

Omics-data machine learning for precise drug response prediction

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ABSTRACT

Detecting predictive biomarkers from multiomics data is important for precision medicine, to improve diagnostics of complex diseases and for better treatments. This needs substantial experimental efforts that are made difficult by the heterogeneity of cell lines and huge cost. An effective solution is to build a computational model over the diverse omics data, including genomic, molecular, and environmental information. However, choosing informative and reliable data sources from different types of data is a challenging problem. We propose DIVERSE, a framework of Bayesian importance-weighted matrix tri- and bi-factorization (DIVERSE3 or DIVERSE2) to predict drug responses from data of cell lines, drugs, and gene interactions. DIVERSE integrates the data sources systematically, in a step-wise manner, examining the importance of each added data set in turn. More concretely, we sequentially integrate five different data sets, which have not all been combined in earlier bioinformatic methods for predicting drug responses. Empirical experiments show that DIVERSE clearly outperformed five other methods including three state-of-the-art approaches, under cross-validation, particularly in out-of-matrix prediction, which is closer to the setting of real use cases and more challenging than simpler in-matrix prediction. Additionally, case studies for discovering new drugs further confirmed the performance advantage of DIVERSE.

BIOGRAPHY

Hiroshi Mamitsuka obtained all degrees (B.S., M.E. and PhD) from University of Tokyo, Japan. After working with industry in business data mining for more than 10 years, he joined academia for doing research on machine learning and scientific data mining. Currently he is a professor of Bioinformatics Center, Institute for Chemical Research, Kyoto University, Japan, being jointly appointed as a faculty of School of Pharmaceutical Sciences of the same university. His current research interests are machine learning, data mining and a wide variety of applications.

All are welcome!



In case of questions, please contact Prof Wong Hau San at cshswong@cityu.edu.hk, or visit the CS Departmental Seminar Web at <https://www.cs.cityu.edu.hk/events/cs-seminars/recent-cs-colloquiums>.

