Title: QSAR modeling of antitubercular activity of diverse organic compounds

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Abstract: Tuberculosis (TB) is a worldwide infectious disease that has shown over time extremely high mortality levels. The urgent need to develop new antitubercular drugs is due to the increasing rate of appearance of multi-drug resistant strains to the commonly used drugs, and the longer durations of therapy and recovery, particularly in immuno-compromised patients. The major goal of the present study is the exploration of data from different families of compounds through the use of a variety of machine learning techniques so that robust QSAR-based models can be developed to further guide in the quest for new potent anti-TB compounds. Eight QSAR models were built using various types of descriptors (from ADRIANA.Code and Dragon software) with two publicly available structurally diverse data sets, including recent data deposited in PubChem. QSAR methodologies used Random Forests and Associative Neural Networks. Predictions for the external evaluation sets obtained accuracies in the range of 0.76-0.88 (for active/inactive classifications) and Q(2)=0.66-0.89 for regressions. Models developed in this study can be used to estimate the anti-TB activity of drug candidates at early stages of drug development (C) 2011 Elsevier B.V. All rights reserved.

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