

## Cancer bioinformatics, a potential way for prediction of chemotherapeutic responses in clinics

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Cancers are different etiological diseases with same characteristics of unlimited cell reproductions caused by the abnormalities of genetic molecules in human cells. Bioinformatics plays important role in revealing these abnormalities of genetic molecules for the importance of cancer diagnostics, prognostics and most important, therapeutics. It is a way of profound significance not only with quickness and high-throughput, but also of potential quantitative value of prediction for drug responses and use details. It is the fastest-growing area in recent cancer research. However, many technical and economic drawbacks impede us from reaching the goal of therapeutic benefits in clinics at current stage and will continual to be in the case in nearly future. We in several years before suggest a way of combination of drug sensitivity tests and mathematical computation, bioinformatics to make it more adequate and available. Adhering to this policy, improving of bioinformatics systems is especially important for the benefits of future individual therapy. In general, presently bioinformatics requires rigorous discipline and reasonable routine to make it real work in future clinical practices. Their gaining of popularity and new breakthrough are largely dependent on the progression of these disciplines. After introducing the general backgrounds of current bioinformatics application in cancer research, here we represent our insights and suggestions into the approach, especially their relations with genome-wide analysis, drug sensitivity tests and mathematics-related problems.

### Biography

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