Portable Sequencing System for SARS-CoV-2 Isolates

Minh Tran1, Jared Haas1, Lauren Leone1, Shane Mitchell1, Stephanie Guertin2, David Ashford2, Brad Abramson1, Katharine Jennings1; 1Noblis, Inc., Reston, VA; 2Noblis ESI, Chantilly, VA

Introduction

Sequencing technology requires advanced laboratory facilities and specialized training which increases the end-to-end time to reach actionable insights and limits the regions able to participate in biosurveillance. The rapid rate of mutation of RNA viruses, like SARS-CoV-2, challenges the limits of our current sequencing and software technologies in understanding shifts in these viruses. We suggest that a portable, near real-time, whole genome sequence-based, server independent system would provide solutions to this challenge. The aim of this study was to apply a portable sequencing and analysis system to SARS-CoV-2 isolates. The system converts Oxford Nanopore Technologies reads to high-quality, complete, strain-specific genome sequences.

Methods

1. Obtain Samples in Field
2. Load SC-2 Samples on MinION
3. Generate Consensus Sequence
4. Generate Consensus Sequence
5. Filter Reads
6. Basecalling
7. Annotate & Generate Variants
8. QA/QC
9. Data Visualization & Analysis

*Boxes outlined in green represent the bioinformatics pipeline.*

The pipeline is available for Windows, Mac, and Linux with CPU and GPU based basecalling.

Results

A portable sequencing and analysis system, outfitted in a single, rugged protective case, was assembled with the required equipment to extract and sequence samples. A comprehensive dashboard was developed to visualize and interact with SARS-CoV-2 whole genome sequencing data using the sample metadata and sample lineages obtained from the pipeline. The dashboard accurately visualized the trend of SARS-CoV-2 variants over time. The SARS-CoV-2 genome sequences were also submitted to public repositories such as NCBI and GISAID.

Conclusions

Accurately identifying variants of SARS-CoV-2 through field portable applications allows early detection and tracking of variants, which increases preparedness and is especially beneficial in resource-constrained regions. The system can be customized for different sample types, organisms, scientific questions, visualizations, and physical configuration. As a result, the portable sequencing system is extensible to multiple use cases.

References

Acknowledgments

Learn More


Special thanks to Tetracore for generating SARS-CoV-2 sequence data. Funding for this project was provided by the Noblis Sponsored Research program.

Funding for this project was provided by the Noblis Sponsored Research program.