Detection of Genes by Next Generation Sequencing Based on RNA

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Abstract

Next-generation putting in correct order (NGS) technologies have progressive advantages in terms of producing a lot for a given amount of money, never-before-seen putting in correct order speed, bright and sharp and quality of being very close to the truth or true number in related to the study of tiny chemical instructions within cells analyses. To date, these high-throughput putting in correct order technologies have been complete and thoroughly applied in a variety of ways, such as whole total set of tiny chemical assembly instructions of a living thing putting in correct order, target putting in correct order, tiny chemical assembly instruction inside of living things expression information-gathering, chromatin immune-precipitation putting in correct order, and small RNA putting in correct order, to speed up related to the body function of living things and studying how living things and medicine work together. However, the huge amount of data created by NGS represents a great challenge. This article discusses the available applications of NGS technologies, presents guidelines for data processing pipelines, and makes suggestions for selecting good tools in study of the tiny chemical instructions within cells, small RNA research.

Keywords

RNA seq, Mi-RNA, NGS, Proteomics

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1. Introduction

Sequencing of RNA is one of the most commonly used ways of doing things in life sciences and has been mostly used in cancer research, drug development, and cancer identification of a disease, or its cause and outlook. Driven by different related to the body function of living things and technical questions, the ways of doing things of RNAseq have went forward quickly from bulk RNAseq, laser-captured micro-cut apart RNAseq, and single-cell RNAseq to digital related to space or existing in space RNA information-gathering, related to space or existing in space list of school grades, and direct in the original position putting in correct order [1]. These different technologies have their like nothing else in the world strengths, weaknesses, and good uses in the field of medicine-based cancer-related medical care. To guide cancer people who work to find information to select the most appropriate RNAseq way of doing things for their related to the body function of living things questions, we will discuss each of these technologies, technical features, and medicine-based uses in cancer [2]. We will help cancer people who work to find information to understand the key differences of these RNAseq technologies and their best uses. The field of study of the tiny chemical instructions within cells and proteomics research has gone through neoteric ups and downs as a result of next-generation putting in correct order (NGS), a way of thinking-shifting technology that provides higher quality of being very close to the truth or true number, larger throughput and more applications than the microarray raised, flat supporting surface [3]. The use of lots of machines all working at the same time putting in correct order has more and more been the object of study over the last few years. The NGS technologies are used for more than two, but not a lot of applications, including whole total set of tiny chemical assembly instructions of a living thing putting in correct order, de novo group of people putting in correct order, resequencing, and list of school grades putting in correct order at the DNA or RNA level. For instance, de novo group of people putting in correct order total set of tiny chemical assembly instructions of a living thing of a particular living thing without a reference total set of tiny chemical assembly instructions of a living thing sequence, which may lead to a better understanding at the related to the study of tiny chemical instructions within cells level and may help in describing a possible future event tiny chemical assembly instructions inside of living things, protein coding areas, and pathways. Also, NGS technologies have been widely used to carefully study small RNAs, including identification of differentially expressed micro RNAs (miRNAs), statement about a possible future event of new miRNAs, and note of other small non-coding RNAs. Many classes of small RNAs (sRNAs), such as miRNA, and small interfering RNA (siRNA), have been reported to play an important role in after-translational regulation of genetic instruction inside of a living body's expression. Next generation small RNA putting in correct order (sRNA-seq) technology has now become a gold standard for both sRNA discovery and sRNA information-gathering, because it can

sequence the whole thing that makes something else complete or perfect of sRNAs in a sample with high sensitivity [4].

2. Conclusion

NGS technologies provide opportunities for understanding group of similar living things and complex sicknesses. Although different companies put into use different raised, flat supporting surfaces with having a unique quality features and advantages, depend on the number of reads and the read length to make sure of device made up of smaller parts quality and quality of being very close to the truth or true number. In order to make the best use of NGS data, the design of the best design available now bioinformatics pipelines to extract meaningful related to the body function of living things understandings of deep things will be a significant topic in the following years. In the end, NGS could tell about human related to the study of tiny chemical instructions within cells information and help to explain the function of the total set of tiny chemical assembly instructions of a living thing, which may provide medically helpful diets for decorated with a personal touch medicine in the future.

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