Using Artificial Neural Networks to Predict Minimum Inhibitory Concentration of Candidate Antibiotics against E. coli and X. alfalfae

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Artificial neural networks, models of which were experimentally calibrated by the author, train homeostatic variable sets to examine the relationship between variations in incubation conditions and the minimum inhibitory concentration (MIC) of selected gram-negative bacteria. MICs of bacteria vary, based upon the tested antibiotic that is subjected to the cell. The species, namely Escherichia coli and Xanthomonas alfalfae, were selected as resazurin-reactive bacteria of which X.alfalfae's MIC is found to be a novel result in this work. E. coli and X. alfalfae were tested against antibiotics Kanamycin and Ampicillin in preliminary trials, respectively, as Kanamycin is a cell-wall acting agent and Ampicillin is protein-inhibiting. The author proposes that not only will the relatively unstudied X. alfalfae result in a MIC of no greater than 5 g/mL against Kanamycin A, but further that machine learning techniques through neural networks shall yield a limited error in predicting the MIC, as measured by the network's cost function. The input variables to the ANN consist of temperature, light intensity of the incubation chamber, and the McFarland turbidity of the bacterial cultures before testing, a means of examining the opacity of an enriched media, among other variables. The author concluded the MIC of X. alfalfae against Kanamycin A to be between 0.24 and 0.49 g/mL when subject to homeostatic conditions, with ANN results sustaining the significant applicability of predictive modeling to the spread of bacterial infections.