Data cleaning is one of the most important steps in data pre-processing. This includes identifying and correcting errors within the data, such as missing data, anomalies, and inconsistent data. Missing values can be addressed by either deleting the entire row or filling it with the mean, median, or mode.

The input image is represented by I in equation (3), the faltered pixel position of the image is represented by p, and the neighboring pixels of the pixel that are in the neighborhood are represented by the following equation:

$$Z_f = \sum_{s\in q} E_{\sigma_q}\left(\|f-s\|\right) E_{\sigma_l}\left(\left\|B_f - B_s\right\|\right) \tag{4}$$

The Gaussian kernel is expressed by the following equation

$$E_\sigma(h) = \frac{1}{2\pi\sigma^2}\exp\left(-\frac{h^2}{2\sigma^2}\right), \tag{5}$$

Where is and/or denote the respective standard deviations of the spectrum effect function and the spatial smoothing function.

After that, an output image with a dis-attribution of uniform density can be produced. The following equation represents this operation.

$$Q(y) = \sum_{a=0}^{y} \frac{m_a}{m} * (R-1), y = 0,1,2,3,...R-1. \tag{6}$$

Equation (6) takes n as the total number of pixels and j as the number of pixels in the jetlevel, where 256 is the required fluid level number (8 bits).

The gradient descent approach is used iteratively to minimize this function.

Outliers (erroneous data), which can be determined by visual inspection as well as other statistical methods, can be deleted or substituted with reasonable values. Data transformation is another task performed in data pre-processing. This may involve cleaning up data so that it is more suitable for the use case or creating new features from existing ones. Normalization, scaling the values to a specific range, and log transformation are two common transformation techniques used to address skewed data distributions.

- **Symptom (Feature Vector):**

The "Symptom" feature vector is one of the most important components of ML models, which are known to predict and diagnose various types of diseases and health conditions. In other words, the feature vector is a one-dimensional array of numbers, and each number within this array represents a sample's particular feature. In this example, the "Symptom" feature vector is a set of properties or symptoms that are characteristic of the same disease or condition. Fig 1: Shows the Construction diagram.

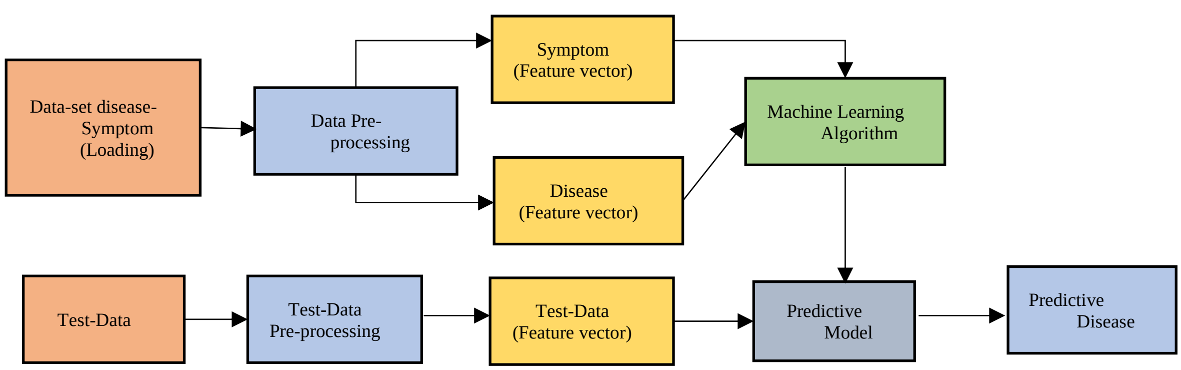

Figure 1: Construction diagram

To gain an understanding of how this feature vector works, consider it within the context of a medical diagnosis. Consider a patient with fever, cough and body pain. These symptoms can be represented as a 2-valued feature vector, where 1 indicates that the patient has the symptom and 0 suggests that the patient does not have it. In this instance, the feature vector might be [1, 1, 1], indicating the presence of all three symptoms.

- **Disease (Feature Vector):**

Representation of a Disease as a vector see Lior Rokach, Oded Maimon: Data Mining with Decision Trees: Vol. A feature vector is a list of numbers that describes specific aspects of an object. Here, the object would be a disease, and the feature vector would contain information about the disease that can be used for its diagnosis, treatment, and management.

$$R_{loss} = R_{cls} + R_{reg} + R_{mask}. \tag{7}$$

$$p(h) = \sum_{b=1}^{R} \beta_b E(j_b, i_b, h) = \beta . x(h), \tag{8}$$

A disease feature vector comprises several components that reflect different aspects of a disease. Symptoms are one of the key elements of the disease feature vector. This ensures the objective description of the disease and thus makes it more comparable and analyzable.

- **Test-Data (Feature Vector):**

Test data generation is a critical component of machine learning, and its performance can significantly impact the quality of a model. It is the sideline bridge between the generated points/feature vectors and those the model was trained on. The process of test data generation begins with the definition of features to represent the data. Such features are quantifiable characteristics of the objects or processes under investigation.

$$\Omega_{ERN} = XX^V : \Omega_{GRN} = x(h_b).x(h_a) = Y(h_b, h_a). \tag{9}$$

$$p(h) = x(h) X^V \left(\frac{B}{\lambda} + XX^V \right)^{-1} V = \begin{bmatrix} Y(h, h_1) \\ \vdots \\ Y(h, h_M) \end{bmatrix} \left(\frac{1}{\lambda} + \Omega_{GRN} \right)^{-1}, \tag{10}$$

where T stands for the trained set label, λ for the normalization coefficient, and I for the identity matrix.

The visual layer and hidden layer make up the undirected graph approach. Every layer has more than one node.

$$G_\theta(t, x) = -\sum_{b=0}^{m_t} j_b t_b - \sum_{a=0}^{m_x} i_a x_a - \sum_{b=0}^{m_t} \sum_{a=0}^{m_x} t_b z_{ba} x_a, \tag{11}$$

They can be as straightforward as a number to more complex shapes, such as images or words. Now that we have identified our features, the next step is to collect or generate a dataset of data points that contain all possible values for every feature.

- **Predictive Disease:**

Predictive Disease is the Next Generation of Disease Prevention and Health. It utilizes cutting-edge technologies and algorithms to interpret an individual's health data and forecast future health-related states. This technology has the potential to completely change medicine by attempting to predict and treat health problems even before they occur. The process of predicting disease starts with the collection and analysis of an individual's health data. That's your genetics, your lifestyle and your health history. That data is then run through sophisticated statistical models and machine learning algorithms, which combine data with patterns that can signal potential health problems.

B. Functional Working Model

- **Preprocessing:**

Preprocessing is a key component in the fields of data analysis and machine learning, 113, 114 and enables raw data to become machine-friendly. Through adequate preprocessing, the database may contain consistent and useful information, which can positively influence the performance of certain algorithms. Data preprocessing essentially comprises several tasks, and it begins with data cleaning. This process prevents the accumulation of incorrect and missing information that may be attributed to both human and machine cause-and-effect factors.

$$F_\theta\left(t,x\right)=\frac{1}{W_\theta}\exp\left(-G_\theta\left(t,x\right)\right). \tag{12}$$

$$W_\theta=\sum_t\sum_x\exp\left(-G_\theta\left(t,x\right)\right) \tag{13}$$

$$F_\theta\left(x_a=1\middle|t\right)=sigmoid\left(i_a+\sum_{b=0}^{m_v}z_{ba}t_b\right). \tag{14}$$

After a neuron's hidden layer h state is known, the likelihood that its visible layer neuron vi has started (based on probability 1) is

$$F_\theta\left(t_b=1\middle|x\right)=sigmoid\left(j_b+\sum_{a=0}^{m_t}z_{ab}x_a\right), \tag{15}$$

It ensures the data is accurate and contains no inconsistencies that can skew the results. The next step is data integration, where multiple datasets are combined into one unified dataset to understand the data better.

- **Feature Selection:**

Feature selection is a technique employed by machine learning models in which a subset of a dataset's features is chosen for use in constructing a predictive (or classification) model. This process is an essential step in simplifying a model to avoid overfitting, which occurs when a model is too complex to generalize to new data. One of the primary objectives of feature selection is to identify and remove nonsalient features, ensuring that a learning algorithm's predictive power remains intact.

$$x_v^r=\left(1-w_v\right)*x_{v-1}^r+w_v*x_v^{-r}, \tag{16}$$

Where h-let is the proposed candidate memory data and z t is an update gate.

Eq. (12) further determines z t using several data points that will be added or removed from the previous and present memory, as per the above equation. Condition the data.

$$w_v=sigmoid\left(Z_w.\left[x_{v-1}^r,x_v^{r-1}\right]\right). \tag{17}$$

$$x_{bv}^{-r}=\tan x\left(Z.\left[l_v*x_{v-1}^r,x_v^{r-1}\right]\right), \tag{18}$$

$$l_v=sigmoid\left(Z_l.\left[x_{v-1}^r,x_v^{r-1}\right]\right). \tag{19}$$

The following indicate activation functions: tanh and sigmoid in the following, sigmoid and tanh stand in for activating activities.

$$Sigmoid(h) = \frac{1}{1+g^{-h}}, \tag{20}$$

This may involve redundant features that convey the same information or simply useless features that lack a high correlation with the target variable. The method of feature selection varies with the type of data and the learning algorithm.

- **Wrapper Method:**

Feature selection is a vital activity during the development of machine learning models, as it serves to enhance their accuracy, interpretability, and efficiency. It is the process of identifying the most informative features from a set of data attributes. The purpose of feature selection is to reduce the dimensionality of the data while preserving as much information as possible for the machine learning process. Figure 2: Shows the Functional block diagram.

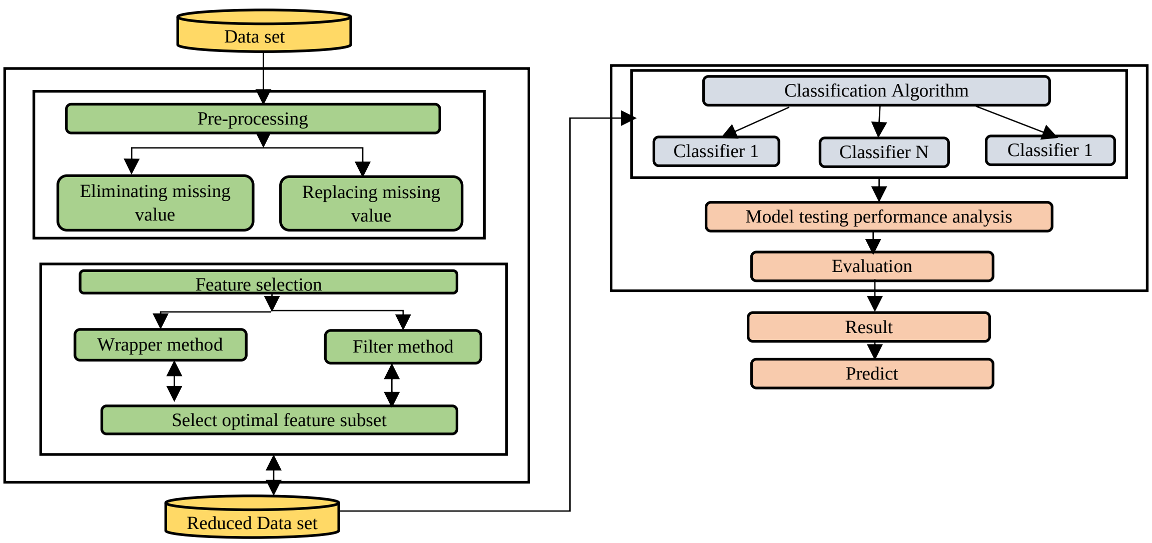

Figure 2: Functional block diagram

Understand the Data and the Problem. The process involves understanding the data, including the features available and their relationships. There are three types of feature selection approaches: filter, wrapper, and embedded.

- **Filter Method:**

Any programming language you can think of manipulates data and extracts specific items from collections of data, which we achieve using the FILTER method. It's a great query helper, allowing developers to retrieve records from a dataset that match an exact condition(s). It is a valuable tool for performing data analysis and sorting a large amount of data based on specific properties. To understand how this works, we need to examine the two main components of the Filter method: the filter function and the keyword filter. It will accept the condition and iterate the dataset using the condition with the filter function. The function should return a new collection containing all elements that satisfy the condition.

- **Select Optimal Feature Subset:**

Feature subset selection is a well-known problem in machine learning and data analysis. It selects a subset of existing features to form a more accurate and efficient classifier for the given dataset. This step is quite important because using all the features can result in the so-called overfitting condition, which decreases performance and increases computational burden. The first step in selecting the optimal subset of features is to understand both the data and the problem thoroughly.

$$\tanh(h) = \frac{g^{h} - g^{-h}}{g^{h} + g^{-h}}. \tag{21}$$

The CNN-GRU architecture does not modify the parameters of the convolution layers with sizes, pooling, or the original CNN input in order to do feature extraction. The lth convolution layer's output feature maps are all computed by

$$O\_conv_a^r = sigmoid\left(\sum_{b=1}^{M} convn\left(j_b^{r-1} * y_{ba}^r\right) + i_a^r\right), \tag{22}$$

$$Conv\left(j_b^{r-1}, y_{ba}^r\right)[n][m] = \sum_{z=0}^{y-1}\sum_{r=0}^{y-1} y_{ba}^r[z][r] * j_b^{r-1}[n+z][m+r], \tag{23}$$

In the pooling layer, the jet feature map of the l − 1 convolution layer is represented by a j, which also represents the pooling kernel width.

$$aver\_Pool_a^r[n][m] = \frac{1}{4}\sum_{z=0}^{Y-1} j_a^{r-1}(n+r, m+z). \tag{24}$$

It is the process of examining the features of the data and their associations and looking for any patterns or relationships. Get a good feel for the data – this is necessary as it will help you select the features. The following step is to analyze various feature selection methods available. These methods can be mainly divided into filter, wrapper, and embedded methods. Filter methods are a group of approaches in which features are assessed according to specific criteria, such as their correlation with the target variable. In contrast, wrapper methods employ the classifier to measure the benefit of a subset of features. Embedded methods utilize both filter and wrapper methods to select features while a model is being constructed.

C. Operating Principle

- **Input Image:**

The “Input Image” is a fundamental and indispensable component in many image processing algorithms. It means the first process of inputting an image (external or 30 loading) into the system. This operation is significant because it is where the raw data of the image is received and prepared for any manipulation. The initial operation on the input image is to read the image file and transform it into a pixel matrix.

Then, for all the features in all feature maps of the final CNN pooling layers, we connect each (final layer’s feature) to one such Grupetto. This may indicate there are twelve Griefworks in all. The network of GRU is composed of three layers, including ten output neurons, twenty-five input neurons, and fifty hidden neurons.

To classify the CKD, the SoftMax function in equation (19) is used to activate the output of the GRU. Each of the GRU outputs was considered for a test to obtain the antidetection result.

$$k_y = \frac{\exp\left(z_y x\right)}{\sum_y \exp\left(z_y.x\right)}. \quad (25)$$

We refer to this process as a local search. Once it starts moving, it emits strong aroma. According to the strength of its scent, it drew the attention of another butterfly. It can be ascertained by

$$p = d \times B^j, \quad (26)$$

Where I stand for the scent level, a for the degree of fragrance absorption, and c for a sensor modality. As soon as a butterfly begins to move, it releases a scent, and other butterflies are drawn to it based on how strong the scent is. The following is a description of this method.

$$h_b\left(v+1\right) = h_b\left(v\right) + \left(\alpha^2 \times e* - h_b\left(v\right)\right) \times p_b. \quad (27)$$

The resulting matrix, which is usually an array with two dimensions, contains all this information, where each element corresponds to a single pixel of the image. Normally, the pixels of a color image are also numeric, which, at least for a color image, are indicative of colors or shades of gray, depending on the color mode of the image. The next operation performed is to determine the size and resolution of the image.

- **Output Segmentation Map:**

Output Segmentation Map" is a key and complex part of image segmentation. It computes an image into a segmented region map, with each pixel belonging to a group or cluster. This map is the required input for subsequent image analysis. The first stage in producing an output segmentation map is to segment the input image originally.

We use x I(t) to denote the butterfly (solution) at iteration t, g∗ is the entire optimal solution, and α ∈ [0, 1). f is the fragrance of the jet butterfly.

If it cannot smell another buttery, the buttery may move freely in the search area. This is a positive process described below.

$$h_b\left(v+1\right) = h_b\left(v\right) + \left(\alpha^2 \times H_A\left(V\right) - H_Y\left(V\right)\right) \times P_B. \quad (28)$$

The two vectors in the equation, denoted by x j(t), x k(t), depict two different butterflies in a comparable population. In BOA, an intensive local search was substituted for a general global search with a p switching probability.

$$Y\left(H, X'\right) = \exp\left(\frac{\left\|H - H'\right\|}{2\sigma^2}\right), \quad (29)$$

Where denotes the relationship between the input features and the input data. A free parameter is σ. For the classification of data, the Radial Basis Function (RBF) was utilized. The closest neighbor in the characteristics vector was located by using the Euclidean distance function (Di).

$$C_b = \sqrt{\left(h_1 - h_2\right) + \left(k_1 - k_2\right)^2}, \quad (30)$$

Typically, this is accomplished using supervised or unsupervised techniques. In a supervised setting, segmentation relies on a set of known classes or labels. Unsupervised In contrast, in an unsupervised manner, regions are detected based on the similarities of pixel values. After the first segmentation, each pixel in the image is assigned to a specific area, thereby forming the segmentation map. This is achieved by comparing features of the pixel, i.e., color, texture, and shape, to the features of regions recognized in the initial segmentation. The pixel is then assigned to the most similar feature region.

- **Down-Sampling:**

Decimation, also known as down-sampling, is an essential component of digital signal processing (DSP); however, limited effort has been made to reduce the energy consumption of traditional digital decimation architectures. The process separates samples of the original input, preserving important information. It is typically done to make the signal easier for subsequent processing or transmission. Figure 3: Shows the Operational flow diagram.

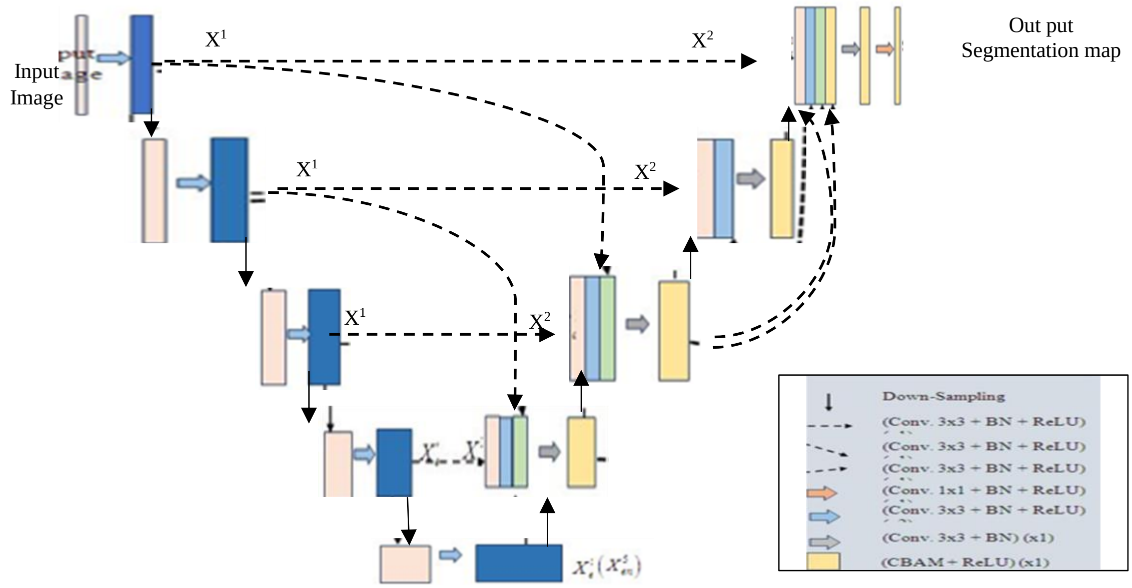

Figure 3: Operational flow diagram

The down-sampling process consists of two basic steps: filtering and sampling. The signal passes through a low-pass filter in the first step to eliminate high-frequency information above the desired bandwidth. It also helps in reducing aliasing, where high frequencies can appear to be low frequencies in the sampled input.

- **CBAM (Convolutional Block Attention Module):**

CBAM (Convolutional Block Attention Module) is a novel technique in deep learning that improves the generalization power of convolutional neural networks (CNNs). It was coined by W. Woo et al. CBAM: Convolutional Block Attention Module DAS-att Module Dey et al.336 The author is with the Department of Computer Science & Engineering, M. S. Ramaiah Institute of 337 Technology, Bangalore, Karnataka, India, E-mail: {sais, gururajh.e}@msrit.edu 338 Prakash et al.

As we consider narrowband block-fading propagation, IS1 will not exist, and the discrete-time equivalent $(7) $ of the received signal can then be expressed as.

$$k = Xh + m \in D^{M_l}, \tag{31}$$

Where n ∼ CN (0Nr×1, σ2 n IN r) is the AWGN vector and H ∈ C indicates the MIMO channel matrix. The formula for the normalized SNR in relation to the maximum average transmit power is γ =

$$H = \frac{1}{\sqrt{L_{LP}}} P_{PF} Q_i \left(P_{II} q \right) = \frac{1}{\sqrt{R_{LP}}} H, \tag{32}$$

In this quantization scheme, with the increase of the quantization resolution, the decrease of the power of the additive noise is proportional to the variety of input. Practically, such behavior is reasonable and promotes the adoption of this methodology.

$$F = S_f \left(o \right) \approx \Upsilon_f o + g \in D^N. \tag{33}$$

The core idea of CBAM is to attend to informative features and suppress less useful ones. This is achieved by utilizing two complementary attention modules: Channel attention and Spatial attention—the Channel Attention module attempts to learn the significance of each channel in a feature map.

- **ReLU (Rectified Linear Unit):**

ReLU stands for Rectified Linear Unit, and it is a type of activation function in artificial neural networks; its benefits include enabling non-linear operations when using neural cells like artificial 'neurons.' The operation takes a real number as input and returns the maximum of the number and 0, clearing all negative values. Mathematically, this is defined as f(x)=max(0,x). The ReLU activation function is well-known for its simplicity and efficiency and is widely used in various deep learning models. For positive inputs, as it has a constant gradient value of 1, this accelerates the training and prevents the vanishing gradient problem.

4 Result and Discussion

The proposed model, KNN-ACO (KNN-based ant colony optimization), has been benchmarked against the available RBF-DE (Radial Basis Function differential evolution), SVM-GA (Support Vector Machine genetic algorithm), and CNN-BP (Convolutional Neural Network backpropagation).

4.1. Accuracy

Performance, in terms of the accuracy of a machine learning algorithm, is a crucial measure for any application. Within the optimization of algorithms for detecting urea in biomedical applications, accuracy refers to the degree to which an algorithm accurately identifies and measures the amount of urea in a sample. It is important since even small measurement errors can lead to significant consequences for medical diagnosis and treatment. Thus, the accuracy of urea detection algorithms must be very high to achieve reliable and useful results. Table 2 Comparison of Accuracy of the proposed and existing models.

Table 2: Comparison of accuracy (in %)

No. of Inputs	RBF-DE	SVM-GA	CNN-BP	KNN-ACO
100	71.33	73.26	74.71	82.48
200	71.00	71.76	74.12	80.61
300	69.66	70.65	73.14	79.78
400	68.52	70.27	71.93	78.87
500	67.47	69.26	70.79	77.95

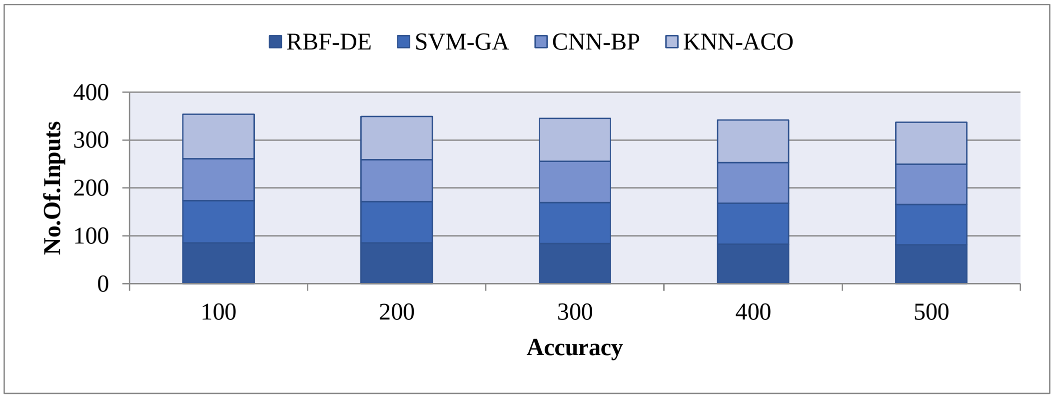

Figure 4: Computation of the accuracy

4.2. Sensitivity

In addition to accuracy, sensitivity is another crucial technical performance metric for enhancing machine learning-based algorithms in urea detection. Specificity is defined by the algorithm's ability to detect slight changes in urea content and accurately quantify them. "Sensitivity" refers to the ability to detect small changes in the concentration of urea; in medical diagnosis, the ability to detect small amounts of a substance becomes extremely important. Table 3 Comparison the Sensitivity comparison of different models is demonstrated in. Figure 5 Shows the Computation of the Sensitivity.

Table 3: Comparison of sensitivity (in %)

No. of Inputs	RBF-DE	SVM-GA	CNN-BP	KNN-ACO
100	75.33	81.26	78.71	86.48
200	75.00	79.76	78.12	84.61
300	73.66	78.65	77.14	83.78
400	72.52	78.27	75.93	82.87
500	71.47	77.26	74.79	81.95

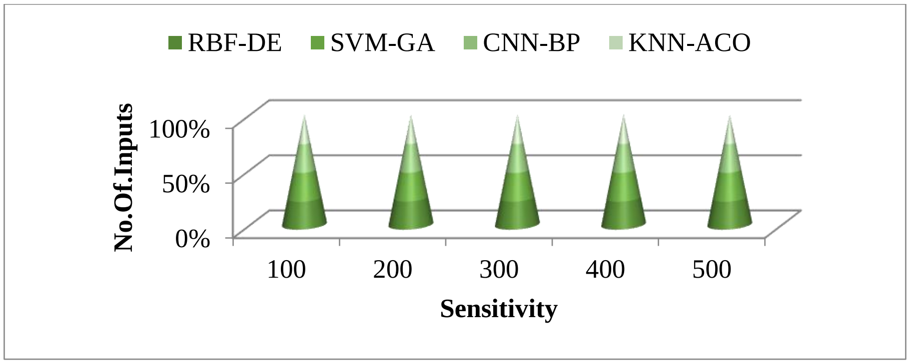

Figure 5: Computation of the Sensitivity

4.3. Speed

In medical diagnosis and treatment, timing is everything. Thus, the speed of a machine learning algorithm is an important performance factor for urea detection in biomedical applications. The algorithm must be capable of rapidly processing and interpreting large volumes of data to achieve fast and effective outcomes. Indispensable in emergencies, when fast and accurate urea measurements can help reduce patient complications. Table 4 Comparison of Speed between existing and proposed models. Figure 6 Shows the Computation of the Speed.

Table 4: Comparison of speed (in %)

No. of Inputs	RBF-DE	SVM-GA	CNN-BP	KNN-ACO
100	82.33	85.26	83.71	89.48
200	82.00	83.76	83.12	87.61
300	80.66	82.65	82.14	86.78
400	79.52	82.27	80.93	85.87
500	78.47	81.26	79.79	84.95

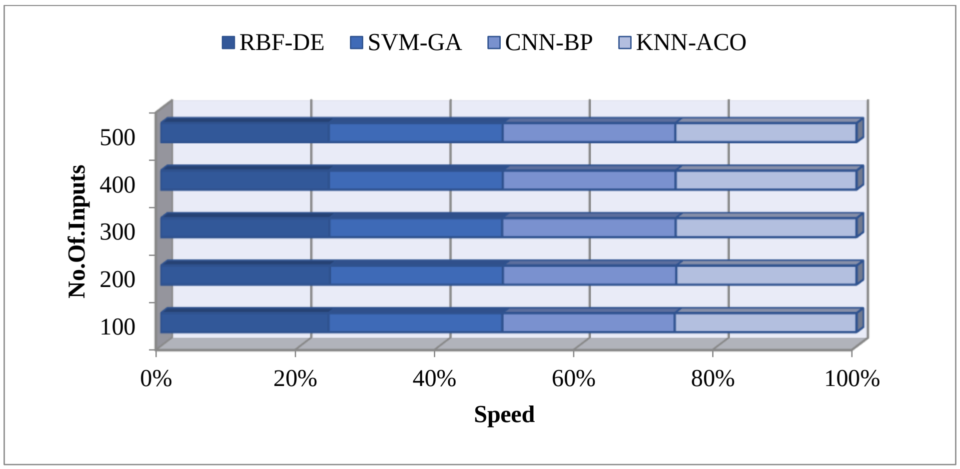

Figure 6: Computation of the speed

4.4. Robustness

The reliability of a machine learning algorithm refers to how well it performs and delivers consistent results in actual projects. When detecting urea for biomedical applications, the algorithm should be robust against different sample types, conditions, etc., that can affect the reliable measurement. A good algorithm should also be able to handle noise and outliers in the database to obtain a dependable quality and consistent result. It is essential for the further clinical application of the algorithm. Table 5 Comparison of Robustness between Existing and Proposed Models. Figure 7 Shows the Computation of the Robustness.

Table 5: Comparison of robustness (in %)

No. of Inputs	RBF-DE	SVM-GA	CNN-BP	KNN-ACO
100	85.33	88.26	87.71	92.48
200	85.00	86.76	87.12	90.61
300	83.66	85.65	86.14	89.78
400	82.52	85.27	84.93	88.87
500	81.47	84.26	83.79	87.95

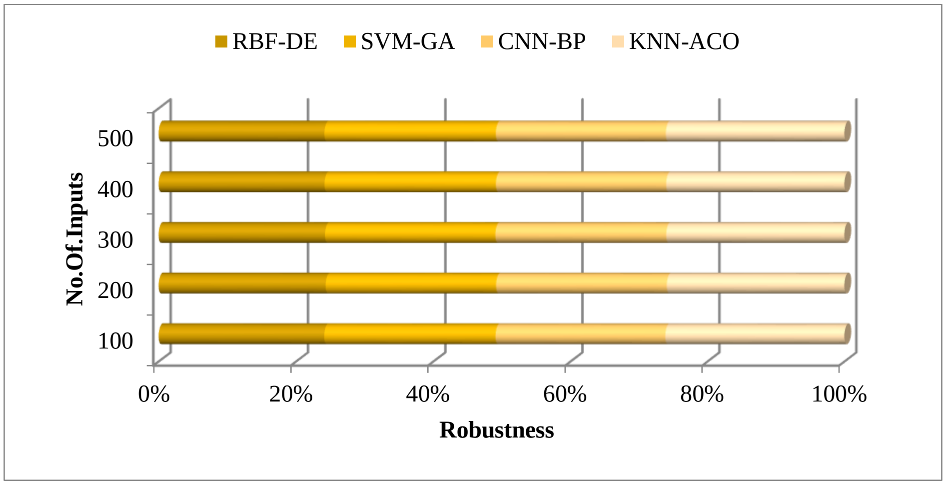

Figure 7: Computation of the robustness

5 Conclusion

In summary, we have demonstrated the potential utility of machine learning algorithms for enhancing urea detection in biomedical applications. By fusing multi-modality data with proper feature generation, these algorithms can monitor and measure urea levels in body fluids that are often difficult to measure in a clinical case study. Furthermore, in recent years, with the development of deep learning architectures, such as convolutional and recurrent neural networks (RNN), researchers have been able to enhance the accuracy of these processes by accurately tracking the complex patterns hidden behind the data. However, challenges remain to be addressed to fully harness the power of utilizing machine learning modeling for the detection of urea in biomedical systems. These procedures will involve the accumulation of more significant multiparameter datasets, the validation and standardization of algorithms, and the removal of biases in the algorithms through testing of the training data. Hence, more research should be carried out and collaborations encouraged between medical experts and machine learning experts to develop efficient and effective methods for identifying urea. These enhancements in the performance of urea detection operations, provided by machine learning-aided learning- aided algorithms, were encouraging and may serve to greatly improve the field of medical diagnostics and treatment, benefiting patients in healthcare. The future is bright for biomedical engineering, and it is poised to set the pace in spurring greater innovation in healthcare through its interdisciplinary scope.

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