Editorial

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Next-Generation Sequencing and its Applications

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Editorial

NGS is new innovation for DNA and RNA sequencing and variation/ transformation recognition. This innovation consolidates the benefits of interesting sequencing sciences, distinctive sequencing networks, and bioinformatics technology. Such a blend permits a massive parallel sequencing of different lengths of DNA or RNA arrangements or even whole genome within a moderately short period of timeframe. It is a progressive sequencing innovation after Sanger sequencing. NGS includes a several significant steps in sequencing. For instance, DNA NGS includes DNA fragmentation, library preparation, massive parallel sequencing, bioinformatics analysis, and variation/ mutation annotation and interpretation.

DNA fragmentation

DNA fragmentation is utilized to break the focused on DNA into many short segments, generally 100–300 bp in length. Various strategies can be utilized to accomplish this. DNA can be divided utilizing mechanical techniques, enzymatic digestion, or different strategies. For instance, sonication can be utilized to break DNA into short segments. The short segments pertinent to the targeted DNA sequences are pulled out utilizing complementary probes of various designs. This strategy is normally alluded to as hybridization capture assay. Another strategy includes polymerase chain response (PCR) amplification. In this strategy, numerous sets of preliminaries are utilized to intensify the focused on DNA sections utilizing PCR. The PCR items fill in as short portions of targeted DNA. This technique is typically called amplicon assay. The DNA sections are then utilized for library preparation.

Library arrangement

Library preparation is a cycle by which DNA segments are changed so that every DNA sample can have an example explicit list like example sample identification which assists with distinguishing the patient from whom DNA sequencing was performed. This cycle additionally permits the sequencing connectors to be added to the DNA portions. Such change permits the sequencing preliminaries to tie to all the DNA fragments and empowers massive parallel sequencing later.

Sequencing

Massive parallel sequencing is performed utilizing a NGS sequencer. The library is transferred onto a sequencing network in a specific sequencer. Various sequencers have diverse sequencing frameworks. For instance, Illumina NGS sequencer utilizes stream cells and Ion Torrent NGS sequencer utilizes sequencing chips. Nonetheless, its objective is something similar, which is to permit massive parallel sequencing of all the DNA sections simultaneously. The arrangement data produced from such massive parallel sequencing is broke down utilizing bioinformatics programming.

Bioinformatics analysis and data interpretation: Bioinformatics analysis is a cycle including base calling, read arrangement, variation recognizable proof, and variation annotation. During this cycle, the arrangement data is contrasted with a human genome reference succession to distinguish whether there are any variations/transformations in the focused on groupings. All data from each sequenced fragment is sorted out to create last sequencing results for the full length of the focused on DNA. The final sequencing results are sent back to the client for interpretation. The annotation and interpretation processes are set to distinguish every variation and their conceivable natural/ clinical importance.

Clinical utilization of NGS

- Expression analysis
- Chromatin Immuno Precipitation (ChIP)- seq
- Methylation
- *De novo* genome sequencing
- Metagenomics
- Non-intrusive prenatal testing
- Disease gene identification
- Human disease and health
- Single molecule and long read sequencing

