



Virtual Training 25
Mobile Labs and Field Sequencing during Outbreaks

The European Mobile Laboratory: field experience in emerging infection surveillance and response

Dr Sophie Duraffour - 15 April 2026

Intended Learning Objectives

Specific objectives of this session:

1. Learn about the European Mobile Laboratory | EMLab

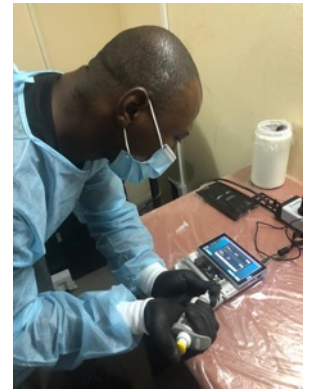


World Health
Organization

GOARN
Global Outbreak Alert and Response Network



1. Learn about experiences of sequencing during outbreaks



1. Learn how the field settings led to develop a new tool for nanopore data analysis



Outline



This session consists of the following elements

1. **Introduction** to the EMLab: goals, deployments and future directions
1. **Examples** of Nanopore field sequencing for surveillance and outbreaks: the EMLab perspective of the last 10 years
1. **Integrate** new tools: ViMOP pipeline, enhancing global Nanopore viral genomic surveillance



1. Introduction to the EMLab: goals, deployments and future directions



EMLab | BNITM



Hamburg, Germany



The Bernhard Nocht Institute for Tropical Medicine



WHO Collaborating Center for Arbovirus and Hemorrhagic
Fever Reference and Research



Global Outbreak Alert and Response Network



EMLab: European Civil Protection Pool (ECPP) certified since 2023



EMLab | type II



Rapid Response Mobile Labs (RRMLs)

WHO / GOARN classification

- Capacity & throughput
- Mobility, transportability, speed
- Self sufficiency
- Biosafety/biosecurity standards



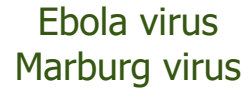
Type I



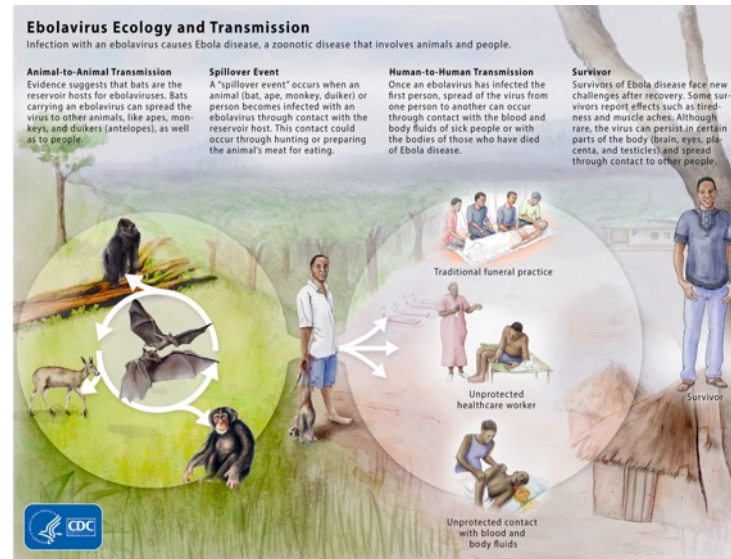
Type II



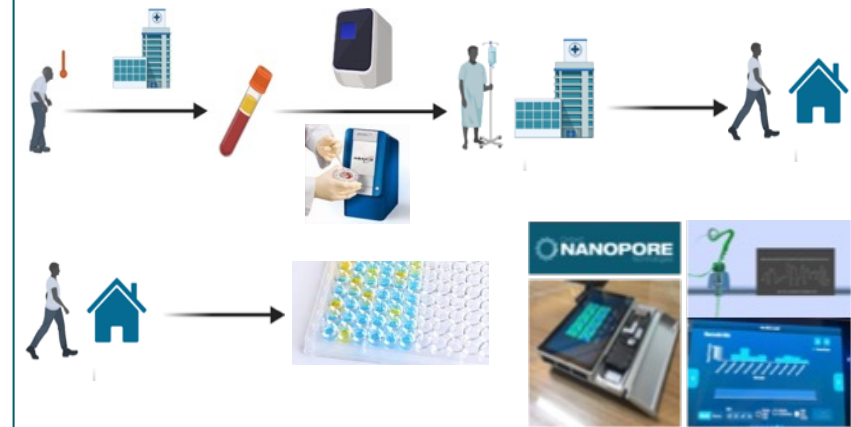
Types III–V



Viral hemorrhagic fevers (VHFs) and others emerging pathogens



Support health-systems



Capacity development

>100 experts
22 Countries



15 missions since 2014
275 deployments done



Copyright: @BNITM



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EMLab | concept

- Rapid Response Mobile Laboratory (RRML)
- Box based
- Field deployable
- Viral pathogens up to risk group 4 (RG4)
- ~ 25-35 boxes per unit
 - Sequencing module: 9 boxes
- Highly mobile
- Flexible modules
- European Civil Protection Pool (ECPP) certified
- Not self-sufficient



Copyright: @BNITM

EMLab | lab content



State-of-the-art diagnostics and sequencing laboratory deployable where needed



Support modules:

Tech support
Office
PPE
Consumables
Cold chain
...

EMLab | deployment mechanisms

START: request for assistance (RFA) - Public Health, Civil Protection & Humanitarian Aid, Bilateral Agreements

GOARN



ECPP



Bilateral



HAND raised → deployment only if country requesting help accepts the offer

EMLab | Teams and rotations

Mobilisation

BNITM: Ops & HR

Field: 5-12, rotation - TL & deputy

Log: On-site



Operations

Detection of viral pathogens up to Risk group 4

Work closely with on-site partners

- MoH, WHO, MSF, etc

Provide a range of services

- Real-time RT-PCR, POC, RDT, hematology, biochemistry, sequencing

Capacity building

- Training local staff, infrastructure and reagents

Operational Research

- Diagnostic tests evaluation
- Clinical trials
- Research studies
- Molecular epidemiology
- Sample storage

Preparedness

- Refurbish & upgrade units
- Training
- TTX, SimEx, Field Ex, Modex

EMLab | pool of volunteers preparedness

EMLab training

- 5-days
- Hosted at BNITM
- Theory and hands-on
- SOPs
- Lectures
- Scenario with 10-years deployment experience



Latest trainings

2024 – 36 staff (incl. RKI joint training)

2026 – coming up – 12 staff



EMLab | global exercises & network



Attendance - most recent examples

2023 – ECPP ModTTX Slovenia

2023 – RRML TTX Berlin, Germany

2023 – RRML SimEx Türkiye

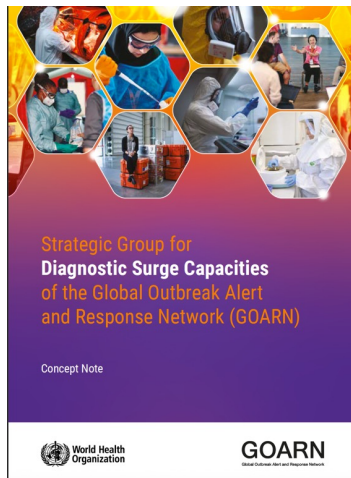
2023 – ECPP Medical MODEX Field Exercise Çanakkale, Türkiye

2023 – EMLab certified within the ECPP

2024 – RRML WHO/GOARN SimEx Kachreti Georgia



Network for RRMLs: GOARN-DiSC (Diagnostics Surge Capacities)



GOARN-DiSC Coordination Board setup. Feb 2025 Amman, Jordan



<https://iris.who.int/handle/10665/380418>

<https://goarn.who.int/documents>

<https://www.who.int/europe/publications/i/item/WHO-EURO-2023-2947-42705-59553>

EMLab | future directions



- Strengthen network to maintain expertise
- Share knowledge: network expansion



High Containment Mobile Laboratory Strategy for Rapid Outbreak and Epidemic Response in Brazil and South America

17 Pages • Posted: 12 Jul 2025 • Last revised: 15 Jul 2025

[Matheus Bezerra](#)

Oswaldo Cruz Foundation (FIOCRUZ) - Aggeu Magalhães Institute

- Upgrade modules



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2. Nanopore field sequencing for surveillance and outbreaks: an EMLab perspective of the last 10 years



What drives EMLab activities



Partnership & trust: transparency & sustainability

Preparedness: laboratory capacities where needed

In-country surveillance: real-time sharing & awareness

Early detection & response: rapid intervention in public health emergencies

Joint research: translate findings into improved surveillance systems & awareness

Create impactful changes: community engagement & better health

Logistics | to consider

Temperature?

Humidity?

Dust?

Uninterrupted power access?

Limited working space?

Cold-chain?

Infrastructure

- Tent-based?
- Building?
- Container?



Technical | many samples, many viruses, many...

Viruses & Sample types



Plasma, serum,
whole blood

Urine

Mouth swab,
saliva

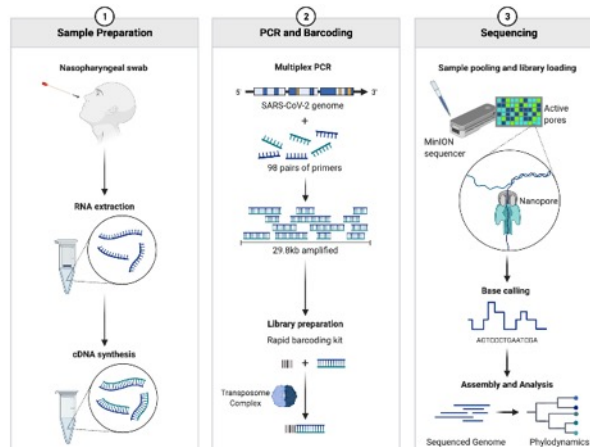
Lacrimal fluid

Vaginal swab

Seminal fluid

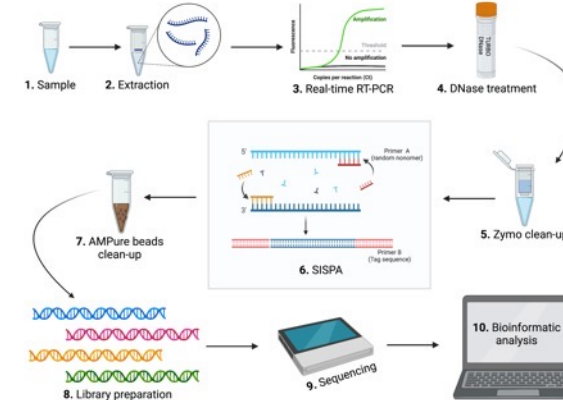
Amplicon-based - targeted

Specific target known and "conserved"
Ex: Ebola virus, SARS-CoV-2 ,
Influenza



Metagenomic - non-targeted

Target known or unknown
no amplicon available / no target enrichment
Ex. Lassa virus / no PCR-detection



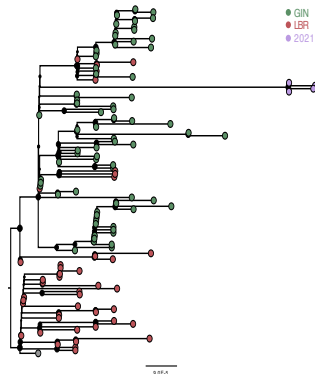
Backbone

Documentation
SOPs
Ethics
Nagoya
....



Molecular epidemiology

Complete genomes?



- Origin of the outbreak?
- Linkage to others cases?
- Spillover event?
- Chains of transmission
- Guide public health response
- Stimulate countermeasure development

Choosing one technology | nanopore

- SOPs
 - Device & analysis capacity
 - Data storage
- Robust in environnement
 - Internet / network access?



Sequencing devices

Mk1C

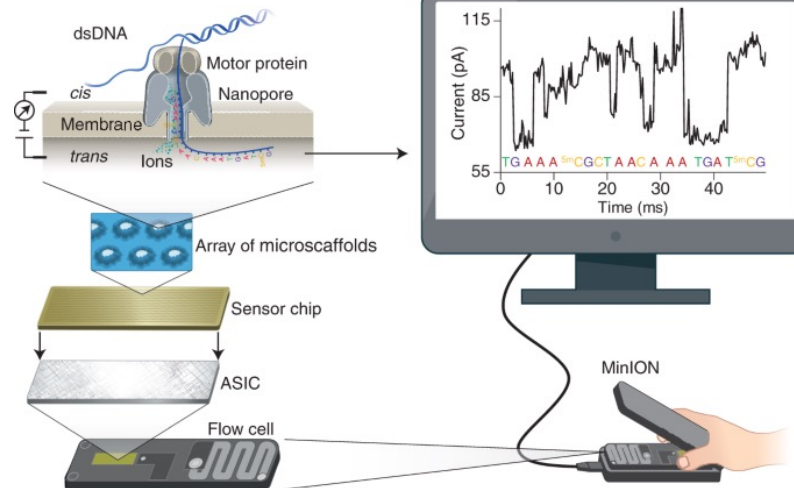


Mk1B



Mk1D

How does it work?



Analysis



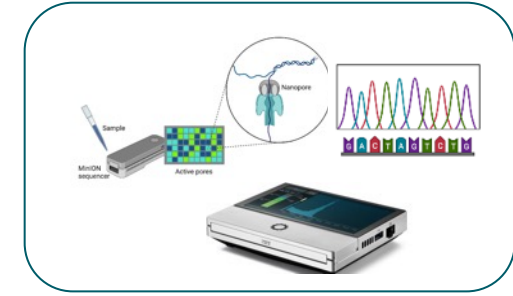
Cumulative knowledge | field sequencing



Guinea 2014-2016



Joint training Guinea-Nigeria 2021



2014-2016

Ebola
Guinea
Amplicon

2018-2020

Lassa
Nigeria
Metag.

2021

Ebola
resurgence
Guinea
Amplicon
Metag.

2021-today

SARS-CoV-2
Guinea
Nigeria
Amplicon

2021

Marburg
Guinea
Metag.

2022-2023

Emerging
viruses
Guinea
Metag.

2024-today

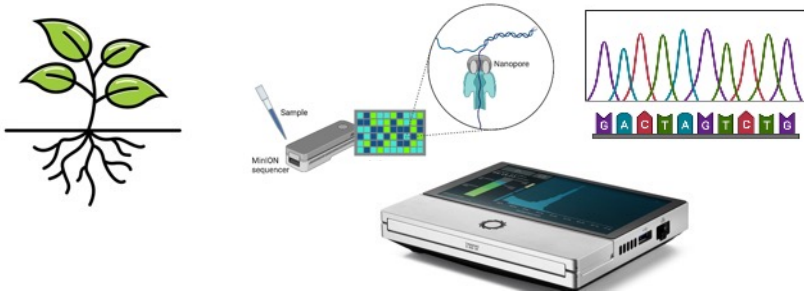
Emerging
viruses -
mpox
Guinea
Metag.
Amplicon

Emergency

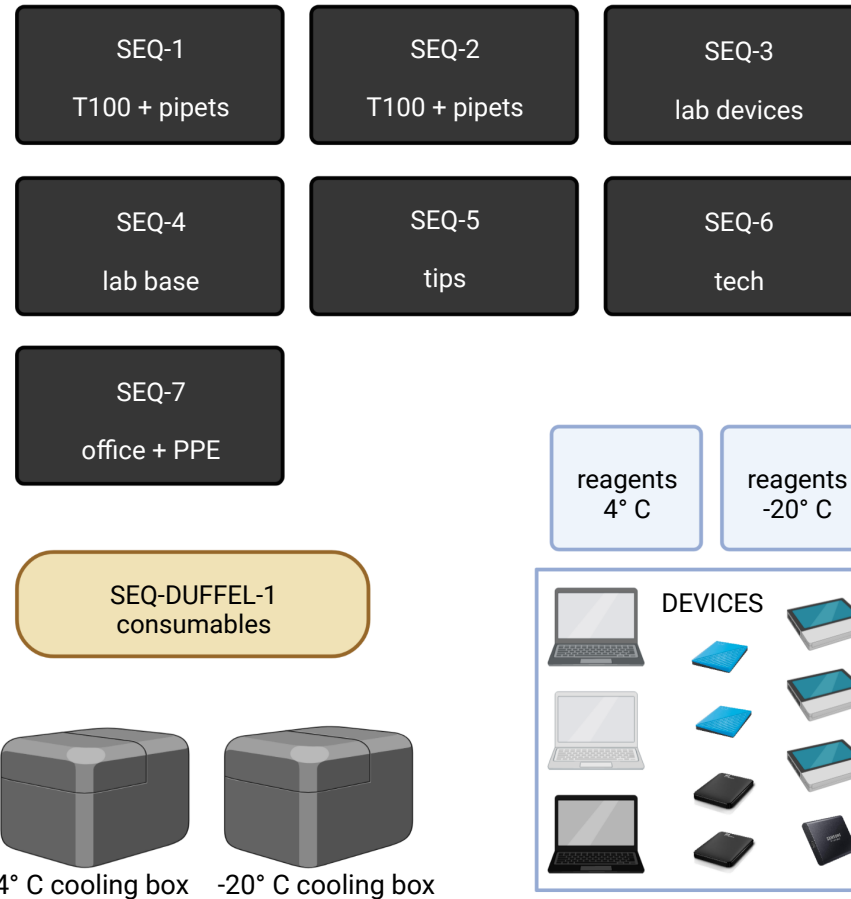
Non-emergency

Field sequencing unit design | mobile or fixed

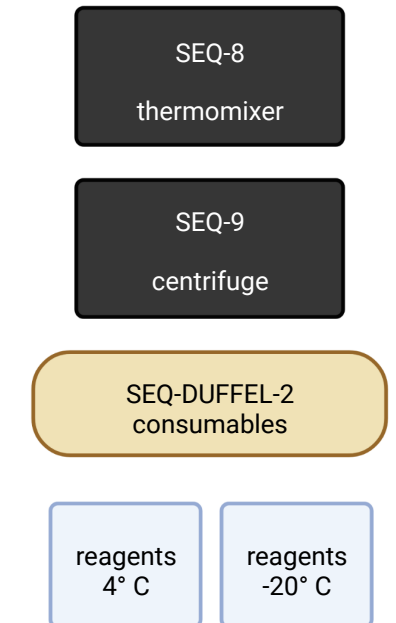
Nanopore sequencing



Amplicon-based



Metagenomics



Field sequencing | mobile tent setup



MODEX exercise – ECPP certification
17-22 September, 2023
Çanakkale, Türkiye

Field sequencing | fixed lab setup



Irrua Specialist
Teaching Hospital
Nigeria

Yearly Lassa fever
epidemic
monitoring



EMLab legacy | Guinea

2014-2016

Ebola virus disease West-Africa – EMLab

2017

EMLab legacy Gueckédou: lab locally run

2021

Resurgence of Ebola

Detection of Marburg

Nanopore sequencing start

2021-22

Covid-19 variant monitoring

Since 2020

Increased detection of Lassa cases

2023

Support to Yellow fever, Dengue, and other relevant emerging RNA virus

2024 - today

Additional support to mpox virus, and other relevant emerging viruses



From punctual support during outbreaks to fixed setup with nanopore sequencing

Ebola resurgence 2021 | the unexpected

New Ebola outbreak declared in Guinea

14 February 2021



Copyright: @BNITM



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Deployment nanopore sequencing following request for assistance



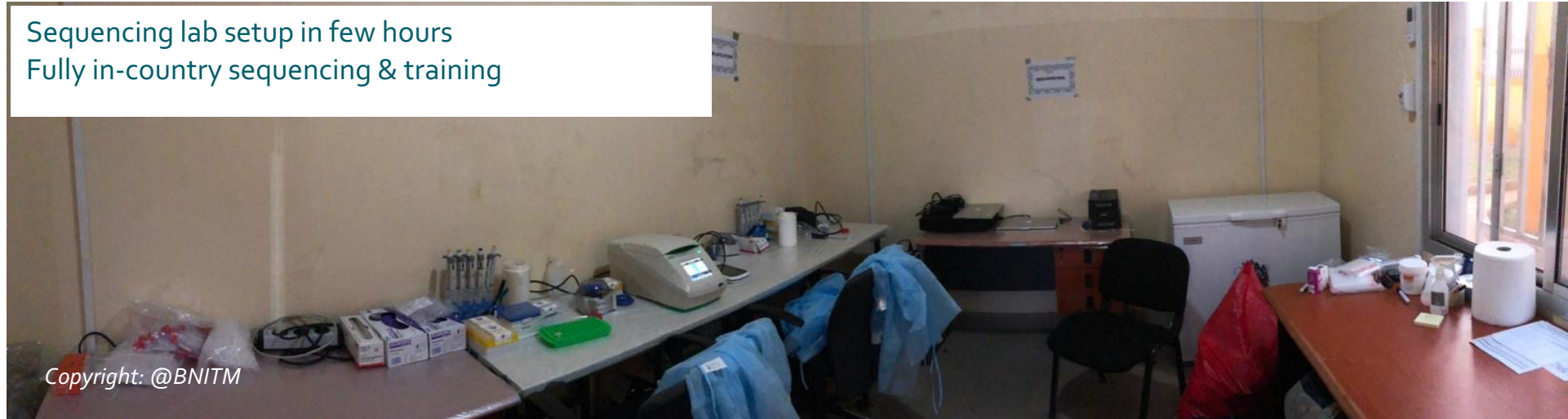
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In how many hours was the mobile sequencing lab setup and operational from landing in the country?

Ebola 2021 | seq lab setup in 24hr

Sequencing lab setup in few hours
Fully in-country sequencing & training



Ebola resurgence 2021 | the unexpected

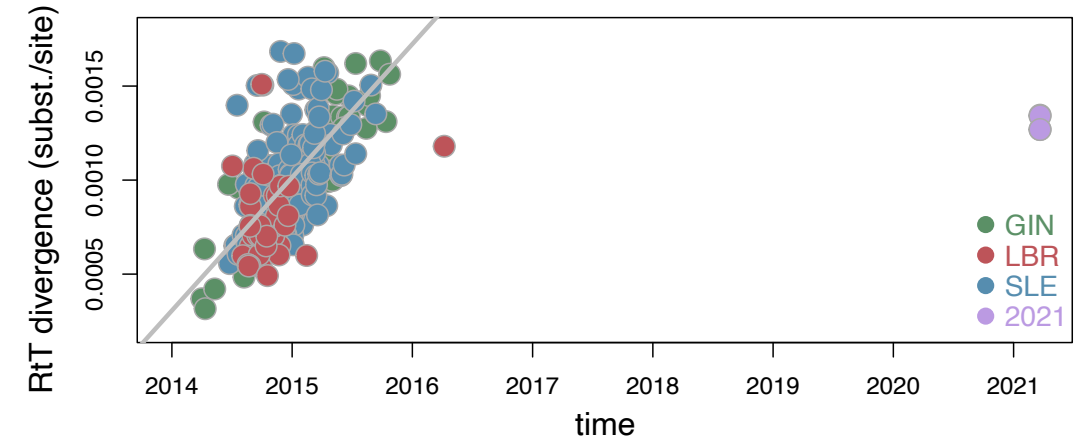
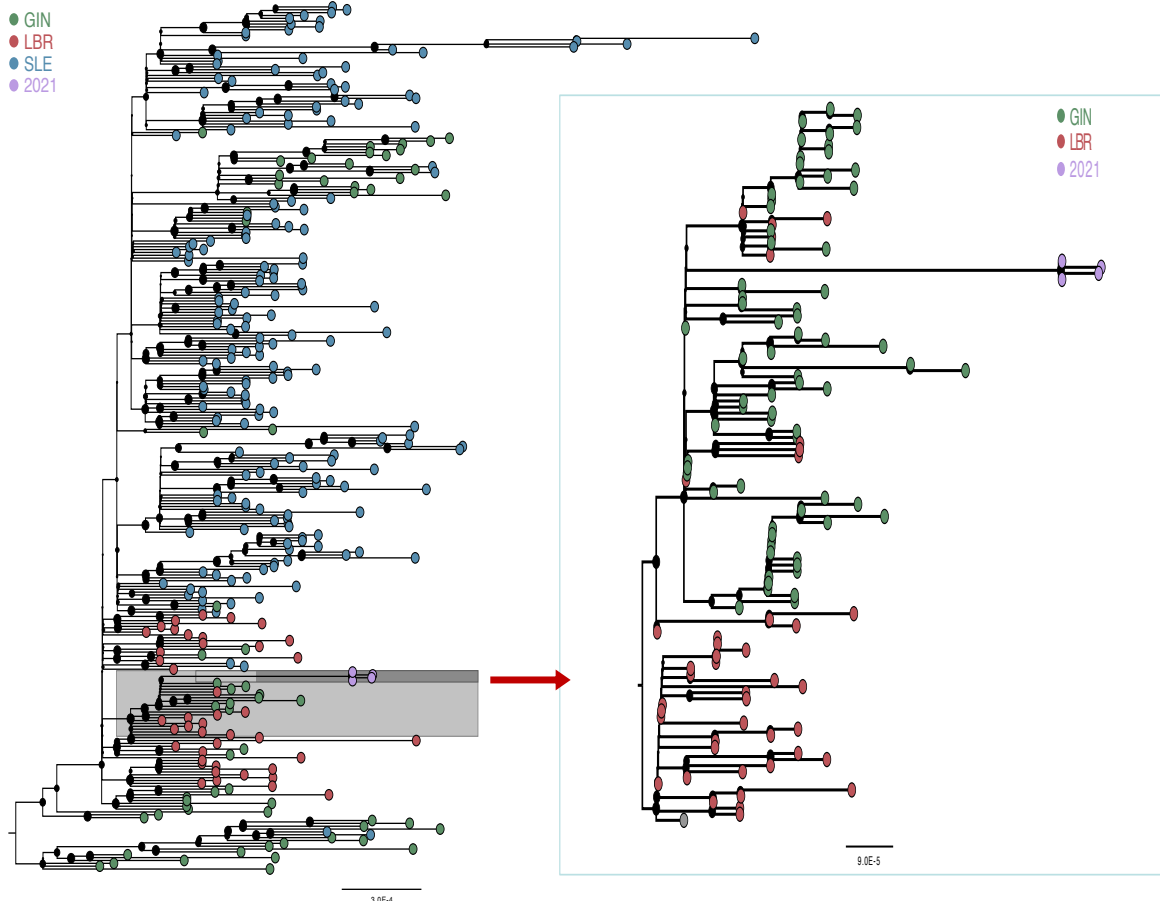
nature

Article | Published: 15 September 2021

Resurgence of Ebola virus in 2021 in Guinea suggests a new paradigm for outbreaks

Alpha Kabinet Keita , Fara R. Koundouno, [...] N' Faly Magassouba

Nature 597, 539–543 (2021) | [Cite this article](#)



- Resurgence related to virus 2014-2016
 - 6.4-fold vs Koropara 2016 5.5-fold
- No new introduction from animal
- First time this has ever been reported
- Epidemiological investigations not conclusive
- Caution against stigmatization

From Ebola to SARS-CoV-2 | keep new capacity

March 2021 until Dec. 2022

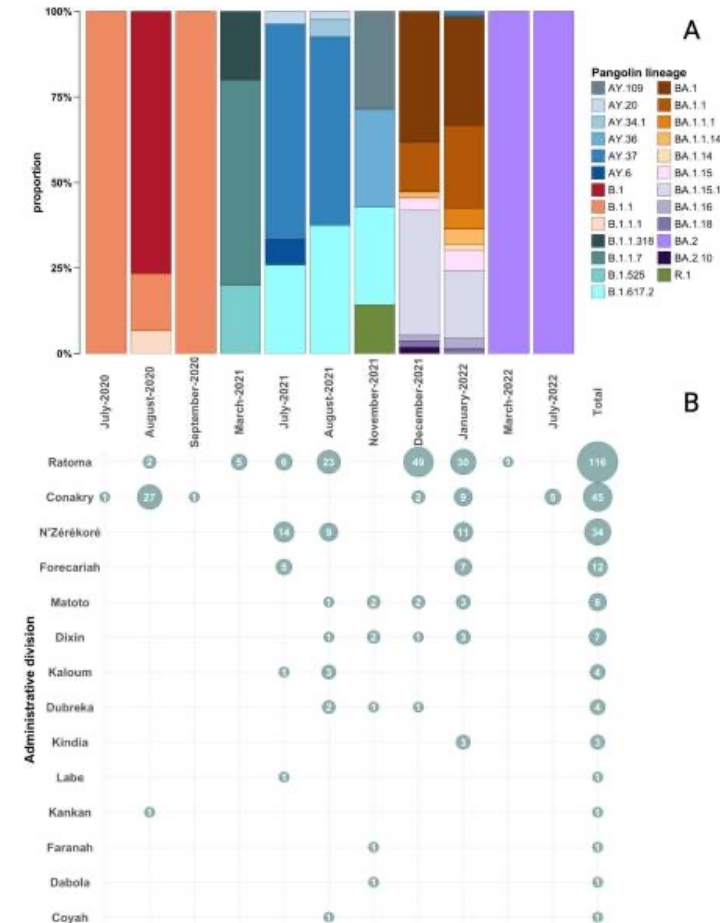
11 EMLab teams
32 experts deployed
26 shipments to Guinea
5 local trainees

amplicon-based

all done in-country incl. analysis
Hub for training: Nigerian collaborators



Overview of SARS-CoV-2
genomic surveillance



[doi: 10.1038/s41598-026-46736-y](https://doi.org/10.1038/s41598-026-46736-y)

Magassouba et al., Sci Rep. 2026

Mobile to fixed lab | today's setup in Guinea



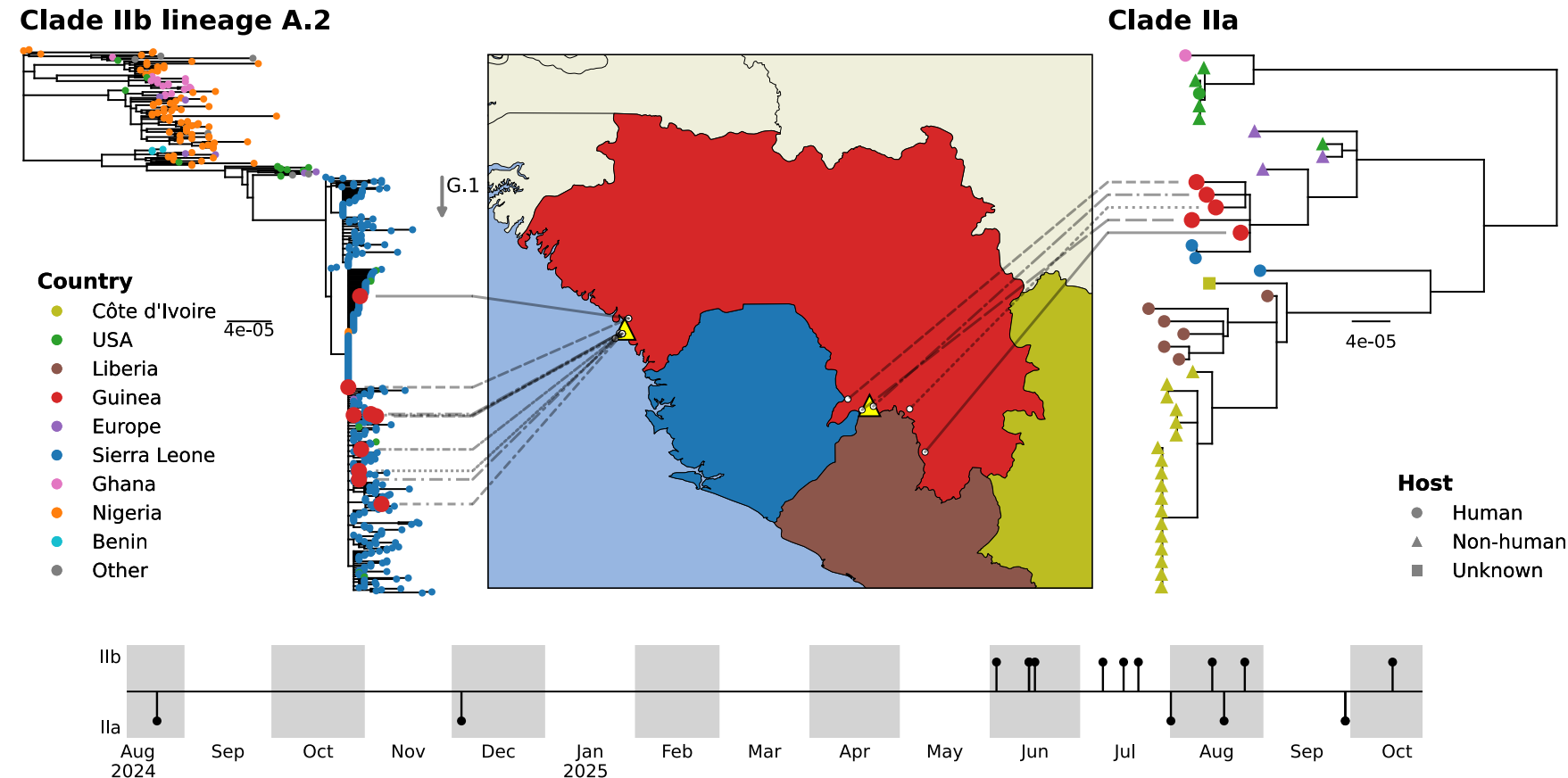
Keep it going | mpox Guinea 2024 - today

Two clades require distinct public health measures

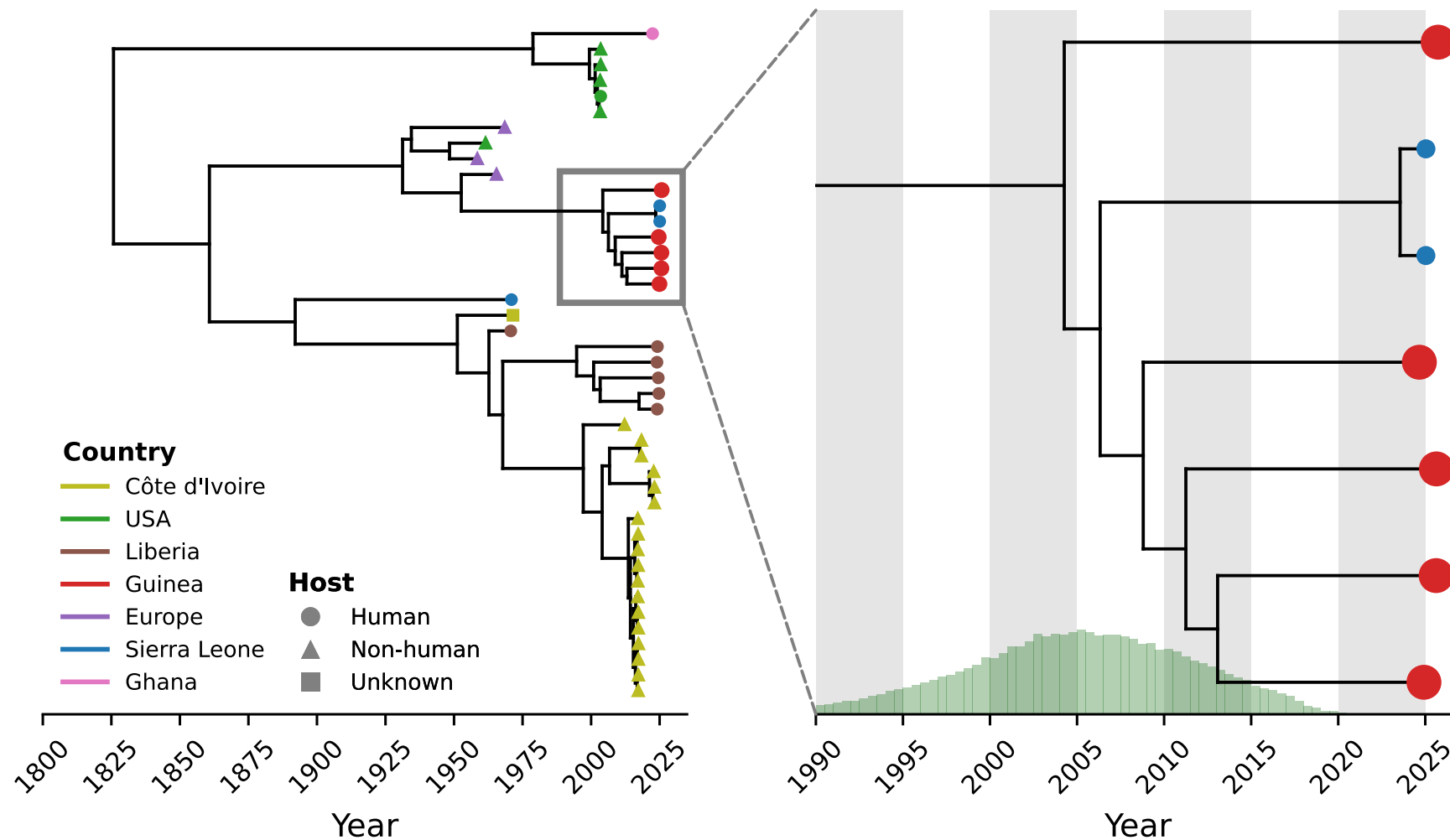
- Human-to-human transmission
- Zoonotic spillover

Capacities

- de-centralized testing
- in-country sequencing



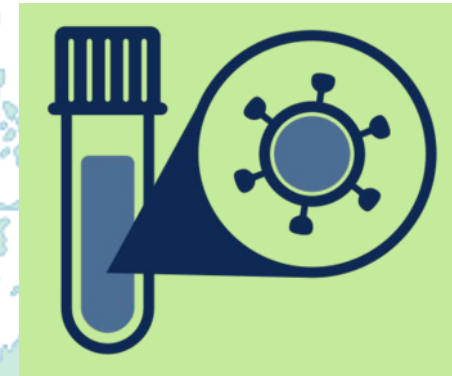
mpox Guinea 2024 - today | clade IIa



3. Integrate new tools: ViMOP pipeline, enhancing global Nanopore viral genomic surveillance

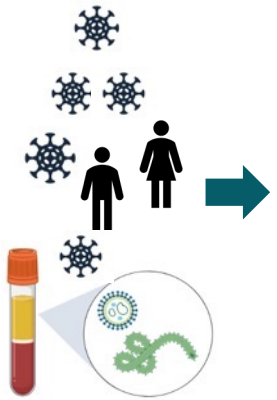


ATCGAACTTAACGT
ATCGAACTTAACGT



A solution to ease **mobile** data analysis = **in-country**

Untargeted sequencing



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Analysis process

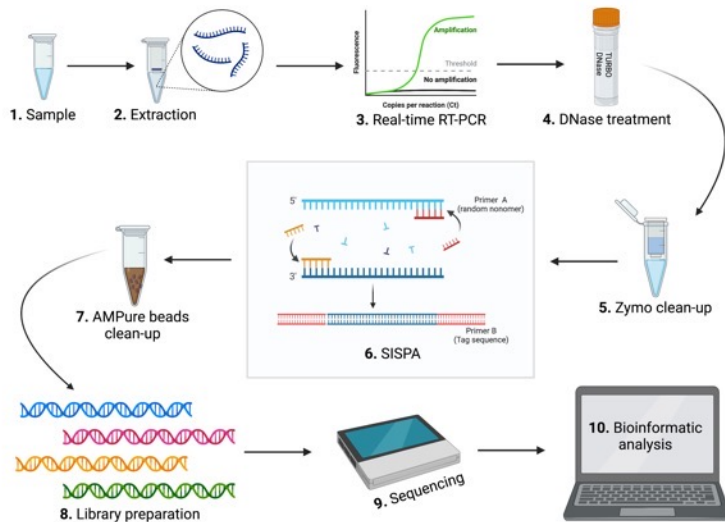


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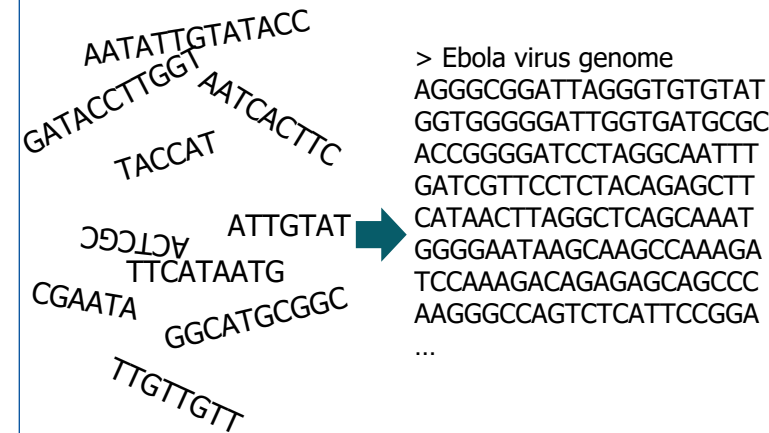
Reporting

Phylogeny



Fastq files

Genome assembly



Customized solutions

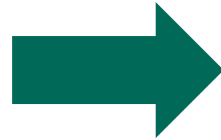
Requirements for the field analysis pipeline

Technical

- Detect all viruses
- Correct genomes

Usability

- Run offline on a laptop (no internet)
- Simple setup and updates
- Data storage
- Easy to use
- Clear output (report)
- Robustness in environment



Virus **M**etagenomics for **O**utbreaks **P**ipeline



<https://doi.org/10.1093/bioinformatics/btaf687>

Bioinformatics 

Article Navigation

JOURNAL ARTICLE

ViMOP: a user-friendly and field-applicable pipeline for untargeted viral genome nanopore sequencing 

Nils Peter Petersen , Mia Le, Annick Renevey, Ehizojie Emua, Sarah Ryter, Giuditta Annibaldis, Jacob Camara, Sanaba Boumbaly, Cyril Erameh, Tanja Laske, Jan Baumbach, Philippe Lemey, Stephan Günther, Sophie Duraffour, Liana Eleni Kafetzopoulou

Author Notes

Bioinformatics, Volume 42, Issue 1, January 2026, btaf687, <https://doi.org/10.1093/bioinformatics/btaf687>

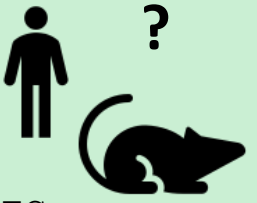
Published: 29 December 2025

ViMOP | Virus Metagenomics for Outbreaks Pipeline

host removal

metagenomic reads

~~CCG~~CGCC
~~CC~~TC
ACGTC CGTTC
ACAA TCGC TCTTT
AAGTCT ~~CGG~~
CCTTTG



viral reads

de novo assembly

viral reads

ACGTC ACAA CGTTC
GTCCG CAATG TCGC
CGG

↓ ↓ ↓

ACGTCCGG ACAATG CGTTCGC

contigs

data base search

contigs + DB

ACGTCCGG
ACAATG
CGTTCGC



↓

> Ebola virus
CGTACGTGCGGCTTTG...

reference genomes

guided assembly

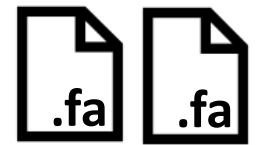
reads + references

CGTACGTGCGGCTTTG...
CGTAC CCTT
CGT CGGCC
CGTCC CTT
CGTACGTC TTG...

↓

CGTACGTCCGGCCTTG...

consensus genomes



Report + Genomes



<https://doi.org/10.1093/bioinformatics/btaf687>

ViMOP | Setup



Nextflow pipeline



User interface with EPI2ME
from ONT



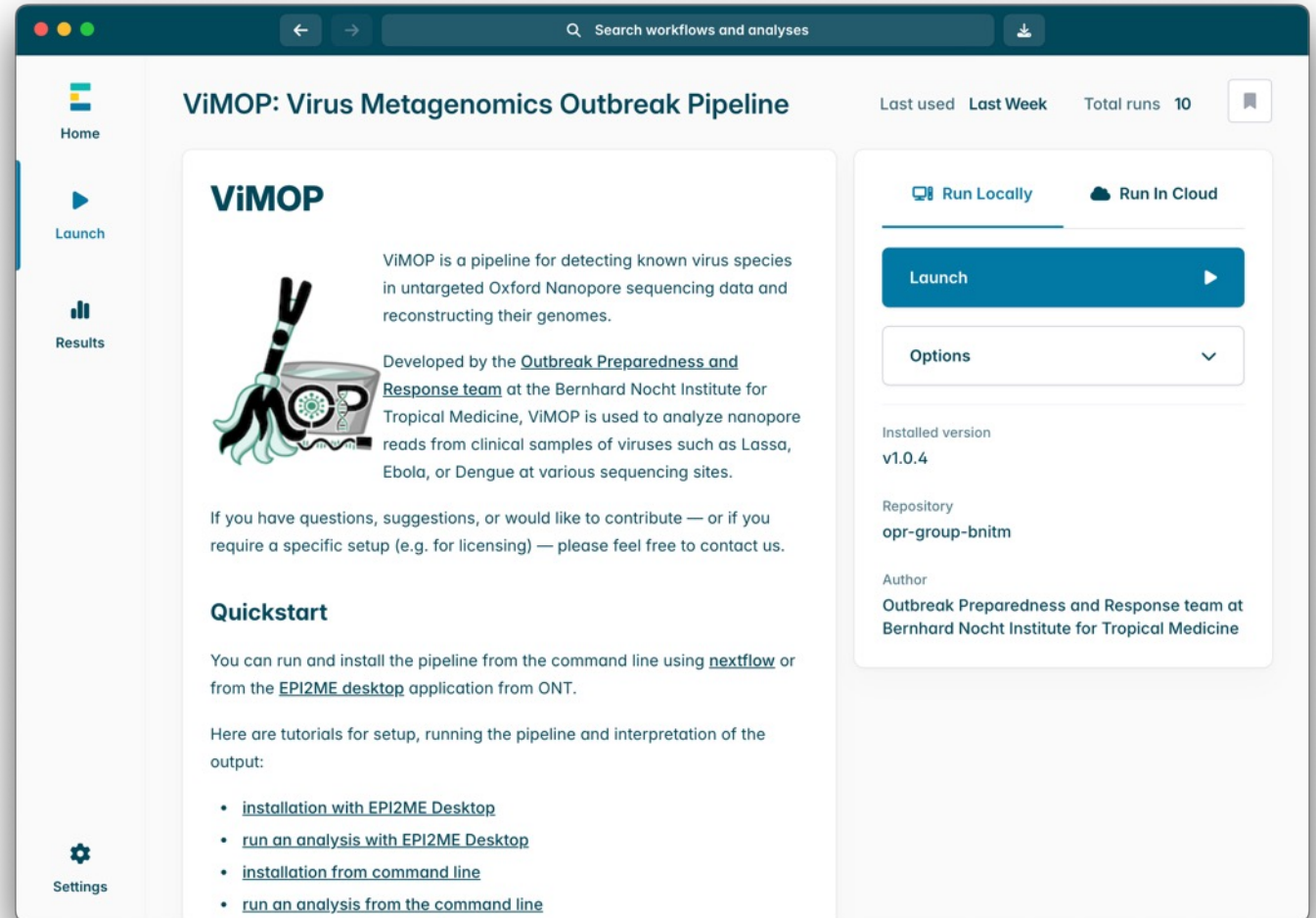
Operates (offline) on a laptop
(≥ 16 CPU, 30GB RAM)



Installation and set up in <25 clicks



(Optional offline installation with a
hard drive – not preferred)



The screenshot shows the ViMOP web interface. The header includes a search bar and navigation links. The main content area is titled "ViMOP: Virus Metagenomics Outbreak Pipeline" and contains a description of the pipeline, its development by the Outbreak Preparedness and Response team, and a quickstart section with links to installation and analysis instructions. The right sidebar shows options to run locally or in the cloud, a launch button, and details about the installed version (v1.0.4), repository (opr-group-bnitm), and author (Outbreak Preparedness and Response team at Bernhard Nocht Institute for Tropical Medicine).

ViMOP: Virus Metagenomics Outbreak Pipeline

Last used Last Week Total runs 10

Run Locally Run In Cloud

Launch

Options

Installed version
v1.0.4

Repository
opr-group-bnitm

Author
Outbreak Preparedness and Response team at
Bernhard Nocht Institute for Tropical Medicine

ViMOP

ViMOP is a pipeline for detecting known virus species in untargeted Oxford Nanopore sequencing data and reconstructing their genomes.

Developed by the [Outbreak Preparedness and Response team](#) at the Bernhard Nocht Institute for Tropical Medicine, ViMOP is used to analyze nanopore reads from clinical samples of viruses such as Lassa, Ebola, or Dengue at various sequencing sites.

If you have questions, suggestions, or would like to contribute — or if you require a specific setup (e.g. for licensing) — please feel free to contact us.

Quickstart

You can run and install the pipeline from the command line using [nextflow](#) or from the [EPI2ME desktop](#) application from ONT.

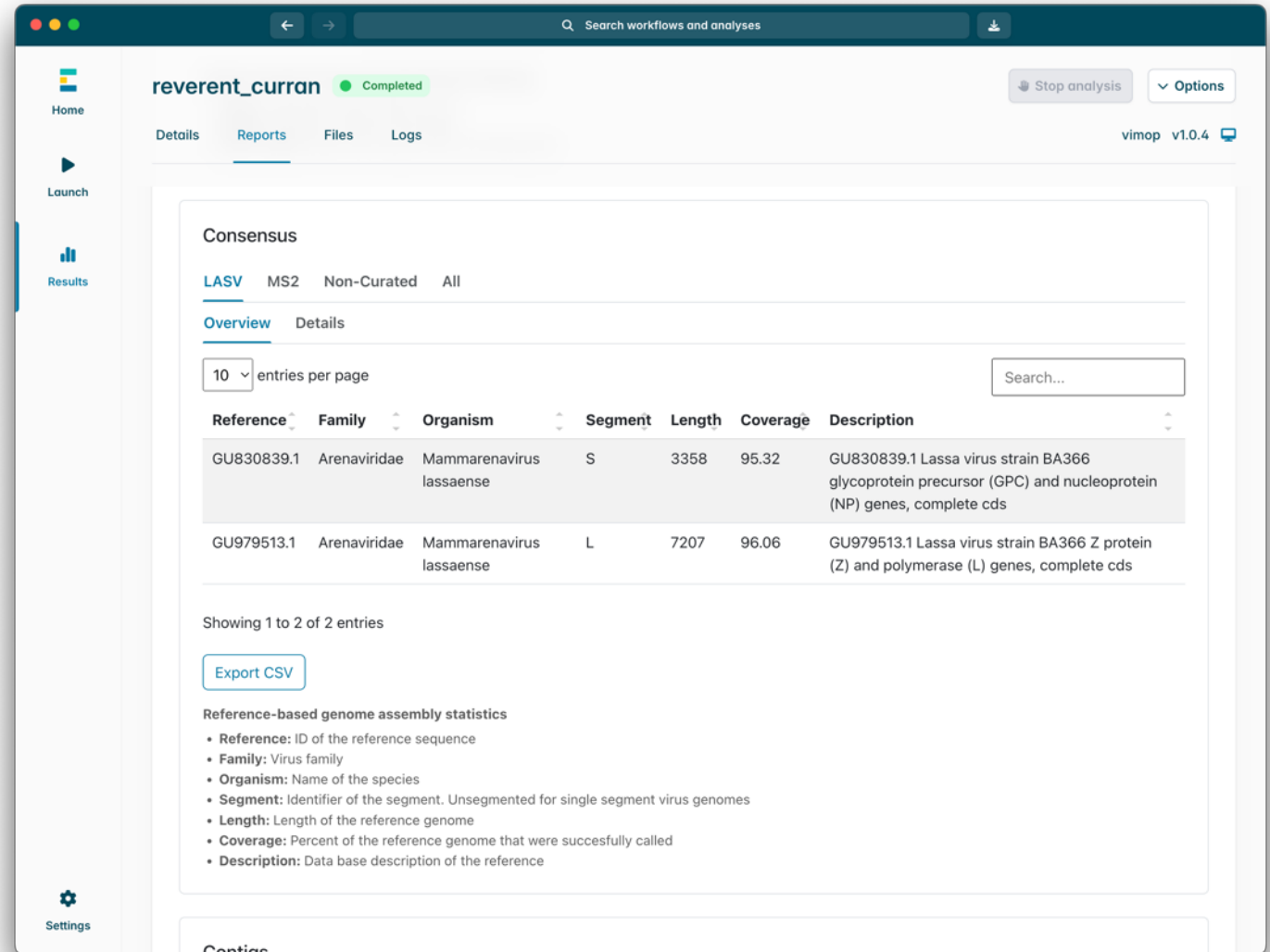
Here are tutorials for setup, running the pipeline and interpretation of the output:

- [installation with EPI2ME Desktop](#)
- [run an analysis with EPI2ME Desktop](#)
- [installation from command line](#)
- [run an analysis from the command line](#)

ViMOP | Report



HTML report with all
relevant results



The screenshot displays the ViMOP web interface. At the top, there's a search bar and a 'Search workflows and analyses' button. The main header shows the analysis name 'reverent_currant' with a 'Completed' status. Below this, there are tabs for 'Details', 'Reports', 'Files', and 'Logs'. The 'Reports' tab is active, showing a 'Consensus' section. Under 'Consensus', there are filters for 'LASV', 'MS2', 'Non-Curated', and 'All'. The 'Overview' sub-tab is selected. A table lists two entries with columns for Reference, Family, Organism, Segment, Length, Coverage, and Description. Below the table, it says 'Showing 1 to 2 of 2 entries' and provides an 'Export CSV' button. A 'Reference-based genome assembly statistics' section lists key metrics: Reference, Family, Organism, Segment, Length, Coverage, and Description.

reverent_currant Completed Stop analysis Options

Details Reports Files Logs vimop v1.0.4

Consensus

[LASV](#) [MS2](#) [Non-Curated](#) [All](#)

[Overview](#) [Details](#)

10 entries per page

Reference	Family	Organism	Segment	Length	Coverage	Description
GU830839.1	Arenaviridae	Mammarenavirus lassaense	S	3358	95.32	GU830839.1 Lassa virus strain BA366 glycoprotein precursor (GPC) and nucleoprotein (NP) genes, complete cds
GU979513.1	Arenaviridae	Mammarenavirus lassaense	L	7207	96.06	GU979513.1 Lassa virus strain BA366 Z protein (Z) and polymerase (L) genes, complete cds

Showing 1 to 2 of 2 entries

[Export CSV](#)

Reference-based genome assembly statistics

- **Reference:** ID of the reference sequence
- **Family:** Virus family
- **Organism:** Name of the species
- **Segment:** Identifier of the segment. Unsegmented for single segment virus genomes
- **Length:** Length of the reference genome
- **Coverage:** Percent of the reference genome that were successfully called
- **Description:** Data base description of the reference

Contigs

ViMOP | Benchmarking

Organism (Gbank ID)	Tool mutation rate	Genome recovery [%]			Sequence identity [%]		
		INSaFLU-TELEVIR	ViMOP	VirDetector	INSaFLU-TELEVIR	ViMOP	VirDetector
SARS-CoV-2 (OX637002.1)	0	95.77	96.02	99.85	100.00	100.00	100.00
	5	95.5	96.01	99.83	99.99	100.00	100.00
	10	94.98	96.01	99.24	99.96	100.00	100.00
	15	63.68	95.57	99.14	99.87	100.00	99.99
	20	no consensus	89.68	89.39	no consensus	100.00	99.86
	25	no consensus	47.79	45.81	no consensus	99.15	99.20
	30	no hit	no hit	no hit	no hit	no hit	no hit
DENV (NC_001474.2)	0	89.25	89.45	no hit	100.00	100.00	no hit
	5	89.18	89.43	no hit	100.00	100.00	no hit
	10	89	89.24	no hit	100.00	100.00	no hit
	15	65.27	89.21	no hit	99.86	100.00	no hit
	20	no consensus	87.03	no hit	no consensus	100.00	no hit
	25	no consensus	17.66	no hit	no consensus	100.00	no hit
	30	no hit	no hit	no hit	no hit	no hit	no hit
LASV L (MG812630.1)	0	69.82	86.77	no hit	99.90	100.00	no hit
	5	no consensus	86.77	no hit	no consensus	100.00	no hit
	10	no consensus	86.77	no hit	no consensus	100.00	no hit
	15	no consensus	86.59	no hit	no consensus	100.00	no hit
	20	no hit	85.81	no hit	no hit	99.98	no hit
	25	no hit	39.67	no hit	no hit	100.00	no hit
	30	no hit	no hit	no hit	no hit	no hit	no hit
LASV S (MG812631.1)	0	66.73	79.92	no hit	99.96	100.00	no hit
	5	no consensus	79.92	no hit	no consensus	100.00	no hit
	10	no consensus	79.92	no hit	no consensus	100.00	no hit
	15	no consensus	79.34	no hit	no consensus	100.00	no hit
	20	no hit	70.14	no hit	no hit	99.96	no hit
	25	no hit	no hit	no hit	no hit	no hit	no hit
	30	no hit	no hit	no hit	no hit	no hit	no hit

ViMOP | Testing, implementation & upgrade

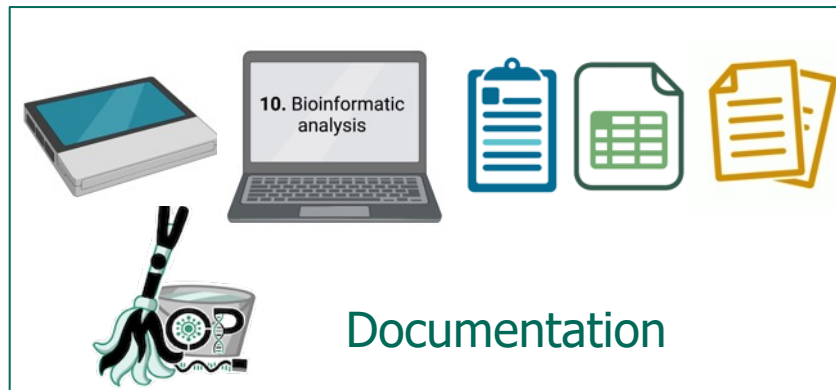
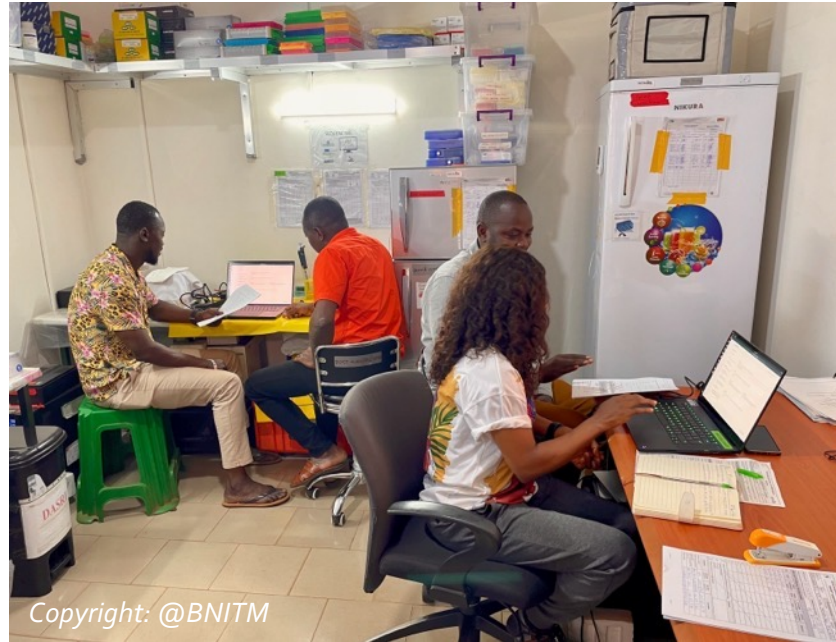
One week training in 2025
Guinea

Participants from Guinea and
and Nigeria

Feedback and improvements

Integration in the EMLab

Since 2026, upgrade ongoing



In summary

List of learning points in this session:

In relation to the **EMLab**:

- Core activities, mechanisms of activation, deployment, staffing and operations
- Future directions

In relation to **field experiences using nanopore sequencing**

- Preparedness activities
- Long-term training for in-country ownership
- Sequencing data at quality: stringent QAM and balance politics/reality
- Need for a home base with experts

If you combine both topics, expertise combined to develop solutions such as **ViMOP**

[illegible]

- # (Drowning in) SOPs
- 
- An illustration depicting a person's arm and hand reaching upwards from a chaotic sea of papers and documents. The papers are scattered all around, some floating in the air and others piled up. The background is a solid teal color. A semi-transparent grey banner at the top contains the text "(Drowning in) SOPs". Two yellow squares are also visible: one in the top right corner and one on a document in the lower left.

Data storage



Further reading

Specific further reading for this session (e.g. Book, article, blog, video, etc.)

- www.emlab.eu/
 - Revamping ongoing – bear with us – launch in 2026
 - Wanna join the pool of EMLab volunteers?
- ViMOP – untargeted viral genome nanopore sequencing
 - <https://github.com/opr-group-bnitm/vimop>
 - <https://doi.org/10.1093/bioinformatics/btaf687>

EMLab



ViMOP



References

- RRMLs into global health security:
 - Storozhenko et al., 2025: doi: 10.1136/bmjgh-2025-022083
- A snapshot of logistics behind EMLab field sequencing setup
 - Magassouba et al, 2026: doi: 10.1038/s41598-026-46736-y
- High Containment Mobile Laboratory Strategy for Rapid Outbreak and Epidemic Response in Brazil
 - Bezerra et al., 2026 - preprint: <http://dx.doi.org/10.2139/ssrn.5345070>
- Overview of RRMLs in EU and Africa:
 - Trojnacki et al, 2025: doi: 10.1186/s42522-025-00180-6



Outbreak Preparedness
Response Group



Whole network

CoSyBio CoSyBio



LIV



Guinea

Centre de Recherche en
Virologie (CRV-LFHVG)

Laboratoire de Gueckédou
(LFHV-GKD)

Laboratoire de N'Zérékoré
(LFHV-HRNZE)

Nigeria

Irrua Specialist Teaching
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GOARN



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RKI



ARTIC network



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