

Katedra aplikovanej informatiky, FMFI UK
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Computational approaches for improving cancer treatment.

From graphs to new drugs and increased survival

Abstract: Cancer development is a multi-step process that leads to uncontrolled tumor cell growth. Multiple pathways are involved; typically some signaling and regulatory pathways are activated, while others are suppressed. Systematically exploring these networks of proteins will lead to better understanding of disease initiation and progression, and in turn more effective patient treatment.

To address these challenges, we developed a system for an integrative analysis, prediction and characterization of molecular signatures and relevant protein-protein interactions, microRNA:gene interactions, and resources for rationally identifying drug combinations for cancer treatment.

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