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Computational Methods for Personalized Medicine in Cancer Research

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Abstract

Personalized medicine is a medical procedure that stratify patients into different groups with specific treatments relied on their predicted response or risk of disease. To support researches in personalized medicine and manufacture viral vaccines and other products of biotechnology (e.g., drug), both tumors and cell lines, which are grown from the tumors, are used. With rapid growth of biomedical and clinical data, many computational methods have been proposed to identify candidate disease-associated cellular components, to predict novel targets of drugs, to predict response of drugs, or to repurpose the use of drug for other diseases, etc.... Specially for personalized medicine, computational methods have been proposed to classify patients into different subtypes according to genomic, epigenomic profiles and/or drug responses on cell lines or patient tumors [1-5], and therefore able to predict response of untested drugs [6], drug synergy [7] as well as to identify predictive genomic features and treatment for each group of patients. Among diseases, cancer is a complex genetic disease and has been received most focus in personalized medicine research [8]. In addition, many data resources for are publicly available for the research such as CCLE [9], COSMIC [10], TCGA [11] and GDSC [12].

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Keywords

Personalized Medicine, patient stratification, cancer research, drug response, computational methods

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