

Docket #: S24-053

Computational Pipeline for Accelerated Identification of Disease-causing Variants with Ultra-Rapid Nanopore Genome Sequencing

Rapid whole genome nanopore sequencing and data analysis is a platform developed at Stanford that delivers genomic results quickly. Combining optimized sample preparation, nanopore-based sequencing, and automated analysis, this technology enables fast genetic diagnostics for critically ill patients.

Applications

- Whole Genome Diagnostics

Advantages

- Fast Turnaround Time
- Comprehensive Variant Detection
- High Yield of Disease Associated Variants

Innovators

- Sneha Goenk

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