

**Title :**

## **SMRT Sequencing- An Era of more Continuity & Completeness**

**Abstract:**

Single-molecule, real-time sequencing developed by Pacific BioSciences offers longer read lengths than the second-generation sequencing (SGS) technologies, making it well-suited for unsolved problems in genome, transcriptome, and epigenetics research. The highly-contiguous *de novo* **assemblies** using PacBio sequencing can close gaps in current reference assemblies and characterize structural variation (SV) in personal genomes. With longer reads, we can sequence through extended repetitive regions and detect mutations, many of which are associated with diseases. Moreover, PacBio transcriptome sequencing is advantageous for the identification of gene isoforms and facilitates reliable discoveries of novel genes and novel isoforms of annotated genes, due to its ability to sequence full-length transcripts or fragments with significant lengths. Additionally, PacBio's sequencing technique provides information that is useful for the direct detection of base modifications, such as **methylation**. The advent of PacBio sequencing has made available much information that could not be obtained via SGS alone.