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PTMLIF model of Metabolic Reaction Networks and ChEMBL Antibacterial Compounds

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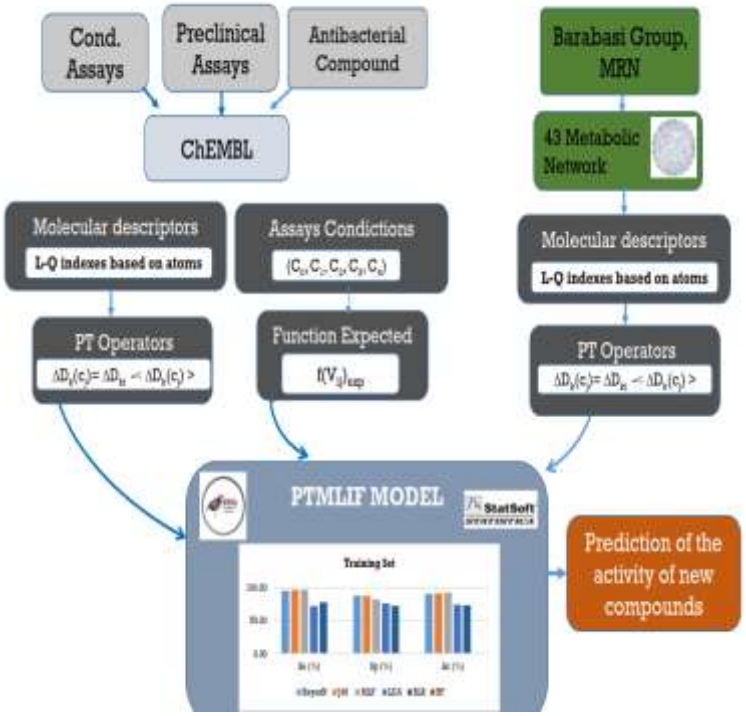
Graphical Abstract



Abstract.

Antimicrobial resistance has prompted research and development of new antibiotic treatments. Efforts to discover new drugs with antibacterial activity have generated large data sets from multiple preclinical trials with different experimental conditions. Predicting the activity of new chemical compounds on pathogenic microorganisms with different Metabolic Reaction Networks (MRNs) has become an important objective in the field. PTMLIF (Perturbation Theory, Machine Learning and Information Fusion) models are the combination of perturbation theory with machine learning and information fusion. In this document, we merge >100000 preclinical antibacterial assays from the ChEMBL database with the structural information for >40 MRNs of different microorganisms reported by the Barabási group. Non-linear PTMLIF models were applied applying Random Forest (RF), J48-decision tree, and Bayesian Network (BN) algorithms. BN, and RF models presented better results. specificity (>88%), sensitivity (>95%), AUROC (>95%). and accuracy (~90%), In this work we also demonstrated the power of information fusion of experimental characteristics of drugs/compounds and MRN for the prediction of antibacterial activity of chemical compounds.

Keywords: Machine Learning; Perturbation Theory; Antibacterial activity; Information Fusion; Bayesian Network; Random Forest.

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