

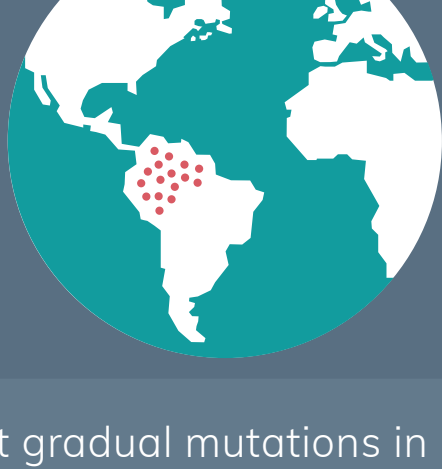
Infectious disease surveillance

Outbreaks of infectious disease are an ongoing risk.

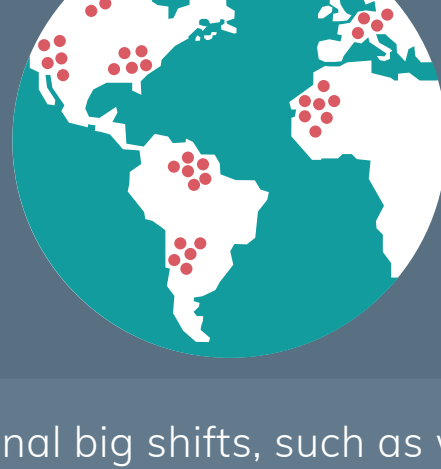
Novel variants of existing pathogens, or entirely new pathogens with pandemic potential, are of particular concern because of the time needed to understand the disease and to develop control measures and treatments.

Influenza surveillance

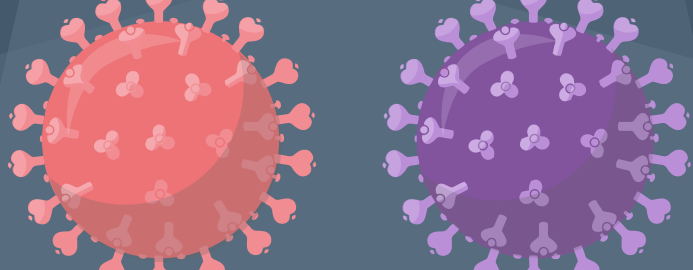
Influenza is a global health concern.



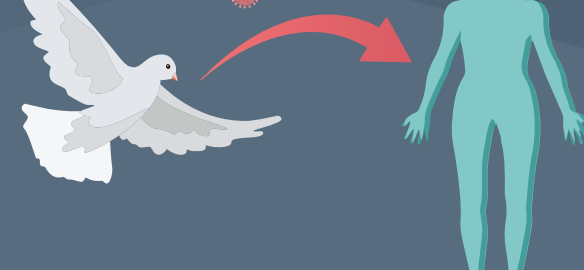
Constant gradual mutations in influenza viruses, combined with seasonal weather, drive regular **epidemics**.



Occasional big shifts, such as when an animal influenza virus gains the ability to infect humans, can cause **pandemics**.



There are two main strains of influenza virus, A and B, that are responsible for seasonal epidemics.



Avian influenza, which causes heavy losses in birds, is of particular concern as a potential emerging pathogen in humans.

Genomic surveillance of influenza enables:



Prediction of future outbreaks: Viral genome sequencing enables ongoing surveillance and identification of new emergent strains, such as monitoring avian influenza spillover into humans.



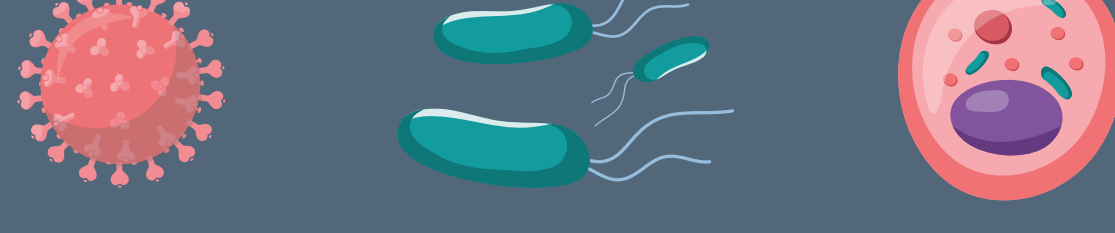
Seasonal surveillance: Monitoring allows a better understanding of the evolution and epidemiology of seasonal influenza.



Vaccine development: Genomic surveillance of circulating viruses can aid the development of new vaccines before an outbreak occurs.



Influenza genomes can be difficult to characterize with traditional short-read sequencing technology as segments cannot be sequenced end-to-end, making it challenging to identify variants with high accuracy. Samples may also need to be sent to a separate facility for sequencing, leading to long turnaround times.

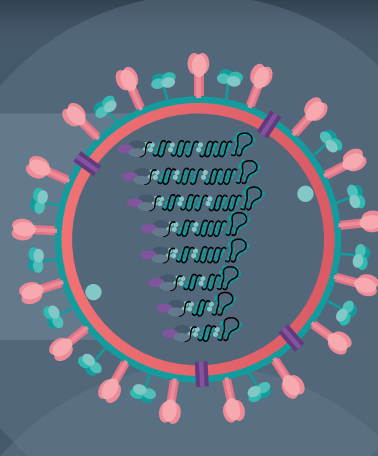


Nanopore sequencing has delivered actionable insights into pathogen surveillance and outbreaks around the world, including viral (e.g. swine influenza), bacterial (e.g. *Mycobacterium tuberculosis*) and fungal pathogens (e.g. *Candida* spp.).



Benefits of nanopore sequencing for viral genomes:

Resolve even the most complex viral genomes, such as segmented viruses, with long nanopore reads



Sequence in your own lab with simple, complete workflows



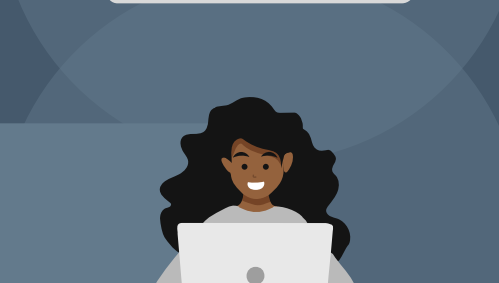
Flexible, scalable and portable devices that enable sequencing at the point of an outbreak



Immediate and easy analysis; the workflow provides an easy to interpret report



Keep data in house



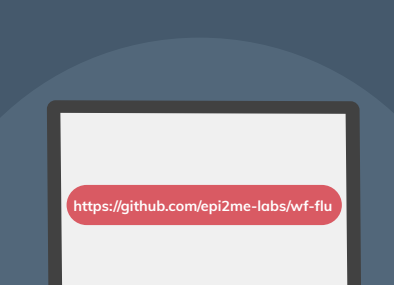
Access efficient, cost-effective influenza surveillance



Influenza virus whole-genome sequencing with Oxford Nanopore: complete workflow

Extract RNA

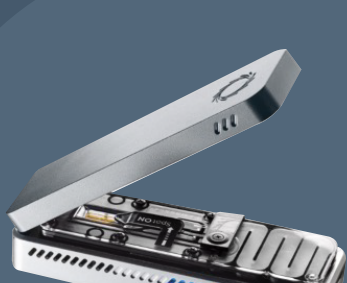
Analyze with the wf-flu analysis workflow



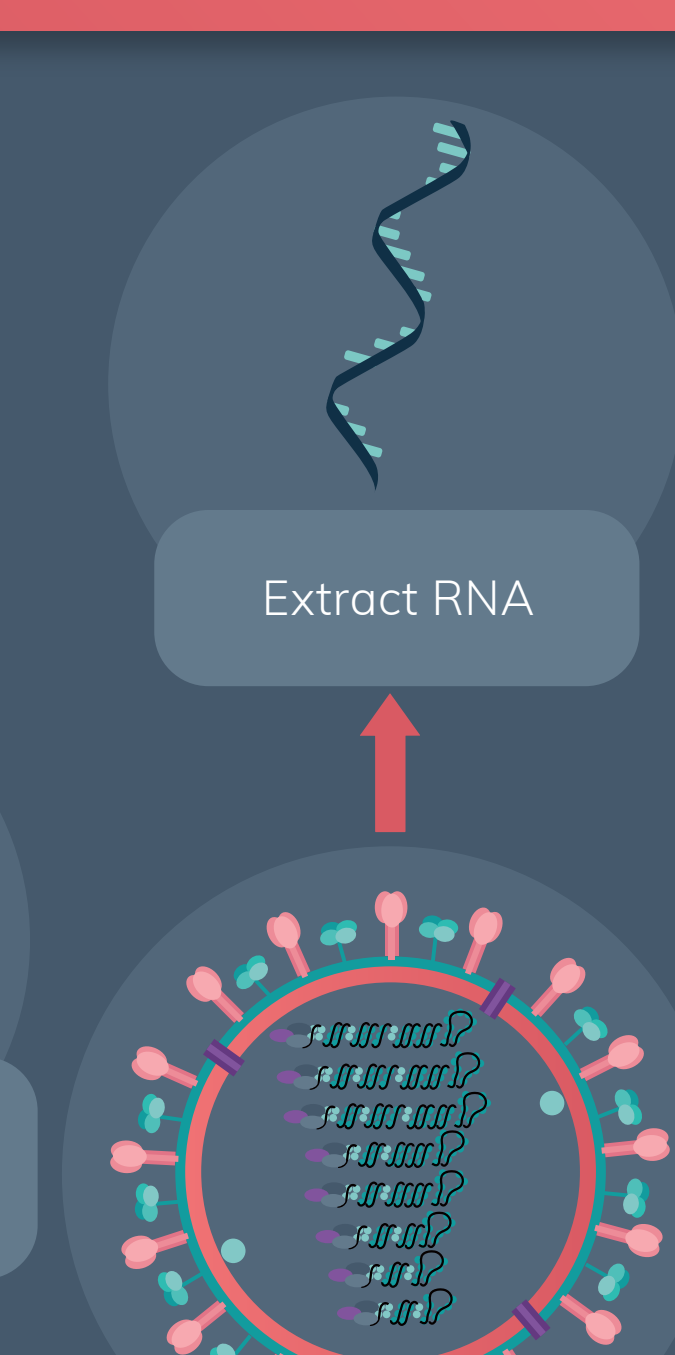
Perform RT-PCR



Sequence up to 96 samples on a single MinION Flow Cell



Ligate barcode adapters using the Oxford Nanopore Native Barcoding Kit



[Click here to find out more.](#)