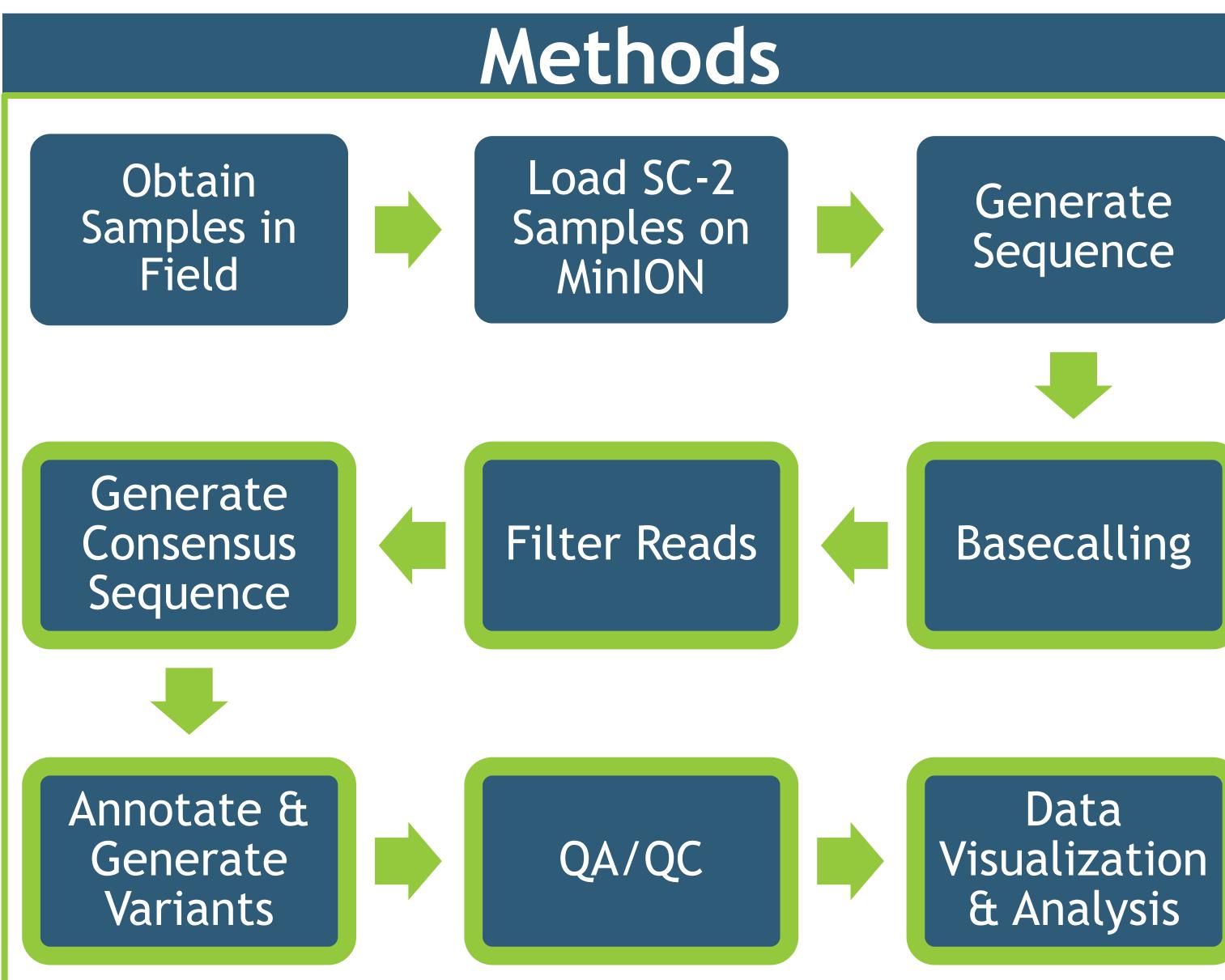
Introduction

Sequencing technology requires advanced laboratory facilities and specialized training which increases the endto-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.



Boxes outlined in green represent the bioinformatics pipeline.

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



NOD 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

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.



Comprehensive Deckhoord for Viewelizing and Interacting with CADC COV 2 Comprise Conversing Date
Comprehensive Dashboard for Visualizing and Interacting with SARS-COV-2 Genomic Sequencing Data.

Filters	Samples (i)	Samples (i) Delta Lineages (i)		GISAID 👔 GenBank 👔	States Represe	nted	Gender 🤅)	Age 🛈	
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Variant Classification	MD-Noblis-S477B0		B.1.1.7		Being Monitored	VA	origino	interre	a origino con	0.5714
Variant of Concern	MD-Noblis-S478B1	.0 MD	B.1.1.7		Being Monitored	WA				0.4594
Variant Being Monitored	MD-Noblis-S486B1	.8 MD	B.1.526	Variant	Being Monitored	СА				0.1812
Others	MD-Noblis-S517B0	2 MD	B.1.1.7	Variant	Being Monitored	PA				0.5714
others	MD-Noblis-S521B0	9 MD	B.1.617.2		of Concern	CA				0.1812
	MD-Noblis-S548B1	.0 MD	AY.25	Variant	of Concern	ТХ				0.1667
	MD-Noblis-S549B1	MD-Noblis-S549B11 MD		AY.25 Variant of Concern		NJ				0.2581
	MD-Noblis-S550B1	.2 MD	AY.25	Variant	of Concern	PA		0.8966		

Results

Version: 1.3 | Last Updated: 12/27/2021 | Source: Noblis

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.

Portability

Availability

Biosurveillance Participation

Learn More

Noblis Portable Sequencing:



Noblis Bioportal:



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