[P5] Predicting drug side-effect profiles from the integration of chemical and biological spaces

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Drug side-effects, or adverse drug reactions, have become a major public health concern. It is one of the main causes of failure in the drug development, and of drug withdrawal once they have reached the market. Therefore, the identification of potential severe side-effects is a challenging issue, and there is a strong need to develop computational prediction methods of potential side-effects at many stages of the drug development process.

In this study we develop a new statistical method to predict potential side-effect profiles of drug candidate molecules based on their chemical structures and target protein information on a large scale. We propose kernel-based and sparsity-induced models for multiple responses to deal with heterogeneous data sources. The originality lies in the integration of the chemical space of drug chemical structures and the biological space of drug target proteins in a unified framework. We show the usefulness of the proposed method on the simultaneous prediction of about one thousand side-effects for drugs from their chemical substructure and target protein profiles, and we show that the prediction accuracy consistently improves owing to the proposed models and integration of chemical and biological information. We also conduct a comprehensive side-effect prediction for uncharacterized drug molecules stored in databases, and confirm the prediction results using independent information sources. The proposed method is expected to be useful in the drug development process.