

End-to-End Field Portable Sampling and Genetic Sequencing

Fast, onboard, real-time analysis for biosurveillance applications

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Introduction

Noblis has developed a field-portable DNA sequencing system producing rapid and actionable genomics insights for national defense, homeland security and public health applications. The field-portable system reduces the reliance on facilities-based sample processing and the need for a full-scale, high-performance computing infrastructure, shortening the turnaround time from sample collection to an actionable insight in less than 3.5 hours.

Unique Features

- Deploys pre-computed databases of interest on the laptop to accelerate field classification of samples
- Enables genomic analysis without an internet connection, including metagenomic analysis
- Supports an unlimited number of reference genomes, e.g. antimicrobial resistance, food organisms, high consequence pathogens databases
- Updated and customized quickly

Noblis pre-computed database

A crucial component of the field-portable system is the database of reference genomes used to classify unknown sequences. This capability directly decreases the computational requirements and turnaround time from sampling to results; enabling a rapid and standalone classification of samples that are collected, processed, and sequenced in the field. We significantly reduce the reference database size by using Noblis' BioVelocity® algorithm. As a multiple reference alignment tool, BioVelocity® detects and uniquely identifies small regions (i.e., signatures) specific to an organism at the species level, while ensuring the signatures remain conserved across all the sequences of that species. By only indexing the reference genome signatures, we reduce the database size by 95 percent.

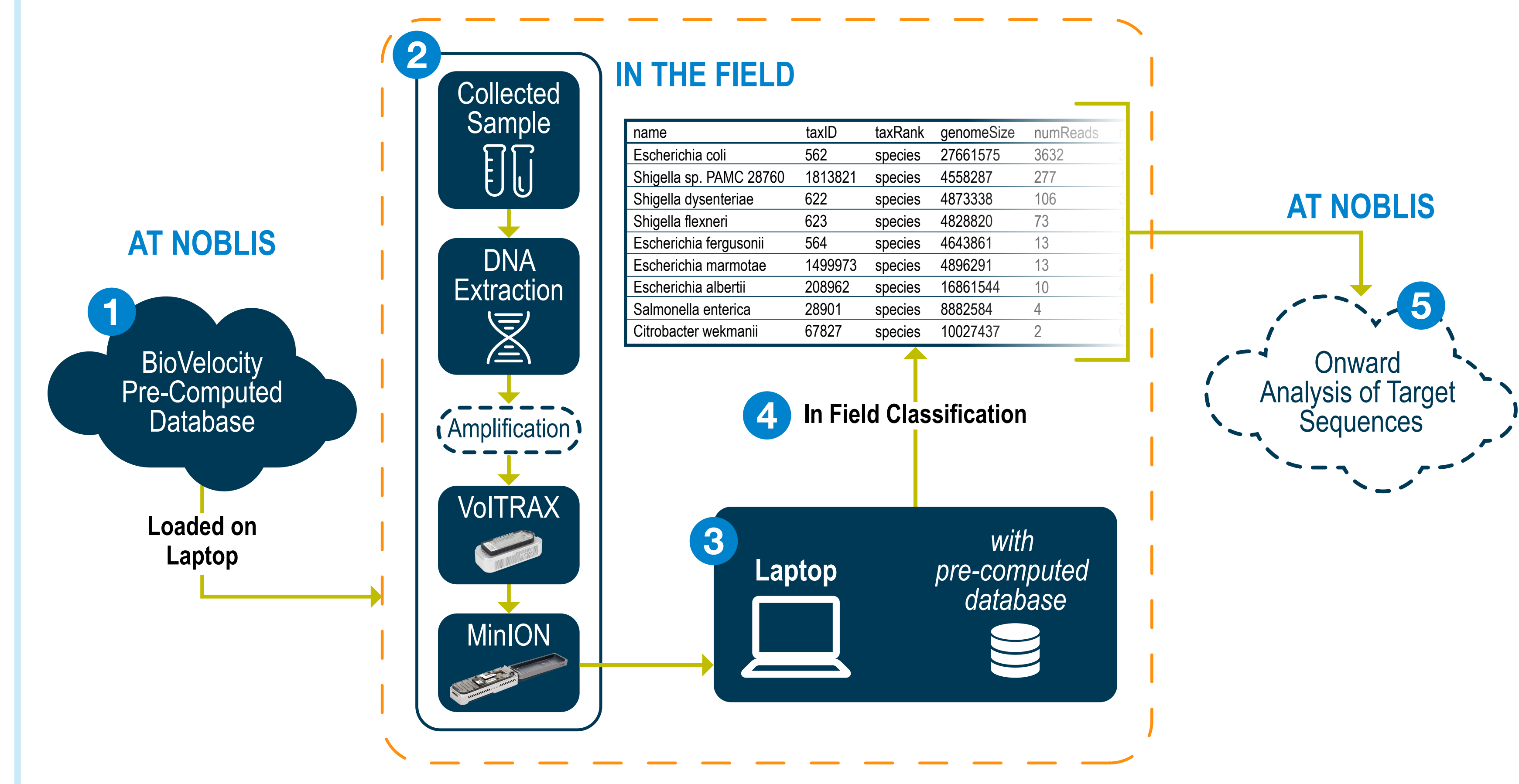


Results & Conclusion

Classifying long reads from the field-portable sequencers against a reference database of small unique signatures of target organisms enables us to identify unknown organism(s) in an unknown sample rapidly and with high confidence. Noblis successfully demonstrated this capability and created unique signature sequences of *Yersinia pestis*. The size of the reference genome was reduced from 65 MB to 150 KB, which is 0.23 percent of its original size. This pipeline is highly customizable and can be updated quickly when new reference data is available.

We developed an end-to-end field sampling, sequencing and fast onboard bioinformatics system enabling identification of biological agents in samples in less than 3.5 hours. The crucial component of the system is a customized reference database reduced by Noblis' BioVelocity® tool that indexes uniquely identifying signatures of one or more specific organisms. By reducing the reference database size, we significantly decreased the computational requirements and turnaround time for sample identification. After creating the signature sequence database of interest, it is deployed to a commercial off-the-shelf laptop so field analysis can be done immediately, without the need for internet access for analysis. This end-to-end system is directly applicable to biosurveillance use cases across the national defense landscape.

Workflow



Portable Genome Sequencing and Analysis System



Specifications

- Provides a complete end-to-end sample analysis in less than 3.5 hours (versus facilities-based sample analysis that may take 24 hours)
- Allows the user to view DNA sequencing results in real time to monitor quality and progress
- Displays results in a user-friendly table to easily identify samples
- Housed in a compact and ruggedized case that contains all the components for field sampling and sequencing, such as miniaturized sample DNA extraction, amplification and automated library preparation
- Portable kit weighs 50 lbs., with exterior dimensions of 32.58 (l)x 18.4 (w)x 11.02 (h) in

Acknowledgement

Special thanks to Noblis' employees - Chris Barnett, Chief Technology Officer; Katharine Jennings; Jane Tang and Sterling Thomas for their support.