

SUPERVISED IDENTIFICATION OF ACINETOBACTER BAUMANNI STRAINS USING ARTIFICIAL NEURAL NETWORK

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ABSTRACT: In hospital environments around the world bacterial contamination is prevalence. One of the most commonly found bacteria is the *Acinetobacter Baumannii*. It can cause unitary tract, lung, abdominal and central nervous system infection. This bacteria is becoming more resistant to antibiotics. Thus, identification of the non-resistant from the resistant bacteria strain is of important for the correct course of treatments. We propose to use the artificial neural network (ANN) for supervised identification of this bacteria. The mass spectra generated from the liquid chromatography mass spectrometry (LCMS) were used as the features to train the ANN. However, due to the massive number of features, we applied the principle component analysis (PCA) to reduce the dimensions. Less than 1% of the original number of features were utilized. The hand out validation method confirmed that the accuracy, sensitivity and specificity are 0.75 respectively. In order to avoid selection biasness in the sampling, 5-fold cross validation was performed. In comparison, the average accuracy is close to 0.75 but the average sensitivity is slightly higher by 0.50.

KEY WORDS: *Acinetobacter Baumannii*, Artificial Neural Network (ANN).

1. INTRODUCTION

Acinetobacter Baumannii is a type of bacteria that is commonly found in hospital environments from the intensive care unit right to the long-term care unit (Thorne et al., 2019). This bacterium can easily colonize the human body with low immune system. It causes severe unitary tract, lung, abdominal and central nervous system infections. Left untreated it can lead to death. Usually these infections can be treated with multiple classes of antibiotic such as cefepime, ceftazidime and ciprofloxacin. However, *A. Baumannii* has demonstrated resistance against most classes of antibiotics (Trinh et al., 2019). Its genome has mutated to create defense