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Enabling rapid and efficient selection of Next generation sequencing algorithms to align sequences to predict differentially expressed genes in cancer

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Abstract

Next-generation sequencing (NGS) has revolutionized technology in genomics; enabling entire genome or sampling of transcriptomes to be sequenced more efficiently than ever before. There are several applications on sequencing include molecular diagnostics to identify the disease condition based on genetic variants and also used in agrigenomics for crop improvement. Although, there are several limitations to use NGS in genomic research include the development of bioinformatics pipelines and algorithms to retrieve, analyze and store large genomic data. Analysis of genomic data typically require bioinformatics pipelines of substantial levels to analyze large data is typically require computing power is most cost effective. While NGS technologies have significant implications on clinical and agricultural data for optimization and availability of appropriate methodologies and tools to analyze, visualize and interpret NGS data are still in their infancy. With an objective of this study was used ovarian cancer sequencing data to analyze clinical variant to predict clinical biomarkers. Here, with focus on implementation of NGS data analysis algorithms, advantages and challenges of implementing NGS.