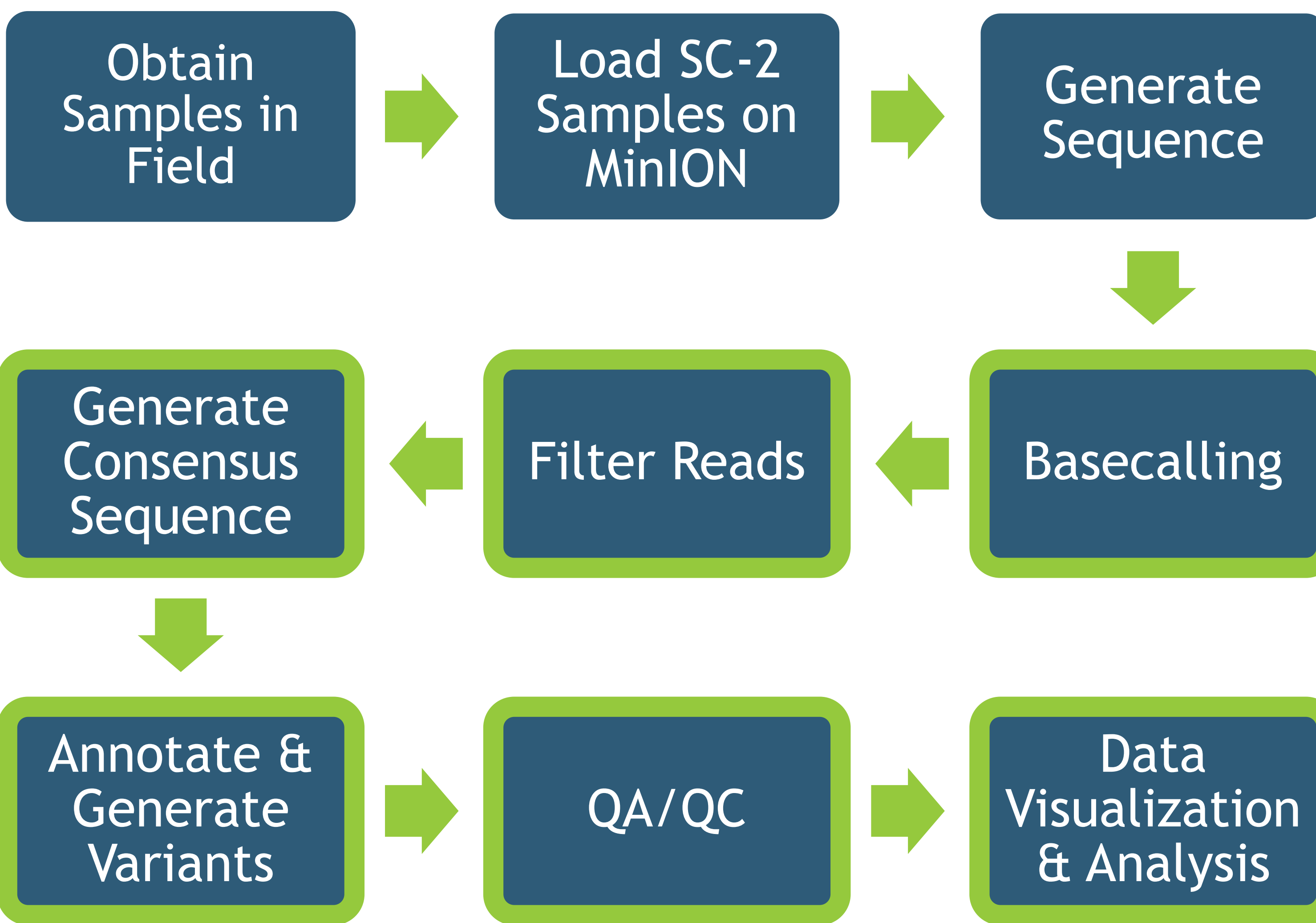


Introduction

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



Boxes outlined in green represent the bioinformatics pipeline.
The pipeline is available for Windows, Mac, and Linux with CPU and GPU based basecalling.

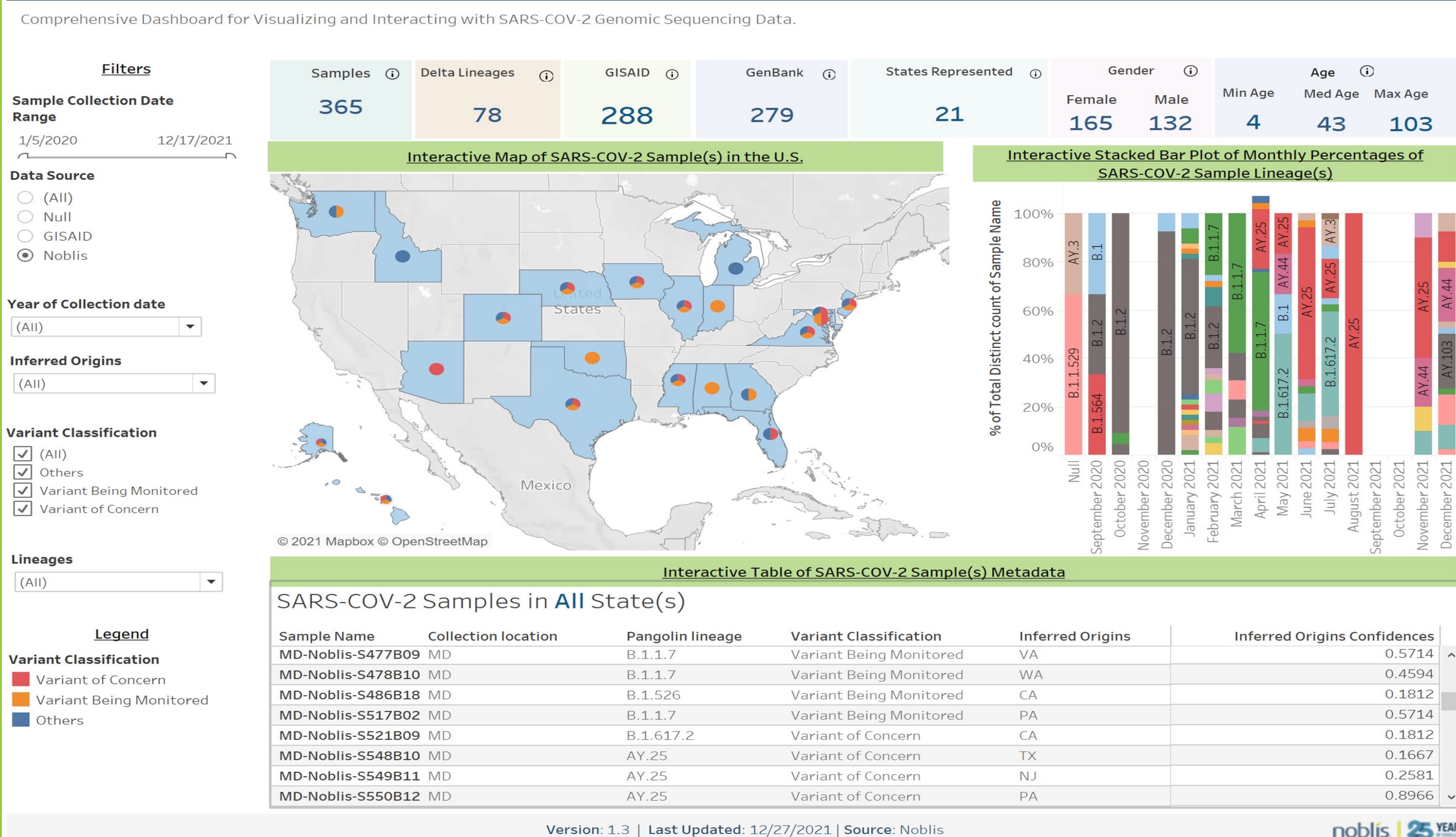


Results

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.

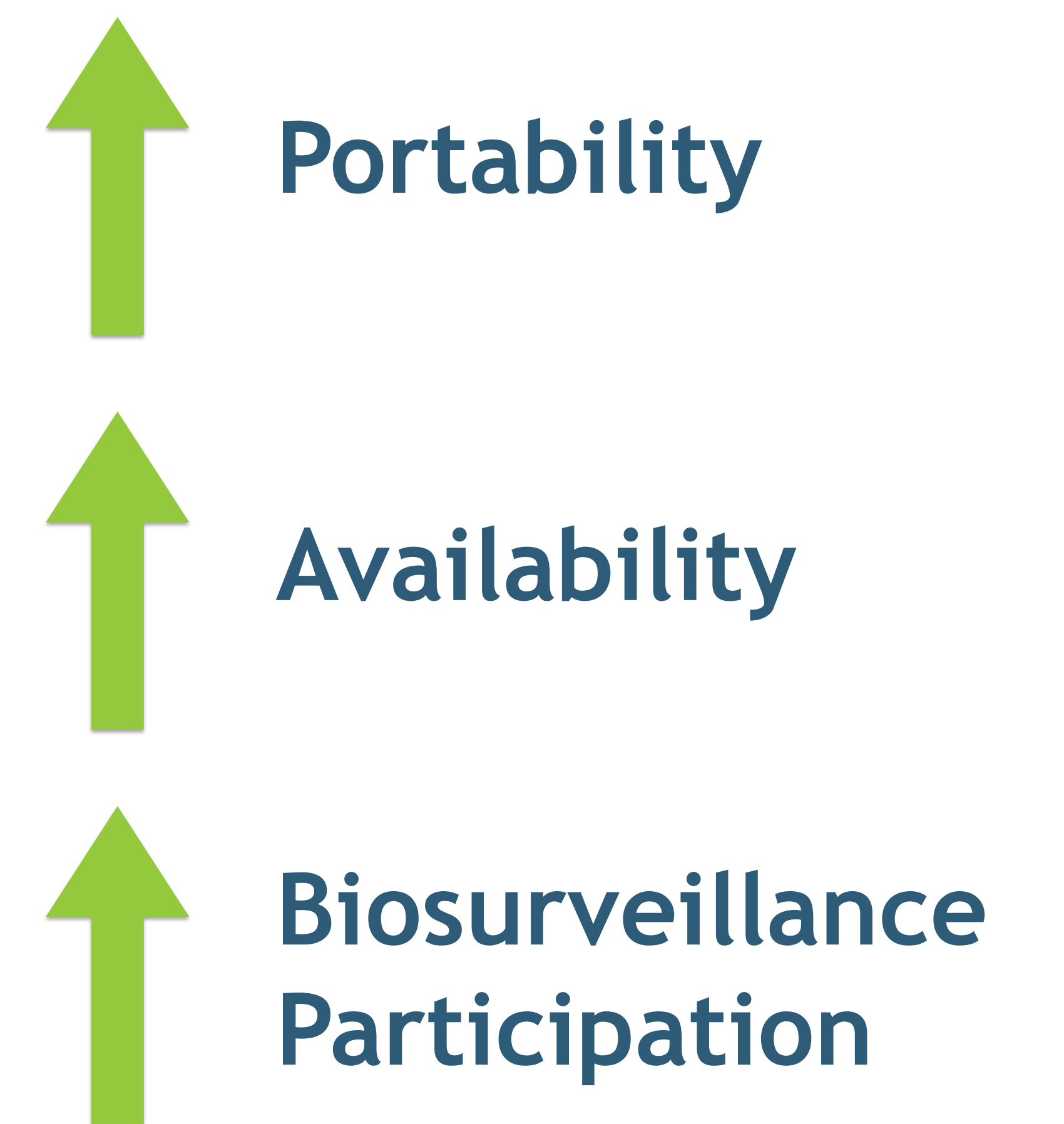


SARS-CoV-2 Genomic Surveillance Dashboard

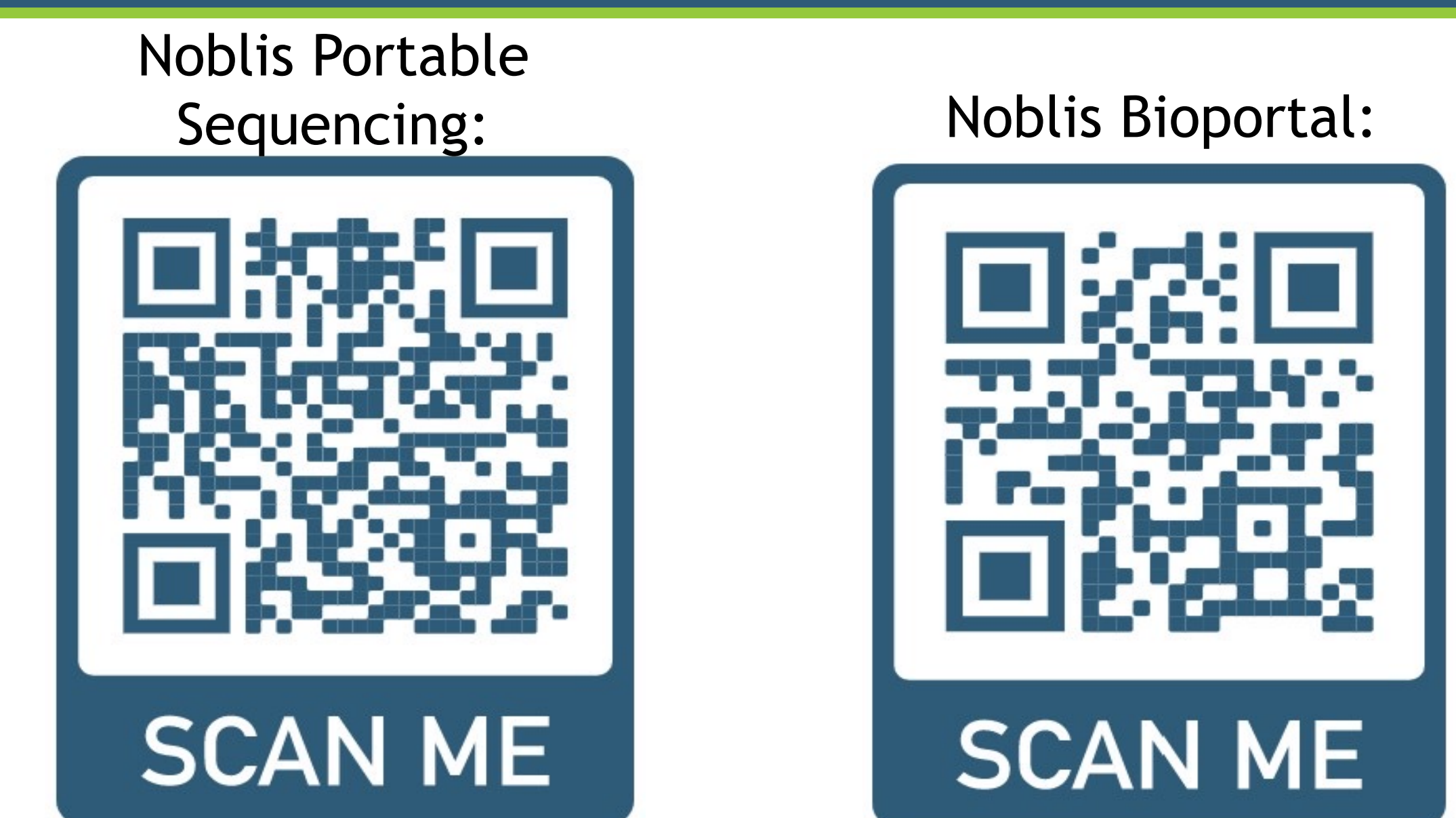


Conclusions

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.



Learn More



References

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