Modeling Quorum Sensing Cycles in Pseudomonas aeruginosa Using Longitudinal Approaches by Measuring Gene Expression

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Quorum sensing (QS) in bacteria is the process of cell-cell communication for the purpose of acquiring information about cellular density in the environment. The detection of cellular density enables bacteria to behave in a synchronous manner to regulate gene expression, allowing for a magnified effect. Pseudomonas aeruginosa is a gram-negative bacterium associated with several human infections such as cystic fibrosis, endophthalmitis, and pneumonia. A method to accurately evaluate QS actives through time was developed and implemented in characterizing the genetic basis of QS in P. aeruginosa. The method developed, referred to as Longitudinal Quorum Sensing Modeling (LQSM), was validated using bacterial cultures with different concentrations of M64, an inhibitor for QS. LQSM adjusted for important factors including bacterial growth and was used to quantify the expression of the causative genes in the QS cycle. This was carried out by using 8 different bacterial strains with certain genes assumed to be associated with QS activity deleted. The approach successfully ranked the gene deletion strains and the results were biologically sound when compared against the P. aeruginosa QS pathway. Certain gene deletion strains had lower curves than others, showing that the deleted genes were highly important in the QS cycle. The study showed that the LQSM approach should be integrated into medical and laboratory devices even if data is continuously collected overtime, since raw data may give incorrect conclusions if it is not statistically adjusted for important covariates such as bacterial growth.

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