



UltraSEQ: Advanced DNA sequencing threat analysis

Bioinformatic software for accurate, science-informed, flexible analysis of genomic datasets

Overview

While DNA sequencing and data generation is becoming routine and inexpensive, low-quality data sources and ineffective collaboration across scientific disciplines make interpretation of this data is non-standardized and expensive.

What remains is an excess of unmaintained, redundant, and niche tools that lack standardization and explainable output.

UltraSEQ

For users who need simple, high confidence, actionable information from genomic data, UltraSEQ provides a flexible system architecture, high-quality data, and algorithms for organism and function identification.

UltraSEQ uses a robust Sequence of Concern database and a learning Threat Identification algorithm to allow researchers to study new DNA sequences safely and responsibly by:

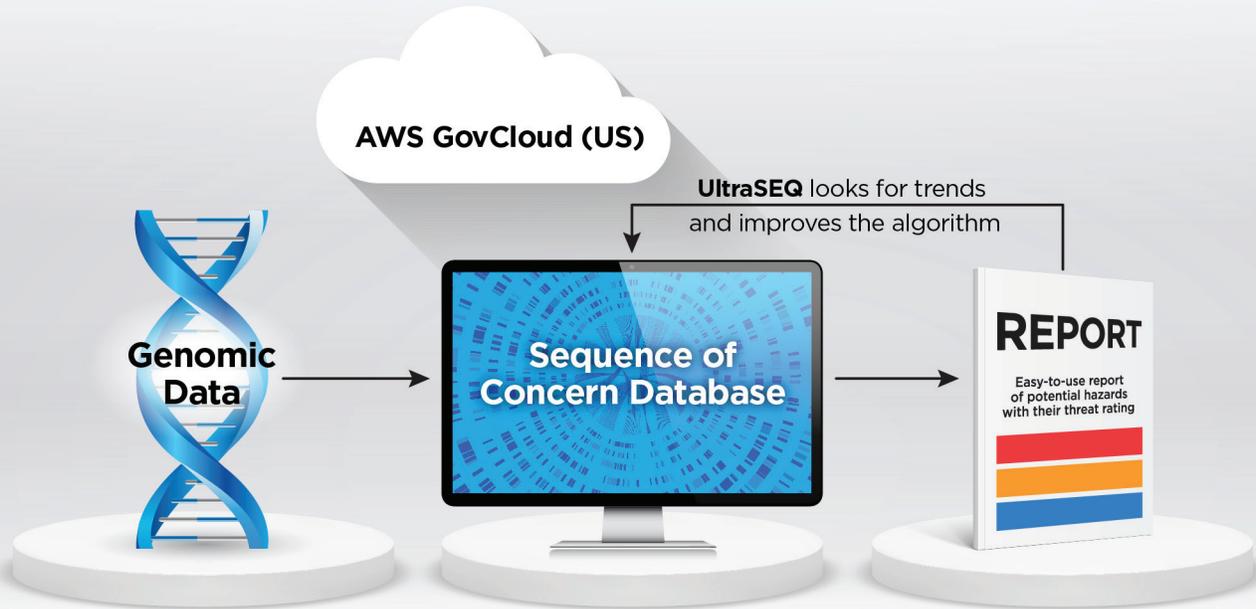
- Reducing the potential for unintended production of DNA sequences of concern
- Quickly and accurately detecting threats
- Protecting against biosecurity risks

The flexible rules engine is rooted in UltraSEQ's proven prediction capabilities backed by trusted biological data curation practices and allows the flexibility to leverage Battelle's pre-installed models (e.g., genetic engineering signature detection) as well as user-defined models for sequence triage.

How it works

The UltraSEQ Threat Identification Algorithm rapidly scans a requested DNA sequence through the proprietary Sequence of Concern Database and looks for matches within the databases. In addition to identifying positive matches, the UltraSEQ algorithm provides information about the types of threats that a gene sequence may present by providing a report that flags and ranks each identified sequence of concern.

Always Improving | UltraSEQ grows with every DNA sequence it processes, discovering trends and building the algorithm.



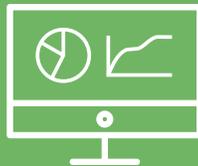
The UltraSEQ Advantage

HIGH FLEXIBILITY



- Individual user-focused and logical sequence triage
- Confidence tuned to level of tolerance
- Adaptable to sequencing hardware

EXPLAINABLE, EFFICIENT RESULTS



- Machine and human-readable science-backed information
- Trusted, interpretable answers
- Novel threat detection

UNRIVALED PERFORMANCE



- Non-reliance on agent blacklists
- Trace and coarse-level taxonomy explorations
- Rapid sample analysis and sequence triage