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Artificial intelligence and artificial immune systems: transforming tuberculosis diagnosis

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Abstract

Tuberculosis (TB) is one of the world's deadliest infectious diseases, making rapid and accurate diagnosis essential for its control. However, challenges such as a lack of infrastructure and qualified professionals hinder detection, especially in low- and middle-income countries. In this scenario, Artificial Intelligence (AI) and Artificial Immune Systems (AIS) emerge as innovative tools to enhance TB diagnosis. AI has been applied to the analysis of chest X-rays and molecular tests, increasing accuracy and reducing diagnosis time. Deep learning algorithms can identify subtle patterns in medical exams, achieving accuracy levels comparable to those of specialists. Meanwhile, AIS, inspired by the human immune system, stands out for their adaptability and continuous learning, making them highly effective in recognizing complex cases. Artificial intelligence has enormous potential to improve the diagnosis and treatment of tuberculosis, making medical care more efficient and accessible. This study presents solutions that can enhance diagnostic accuracy and efficiency, enabling faster and more targeted interventions. By combining these technologies with traditional methods, efforts to combat tuberculosis can be optimized, reducing its spread and global mortality.

Keywords

Disease Detection; Healthcare Efficiency; Medical Innovation; Negative Selection Algorithm.

Introduction

Tuberculosis (TB) remains one of the world's deadliest infectious diseases, with millions of new cases and hundreds of thousands of deaths annually (WHO, 2023). Early and accurate diagnosis is crucial for disease control, but many countries face challenges such as a lack of medical infrastructure, a shortage of qualified professionals, and difficulties in accessing advanced technologies. In this context, artificial intelligence (AI), and more specifically, Artificial Immune Systems (AIS), are emerging as promising tools to revolutionize tuberculosis diagnosis, offering rapid, accurate, and accessible solutions.

Caused by the bacterium Mycobacterium tuberculosis, it primarily affects the lungs, although it can affect other organs such as the kidneys, meninges, and bones. Transmission occurs through the air when an infected person coughs, sneezes, or speaks, releasing droplets contaminated with the bacillus (Fuzinatto et al., 2024). The most common symptoms include a persistent cough lasting more than three weeks, fever, night sweats, weight loss, and fatigue. In severe cases, hemoptysis (coughing up blood) may occur.

Traditional tuberculosis diagnosis is performed through clinical, radiological, and laboratory tests, such as sputum smear microscopy and the Xpert MTB/RIF rapid molecular test. Treatment is based on a combination of antibiotics, including rifampicin, isoniazid, pyrazinamide, and ethambutol, administered for a minimum period of six months (Fuzinatto et al., 2024). Adherence to treatment is crucial to prevent the development of resistant strains, such as multidrug-resistant tuberculosis (MDR-TB).

Despite advances in diagnosis and treatment, tuberculosis remains a leading cause of mortality from infectious diseases worldwide. According to the World Health Organization (WHO, 2023), in 2021, approximately 10.6 million people fell ill with tuberculosis, and 1.6 million died from the disease. The COVID-19 pandemic has further exacerbated the scenario, with disruptions in health services and a reduction in the diagnosis and treatment of tuberculosis cases.

AI, particularly through techniques such as deep learning, has been applied to analyze medical images, such as chest X-rays, which is one of the most common methods for identifying suspected tuberculosis. AI algorithms can detect subtle patterns in images that may go unnoticed by the human eye, identifying pulmonary lesions characteristic of the disease with high accuracy. Recent studies show that AI-based systems can achieve accuracy rates comparable to or even higher than those of experienced radiologists, reducing the

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time required for diagnosis and minimizing errors (Smith et al., 2023). For example, Smith et al. (2023) demonstrated that an AI algorithm developed to analyze chest X-rays achieved a sensitivity of 95% and a specificity of 88% in detecting tuberculosis, outperforming the accuracy of traditional methods of human analysis.

In addition to X-rays, AI is also being used to analyze data from molecular tests, such as the Xpert MTB/RIF, which detects the presence of the tuberculosis bacillus and its resistance to rifampicin (WHO, 2023). Algorithms can process large volumes of laboratory data, identify patterns, and provide results more quickly and efficiently. This is especially useful in resource-limited regions, where manual processing capacity is limited. A 2023 report by the World Health Organization (WHO) highlighted that the integration of AI into molecular tests can reduce diagnosis time by up to 50%, facilitating early treatment initiation.

Another promising application of AI is in screening at-risk populations. Intelligent systems can analyze demographic, clinical, and epidemiological data to identify individuals more likely to develop tuberculosis, directing prevention efforts and early diagnosis. This is particularly relevant in endemic areas, where early detection can interrupt the chain of transmission. The study published in 2022 by Jones et al. showed that an AI model developed to predict the risk of tuberculosis in vulnerable populations achieved an accuracy of 92%, demonstrating its potential to optimize the allocation of resources in public health.

Inspired by the workings of the human immune system, Artificial Immune Systems (AIS) are computational algorithms that mimic biological processes, such as learning, memory, and pattern recognition, to solve complex problems (Soares et al., 2025; Almeida et al., 2024). In the context of tuberculosis, these systems have proven particularly effective, overcoming many of the limitations of traditional techniques.

AIS are capable of analyzing large volumes of data, such as chest X-ray images, molecular test results, and clinical data, identifying patterns associated with tuberculosis with high accuracy. Unlike other AI techniques, such as conventional neural networks, AIS stand out for their dynamic adaptation and continuous learning capabilities. They can evolve over time, adapting to new data and improving their effectiveness, without the need for extensive reprogramming. This is especially useful in scenarios where data can vary significantly, such as in different populations or geographic regions.

One of the main advantages of AIS is their ability to handle incomplete or noisy data, a common challenge in resource-limited areas. For example, in regions where the quality of chest X-rays may be compromised by old equipment or a lack of maintenance, AIS can still provide reliable diagnoses. Something that other AI techniques may not be able to achieve with the same efficiency. In addition, AIS are particularly effective in detecting complex cases, such as extrapulmonary tuberculosis or latent infections, which are more difficult to identify with traditional methods.

Another aspect that differentiates AIS is their ability to integrate with other technologies. They can be combined with molecular tests, such as the Xpert MTB/RIF, to increase diagnostic accuracy and reduce the time required to obtain results. A recent study published in 2023 by Lee et al. demonstrated that an artificial immune system integrated with molecular tests achieved 98% accuracy in detecting tuberculosis, outperforming conventional methods. This integration allows not only the identification of the presence of the disease but also the detection of drug-resistant strains, a critical factor for effective treatment.

Furthermore, AIS are highly scalable and can be implemented on portable or cloud-based platforms, facilitating their use in remote areas or areas with limited infrastructure. This contrasts with other AI techniques that may require advanced hardware or stable internet connections. The portability and accessibility of AIS make them a viable solution for low- and middle-income countries, where tuberculosis is most prevalent.

Despite the advances, the use of AI and AIS in tuberculosis diagnosis still faces challenges. The quality of the data used to train the algorithms is fundamental, and the lack of diverse and representative datasets can limit the effectiveness of these tools in different populations. In addition, it is necessary to ensure that AI-based solutions are accessible and integrated into existing health systems, especially in underdeveloped and developing countries, where the burden of tuberculosis is higher. A recent report by the Bill & Melinda Gates Foundation (2023) highlighted the need for investments in digital infrastructure and training of health professionals to ensure the effective adoption of AI in the fight against tuberculosis.

In summary, Artificial Intelligence and Artificial Immune Systems have the potential to transform tuberculosis diagnosis, making it faster, more accurate, and more accessible. However, for this technology to reach its full potential, investments in research, infrastructure development, and collaboration between governments, health institutions, and technology companies are needed. The combination of AI with traditional tuberculosis control strategies can be a decisive step towards reducing the global impact of this disease. This study aims to present a solution, based on these technologies which can increase the accuracy and efficiency of diagnosis, allowing for faster and more targeted interventions.

Materials and Methods

This study adopts a quantitative approach, based on the statistical analysis of structured epidemiological data obtained from the SINAN/DATASUS database. A total of 109,345 samples related to confirmed tuberculosis cases in Brazil were used, encompassing clinical, demographic, and laboratory variables. The proposed method, based on the Negative Selection Algorithm (NSA), was implemented in a computational environment and evaluated through repeated statistical simulations, focusing on objective metrics such as accuracy, processing time, and classification performance. As it does not involve the collection of subjective data or interpretative qualitative analysis, the study is fully aligned with the quantitative research paradigm.

Biological Immune System: The biological immune system is a complex set of cells, tissues, and organs that work in harmony to defend the body against infections, diseases, and harmful substances, such as viruses, bacteria, and cancerous cells. The main function of the immune system is to identify and destroy these invaders while preserving the body's cells

(Murphy and Weaver, 2017). The functioning of this system can be divided into two lines of defence: innate immunity and adaptive immunity.

Innate immunity is the first line of defence and responds quickly to any invading pathogen without the need for specific recognition. It is composed of physical barriers, such as the skin and mucous membranes, which prevent the entry of pathogens, and specialized cells, such as phagocytes (neutrophils and macrophages), which engulf and destroy microorganisms (Murphy and Weaver, 2017). In addition, innate immunity involves proteins such as the complement system. The complement system consists of a set of plasma proteins that can be activated by different pathways and acts by marking pathogens for destruction, promoting inflammation, and facilitating phagocytosis. However, the innate immunity response is general and non-specialized, that is, it does not have the ability to remember a previously encountered pathogen (Janeway et al., 2001).

On the other hand, adaptive immunity is more specific and highly specialized. When innate immunity is not sufficient to eliminate a pathogen, adaptive immunity comes into play, promoting a more targeted response. It involves T and B cells, which are responsible for recognizing and eliminating pathogens more effectively. T cells help destroy infected cells, while B cells produce antibodies, which are proteins that bind to pathogens and neutralize their actions (Alberts et al., 2002). In addition, adaptive immunity has the capacity for immunological memory, that is, the immune system recognizes the pathogen it has previously encountered, allowing for a faster and more efficient response in the event of a reinfection (Murphy & Weaver, 2017).

These two lines of defence act complementary. Initially, innate immunity blocks the invader, and subsequently, adaptive immunity provides a more specific and lasting response. The immune system also relies on organs such as the bone marrow, which produces blood cells, and the thymus, where T cells mature, in addition to lymph nodes and the spleen, which help coordinate immune responses (Medzhitov & Janeway, 2000).

Although the immune system is highly efficient, it can exhibit failures. Autoimmune diseases, such as lupus and rheumatoid arthritis, occur when the immune system mistakenly attacks the body's own cells. In addition, some infections or cancers may escape immune detection due to mutations in pathogens or cancerous cells. However, in general, the immune system is essential for maintaining health and protecting against disease.

Artificial Immune Systems: Artificial Immune Systems (AIS) are computational systems that seek to simulate the functioning of the biological immune system in a digital environment. They utilize artificial intelligence (AI) techniques to solve complex problems adaptively, that is, with the ability to learn and adjust to new situations, just as the human immune system reacts to pathogens and other threats (De Castro and Timmis, 2002). Inspired by the biological processes of pattern recognition, memory, and learning, AIS has been applied in various fields, including medicine, cybersecurity, and disease diagnosis.

AIS operate in a similar approach to the biological immune system, where they seek to identify and neutralize threats or problems within a system. The fundamental principle of these systems is self-organization and continuous learning, which allows them to evolve over time, just as the immune system adapts throughout an organism's life. The architecture of AIS is generally composed of three main elements: detection, response, and memory.

Detection: just as cells of the biological immune system identify pathogens and other harmful cells, AIS use machine learning algorithms to detect patterns or anomalies in input data, such as signs of intrusion or anomalous behaviors.

Response: after detection, the AIS takes action to mitigate the problem, similar to the immune response process in the body. This may involve modifying a behavior or applying a solution.

Memory: one of the most interesting features of AIS is their ability to store information about previous threats and use these memories to improve responses in future interactions. This is comparable to the immunological memory of the biological immune system, where the body recognizes past pathogens and responds more effectively in subsequent infections.

The biological immune system is composed of a network of cells and molecules that communicate with each other to protect the body against pathogens and other foreign agents. This system is highly adaptive, utilizing specialized cells, such as T and B lymphocytes, to identify, attack, and remember invaders (Murphy & Weaver, 2017). In addition, the immune system is capable of mounting a rapid response to acute infections and maintaining immunological memory to protect the organism against reinfections (Alberts et al., 2002).

AIS replicates this capacity for adaptation and response through machine learning algorithms and artificial neural networks. While the biological immune system deals with pathogenic agents such as viruses and bacteria, AIS can be used to solve problems in different areas. For example, detection of failures in computing systems, prevention of cyberattacks, and even in the diagnosis of diseases, such as tuberculosis, through the analysis of clinical data (Janeway et al., 2001). Just as the human immune system adapts and responds to new pathogens, AIS can also learn from data and improve their responses over time.

Although the biological immune system is more complex and involves a vast network of cells and organs, AIS share the idea of continuous learning, pattern identification, and adaptation to new information. In addition, both systems have the ability to protect and defend the organism, whether against physical pathogens or digital threats.

AIS has several practical applications. In the healthcare field, for example, they are used to analysing large volumes of medical data, such as X-ray images or laboratory test results, to identify diseases more efficiently and quickly (Jones et al., 2022). They have also been applied in the development of intelligent screening systems, where algorithms identify populations at risk for diseases such as tuberculosis, providing early diagnoses and facilitating the allocation of resources in regions lacking infrastructure.

Although Artificial Immune Systems do not possess the biological complexity of the human immune system, they share the central concept of adaptation, learning, and response to threats. By combining artificial intelligence techniques with the principle of responding to threats, AIS has the potential to revolutionize several areas, especially medicine and digital

security, offering innovative and adaptive solutions. The ability of these systems to evolve and improve over time makes them promising tools in the early diagnosis of diseases and in the protection of computing systems.

Negative Selection Algorithm: The negative selection algorithm is a technique inspired by the functioning of the biological immune system and is commonly used in Artificial Immune Systems (AIS) and other areas of artificial intelligence to solve optimization and learning problems. The central idea of the algorithm is based on the process of immunological selection that occurs in the human immune system. In which cells of the immune system are trained to recognize and eliminate substances foreign to the organism (antigens), while preserving the body's own cells (self-antigens) (Bauer et al., 2005).

In the biological immune system, the body must ensure that its immune cells, such as T lymphocytes, do not attack the body's own cells (Janeway et al., 2001). To this end, the immune system undergoes a process called central tolerance, where cells that react against the organism itself (autoimmunity) are eliminated, while those that recognize pathogens or foreign substances are maintained and strengthened. Analogously, in the context of negative selection algorithms, the idea is to create a set of possible solutions to a problem and then eliminate the solutions that are not desired or that are autoimmune, that is, those that are not able to solve the problem efficiently (De Castro & Timmis, 2002). The algorithm then selects the best solutions that can address the problem effectively, based on a process of eliminating solutions that do not meet the established criteria.

Steps of the Negative Selection Algorithm:

1. **Generation of antigens and receptors**: the algorithm begins by generating a set of possible solutions (called antigens) to the problem. Each solution represents a point in the solution space of the problem to be solved. In parallel, receptors are generated that represent a simplified representation of the possible solutions (De Castro & Timmis, 2002).
2. **Conformity evaluation**: the algorithm checks the similarity between the proposed solutions (antigens) and the set of previously accepted solutions or those that have already been identified as valid (the body itself or the ideal solution). If a solution is too similar to a previously known one (self-antigen), it is considered "unfit" and is discarded (Bauer et al., 2005).
3. **Selection of valid solutions**: the solutions that have not been discarded, that is, those that have characteristics sufficiently different from the previous solutions, or that are foreign to the system, are selected to proceed in the optimization or learning process (De Castro & Timmis, 2002). These solutions can then be used as a basis for the next iteration of the algorithm, promoting improvements.
4. **Learning and refinement**: the algorithm continues to adjust the selected solutions, continuously looking for new alternatives or improvements. This process is repeated until a convergence criterion is reached, that is, until the solution considered optimal or good enough is found (Bauer et al., 2005).

This type of algorithm is used in a variety of contexts; in the field of supervised learning, the algorithm can be used to refine data sets, discarding those examples that are redundant or irrelevant to the classification task (Bauer et al., 2005).

The negative selection algorithm has two distinct steps, the first being censoring, and the second monitoring. Censoring generates a set of detectors, where each detector is a string that does not correspond to any of the detected data. The monitoring phase monitors the protected data by comparing it with the detectors, where, in the event of a change a detector is activated (Forrest et al, 1994). Figure 1 shows the flowchart of the censoring and monitoring phase, respectively, on the left and right side (Forrest et al, 1994).

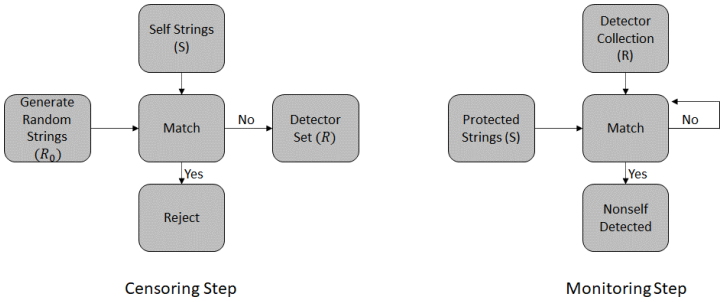

Figure 1. Censoring and Monitoring Steps.

The match concept, presented in the censorship and monitoring phase, can be perfect when the match between the two strings of equal sizes with identical symbols occurs. This case is considered extremely rare. The other case occurs when the match is considered partial, and occurs when *r* close matches, has corresponding symbols and positions, so any two chains *(x,y)* are matched and considered true when *x* and *y*, correspond at least to *r* nearby locations (Forrest et al, 1994). Therefore, the probability of any two P_m strings, can be calculated by Equation 1.

$$P_m \approx \left(\frac{\left(\frac{(l-r)(m-1)}{m+1} \right)}{m^r} \right) \quad \text{Equation 1}$$

Note that, l corresponds to the number of symbols in the string (length); *m* corresponds to the number of symbols of the alphabet; and *r* is the next matching number required to match (Forrest et al, 1994). The affinity rate of T_{af} chains, given the proximity match, can be calculated, based on Equation 2.

$$T_{af} = \left(\frac{A_n}{A_t} \right) 100\% \quad \text{Equation 2}$$

where, A_n corresponds to the number of normal chains in the problem, the own strings; and corresponds A_t to the total number of chains of the problem, the own and non-own chains (Bradley, Tyrrell, 2002). The quantification of the affinity of the analyzed patterns (Q_{af}) should be made considering $Q_{af} \geq T_{af}$, and can be calculated using Equation 3.

$$Q_{af} = \frac{\sum_{i=1}^{L} V_c}{L} 100\% \quad \text{Equation 3}$$

which V_c corresponds to the corresponding variables; L corresponds to the total amount of variables; $\sum_{i=1}^{L} V_c$ corresponds to the sum of the corresponding variables (Soares et al, 2025).

Database: The database of DATASUS (Department of Informatics of the Unified Health System - SUS) with cases of tuberculosis since 2001, especially from the Information System for Notifiable Diseases (SINAN), is a platform that collects, organizes, and makes available information on the incidence and distribution of notifiable diseases, such as tuberculosis, in Brazil (Brasil, 2023). SINAN is a disease monitoring and management tool, and one of the main sources of data on cases of tuberculosis and other health problems in the country.

SINAN's central objective is to centralize information on compulsory notifiable diseases, including tuberculosis, and enable monitoring of its evolution. This database contains records of confirmed, suspected, and discarded cases, as well as data on treatments, clinical evolution, demographic, and epidemiological characteristics of patients, among other parameters. By being fed by health professionals, it allows for the elaboration of accurate statistics on the rates of incidence, mortality, and resistance of the tuberculosis bacillus (Brasil, 2023).

The database with 109,345 samples of tuberculosis cases since 2001 contains detailed information of each patient who had the diagnosis of tuberculosis confirmed in several regions of Brazil. Each sample contains a series of parameters that allow the evaluation of the patterns of occurrence and treatment of the disease. Among these parameters, we can highlight:

1. Demographic data: age, sex, race/ethnicity, and municipality of residence of the patient.
2. Clinical characteristics: symptoms presented, such as persistent cough, fever, and night sweats, among others.
3. Treatment history: information on adherence to treatment, type of therapeutic regimen used (directly observed treatment, for example), treatment time, drug resistance, and evolution of the clinical picture.
4. Epidemiology and comorbidities: data on the presence of other associated conditions, such as HIV, and history of contact with patients diagnosed with tuberculosis.
5. Types of tuberculosis: classification of the type of tuberculosis (pulmonary, extra pulmonary), bacilliferous or non-bacilliferous form, among others.

These data are of utmost importance to understand the behavior of the disease over time, identify more vulnerable populations, and improve prevention and treatment policies (Brasil, 2023). With 109,345 samples, the database offers a substantial amount of information, which makes it possible to carry out robust epidemiological analyses. The samples are not just raw numbers; each of them includes a set of variables that make up the patterns to be evaluated, such as:

Diagnostic Patterns: identification of areas with the highest number of diagnosed cases.

Epidemiological Patterns: study of incidence and mortality rates, relating them to factors such as age, sex, and socioeconomic conditions.

Treatment Patterns: monitoring the effectiveness of treatments performed, the occurrence of drug resistance, and the impact of different therapies.

These parameters offer a detailed view of the tuberculosis epidemic in Brazil and help to identify trends and areas with the greatest need for intervention (Brasil, 2023).

The SINAN database provides a large amount of data that can be used to optimize the diagnosis, treatment, and control of tuberculosis, in addition to providing important insights into the epidemiology of the disease. The analysis of these data is fundamental to improving public health strategies and strengthening the fight against tuberculosis in the country. Through the SINAN database, we extracted the data necessary for this work according to Table 1.

Table 1. Pre-processing steps performed to build the final data set.

Attribute	Description
RAIOX_TORA	Result of chest X-ray at the time of notification (code 3 refers to other changes not compatible with tuberculosis)
AGRAVAIDS	AIDS associated with tuberculosis at the time of the notification
AGRAVALCOO	Alcohol consumption associated with tuberculosis at the time of the notification
AGRAVDIABE	Diabetes associated with tuberculosis at the time of the notification
AGRAVDOENC	Mental disease associated with tuberculosis at the time of the notification
AGRAVOUTRA	Other diseases associated with tuberculosis at the time of the notification
HIV	Result of serology for the acquired immunodeficiency virus, performed before or after the notification of TB. It aims to assess HIV co-infection
HISTOPATOL	Result of histopathological examination for diagnosis of TB
AGRAVDROGA	Other drug consumption associated with tuberculosis at the time of the notification
AGRAVTABAC	Tobacco consumption associated with tuberculosis at the time of the notification

Results and discussion

In this section, we present the tests performed on the samples collected from the database originating from the SINAN database. All experiments were conducted on a computer equipped with a 13th generation Intel(R) Core(TM) i7-1355U processor, with a frequency of 1.70 GHz, 16 GB of RAM, and a 64-bit Windows 11 operating system. The implementation of the proposed method was carried out in the MATLAB® software.

Test Suite

The test suite used to evaluate the method proposed in this article is composed of the database samples generated from those collected in the laboratory, as described in Section 2.4. This set includes a total of 109,345 samples, as detailed in Table 2. Thus, a set of detectors was generated using 30% of the signals (baseline), and the parameters used for the tests are presented in Table 3.

Table 2. Set of tests

Features Database	Sample
Normal	8.218
Contaminated	101.127
Total	109.345
Number of points in each sample	10

Table 3. Parameters.

Parameters	Value
TAf	70%
ε	3%

Letting *TAf* be the affinity rate and ε the deviation. To evaluate the proposed methodology, simulations were performed considering the configuration of the Negative Selection Algorithm (NSA). The input variables employed in

this study are listed and described in Table 1, with each row corresponding to an individual data sample. A total of 18,000 samples were utilized, of which 30% (5,400 samples) were allocated to the censoring phase and the remaining 70% (12,600 samples) to the monitoring phase, in accordance with the proposed methodology. To enhance the robustness and statistical reliability of the results, the simulations were performed over 30 independent iterations. The classification performance is detailed in the confusion matrix presented in Figure 2.

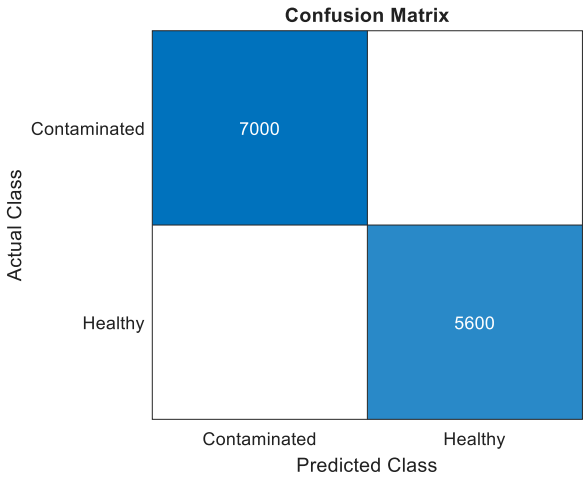

Figure 2. Confusion Matrix.

The data collected throughout these executions allows for a detailed analysis of the system's behavior. The results from these simulations are presented in an organized manner in Table 4, enabling a better understanding of the impacts of the adopted configuration.

Table 4. Results obtained in ASN.

Samples Tests	Ratings proper	Ratings Non-proper	Correct ratings	Accuracy (%)	Processing time (ms)
12600	7000	5600	12600	100	0.376288

In order to ensure the veracity of the results, the results in Table 4 show the average values obtained by a cross-reference test, performed 30 times during the execution of the NSA for the detector set. We note that the NSA performs well, with an accuracy rate equal to 100% for the best configuration. The number of detectors used in the censorship phase directly influences the fault diagnosis process. Thus, we suggest using 30% of the information in the database to generate the detector set, aiming to give robustness to the system. That is, the more knowledge available in the learning phase, the more efficient the NSA diagnosis process will be.

Finally, we highlight that the NSA is executed in less than 0.38 milliseconds, which allows the application of this system in real-time, as decisions must be made in a short time frame in situations of widespread contamination.

Conclusions

The Negative Selection Algorithm (NSA), inspired by the biological immune system, is a powerful tool for solving complex problems. In this work, we proposed a novel NSA-based approach for the detection and diagnosis of tuberculosis. The method achieved a 100% success rate in its best configuration, demonstrating exceptional accuracy and reliability.

Although the sensing phase requires more computational time, it is executed offline and does not impact real-time performance. The monitoring phase, responsible for processing acquired signals, operates in under 0.37 milliseconds, enabling real-time disease detection.

These results have significant implications for clinical practice: the high accuracy reduces the risk of misdiagnosis, while the system's speed supports rapid decision-making in healthcare settings. The proposed method offers a robust and efficient alternative to traditional diagnostic procedures, reducing dependence on time-consuming laboratory tests and enabling earlier interventions. Therefore, this work represents a meaningful advance in clinical diagnostics by introducing a promising intelligent system that can be integrated into real-world medical applications and extended to the diagnosis of other diseases in future research.

Moreover, the proposed computational architecture demonstrates high technological transferability. Its modular and lightweight design allows easy adaptation to different hardware platforms, including embedded systems and portable diagnostic devices. This feature supports the implementation of the method in resource-limited healthcare environments, such as rural clinics or mobile units, expanding the technology's reach and promoting greater equity in access to quality diagnostics.

However, some limitations must be considered. The system was evaluated using a controlled dataset, which may not fully reflect the variability found in real-world clinical environments. Additionally, adapting the method to different diseases may require specific tuning of the NSA parameters. As future directions, we propose large-scale clinical validation, integration with portable monitoring devices, and the combined use of other artificial intelligence techniques to enhance the system's sensitivity and generalizability across diverse medical contexts.

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