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Machine learning for assessment of antimicrobial susceptibility: A novel bioinformatics approach against antimicrobial resistance

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To the Editor

Antimicrobial resistance (AMR) is one of the growing challenges of modern medicine, which causes thousands of deaths worldwide annually [1, 2]. To treat microbial infections, health specialists must prescribe effective antibiotics to patients on time. Microbiology laboratories should perform antimicrobial susceptibility tests on bacteria isolated from patients to select appropriate drugs [3]. Rapid detection of bacteria and their pattern of sensitivity to antibiotics play an essential role in the treatment of microbial infections [3]. Conventional antibiotic susceptibility testing method including disk diffusion is culture-based and take a long time (usually about 24 hours) to determine suitable drugs prescription [4]. In acute infectious diseases, physicians usually immediately begin experimental treatment including possible antibiotic therapy with high-sure therapeutic probability potential based on the patient's clinical symptoms. Improper administration or overuse of antibiotics could lead to the release of bacterial toxins such as bacterial lipopolysaccharide, the spread of bacteria, increased antibiotic resistance, and even death [3]. Therefore, one of the main challenges in detecting microbial resistance is obtaining a reliable antibiotic susceptibility pattern in several minutes or hours via simple and inexpensive tools [4].

Meanwhile, predict of AMR phenotypes by growth-independent methods can reduce the diagnostic cycle time [5]. Ma-

chine learning (ML) is a subfield of artificial intelligence that using the development of algorithms can build a prediction model via training datasets [6-9]. Previous research showed that ML models can predict AMR phenotypes using bacterial genome sequence data [2]. Because microbial species behave differently against different environmental factors or physio-chemicals variables like light, pH, and temperatures, this method can be used to detect microbial resistance behavior in microscopic micro-ecosystems using ML techniques [10]. It is expected that in the future develop an ML-based image/video classification algorithm by analyzing the movement of microbes under specific conditions. Bacteria can sense and respond to chemical slopes in their surroundings. For example, "Brownian motion" is a random motion of particles in a fluid affected by temperature, particle size, viscosity, and the motion of liquid molecules [10, 11]. This movement affects bacterial-specific motility like swimming by randomizing the displacement and direction [12]. Without "Brownian motion", a bacterium can only search a small area repeatedly, while the cell wanders into a much larger area with "Brownian motion" [12]. It is suggested to observe the microscopic behavior of bacteria in response to special series of antibiotics. A certain number of bacteria must be incubated in the same fluid medium with a constant volume and temperature. Resistant and susceptible bacteria exhibit phenomenal different behaviors facing different antibiotics. This unique reaction of bacteria could be predict-

able via a developed algorithm and, it is possible to obtain a specific predictive pattern for detecting resistant/sensitive species by processing and classifying input images/videos. Although the use of ML to diagnose, treat, and prevent antibiotic resistance is still in its infancy, ML can be considered as a new and efficient technique to diagnose, treat, and prevent antibiotic resistance [6]. Factors limiting progress in this area include the relative lack of experimental data and the small number of interdisciplinary research in the case of ML and AMR. Therefore, researchers in the future can design studies to assess ML for the assessment of antimicrobial susceptibility as a novel bioinformatics approach against AMR.

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Authors' contributions

Substantial contributions to the conception or design of the work; or the acquisition, analysis, or interpretation of data for the work: MHC, MM, AF, MS; Drafting the work or revising it critically for important intellectual content: MHC, MM, AF, MS; Final approval of the version to be published: MHC, MM, AF, MS; Agreement to be accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved: MHC, MM, AF, MS.

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Availability of data and materials

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Using artificial intelligent chatbots

None.

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