



TOWARDS TIMELY AND ACCURATE PATHOGEN DETECTION

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

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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*

WORKFLOW

nanocas Setup Wizard
Step 1 of 2

1 CREATE DATABASE 2 SUMMARY

Device Selection
Select a device or choose to run without one.
Run without device

Nanopore Location
Enter the directory where Nanopore data is stored.
/path/to/minion/dropbox

File Type
Select the expected input file type. For BAM files, ensure they are aligned to the database sequences.
FASTQ

ALERT SEQUENCES

Sequence file /path/to/file.fasta Sequence Identifier ☐ Alert? Breadth Coverage % T

Next Step

Analysis Information			
Analysis ID	MinION Path	Device	Status
05589795-4f06-4ac9-a3e4-3d7f017f820c	Users → tayabsoomro → Documents → Projects → nanocas_experiments → brucella → nanopore_run	Not specified	Running
<div>Stop Analysis Remove Analysis</div>			

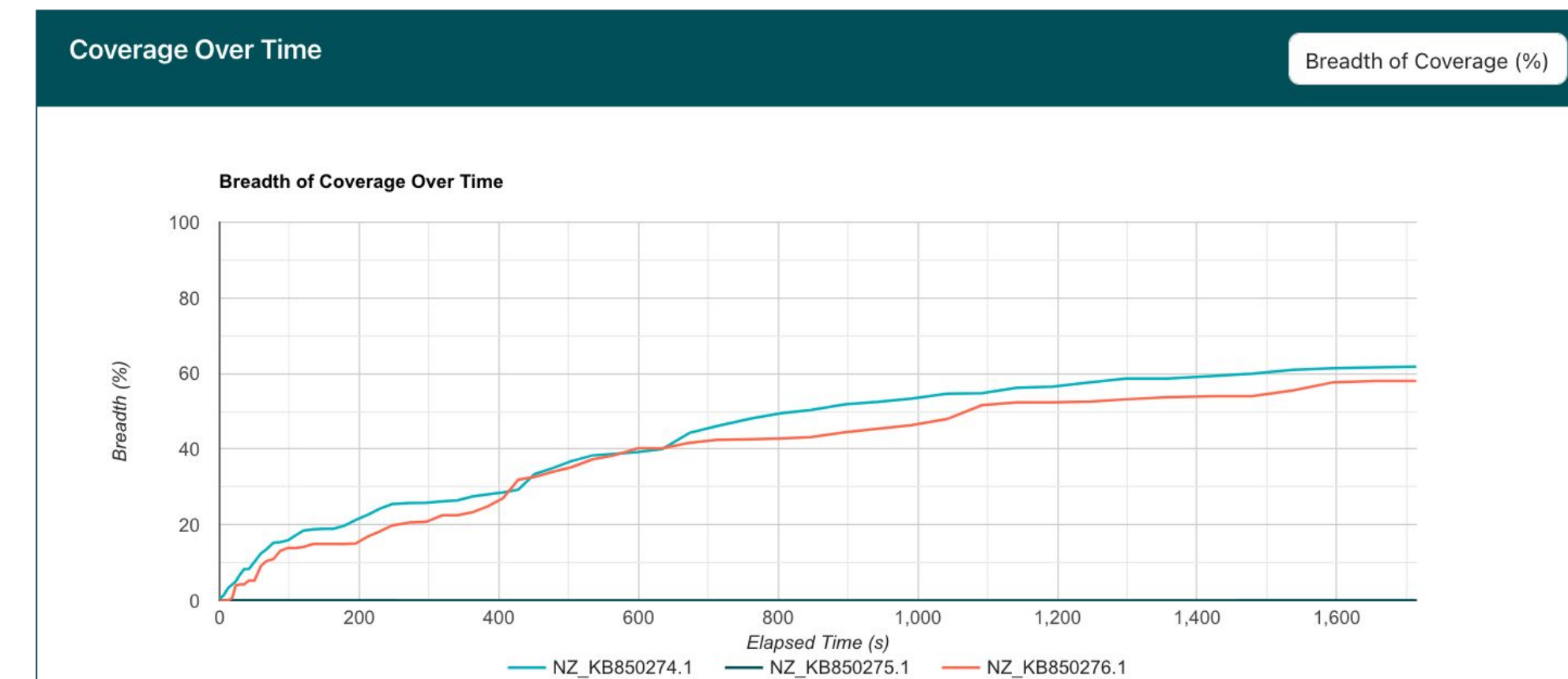


Figure 1 – nanoCAS Workflow. These screenshots showcase the workflow of nanoCAS. The user first specifies sequencing run folder and the alert sequences of interest through FASTA files. The user also specifies the alert threshold (coverage needed to trigger an alert). Then, in the analysis window, the user monitors as the new FASTQ/BAM files are added by the nanopore sequencer to see if any alerts are issued.

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

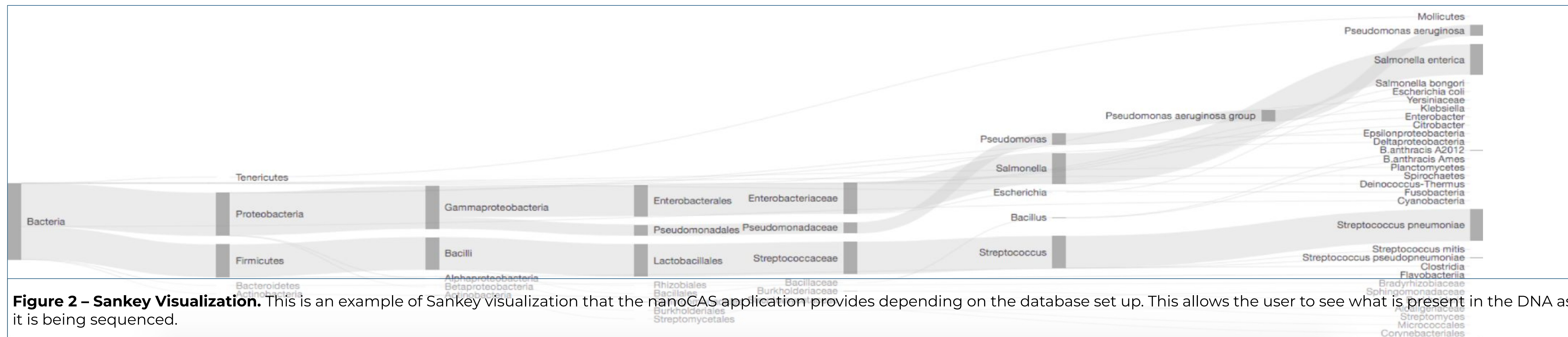


Figure 2 – Sankey Visualization. This is an example of Sankey visualization that the nanoCAS application provides depending on the database set up. This allows the user to see what is present in the DNA as it is being sequenced.