South Asian Journal of Engineering and Technology Research Article

Open Access Full Text Article 152(2025) 21-32 DOI: 10.26524/sajet.2025.15.4

Genomic Surveillance and Prediction of Antibiotic Resistance Trends Using AI Tools

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Article info
Received 25th October 2024
Revised form 20th December 2024
Accepted 2nd February 2025

Keywords
Client experience/fulfilment, CCRF, cost, planning

https://sajet.in/index.php/journal/article/view/308

Abstract

Antibiotic resistance (AMR) is a global public health crisis that threatens the efficacy of many life-saving antibiotics. As resistance patterns continue to evolve and spread, traditional surveillance methods struggle to keep pace with the complexity and scale of the issue. Genomic surveillance, particularly when integrated with advanced Artificial Intelligence (AI) tools, offers a powerful solution to track, predict, and mitigate the emergence of resistant bacterial strains. This paper explores the role of AI in genomic surveillance, highlighting how machine learning and deep learning algorithms can analyze vast genomic datasets to identify resistance genes, mutations, and emerging resistance trends. By combining genomic, clinical, and environmental data, AI-powered models can predict resistance patterns, enabling early detection and more targeted public health interventions. The paper examines various AI techniques, including supervised and unsupervised learning, and their application in forecasting antibiotic resistance in pathogens like Escherichia coli and Mycobacterium tuberculosis. Despite the promising potential, challenges such as data quality, model generalizability, and ethical concerns persist. Nevertheless, the integration of AI into genomic surveillance holds transformative potential for enhancing global efforts to combat AMR, providing real-time insights and more effective strategies for antibiotic stewardship. The paper concludes by discussing future directions for AI in genomic surveillance, emphasizing the need for further research, collaboration, and global data sharing to improve predictive capabilities and combat antibiotic resistance effectively.

INTRODUCTION

Antibiotic resistance is rapidly emerging as one of the most pressing public health threats globally, undermining the effectiveness of many conventional antibiotics and complicating the treatment of infections [1]. The widespread misuse and overuse of antibiotics, along with the natural evolution of bacterial pathogens, have led to the rise of multidrug-resistant (MDR) and extensively drug-resistant (XDR) bacteria [2]. As resistance mechanisms evolve, it becomes increasingly difficult to predict and track the spread of resistant strains. Traditional methods of surveillance, such as culture-based techniques and susceptibility testing, are time-consuming and often insufficient for providing real-time data on resistance trends [3]. In this context, genomic surveillance has become a powerful tool for understanding and tracking the genetic basis of antibiotic resistance. By sequencing the genomes of bacterial pathogens, researchers can identify specific resistance genes, mutations, and genetic markers associated with resistance [4]. However, the growing complexity and volume of genomic data necessitate the application of advanced computational tools, such as Artificial Intelligence (AI), to process and analyze this information efficiently [5]. AI, particularly machine learning and deep learning, offers great potential in predicting the future trajectory of antibiotic resistance by integrating vast amounts of genomic, clinical, and epidemiological data [6]. This paper explores the integration of AI tools into genomic surveillance to enhance the prediction of antibiotic resistance trends, thereby informing better public health responses and strategies to combat the growing threat of AMR.

2. ANTIBIOTIC RESISTANCE AND THE NEED FOR GENOMIC SURVEILLANCE

Antibiotic resistance occurs when bacteria develop mechanisms that render antibiotics ineffective in treating infections [7]. This resistance can occur through mutations in bacterial DNA, horizontal gene transfer (HGT), and biofilm formation. Resistance mechanisms include the production of enzymes such as β-lactamases, which break down antibiotics, changes to cell membranes that block drug entry, and the overexpression of efflux pumps that expel antibiotics from bacterial cells [8]. The rise of multidrug-resistant (MDR) and extensively drug-resistant (XDR) pathogens complicates treatment options, leading to longer hospital stays, higher treatment costs, and increased mortality rates. Genomic surveillance plays a crucial role in understanding the underlying genetic factors that drive resistance [9]. Unlike traditional susceptibility testing, which only identifies resistance phenotypes, genomic surveillance allows for the identification of specific genetic markers, mutations, and resistance genes that contribute to bacterial resistance. By sequencing the genomes of bacterial pathogens, public health officials can track the evolution and spread of resistance, identify new resistance mechanisms, and pinpoint emerging resistant strains before they spread widely [10]. This type of surveillance is particularly crucial in detecting novel resistance profiles and predicting future trends in antibiotic resistance. As such, genomic surveillance is essential for guiding antibiotic stewardship and public health interventions to limit the spread of resistant bacteria and preserve the efficacy of existing antibiotics [11].

3. GENOMIC TECHNOLOGIES IN ANTIBIOTIC RESISTANCE SURVEILLANCE

Recent advancements in genomic sequencing and nanotechnologies have revolutionized the field of antibiotic resistance surveillance [12][13][14]. Next-generation sequencing (NGS) has emerged as a powerful tool for obtaining high-throughput genomic data, enabling the rapid and accurate identification of antibiotic resistance genes in bacterial populations [15]. NGS technologies, such as Illumina sequencing and Oxford Nanopore sequencing, provide comprehensive insights into bacterial genomes, allowing for the detection of both known and novel resistance markers [16]. Whole-genome sequencing (WGS) offers the ability to analyze the entire genome of a pathogen, identifying mutations, resistance genes, and genomic elements associated with resistance [17]. Metagenomics, another genomic technology, allows for the sequencing of environmental samples, providing insights into the diversity of bacterial populations and their associated resistance genes [18]. These technologies enable the surveillance of antibiotic resistance on a global scale, providing real-time data on the spread of resistant pathogens. Databases such as GISAID and the Antibiotic Resistance Monitoring in Europe (EARS-Net) collect genomic data from various sources, creating repositories of resistance profiles that can be used for comparative analysis [5]. Genomic surveillance has become an indispensable tool for tracking resistance trends, identifying new resistance mechanisms, and guiding public health responses to mitigate the impact of antibiotic resistance [15]. As these technologies continue to evolve, they will play an increasingly important role in the fight against AMR.

4. ARTIFICIAL INTELLIGENCE IN GENOMIC SURVEILLANCE

Artificial Intelligence (AI) has gained significant attention in the field of genomic surveillance due to its ability to analyze large and complex datasets. AI tools, particularly machine learning (ML) and deep learning (DL) algorithms, can process genomic data more efficiently than traditional methods, enabling the identification of patterns and trends that might be missed by human analysis [19]. ML algorithms, such as supervised and unsupervised learning, are commonly used to analyze genomic data and predict the presence of antibiotic resistance genes or mutations [20]. Supervised learning techniques involve training algorithms on labeled datasets, allowing the model to recognize specific patterns associated with resistance. Unsupervised learning, on the other hand, allows the model to identify previously unknown resistance patterns by analyzing unlabeled data [21]. Deep learning, a subset of ML, uses neural networks to analyze complex genomic sequences and can be particularly useful in identifying novel resistance mechanisms or mutations that may not be evident through traditional methods. AI can also be used to integrate genomic data with other types of data, such as clinical and environmental data, to create more comprehensive models for predicting resistance trends. By automating the analysis of genomic surveillance data, AI tools not only improve the speed and accuracy of resistance detection but also enable more effective and timely responses to emerging threats in antibiotic resistance [22].

5. AI MODELS FOR PREDICTING ANTIBIOTIC RESISTANCE TRENDS

AI-based models for predicting antibiotic resistance trends have become an essential tool for forecasting the future trajectory of AMR [23]. By analyzing large datasets that include genomic, clinical, and epidemiological information, machine learning algorithms can predict which bacterial strains are most likely to develop resistance and which antibiotics are at greatest risk of becoming ineffective.

Supervised learning algorithms, such as random forests and support vector machines, are often employed to train models on historical data, allowing them to identify patterns and make predictions about the spread of resistance [23]. These models can integrate genomic data, such as the presence of specific resistance genes, with clinical data, including antibiotic usage patterns, to predict how resistance will evolve in different settings. Additionally, AI models can incorporate environmental factors, such as hospital and community environments, to forecast resistance dynamics. One example of AI models in action is the prediction of future resistance in pathogens like Escherichia coli and Mycobacterium tuberculosis, where models have been used to predict the development of resistance to first-line antibiotics, guiding more effective antibiotic stewardship [23]. As AI tools become more sophisticated, they can provide near real-time predictions of resistance trends, helping public health officials make informed decisions about antibiotic use, prevention strategies, and the allocation of resources to combat AMR [22].

6. CHALLENGES AND LIMITATIONS OF AI IN GENOMIC SURVEILLANCE

Despite the promising potential of AI in genomic surveillance for predicting antibiotic resistance, several challenges and limitations must be addressed for successful implementation [22]. One of the key challenges is data quality and availability. AI algorithms rely heavily on large, high-quality datasets to generate accurate predictions. However, genomic data may be incomplete or inconsistent, leading to biased or inaccurate models. Additionally, the lack of standardized data collection methods across different regions and institutions complicates the integration of genomic surveillance data into AI models [24]. Ethical and privacy concerns also pose significant barriers to the widespread use of genomic surveillance. The collection of genomic data, especially from human patients, raises issues of consent and data security, particularly when dealing with sensitive health information [25]. Another challenge is the generalizability of AI models. Algorithms trained on data from specific geographic locations or populations may not be applicable in other regions with different bacterial strains, resistance profiles, and healthcare practices. This limitation underscores the need for continuous model validation and refinement. Finally, there is a challenge in integrating genomic data with clinical and environmental data, which is often stored in disparate formats and systems. Overcoming these challenges will require the development of robust data-sharing frameworks, improvements in data standardization, and advancements in AI algorithms that can adapt to different data types and settings [26].

7. APPLICATIONS OF AI-POWERED GENOMIC SURVEILLANCE IN PUBLIC HEALTH

AI-powered genomic surveillance has transformative potential in public health by enabling early detection of antibiotic resistance outbreaks and facilitating real-time monitoring of resistance trends. AI tools can rapidly analyze genomic data from bacterial isolates and predict the emergence of new resistant strains, allowing for quicker responses to potential outbreaks [22]. This proactive approach can help prevent the widespread dissemination of resistant pathogens in hospitals and communities. AI models can also assist in identifying the sources and pathways of resistance spread by analyzing genomic data from diverse settings, such as healthcare facilities, agricultural environments, and wastewater treatment plants [6]. By integrating clinical data with genomic information, AI can predict which antibiotic resistance patterns are likely to emerge in specific populations, informing targeted interventions and antibiotic stewardship programs. For example, AI algorithms have been used in surveillance systems like the WHO’s Global Antimicrobial Resistance Surveillance System (GLASS) to monitor resistance trends across countries, guiding global efforts to combat AMR [27]. Moreover, AI tools can support the real-time tracking of antimicrobial usage and the efficacy of interventions, enabling health authorities to adapt their strategies based on current trends [15]. As AI-powered genomic surveillance continues to evolve, it is expected to play an increasingly vital role in early warning systems, helping to mitigate the impact of AMR and improve public health outcomes worldwide [28].

8. FUTURE DIRECTIONS AND RESEARCH NEEDS

The future of AI in genomic surveillance for antibiotic resistance holds exciting potential but requires further research and development to address existing challenges. One of the most promising directions is the integration of multi-omics data, combining genomic, transcriptomic, proteomic, and metabolomic data, to provide a more comprehensive understanding of resistance mechanisms [29]. By incorporating additional layers of biological data, AI models can make more accurate predictions about resistance development and bacterial behavior. Another area for improvement is the enhancement of model accuracy through the inclusion of larger and more diverse datasets, particularly from underrepresented regions and low-income settings [30]. This will ensure that AI tools are globally applicable and can be used to monitor resistance in diverse populations. Advances in deep learning and neural networks may also lead to more powerful predictive models, capable of identifying complex patterns in genomic data that are not readily apparent [31]. Additionally, there is a need for greater collaboration between researchers, clinicians, and policymakers to create standardized frameworks for data sharing, ensuring that AI tools can be applied in a wide range of settings. Finally, continuous efforts to refine AI algorithms and validate their predictions in real-world scenarios will be crucial for the successful integration of AI-powered genomic surveillance into routine public health practices [32].

9. CONCLUSION

The integration of AI tools into genomic surveillance represents a promising and transformative approach to addressing the global threat of antibiotic resistance. By leveraging AI's ability to analyze vast amounts of genomic data, public health authorities can predict resistance trends, identify emerging resistant strains, and implement timely interventions to mitigate the spread of antimicrobial resistance (AMR). AI models that combine genomic, clinical, and environmental data offer a more comprehensive and dynamic understanding of antibiotic resistance, which is crucial for improving stewardship strategies and informing clinical decisions. While challenges such as data quality, model generalizability, and ethical considerations remain, advancements in AI technology and collaborative efforts across disciplines will continue to push the boundaries of what is possible in AMR surveillance. As AI tools become more refined and integrated into public health systems, they have the potential to revolutionize the fight against antibiotic resistance, providing more accurate predictions, faster responses, and ultimately, better outcomes for global health.

Acknowledgement

Nill

Funding

No funding was received to carry out this study.

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