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Cancer treatment in the era of precision medicine

Traditional approach to cancer treatment generally involves "one-size-fits-all" treatments and procedures (e.g., chemotherapy, radiation therapy, and surgery), which is focused largely at fighting a particular type of cancer (e.g., liver, lung, colorectal). However, this approach ignores the unique nature of an individual patient's cancer, despite the fact that the complex genotypic and phenotypic heterogeneity of an individual patient's cancer/tumor has a profound influence on the clinical responses to targeted anticancer therapies. Genetic sequencing of tumors is conducted for only a small number of patients (~2%), and the large number (>4.5 M) of options and potential for drug-drug interactions have precluded widespread adoption of combination therapies. Current approach to treatment response planning and assessment also lacks an efficient method to consolidate biomarker changes into a holistic understanding of treatment response.

Major goals of successful combination therapy include the ability to: (a) cover most of the patient's aberrations with a minimal number of drugs, (b) achieve enhanced effectiveness through drug synergy, (c) reduce the frequency and severity of adverse events (AEs) and (d) minimize the potential to develop drug resistance. While the majority of research on chemotherapies focus on cellular and genetic mechanisms of resistance, there are numerous patient-specific and tumor-specific measures that contribute to treatment response. Development of effective combination therapy is also challenging because many cancer drugs act on intersecting signaling pathways and thus can potentially interfere or antagonize each other. One approach to identify effective combinations is by precise targeting of synergistic combinations, which exhibit enhanced therapeutic efficacy when combined at lower doses. However, identification of synergistic drug combinations is often a labor- and resource-intensive process. We developed a precise, multimodal computational model that can leverage clinically-available measurements to optimize treatment selection and schedules for patients.

Biography

Igor F Tsigelny is an expert in structural biology, molecular modeling, bioinformatics, structure-based drug design and personalized cancer medicine. He published >200 articles, 4 scientific books and around 15 patents. The book 'Protein Structure Prediction: Bioinformatic Approach' that he edited has been called 'The Bible of all current prediction techniques' by BioPlanet Bioinformatics Forums. His computational study of molecular mechanisms of Parkinson's disease was included in the US Department of Energy publication 'Decade of Discovery' where the best computational studies of the decade 1999–2009 have been described. He is a Professor in the UC San Diego and CSO of CureMatch Inc. (San Diego).

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