Predictive Modelling of Drug Effects and Interactions

Dr. Ping Zhang
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Abstract:
Drug discovery is a time-consuming and laborious process. The lack of efficacy and safety issues are the two major reasons for which a drug fails clinical trials, each accounting for around 30% of failures. By leveraging the diversity of available molecular and clinical data, predictive modelling of drug effects and drug-drug interactions could lead to reduce the attrition rate in the drug development. In this talk, I will present our recent work on predictive modelling techniques for the purpose of understanding and analyzing clinical drug responses (i.e., efficacy and safety). I will focus on three important applications, including drug repositioning, prediction of drug-drug interactions, and personalized medicine. Experimental results demonstrate the effectiveness of our methods, and show that predictive models could serve as a useful tool to generate hypothesis on efficacy and safety profiles of drugs.

Bio:
Ping Zhang is a Research Staff Member at Health Informatics Department, IBM T. J. Watson Research Center. Dr. Zhang graduated with PhD in Computer and Information Sciences at Temple University in the fall of 2012. His advisor was Prof. Zoran Obradovic. His research focuses on Machine Learning, Data Mining, and their applications to Drug Discovery and Health Informatics. He has published more than 20 articles in refereed journals and conferences, including AMIA, BIBM, ECML/PKDD, KDD conferences, and BMC Bioinformatics, JAMIA, Nucleic Acids Research, Proteome Science journals. Dr. Zhang served on the program committees of leading international conferences including SIAM SDM, IEEE BIBM, and ACM BCB.