

KEYNOTE TALK

Monday, October 11, 2021 at 9am

Precision oncology via the tumor transcriptome

Eytan Ruppin
CDSL, NCI, NIH
USA

Abstract: Precision oncology has made significant advances, mainly by targeting actionable mutations and fusion events involving cancer driver genes. Aiming to expand treatment opportunities, recent studies have begun to explore the utility of tumor transcriptome to guide patient treatment. I will introduce a new approach, termed SELECT, which harnesses genetic interactions to successfully predict patient response to cancer therapy from the tumor transcriptome. SELECT is tested on a broad collection of 35 published targeted and immunotherapy clinical trials from 10 different cancer types. It is predictive of patients' response in 80% of these clinical trials and in the recent multi-arm WINTHER trial. In summary, we report the first systematic, transcriptomics-based approach that is predictive across many targeted and immune therapies. The predictive signatures and the code are made publicly available for academic use, laying a basis for future prospective clinical studies. As time permits, I will provide a brief overview of MadHitter, a new approach for guiding precision cancer therapy based on single cell tumor transcriptomics.



Speaker Bio-Sketch: Eytan Ruppin received his M.D. and Ph.D. (Computer Science) from Tel-Aviv University where he has served as a professor of Computer Science & Medicine since 1995, conducting computational multi-disciplinary research spanning a wide variety of topics, including neuroscience, machine learning and systems biology. He joined the University of Maryland in July 2014 as director of its center for bioinformatics and computational biology and moved to the NCI in January 2018 as chief of its newly established cancer data science branch (CDSL). His lab co-identified the first metabolic synthetic lethal (SL) drug target to treat cancer (Nature, 2011), was the first to identify metabolic SLs in cancer in a genome-wide manner (Molecular Systems Biology, 2011) and the first to infer cancer SLs by mining patients tumor data (Cell, 2014). More recently, his research has been focused on developing new computational approaches for SL/transcriptomics based precision oncology (Nat Comm 2018, MSB 2019, Cancer

Cell 2019, NCB 2019, Science Advances 2021, Cell 2021) and for immunotherapy (Nat Med 2018, Cell 2018, JAMA Onc 2019, Nat Cancer 2020). Eytan is a co-founder of a few startup companies involved in precision medicine and cancer drug discovery, including Metabomed, Medaware and Pangea Therapeutics an editorial board member of EMBO Reports and Molecular Systems Biology and a fellow of the International Society of Computational Biology (ISCB).