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Bioinformatics and Computational Tools for Next-Generation Sequencing Analysis in Clinical Genetics

Abstract:

Clinical genetics plays a critical role in the healthcare system by providing conclusive diagnoses for a wide range of rare syndromes. It can also help patients choose the best care/treatment choices by influencing genetics prevention, disease prognosis, and helping in the selection of the best options for care/treatment. Next-generation sequencing (NGS) has transformed clinical genetics,allowing researchers to examine hundreds of genes at once, As compared to traditional Sanger sequencing, this method achieves unparalleled speed and cost savings. Despite the increasing literature on NGS in clinical settings, the goal of this review is to bridge the gap between (bio)informaticians, molecular geneticists, and clinicians by providing a broad overview of NGS technology and workflow. First, we'll take a look at the existing NGS platforms ,The NGS analytical bioinformatic pipelines are then dissected, with a focus on the Algorithms typically used to generate and analyse sequence variants. Finally, the main challenges around NGS bioinformatics be put into context for future improvements Even with the enormous advances in NGS technology and bioinformatics, more bioinformatic Algorithm improvements are needed to deal with complex and genetically diverse diseases.

Introduction:

Next-generation sequencing (NGS) is a technology for determining the sequence of DNA or RNA to study genetic variation associated with diseases or other biological phenomena. Introduced for commercial use in 2005, this method was initially called massively-parallel sequencing, because it enabled the sequencing of many DNA strands at the same time, instead of one at a time as with traditional Sanger sequencing by capillary electrophoresis (CE).

Each of these technologies has utility in todays genetic analysis environment. Sanger sequencing is best for analyzing small numbers of gene targets and samples and can be accomplished in a single day. It is also considered the gold-standard sequencing technology, so NGS results are often verified using Sanger sequencing. NGS enables the interrogation of hundreds to thousands of genes at one time in multiple samples, as well as discovery and analysis of different types of genomic features in a single sequencing run, from single nucleotide variants (SNVs), to copy number and structural variants, and even RNA fusions. NGS provides the ideal throughput per run, and studies can be performed quickly and cost-effectively. Additional advantages of NGS include lower sample input requirements, higher accuracy, and ability to detect variants at lower allele frequencies than with Sanger sequencing.

The speed, throughput, and accuracy of NGS has revolutionized genetic analysis and enabled new applications in genomic and clinical research, reproductive health, and environmental, agricultural, and forensic science **,so we will focus on :**

1- NGS Library

2-NGS Platforms : Second-Generation Sequencing Platforms, Third-Generation Sequencers.

3-NGS Bioinformatics : Primary Analysis ,Quality Control(Read Filtering and Trimming),

Secoundary Analysis (Sequence Alignment, Post-Alignment Processing ,Variant Calling),

Tertiary Analysis(Variant Annotation, Variant Filtering, Prioritization and Visualization)

4- NGS Pitfalls