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Cancer Bioinformatics, its Impacts on Cancer Therapy

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Abstract

Last 20 years, this world has witnessed the rapid progresses of bioinformatics. Cancer bioinformatics is one of such important omics branches for drug developments and clinical applications. Same as other biological techniques or systems, bioinformatics are not omni-potent now. They have their own limits and shortcomings. This article addresses the panorama of bioinformatics in cancer researches and clinical applications. Their advantageous and drawbacks are discussed and highlighted.

Keywords: Cancer bioinformatics; Cancer pathology; Neoplasm metastasis; Cancer stem cells; Drug response; Personalized cancer therapy; Antimetastatic drug development

Introduction

Cancer remains to be a serious human health problem despite great progresses in cancer researches. Cancer is a common disease that claims life about 7-10 million people annually in the world. As a result, cancer remains to be a great medical challenge worldwide [1-3]. Last 20 years, this world has witnessed the rapid progresses of bioinformatics in cancer treatment studies and clinical applications. Since cancer bioinformatics systems and applications have advantages and shortcomings, these shortcomings limit the popularity of cancer bioinformatics in general cancer therapeutic practices worldwide. Many obstacles need to be overcome. This article not only offers a panorama of bioinformatics in cancer researches and clinical applications, but also provided future perspectives for improvements.

Panorama of cancer bioinformatics in personalized cancer therapy (PCT)

Since cancer is a progressive disease with a lot of genetic alterations and molecular abnormalities [4,5], the best therapeutic approaches should target these genetic alterations and molecular abnormalities. However, different types of cancers are caused by different genetic abnormalities, such as mutation, translocation, deletion or replication etc. Thus before an appropriate therapy can be initiated, exact genetic alterations and molecular abnormalities of a specific cancer must be determined. Drug sensitivity testing, cancer bioinformatics, pharmacogenetics and individualized antimetastatic therapies are major parts of PCT that are designed to reveal these genetic alteration and molecular abnormality information and select optimal anticancer drugs [6-9]. Among these categories of personalized cancer therapies, cancer bioinformatics and individualized antimetastatic therapies are underestimated, yet of great clinical significances.

Since 84 anticancer drugs have been licensed in US [10] and 178 anticancer drugs have been approved worldwide (2013) [11], the determination of therapeutic efficacies of various anticancer drugs for individual cancer patient is an ideal model for clinical cancer treatments. Various biological molecules (bioinformatics) have been widely reported to have diagnostic, prognostic and/or therapeutic predictive values in cancer patients [5-9,11-21]. Before initiating antibody therapy (treatment with monoclonal antibodies or polyclonal antibodies) or other type of targeted anticancer drug or biotherapies, [22] it is ideal to know the levels of their targeted antigens or receptors in tumors in order to provide a rational basis for the quality of anticancer treatments [5-9,11-21]. Besides, since the cancer tissue bioinformatics detection methodologies can be varied greatly, bioinformatics technical studies for pinpointing oncogenic status are also an interesting topic presently and in future.

Bioinformatics methods are high throughput assays for identifying the original and causative cancer biomarkers in personalized chemotherapy [9]. It includes mathematical or computational systems to facilitate the deciphering of oncogenic genomic and molecular information [23-25]. To attain this goal, mounting basic and clinical investigations are needed to establish good hospital routines and paradigms to follow. These hospital routines and paradigms need to be easy to be handled, less costly, high-throughput, and as effective as possible.

Future perspectives

Currently, bioinformatics techniques are diversified and standard techniques have not been made uniformity by manufacturers [6]. In order to safeguard the quality and cost of hospital routines, standard guidelines international must be issued every 4-5 years.

Validating and pinpointing the cancer biomarkers or bioinformatics from tumor samples and predicting which targeted anticancer drugs or biotherapies might be specifically targeted are general schemes of cancer bioinformatics applications. To achieve this goal, effectively targeted anticancer drugs are needed. If we have not equipped enough useful targeted anticancer drugs, we cannot properly control cancer growths and metastasis no matter how crystal clear we know the tumor causations by cancer bioinformatics. Development and approval of more effective targeted anticancer drugs are indispensable.

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Since cancer is a genetic disease, finally improvements of our knowledge about human cancer genomes by next generations of sequencing (NGS) [26] are urgently needed. Only by genomic studies of cancer pathogenesis and metastatic cascades, proper medical interventions can be innovated and effectively utilized.

Presently, most cancer bioinformatics testing are referred to tumor tissue assays. With the increasing diversity of bioinformatics technology, we can understand disease progressions by testing cancer patient's blood, urine, or even saliva [11,20,26]. By these bio-sample assays, we can make decisions as easy as possible and as quick as possible.

Individualized cancer therapy by detecting cancer biomarkers or bioinformatics is a modern method and has a great clinical significance. Comparing with therapeutic anticancer drugs and the costs of residents in hospitals (more than $10,000), the costs of standard cancer bioinformatics detection ($100-5000) is relatively low. It is a cost-effective strategy for most early stage of cancer patients [9].

Conclusion

Cancer bioinformatics has been developing rapidly. However, it is still in its infantile stage and no decisive role has been played in clinical cancer treatment. Many new areas for cancer bioinformatics applications will be implemented. But are we ready for that yet? [27,28]

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