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Evolution-informed biomarker discovery for precision oncology

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As one of the leading causes of death worldwide, cancer takes millions of lives each year despite of hundreds of billions of dollars spent on patient care. Major concerns have been raised on under-treatment that leads to disease progression and drug resistance, and over-treatment that exposes patients to unnecessary toxicity with little or no benefit. This situation can be significantly improved by precision oncology, in which treatment regime is tailored to each patient for best outcome. However, discovering bona fide biomarkers to help predict cancer outcomes has been a long-standing mission in cancer research. Although “omics” data generated by high-through biotechnologies offer a valuable source from which genetic markers can be identified, distinguishing spurious markers that show fortuitous statistical associations from biologically relevant markers is a grand challenge. Here, we present a novel framework that integrates evolutionary patterns and statistical association with sparse learning algorithms to assist cancer biomarker discovery. Our methods search beyond human genomes to look for signatures in cancer driver genes across mammals and vertebrates, and incorporate these patterns to discover novel drug targets and cancer biomarkers. When applied to predict therapeutic responses for patients with acute myeloid leukemia and to predict metastasis for patients with prostate cancers, this novel approach gave rise to evolution-informed models that reported lower complexity and higher accuracy than uninformed models. The identified genetic markers also have significant implications in tumor progression and embrace potential drug targets.

Biography

Li Liu is an Assistant Professor of Biomedical Informatics and the Director of the Bioinformatics, Core Facility at ASU. She holds an MD degree in Medicine and an MS degree in Information System. As a trained Clinician and a Bioinformatics Researcher, she fully appreciates the critical roles of genomic medicine and bioinformatics in advancing precision medicine. She and her research team has investigated clinical and molecular signatures of human diseases and developed novel computational methods to discover biomarkers for early diagnosis and accurate prediction of therapeutic responses for individual patients by integrating genomic, phylogenetic, population genetic, statistical and machine-learning techniques.

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