Seminars in Biotechnology BTEC 591 & BTEC 691

"From Cell-Lines to Cancer Patients: Personalized Drug Synergy Prediction"

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13:30

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Resume: Dr. Öznur Taştan received her Ph.D. in 2011, from Carnegie Mellon University, School of Computer Science. Since 2018, she has been with the Sabanci University Computer Science and Engineering and Molecular Biology, Genetics and Bioengineering departments. Before joining Sabanci, she worked as a faculty member at Bilkent University, Department of Computer Engineering, and as a post-doctoral researcher at Microsoft Research New England Lab (Cambridge, MA, USA). She has worked on diverse problems in machine learning for computational biology. She is a recipient of the Young Scientist Research Award of the Science Academy (BAGEP), the UNESCO-L'OREAL National Fellowship for Young Women in Life Sciences, and METU Prof. Mustafa Parlar Foundation Research Incentive Award.

Abstract:

Combination drug therapies are effective treatments for cancer. However, the genetic heterogeneity of the patients and exponentially large space of drug pairings pose significant challenges for finding the right combination for a specific patient. Current in silico prediction methods promise to reduce the vast number of candidate drug combinations for further screening. However, existing powerful methods are trained with cancer cell line gene expression data, which limits their applicability in clinical settings. While synergy measurements on cell lines models are available at large scale, patient-derived samples are too few to train a complex model. On the other hand, patient-specific single-drug response data are relatively more available. In this talk, I will first present our in-house developed deep learning model Matchmaker that is trained on cell line gene expression data and further describe a new model and training strategies for customizing patient drug synergy predictions. The patient-specific models are first trained to learn synergy scores of drug pairs and their single drug responses for a given cell line using drug structures and large-scale cell line gene expression data. Then, the model is fine-tuned for patients with their patient gene expression data and associated single drug response measured on the patient ex vivo samples.