# **NEXT GENERATION SEQUENCING: A SURVEY**

MinolMrinaline Braggs<sup>1</sup>, Shiny D'Souza<sup>2</sup> & Hemalatha N<sup>3</sup>

Abstract-Next generation sequencing is one of the popular topics which is booming around. NGS is a vast topic which describes the sequencing of DNA technology and revolutionises the genomic research. In this modern period, NGS plays a very prominent role in the field of research. This paper gives a brief description on the applications on next generation sequencing and methods of sequencing a DNA.

Keywords-Next generation sequence, DNA, genes, genomes.

#### 1. INTRODUCTION

The science around us is growing fast and NGS is the vast topic in researches regarding living organisms. In the past, the great efforts made to sequence genes were time consuming and meticulous. The time began to change around 1970's, soon after Fredrick Sanger developed efficient techniques to sequence DNA. He was awarded Noble prize for this work in chemistry in 1980. The two papers published by Fredrick Sanger and Alan Coulson on the rapid discovery of DNA sequence paved a way to transform biology by providing a tool to convert complete genes and then entire genomes. This method was further improved by Maxam and Gilbert by another paper presented in the same year.

Next generation sequencing is massively parallel or a deep sequencing that describes a DNA sequencing technology which has revolutionized genomic research. Sequence is determined by parallel sequencing of number of small fragments of DNA. The initial which helps a template for Next generation sequencing is double stranded DNA (Deoxyribonucleic Acid), which can be obtained from different cells. The double stranded nuclear DNA terms as starting material that gives an outline for NGS.

Most of medical, biological and health cares use DNA sequencing as it has large range of applications in the present situation and also it is more accurate, easier, and faster and find more variant with less money. DNA sequencing has multiple applications obtained from different cells. In this modern era Next generation sequencing plays an important role in the field of research. In early days gene sequencing was much difficult, time consuming and more number of labourers were required. But now it is so developed that one can handle anything by his own intelligence.

NGS helps in alteration of genome for analysis of genetics which consist of complicated traits. NGS creates the path to the entire spectrum of genomic alterations for the genetic study of composite traits. In this fast growing NGS technologies, the challenge is to tackle with the analysis of vast production of sequencing database through advanced bioinformatics tools. This paper gives a description on next generation sequencing taken from eight research papers.

### 2. REVIEW OF LITERATURE

Stephan in his paper says that impressive scientific achievements and novel biological applications are enabled by a new generation of non-Sanger based sequencing technologies which has delivered its promise of sequencing DNA at unprecedented speed [1]. But however, for 30 years next generation sequencing overcame the inertia of the field that relied on Sanger sequencing before stepping into limelight. He says at a time when many believed the age of post genomics had arrived, NGS has demonstrated its fabulous potential for the one's working in the life sciences, by the publications of more than 100 research papers in few years. Next generation sequencing publications originated from sites other than the large genome centres. He says that NGS has brought the field of genomics into the laboratories of single investigators. Next-generation sequencing has applications that are immediately relevant to the medical field. Specific cancer alleles can be detected in tissues through ultra-deep sequencing of genomic DNA in cancer genetics. Next-generation sequencing of genomic DNA in cancer genetics.

With fast development and wide applications of next-generation sequencing(NGS)technologies, genomic sequence information is within reach to aid the achievement of goals to decode life mysteries, make better crops, detect pathogens, and improve life qualities says the paper by Liu et al.,[2]. Technologies of these systems are reviewed, and first-hand data from extensive experience, advantages, and applications of NGS are summarized. NGS systems are typically represented by SOLID/Ion Torrent PGM from Life Sciences, Genome Analyzer/HiSeq 2000/MiSeq from Illumina, and GS FLX Titanium/GS Junior from Roche. The next generation sequencing has sequences in the entire transcriptomes expressed under different conditions which are explained by Samuel et al., [3]. Hence the revolution of genomic studies is now successfully carried out due to the many powerful applications of next generation sequencing. In their paper they have provided a description of these exciting new

<sup>&</sup>lt;sup>1</sup> Department of IT and Bioinformatics, Aimit, Mangalore, Karnataka, India

<sup>&</sup>lt;sup>2</sup> Department of IT and Bioinformatics, Aimit, Mangalore, Karnataka, India

<sup>&</sup>lt;sup>3</sup> Department of IT and Bioinformatics, Aimit, Mangalore, Karnataka, India

approaches to understand the functions and properties of genomes. Next generation sequencing evolved in widely ranged applications very fast. ChIP-seq and RNA-seq are the sequence census methods that are becoming highly powerful and qualitative approach to analyse the structures and functions of both transcriptomes and genomes at resolution in maximum. Hence a challenge for informatics is created by the huge amount of data generated by the next generation sequencing. They tell the readers that in future the full potential of next generation sequencing is established by the routine data analysis methods with decrease in sequencing cost and increase in lengths and numbers of sequence reads.

Attia and Saeed in their paper said that NGS can be used to sequence every nucleotide in an individual's DNA, or limited to smaller portions of the genome such as the exome or a preselected subset of gene [4]. And also they explained that many second generation HT next generation sequence platforms are continuously on the horizon. They assumed that in future, HT-NGS technologies with ultra-deep sequencing of genomic DNA will be very helpful for medical purpose like analysis of the disease etiology and development in new drugs. The main challenge is to develop a production of sequence database to advance bioinformatics tools. They also concluded that the researches will be of great value for genetic improvement of animal health and productivity.

The new technologies such as massively parallel DNA sequencing, according to Jay Shendure and Hanlee Ji, are rapidly evolving [5]. Next generation DNA sequencing has the potential to dramatically accelerate biological and bio-medical research, by enabling the comprehensive analysis of genomes, transcriptomes and interactomes to become inexpensive, routine and widespread, rather than requiring significant production-scale efforts. They say that over the past years, next generation DNA sequencing technologies have catapulted to prominence, with adoption of several platforms that individually implement different flavours of massively parallel sequencing. Their paper explains few applications regarding next generation sequencing such as mapping of structural rearrangements, which may include copy number variation, balanced trans-location breakpoints and chromosomal inversions.

Ruffaloet al., in their paperwith a view to comparing existing short read alignment software, they developed a simulation and evaluation suite, Seal, which simulates NGS runs for different configurations of various factors, including sequencing error and coverage [6]. They also developed criteria to compare the performances of software with disparate output structure.

Alan D Radford et al., in their paper of next generation sequencing and their application in the field of virology have given the limitations to the technologies which are costly to be applied for genome projects [7]. As such, genomic projects where largely restricted to high profile organisms, model organisms and human pathogen. New methods of sequencing have been developed with these limitations in mind that have revolutionized our ability to sequence. They say that within a few years there is a possibility of generating many millions of bases of sequence which has opened new opportunities which has made the large scale sequencing projects available to all in any of our fields in biology. In their review, they have given an overview of these methods and looked on their increasing application in virology, especially in virus discovery, genome sequencing and transcriptomes. Next-generation sequencing technologies have revolutionized says Shokralla et al., in his paper of research on NGS [8]. One important part which involves target selection for next generation sequence. The fast era of development and improvements in next generation sequencing technologies may reflect on broader and more applications in DNA research. The analysis of environmental DNA is due to the use of specific gene markers such as species-specific DNA barcodes has been a key application of next generation sequencing technologies in ecological research. Mass sequencing of environmental samples has been at the fore front of ecology and biodiversity research. There are much more opportunities to work on advance NGS which would be benefited in future.

### 3. CONCLUSION

NGS technology is growing faster around the world. The advanced bioinformatics tools support in sequencing the DNA of coming generations. Many authors have worked on NGS and its applications which are majorly helpful in the field of medical, health and biological areas. In the future, we aim to work on the advanced NGS technology and many more applications.

## 4. REFERENCES

- [1] S.C. Schuster, Next-generation sequencing transforms today's biology. Nature methods, vol. 5 no. 1, p.16, 2008.
- [2] L. Liu, Y. Li, S. Li, N. Hu, Y. He, R. Pong, D. Lin, L. Lu, and M. Law, Comparison of next-generation sequencing systems. Biomed Research International, 2012
- [3] S. Marguerat, B. T. Wilhelm, and J. Bähler, Next-generation sequencing: applications beyond genomes. 2008.
- [4] M. L. Metzker, Sequencing technologies--the next generation. Nature reviews. Genetics, vol. 11 no.1, p.31, 2010.
- [5] J. Shendure, and H. Ji, Next-generation DNA sequencing. Nature biotechnology, vol. 26 no.10, p.1135, 2008.
- [6] M. Ruffalo, T. LaFramboise, and M. Koyutürk, Comparative analysis of algorithms for next-generation sequencing read alignment. Bioinformatics, vol. 27 no.20, pp.2790-2796. 2011.
- [7] A.D. Radford, D. Chapman, L. Dixon, J. Chantrey, A. Darby, and N. Hall, Application of next-generation sequencing technologies in virology. Journal of General Virology, vol 93 no 9, pp.1853-1868, 2012.
- [8] S. Shokralla, J. L. Spall, J. L.Gibson, and M. Hajibabaei, Next-generation sequencing technologies for environmental DNA research. Molecular ecology, vol. 21 no.8, pp.1794-1805. 2012.