Application of SARS-CoV-2 NGS

ErasmusMC

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Aims

- Reconstruct the trajectory of SARS-CoV-2 emergence and spread nationally and internationally
- Application of NGS in public health policy making and infection prevention policies
- Monitoring relevant mutations: genotype to phenotype
- Need to do this fast and to share data near to instantly

Amplicon based sequencing

PROTOCOL

Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples

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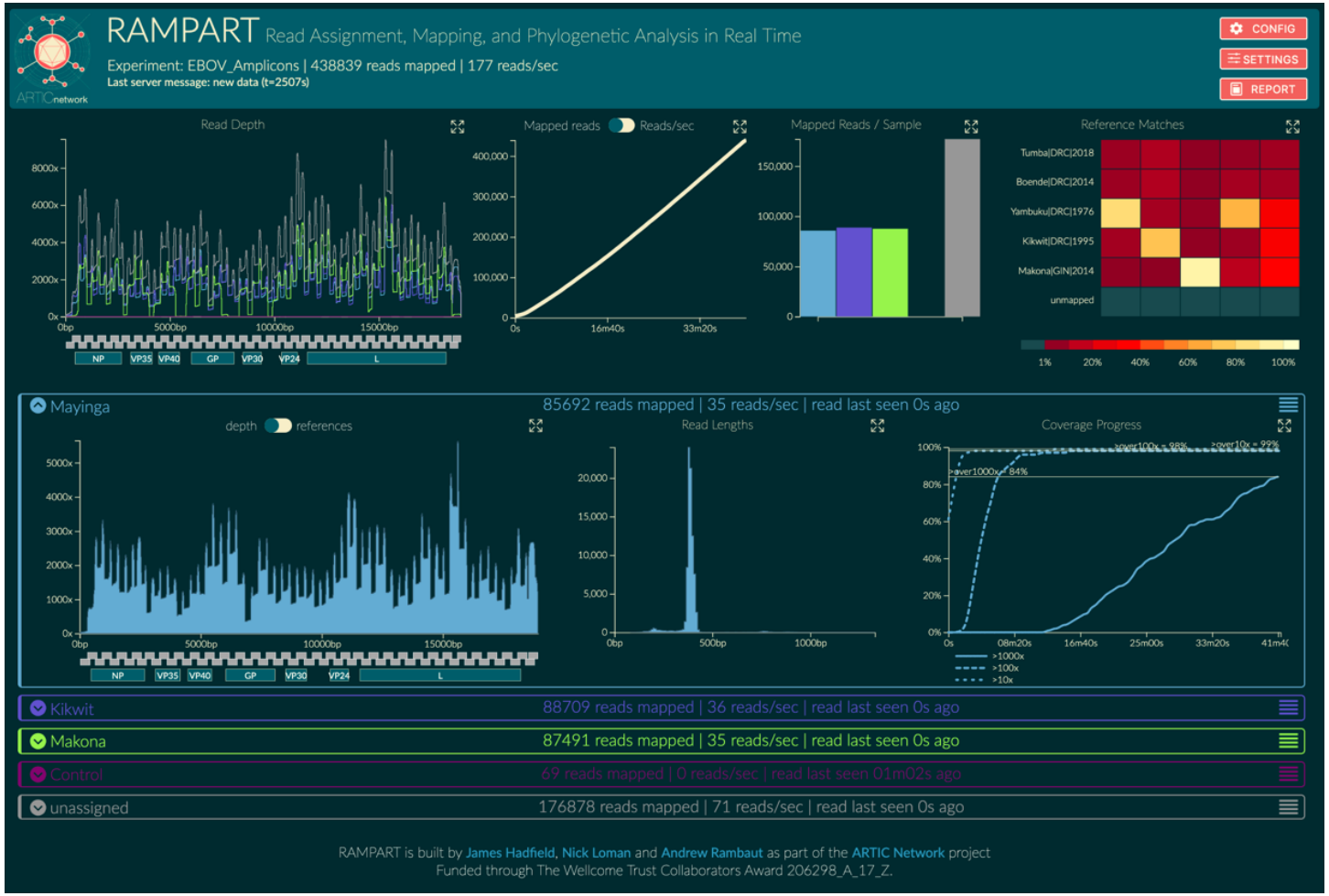
83 overlappende amplicons
500bp
75 bp overlap

Data analysis



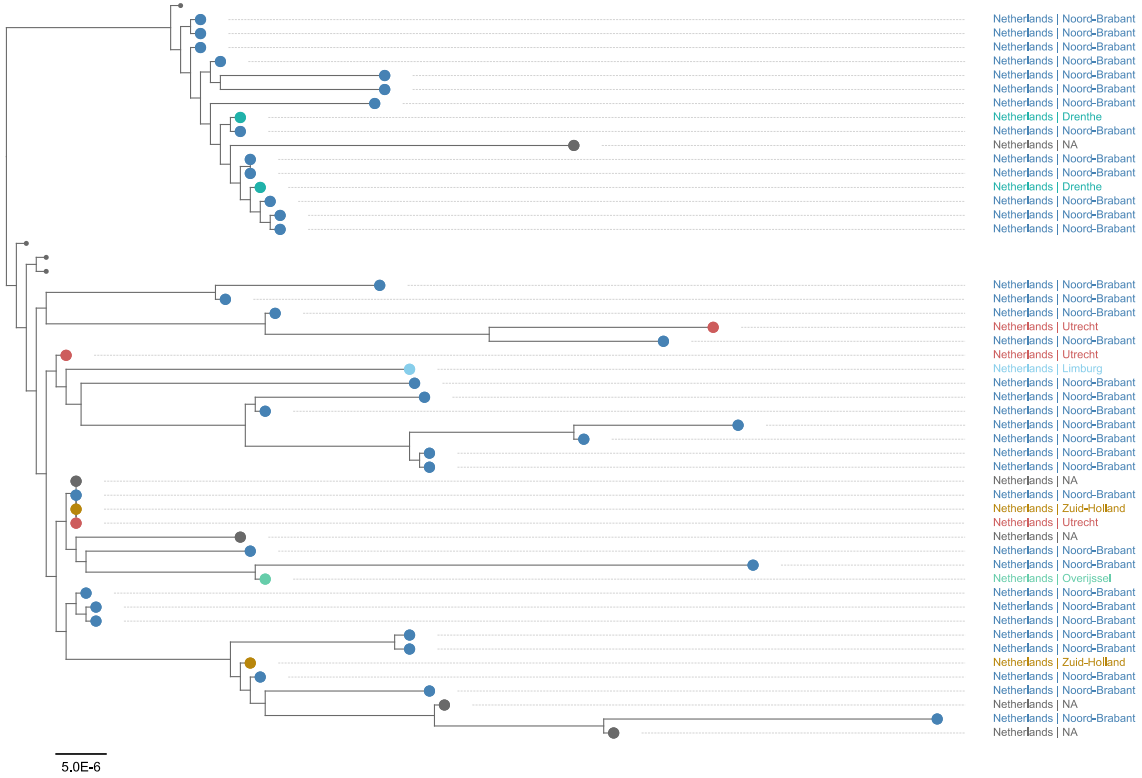
Custom script to automatically collect data from the machine and transfer to the server

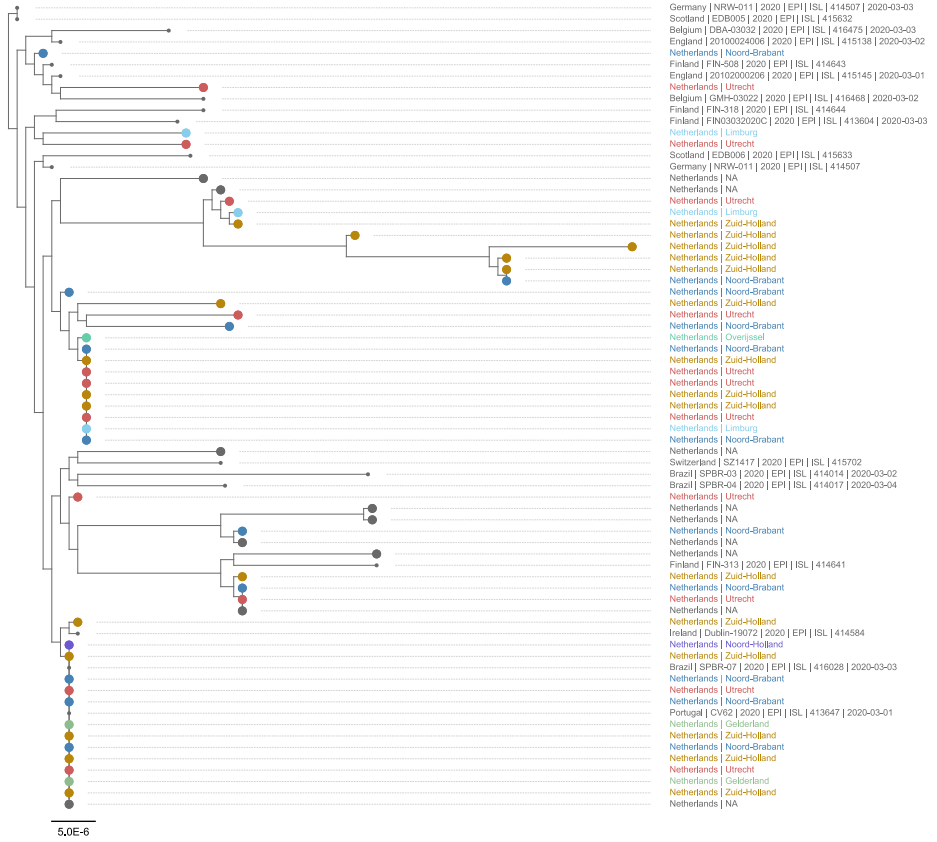
Real-time automated data-analysis:

- Demultiplex
- Trim primers
- Align to reference
- Generate consensus sequence (10x, 30 and 100x coverage)

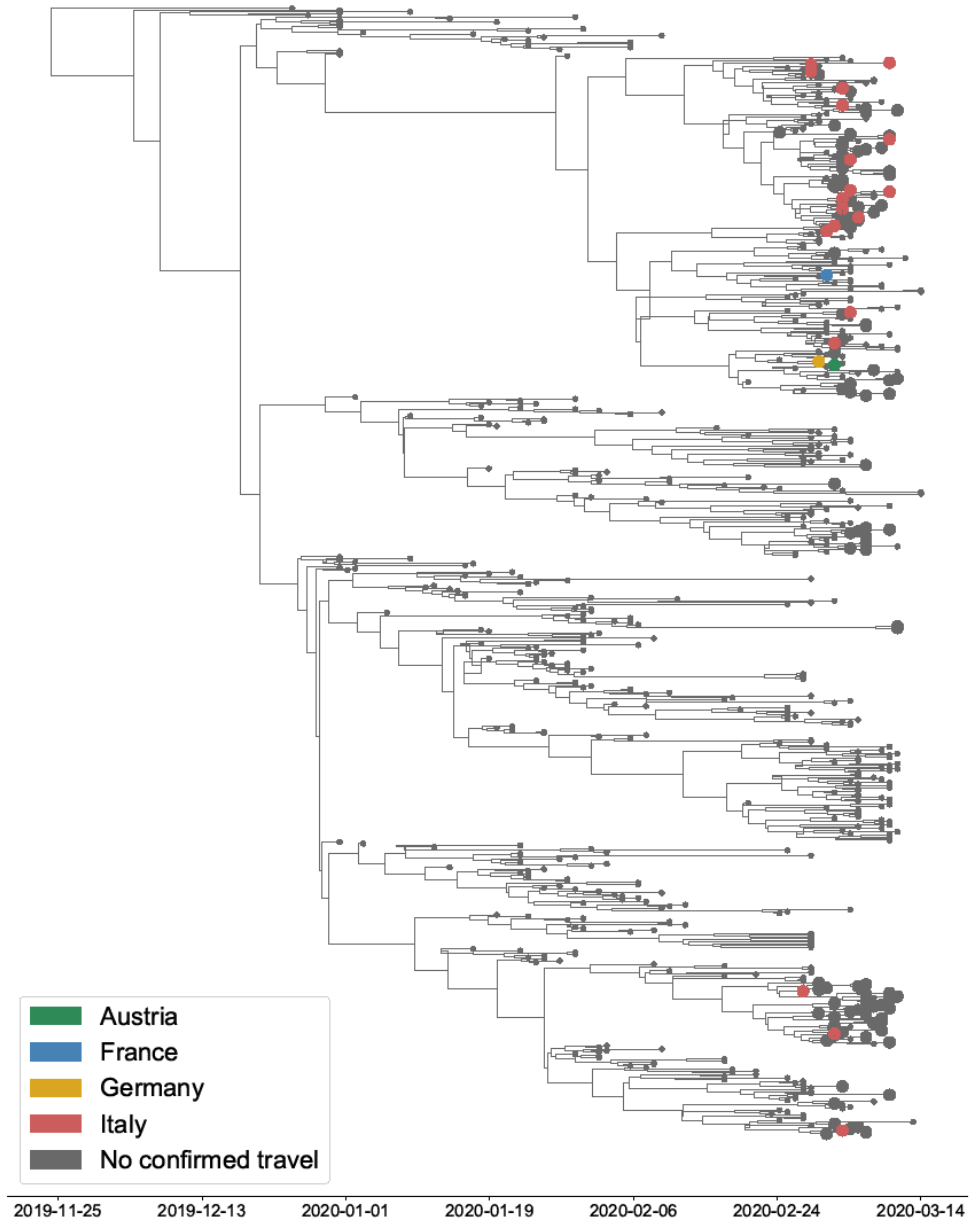
Phase 1: Initial testing of travelers according to the WHO and ECDC case definitions

Phase 2: Inclusion of patients hospitalized with severe respiratory infections





Phase 3: Systematic sequencing during exponential growth phase



Patient

HCW

Other

Instelling A

Instelling B

Instelling C

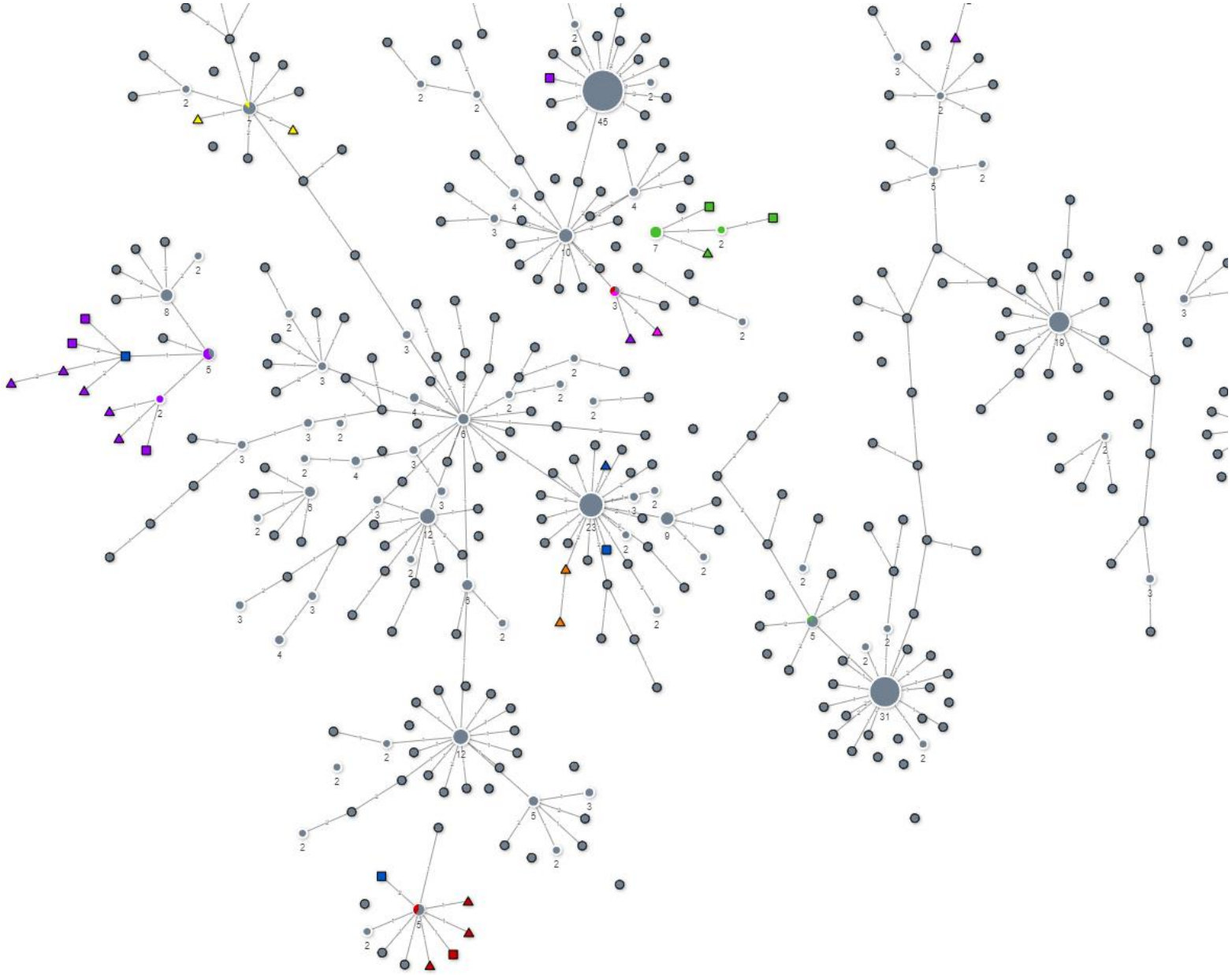
Instelling D

Instelling E

Instelling F

Instelling G

Dutch patient

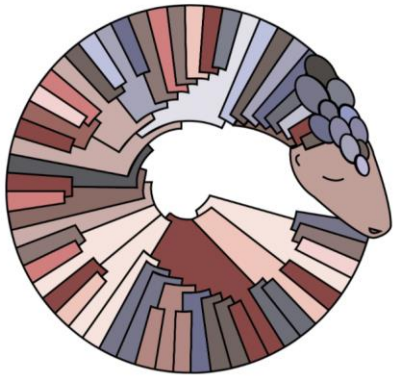


>2 nucleotide afstand onzichtbaar

Dutch situation report

pangolin

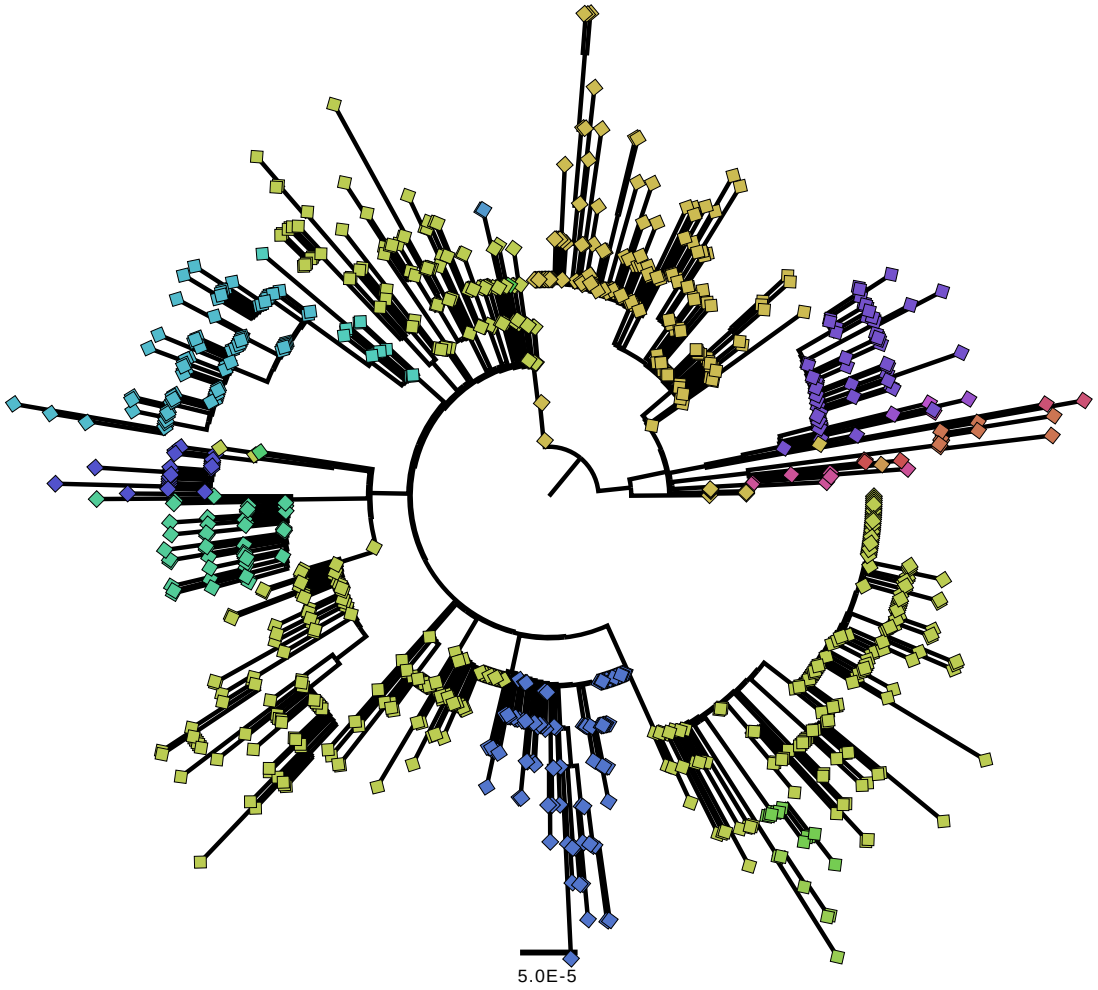
Phylogenetic Assignment of Named Global Outbreak LINeages



Aine O'Toole and Andrew Rambaut

Lineage

- A
- A.2
- A.5
- B
- B.1
- B.1.1
- B.1.10
- B.1.11
- B.1.13
- B.1.22
- B.1.5
- B.1.5.2
- B.1.7
- B.1.8
- B.1.9
- B.2
- B.2.1
- B.2.3
- B.2.5
- B.3
- B.4



Ongoing..

- Monitoring of relevant mutations
- Longitudinal monitoring patients
- Household studies
- Animal studies

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Consortium partners

University of Antwerp

Inserm

中国科学院上海巴斯德研究所
Institut Pasteur of Shanghai
Chinese Academy of Sciences

Institut Pasteur

UNIVERSITY OF OXFORD

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