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Developing timely insights into *Pseudomonas aeruginosa* quorum sensing therapeutics through text mining

Paula Alexandra Jorge^{1,2}, Martín Pérez-Pérez¹, Gael Pérez Rodríguez¹, Florentino Fdez Riverola¹, Maria Olívia Pereira², Anália Lourenço^{1,3}

¹ESEI - Department of Computer Science, University of Vigo, Ourense, Spain; ²CEB - Centre of Biological Engineering, LIBRO - Laboratory of Research in Biofilms Rosário Oliveira, University of Minho, Braga, Portugal; ³CEB – Centre of Biological Engineering, University of Minho, Braga, Portugal; paulajorqe@ceb.uminho.pt

The pervasive growth of antibiotic-resistant is pressing the development of novel strategies to control infectious diseases. Quorum sensing (QS) is a key communication mechanism that allows bacteria to regulate gene expression, and thus many physiological activities e.g. virulence, motility, and biofilm formation. Hence, QS inhibition or quorum quenching is being pursued as a promising strategy to control clinical pathogens. Most available information about drug interactions with QS genes and molecules is scattered in the vast and ever-growing biomedical bibliome. So, text mining and network mining are attractive solutions to identify relevant interactions and generate new hypothesis for antimicrobial research. Here, we describe the implementation of such an automated workflow that extracts key information on *P. aeruginosa* QS-focused antimicrobial strategies from PubMed records. The workflow produces an integrated network, capturing the effect of antimicrobial agents over QS genes, QS signals and virulence factors. Interactions are contextualised by information on the conducted experimental methods and details on the antimicrobials and QS entities retrieved. The public Web-based interface (<http://pcquorum.org>) enables users to navigate through the interactions and look for indirect, non-trivial antimicrobial-QS associations. Currently, the *P. aeruginosa* antimicrobial-QS network contains 439 interactions encompassing 170 different drugs and 72 different QS entities; but it is in continuous, semi-automated growth. It offers a comprehensive picture of emerging anti-QS findings and thus may help in gaining novel understanding and prioritising new antimicrobial experiments.