

Enriched Nanopore Sequencing Using Real-Time Sequence Analysis

The solution is the combination of a Scalable Metagenomics Alignment Research Tool (SMART) with nanopore “Read Until” sequencing to create a point-of-service, real-time selective sequencing platform that can detect and identify pathogens or other DNA/RNA of interest.

What is the Problem?

Real-time selective sequencing, or “Read Until” of individual molecules is made possible by nanopore sequencers, which work by individually reversing the voltage across selected nanopores to reject specific sequences. However, this requires the rapid classification of the first part of the sequencing read to determine whether the molecule should be sequenced or rejected and replaced with a new molecule. Current mapping methods to rapidly identify reads in nanopore sequencing devices require significant computational resources, limiting its generalized use.

What is the Solution?

The solution is the combination of a Scalable Metagenomics Alignment Research Tool (SMART) with nanopore “Read Until” sequencing to create a point-of-service, real-time selective sequencing platform that can detect and identify pathogens or other DNA/RNA of interest. The improved SMART pipeline is the fastest sequence matching tool, enabling sequence identification on the timescale of nanoseconds. Since it can be run on a laptop equipped with a graphics-card, this technology offers the possibility of a real-time point-of-service platform for metagenomic infection identification.

What is the Competitive Advantage?

The competitive advantage of this technology lies in its ability to enable 1-2 log enrichment of non-human sequences through the combination of the enhanced SMART pipeline and nanopore “Read Until” technology. This will significantly speed up pathogen identification, allowing the development of a metagenomics pathogen sequencing platform. This method also enables the use of nanopore sequencing technology in applications such as rapid point-of-service diagnostics for agnostic pathogen detection, class-specific pathogens, and specific sequences.

Patent Information:

Technology ID

BDP 8574

Category

Research Tools
Selection of Available
Technologies
Diagnostic

Authors

Russell Van Gelder

Learn more



References

1. Lee, A.Y., Lee, C.S. & Van Gelder, R.N.(2016) ,
<https://bmcbioinformatics.biomedcentral.com/articles/10.1186/s12859-016-1159-6>,
<https://bmcbioinformatics.biomedcentral.com/>, 17, 292
2. Nakamichi, K., Stacey, A., & Mustafi, D.(2022) ,
<https://www.tandfonline.com/doi/full/10.1080/13816810.2022.2141797>,
<https://www.tandfonline.com/journals/iopg20>, 43, 762-770