Predicting Drug Sensitivity of Cancer Cell Lines via Collaborative Filtering with Contextual Attention

Yifeng Tao\textsuperscript{1,2,†}, Shuangxia Ren\textsuperscript{3,4,†}, Michael Q. Ding\textsuperscript{3}, Russell Schwartz\textsuperscript{1,5,*}, Xinghua Lu\textsuperscript{3,4,6,*}

\textsuperscript{1}Computational Biology Department, School of Computer Science, Carnegie Mellon University
\textsuperscript{2}Joint Carnegie Mellon-University of Pittsburgh Ph.D. Program in Computational Biology
\textsuperscript{3}Department of Biomedical Informatics, School of Medicine, University of Pittsburgh
\textsuperscript{4}Intelligent Systems Program, School of Computing and Information, University of Pittsburgh
\textsuperscript{5}Department of Biological Sciences, Carnegie Mellon University
\textsuperscript{6}Department of Pharmaceutical Science, School of Medicine, University of Pittsburgh
Introduction

• Challenges in predicting drug response of cancer cell lines
  • Robustness
  • Contextual effects
  • Interpretability
Methods

- CADRE: Contextual Attention-based Drug REsponse
  - Collaborative filtering: copes with noisy data
  - Attention mechanism: improves interpretability and performance
  - Pretrained gene embeddings: boosts performance further
Results

- Outperforms competing models
- Effective attention-encoded cell line representation
- Identifies critical biomarkers related to drug resistance