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Sequencing Technologies and their Importance in the Field of Oncology

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ABSTRACT: The molecular level analysis of diseases provides multiple new insights into their genetics and pathogenesis. Revelation of information about abnormal nucleic acid sequences can aid in the discovery of novel conditions, to characterize different versions of the same disorder and also in the development of newer, more effective techniques for controlling and curing the disease. The analysis of cellular transcriptomic data has proven to be a very useful approach in the development of predictive biomarkers for cancer. The introduction and increasing popularity of high-throughput Next Generation Sequencing (NGS) technologies in the past few years has marginally increased the speed and decreased the cost of the sequencing procedure. It has been at the forefront of medical research with huge leaps in the field of cancer genomics. Cancer is the consequence of mutation in the genetic code, DNA based alterations and other factors associated, leading to uncontrolled cell division. The early detection of RNA based alterations is measured using transcriptomic analysis, where Next Generation Sequencing (RNAseq) data computation/ analysis methodologies have been reported as upcoming approaches in cancer genomics. These methods help to gain better insight into the mechanisms and effects of several factors combined, on the problems of metastasis and therapy resistance during progression of the cancer. This additionally has better repercussions for clinical oncology since it can help in easier characterization (on the basis of tumour type), heredity risk predictions, in designing of suitable targeted therapies and overall more informed, genome based clinical trials and treatments. The challenges faced by NGS however, are the complex procedures and inconvenience caused during handling and organizing of the enormous amounts of high-dimensional data (big data) and raises the need for novel computational framework and methods for efficient data analytics. In this review, we discuss about the various sequencing methods employed in the study of cancer genomics and also about their advantages, disadvantages, data analytics and future possibilities.

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