Predicting Cancer Drug Response Using Nuclear Norm Multi-Task Learning

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The future of personalized cancer treatment relies on the existence of computational models that can accurately predict how a patient will respond to a cancer drug, given the genetic makeup of that patient’s cancer. The current state of the art algorithm, Elastic Net, is limited by its inherent inability to exploit the complex relationships between drugs, which affects its accuracy. I propose a novel computational tool, inspired by the human brain, that takes full advantage of the important relationships between drugs to greatly increase the accuracy of its drug response predictions. The increase in accuracy of the proposed method is on average 35% and as high as 61%. The superiority of Nuclear Norm’s predictions is further substantiated by hierarchical clustering analysis which highlights their greater biological interpretability over Elastic Net’s. The biological relevance of Nuclear Norm’s predictions is further validated by Gene Ontology Enrichment Analysis, which shows that Nuclear Norm was able to not only pick up the mechanisms of action for all drugs studied, but for several of them, also their side effects and potentially novel mechanisms of action. In addition, drug response noise analysis helped direct our research and its results are strongly correlated with our prediction results, which stresses the importance of accurate genomic data. The combination of greater accuracy and biological interpretability allows my model to offer novel insights into cancer. Overall, Nuclear Norm represents a significant step forward for computationally driven personalized cancer treatments and should be included as a standard computational tool in cancer research.

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