

TOWARDS TIMELY AND ACCURATE PATHOGEN DETECTION

WHAT

nanoCAS identifies pathogens accurately and in real-time using nanopore sequencing

WHY

Slow and Inaccurate detection costs time and money.

HOW

nanoCAS tracks the nanopore data live, matches it to a custom database, and sends instant alerts when threats are detected, enabling rapid response.

CASE STUDIES

- ➤ Brucella spp.
- > Xylella fastidiosa
- > Sclerotinia sclerotiorum

)			Analysis Information	Analysis Information		
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	nanocas Setu Step 1 of 2		Stop Analysis			
CREATE DATABASE SUMMARY			Coverage Over Time	Breadth of Coverage (%		
			Breadth of Coverage Over Time			
Selection device or choose to run without one.	L.	Nanopore Location Enter the directory where Nanopore data is stored.	80	Image: selection of the se		
hout device		/path/to/minion/dropbox	60 %) (%)			
	File Type		ag 40			
Select the expected input file type. For BAM files, ensure they are aligned to the database sequences.		20				
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Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacterales Enterobacteriaceae	Escherichia	
			Pseudomonadales Pseudomonadaceae	Bacillus	
	Firmicutes	Bacilli	Lactobacillales Streptococcaceae	Streptococcus	Stre
Figure 2 – Sankey	Visualization. This is an exam	ple of Sankey visualization th	at the nanoCAS application provides dep	ending on the database set up. Th	his allows the user to :

it is being sequenced.

USING NANOPORE SEQUENCING TO DETECT PATHOGENS IN REAL-TIME AND ON-SITE

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POWERED BY

- Python 3.8
- React 17.0.2
- Minimap2

FEATURES

- Continuous Real-Time Monitoring — Live data analysis as sequencing run progresses.
- User-Defined Alert **Customization** — Tailor alert thresholds to match the specific requirements.
- Dynamic Data Visualization — Pathogen presence and coverage with graphics

LEARN MORE...

nanoCAS: Detect. Alert. Protect

