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Decoding the human genome

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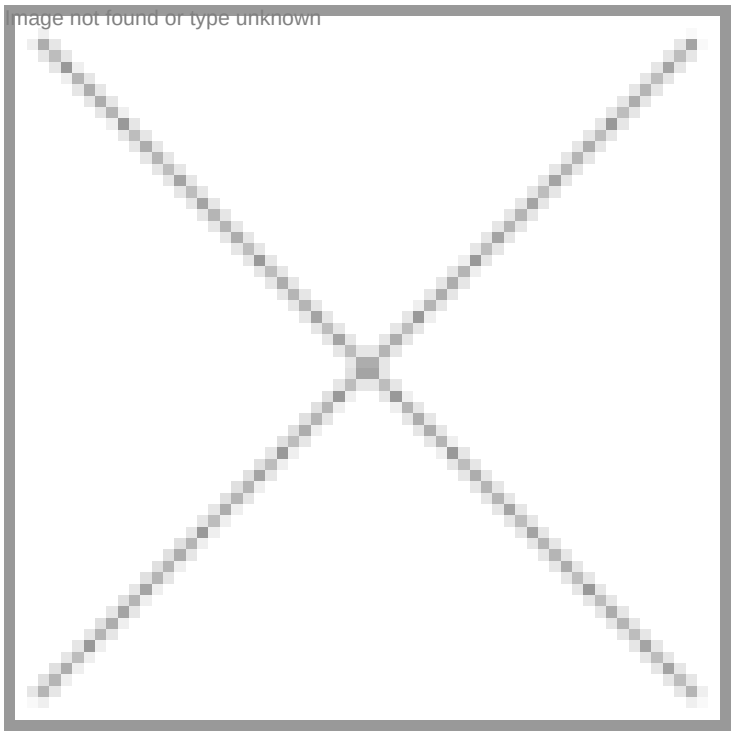

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Ngs

Next generation sequencing has created amazing opportunities in the biological sciences as sequence generation is no longer a bottleneck for biologists

Genesis

The original sequencing methodology, known as Sanger chemistry, uses specifically labeled nucleotides to read through a DNA template during DNA synthesis. Shotgun sequencing was developed during Human Genome Project, in which genomic DNA is enzymatically or mechanically broken down into smaller fragments and cloned into sequencing vectors in which cloned DNA fragments can be sequenced individually. The complete sequence of a long DNA fragment can be eventually generated by these methods by alignment and reassembling of sequence fragments based on partial sequence overlaps.

The Technology

New NGS technologies read the DNA templates randomly along the entire genome. This is accomplished by breaking the entire genome into small pieces, then ligating those small pieces of DNA to designated adapters for random read during DNA synthesis (sequencing-by-synthesis). Therefore, NGS technology is often called massively parallel sequencing.

The Impact

Questions that biologists have sought to answer for decades but were unable to address because of lack of appropriate technologies can now be addressed with NGS. It has become easier and quicker to map genes for diseases that are caused due to alterations in one or a few genes.

Next Generation Sequencing (NGS), also called second generation sequencing, is a term that has come to mean post-Sanger sequencing methods. It has become a shorthand for large amounts of data being generated at incredibly low costs. The initial sequencing of the human genome took around 13 years, an international consortium of researchers and close to 13,500 crore ($2.7 billion) to complete. Since then, sequencing technology has so evolved that a consumer can have his or her entire genome sequenced 00).

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In India, not many companies are working in the field. However, there is immense scope. Professor Partha P Majumder, director of National Institute of Biomedical Genomics and TCG-ISI Center for Population Genomics, Kolkata, and head of the Human Genetics Unit, ISI, Kolkata, says, â€œI think ar high. Many organizations have actually taken the zations getting involved in NGS-related R&D. The) is small in India, therefore, there is very little scope of dialogue and argumentation on NGS.â€?

India can jump into leap, but I would l community of scienti

Although NGS has immense potential, there seems to be several concerns and challenges associated with it, including lack of appropriate statistical methods and analytical pipelines to draw valid and generalizable inferences from the NGS data; lack of storage; lack of robust methodologies for data analyses and high error rates, particularly in regions of sequence complexity. These concerns have paved the way for the emergence of a new generation of sequencing technologies.

Working on NGS

Roche is active in this field with its GS-FLX 454 Genome Sequencer, which was originally called 454. Illumina is also at the forefront with its Genome Analyzer, which was originally with Solexa Technology. Dover has created the Polonator G.007 in collaboration with the Church Laboratory of Harvard Medical School. Furthermore, Helicos BioSciences and Applied Biosystems are also contributing to NGS with their HeliScope platform and SOLiD sequence alignment, respectively.

The companies use a single or a combination of technologies, such as microfluidic DNA sequencing, polony sequencing, millikan sequencing by nucleotide, single-molecule DNA sequencing with engineered nanopores.

Saptarshi Chaudhuri in Bangalore