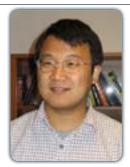
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Bin Li

Takeda Pharmaceuticals International Co., Japan

NGS data process and building/testing drug-sensitivity predictive models for both single agents and drug combinations

Precision medicine approaches to optimize therapeutic efficacy in selected patient populations requires the acquisition and storage of in depth genomic and phenotypic patient information combined with the use of innovative computational platforms for knowledge generation. A critical objective is to discover and clinically apply biomarkers to select patients most likely to respond or least likely to experience adverse events. Here, we discuss various computational efforts to support translational biomarker research for biomarker discovery and the development of predictive signatures for clinical testing. These efforts include: Method evaluation and pipeline building for QC/process clinical NGS data; single agent's predictive modeling for identifying/validating translational biomarkers for patient stratification; building translational research storage platforms to integrate clinical and omics data and; method development and evaluation for drug combination prediction. Combining predictive modeling and translational platform building efforts, computational bioinformatics will be able to support the identification of biomarkers for patient stratification and disease indication selection.

Biography

Bin Li leads a Computational Biology team at Takeda Pharmaceuticals, to support translational research on various Takeda compounds. His team evaluates NGS methods, builds internal pipelines, and selects vendors for clinical data process, for multiple NGS platforms (including WGS, WES, custom panel, and RNA-seq). His team also develops methods and builds predictive models for patient stratifications and disease indication selections. Before joining Millennium, he was a Senior Scientist at Merrimack Pharmaceuticals in Cambridge, MA. Prior to Merrimack, he was a Senior Scientist at Institute for Systems Biology in Seattle, WA.

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