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DSICCR Tuesday Seminar Series

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From cell lines to pharmacogenomics: Transferring deep learning drug response prediction models from cell lines to personalized therapy through molecular pathways

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Computational prediction models built on cancer cell line data create an opportunity for guiding precision medicine for cancer treatment. However, it remains challenging to tailor these models to predict drug response of specific patients.
Here, we present our 3-step framework for modelling drug response for single drugs and for drug combinations on cell lines and transfer learning the models to patient tumors. A key component of a successfully translating a computational framework to the clinic is the explainability of the models. We address this issue by introducing the association of curated molecular pathways with drugs and with cell-lines/tumors based on their genomic information. These curated pathways help bridge the gap between cell lines and personalized treatment.

Tuesday, March 29th, 2022. 12p – 1p. Webcast

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