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Infrared Spectroscopy in Tandem with Machine Learning for Simultaneous Rapid Identification of Bacteria Isolated Directly from Patients' Urine Samples and Determination of Their Susceptibility to Antibiotics

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Abstract : Urinary tract infections (UTIs) are considered to be the most common bacterial infections worldwide, which are caused mainly by Escherichia (E.) coli (about 80%). Klebsiella pneumoniae (about 10%) and Pseudomonas aeruginosa (about 6%). Although antibiotics are considered as the most effective treatment for bacterial infectious diseases, unfortunately, most of the bacteria already have developed resistance to the majority of the commonly available antibiotics. Therefore, it is crucial to identify the infecting bacteria and to determine its susceptibility to antibiotics for prescribing effective treatment. Classical methods are time consuming, require ~48 hours for determining bacterial susceptibility. Thus, it is highly urgent to develop a new method that can significantly reduce the time required for determining both infecting bacterium at the species level and diagnose its susceptibility to antibiotics. Fourier-Transform Infrared (FTIR) spectroscopy is well known as a sensitive and rapid method, which can detect minor molecular changes in bacterial genome associated with the development of resistance to antibiotics. The main goal of this study is to examine the potential of FTIR spectroscopy, in tandem with machine learning algorithms, to identify the infected bacteria at the species level and to determine E. coli susceptibility to different antibiotics directly from patients' urine in about 30minutes. For this goal, 1600 different E. coli isolates were isolated for different patients' urine sample, measured by FTIR, and analyzed using different machine learning algorithm like Random Forest, XGBoost, and CNN. We achieved 98% success in isolate level identification and 89% accuracy in susceptibility determination.

Keywords : urinary tract infections (UTIs), E. coli, Klebsiella pneumonia, Pseudomonas aeruginosa, bacterial, susceptibility to antibiotics, infrared microscopy, machine learning
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