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Recent Advancements in Biomarkers World

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Commentary Article

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Introduction

Biomarkers additionally known as biological markers are biological measures of a biological state. In 1998, the National Institutes of Health Biomarkers Definitions Working Group defined a biomarker as "a characteristic that is objectively measured and evaluated as an indicator of normal biological processes, pathogenic processes, or pharmacologic responses to a therapeutic intervention"[1-4].

Biomarkers can be used to measure and evaluate traditional biological and infective processes, or pharmacologic responses to a therapeutic intervention, and in some cases they may serve as potential drug targets [5]

An ideal biomarker has certain characteristics that make it appropriate for checking a particular disease condition. Ideally, an ideal marker should have the following features:

1. Safe and easy to measure
2. Cost efficient to follow up
3. Modifiable with treatment
4. Consistent across gender and ethnic teams

Biomarker Discovery

Multi-omics solutions are used to discover biomarkers, attending to facilitate researchers to accelerate the process of drug discovery and development [6-8]. By combining multiple technologies such as Next-generation sequencing, Sanger sequencing, Genotyping, Mass spectrometry, we can study variants from genomic to trancriptomic and proteomic levels. These multi-omics solutions enhance the strength of combinational analysis to find sickness related biomarkers for further validation [9-10].

Recent advancements in biomarker discovery

Due to the inherent disadvantage of biomarker various ways have developed like capillary electrophoresis-based single and multidimensional separations coupled with mass spectrometry for performing comprehensive proteomic analysis of clinical specimens [11-14]. In addition to protein identification, monitoring quantitative changes in protein expression is essential for the discovery of disease-associated biomarkers. Comparative proteomics involving measurements in changes of biological pathways or functional processes are further expected to provide relevant markers and networks, molecular relationships among different stages of disease, and molecular mechanisms that drive the progression of disease.

Along with this, computational biology is also essential in the process of translating biological knowledge into clinical practice, as well as in the understanding of biological phenomena at totally different structure and quality scales. A key contribution of computational biology is the discovery of biomarkers for predicting clinical outcomes [15].

The complexity of human biological systems and imperfect instrumentations of high-throughput biological instruments/results have created significant hurdles in biomarker development. This process involves the predictive modelling and integration of different types of data and knowledge for screening, diagnostic or prognostic purposes [16-20]. Moreover, this requires the design and combination of different methodologies based on statistical analysis and machine learning.

CONCLUSION

Biomarkers play a critical role in rising the drug development process as well as in the larger biomedical research enterprise. Understanding the relationship between measurable biological processes and clinical outcomes is vital to expanding our arsenal of treatments for all diseases, and for deepening our understanding of normal, healthy physiology. The FDA continues to promote the use of biomarkers in basic and clinical research, as well as research on potential new biomarkers to use as surrogates in future trials. However, for all their potential to do good- to speed drug development, to reduce exposure to ineffective experimental treatments, and so on-biomarkers present substantial risks when trial designers confuse them with clinical endpoints. Biomarkers may solely serve as true replacements for clinical relevant endpoints if we completely understood the conventional physiology of a biological process, the pathophysiology of that process in the disease state.

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