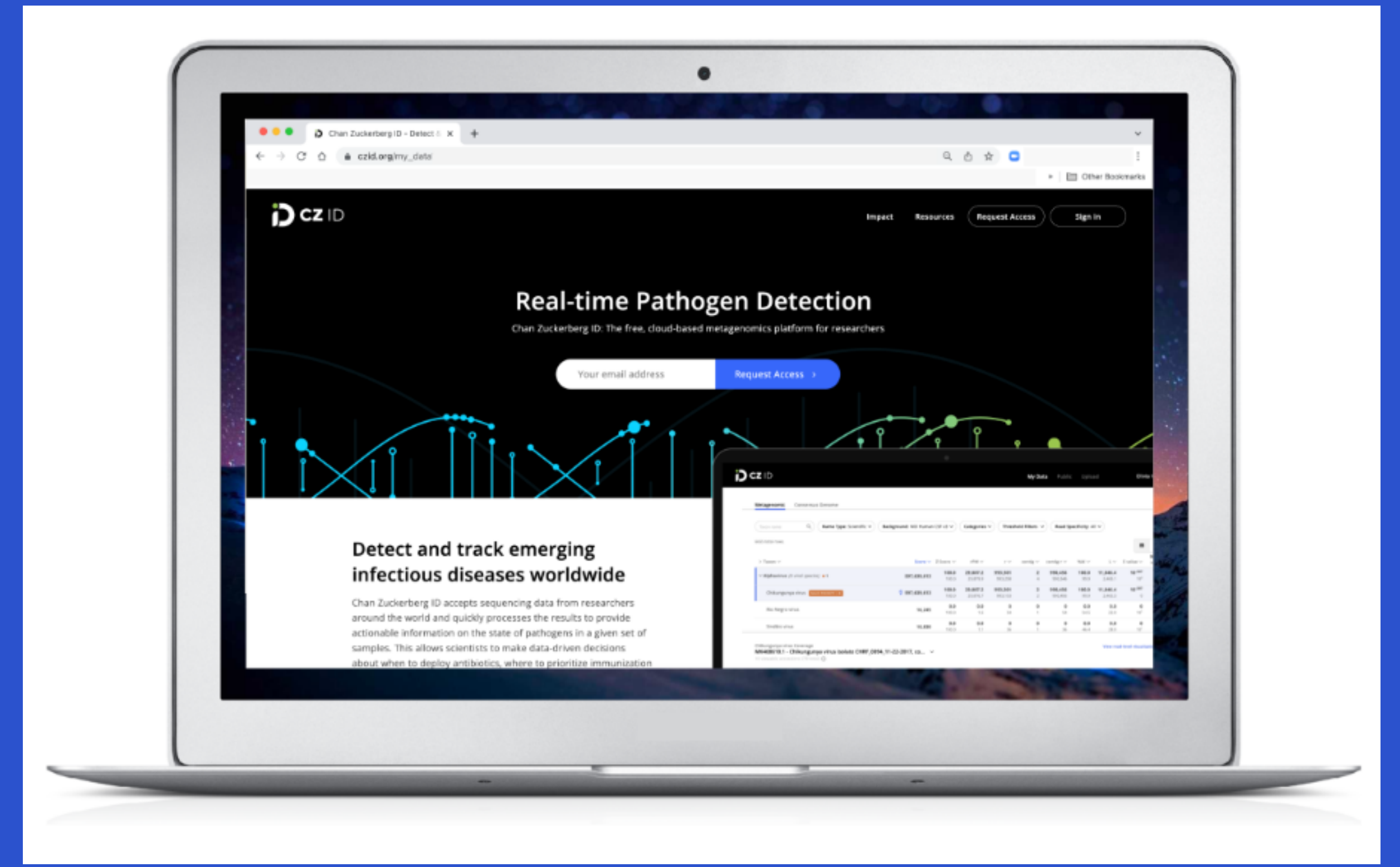




Discover and detect microbes using metagenomics without bioinformatics expertise



CZ ID: a free cloud-based metagenomics platform that enables hypothesis-free microbe detection

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BACKGROUND

Metagenomics has enabled the rapid, unbiased detection of microbes helping to investigate mystery illnesses, emerging biological threats, disease outbreaks, and microbial landscapes. CZ ID is a project of CZ Biohub and the Chan Zuckerberg Initiative. Together, we use technology and training to enable scientists to access high-resolution, actionable insights that accelerate the detection, identification, and tracking of infectious disease.

Investigate the world's biggest health questions



The new **CZ ID Nanopore metagenomics module** lets researchers upload and automatically analyze ONT samples in the cloud from anywhere in the world.



FEATURES

Feature	CZ ID	EDGE	BV-BRC	INSAFLU
Host filter	✓	✓		✓
Assembly	✓	✓		
Species info	✓		✓	✓
Filter report	✓			
BLAST	✓		✓	
Taxon ID nucleotide	✓	✓	✓	✓
Taxon ID protein	✓			
Pathogen tag	✓			
Coverage viz	✓	✓		✓
Alignment viz		✓		✓

Feature comparison among cost-free web platforms that offer fast metagenomic data analysis and management.

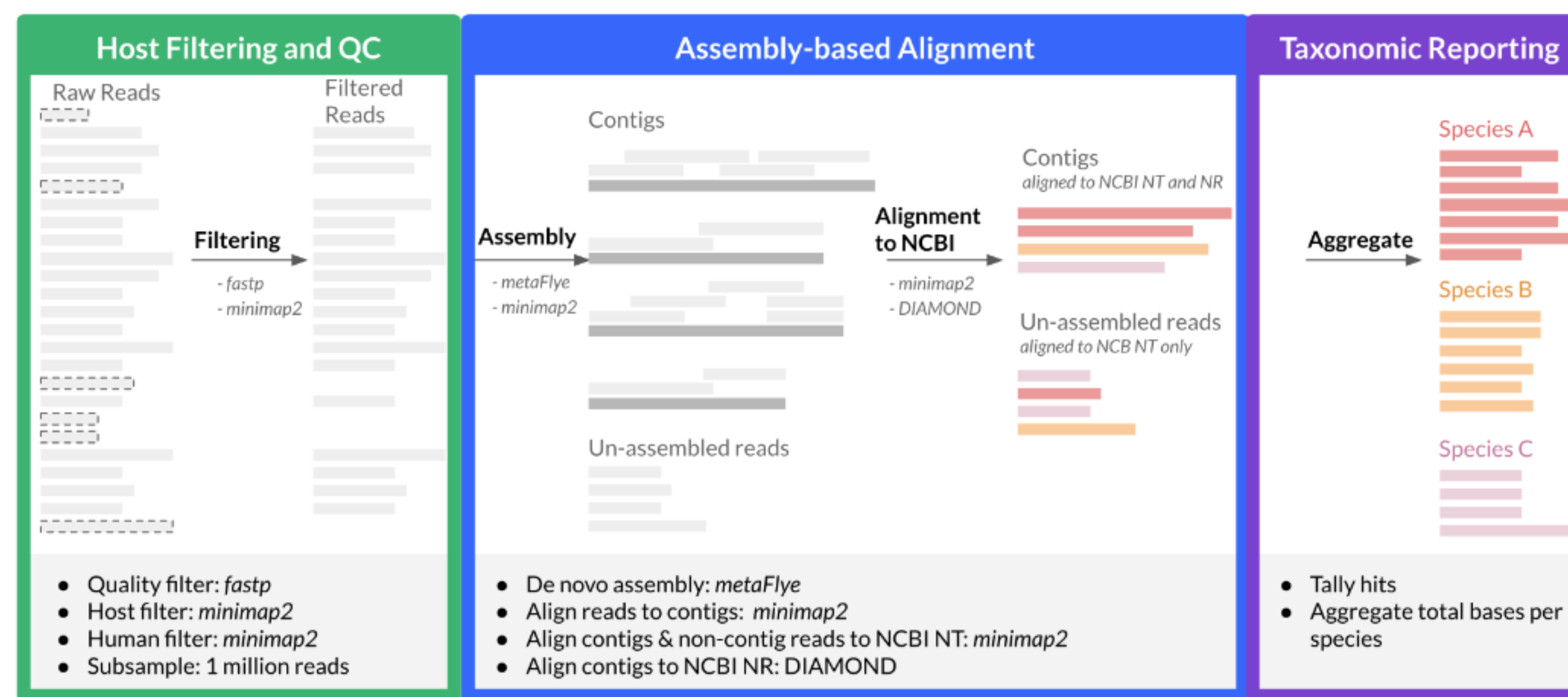
Open-source code

Pipeline <https://github.com/chanzuckerberg/czid-workflows>
Web app <https://github.com/chanzuckerberg/czid-web>
ONT heatmap <https://github.com/katrinakalantar/czid-ont-heatmap>

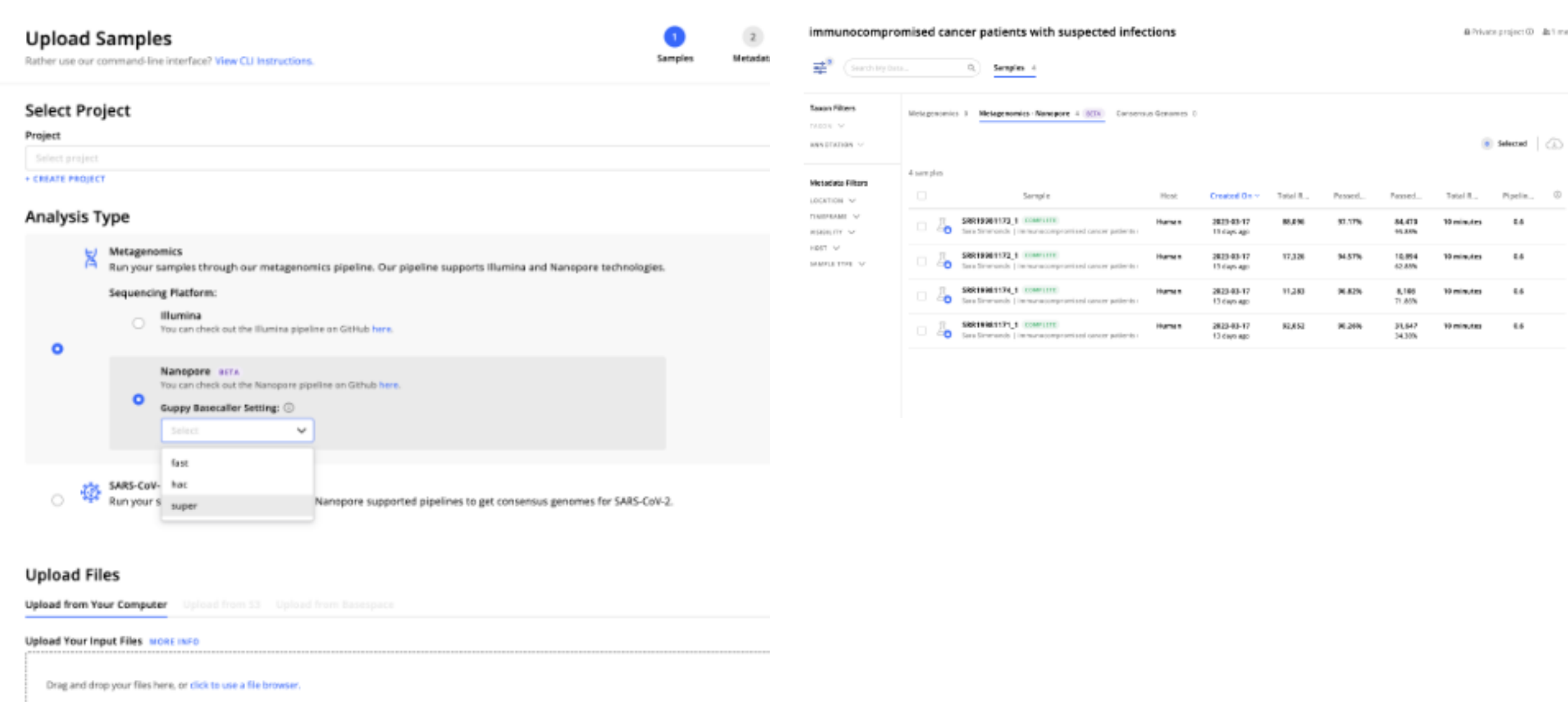
Acknowledgements

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CZ ID NANOPORE METAGENOMICS PIPELINE

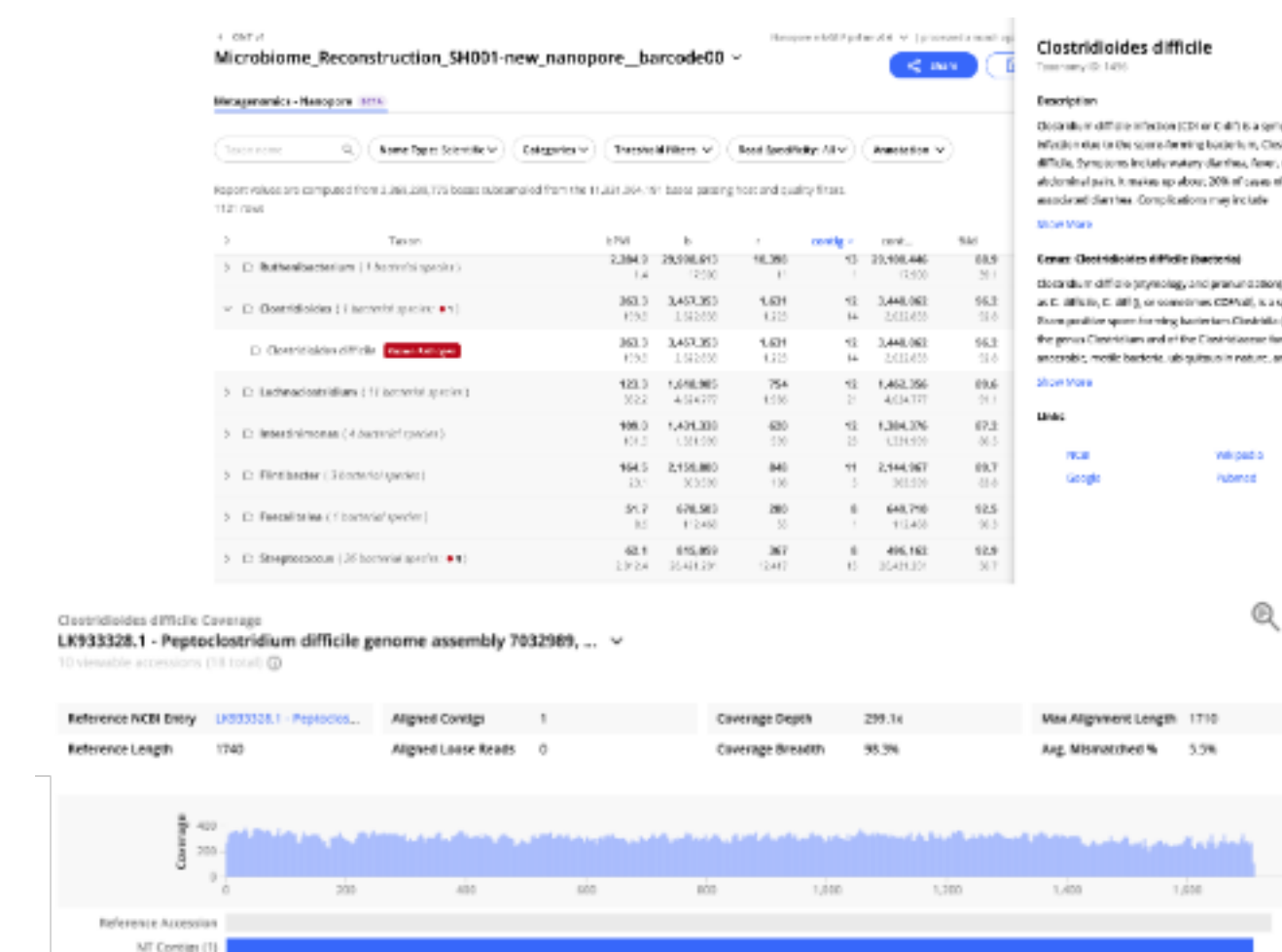


USER INTERFACE

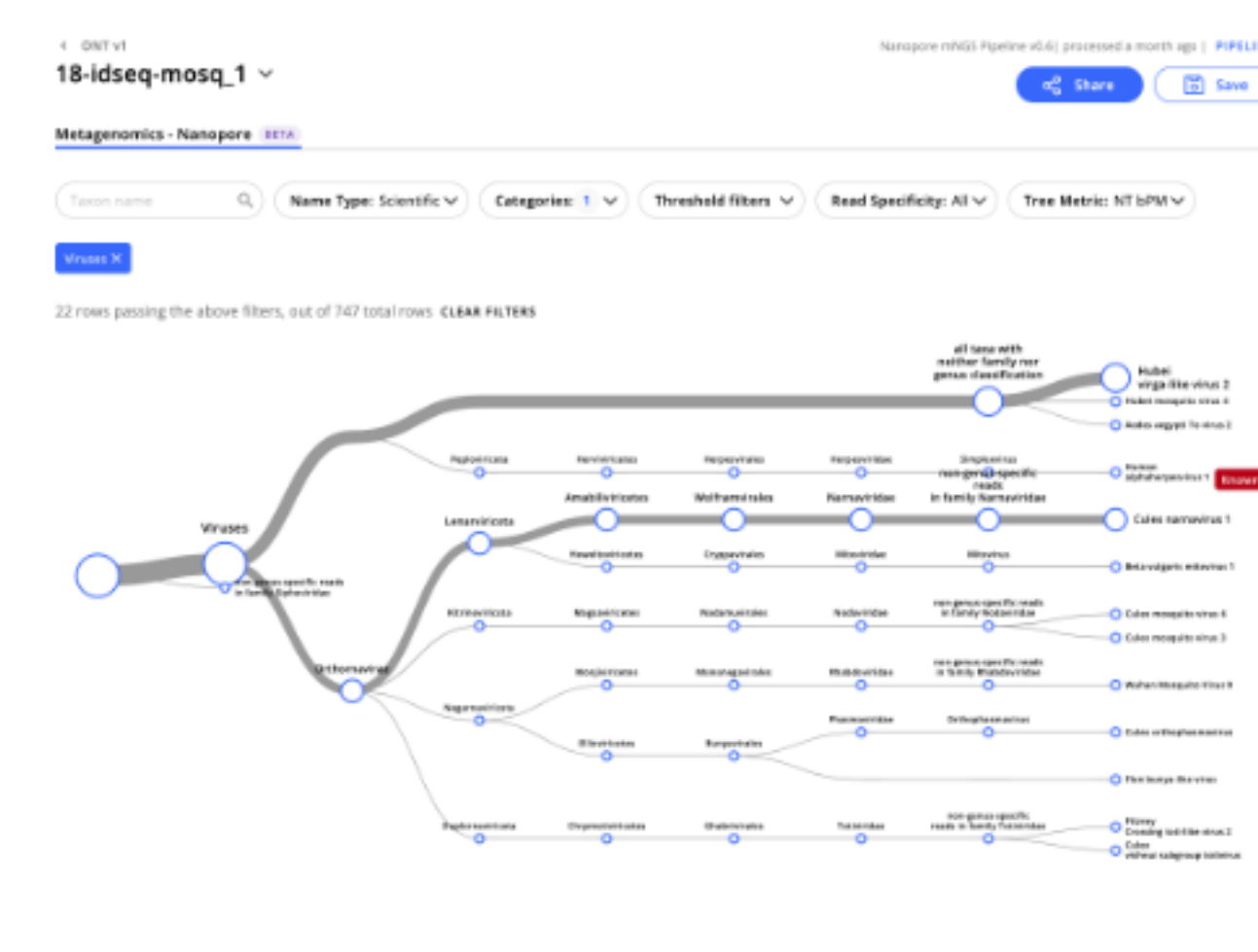


Simple sample upload and cloud-based data processing

Data management for projects and samples



Sample report includes identified taxa, taxon abundances, and genome coverage visualizations

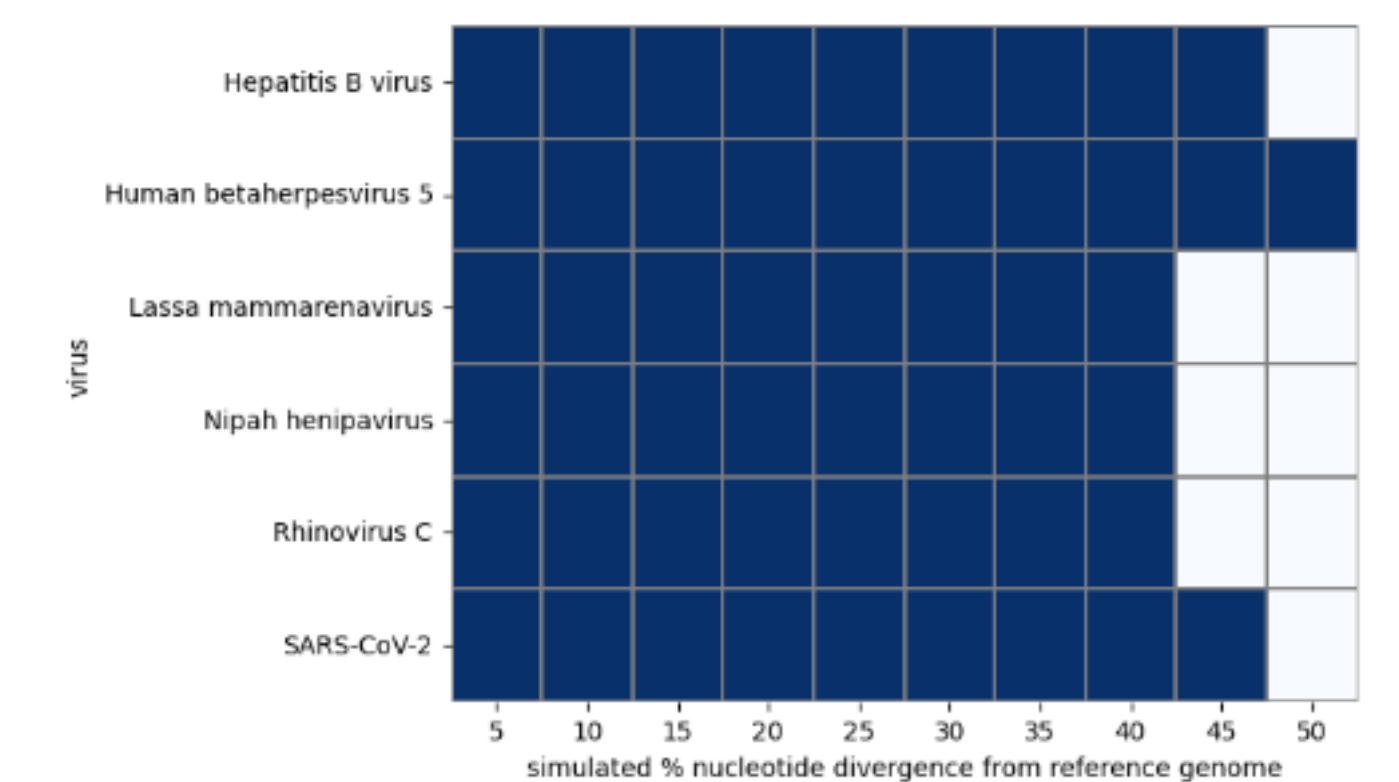


Taxonomic tree view provides a phylogram of the taxonomic hierarchy of microbes identified in a sample

DIVERGENT VIRUSES

Question
Can CZ ID Nanopore metagenomics module detect divergent viruses?

- Approach**
- Six viruses of interest
 - Reference genomes from NCBI
 - Mutated to obtain artificial diversity
 - Simulated Nanopore reads generated
 - Merged with real human serum data



Results
CZ ID detected viruses up to 40-50% divergent by aligning translated nucleotide sequences to the NCBI protein (nr) database.

Conclusion
CZ ID is the only free tool that finds matches to protein sequences - enabling the detection of divergent taxa.

COMING SOON



Heatmaps to compare across samples and filters to refine your analysis

