Doctoral School of Information and Biomedical Technologies Polish Academy of Sciences

Subject
Machine learning methods for identification of effective drug combinations in immuno-oncology

Supervisors, contact, place of research
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Project Description

Thanks to the significant progress in medicinal chemistry, we have now available a plethora of compounds that can target individual biochemical reactions in the organism with relatively high specificity. It could appear that specific biochemical interventions, which alter specific biochemical processes, provide an attractive opportunity to induce specific, therapeutically desired, cellular responses. In practice, however, clinical outcomes of many drugs with high molecular specificity have been different than originality hoped for, if not disappointing (Kenakin, 2013). Low efficacy of drugs that target specific biochemical reactions can be, to a considerable degree, attributed to a highly cross-wired architecture of cellular processes: single biochemical process drives, and is driven by, a number of other processes (Amit, 2013; Komorowski, 2019). Therefore, the design of pharmacological interventions aimed to induce specific cellular responses may require more sophisticated strategies, even when compounds with high molecular specificity are at hand.

Drug combinations are seen as a promising approach. Unfortunately, screening combinations is difficult because the number of experiments grows exponentially with the number of drugs and doses. Screening a relatively small number of combinations and using a model to predict the rest has a fair potential to overcome this combinatorial explosion problem. The main goal of the PhD project will be to to refine statistical methods for the facilitation combinatorial drug screening as well as to deliver their robust and portable software implementations. The project provides a tangible opportunity to deliver generally applicable tools to improve cost-effectiveness of combinatorial drug screening.

Collaborators
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