CHASING THE CLONES

How ECDC is investigating* cross-border outbreaks of tuberculosis caused by *Mycobacterium tuberculosis* clones.

DISEASE SURVEILLANCE AND REPORTING

An EU Member State informs ECDC in Stockholm about a cluster of multidrug-resistant TB (MDR TB).**

ECDC contacts its TB network: Are there cases with the same characteristics in other Member States?

NO → Isolated national cluster, no further action from ECDC.

YES → Fictitious scenario
Potential cross-border outbreak! Nine countries report cases with the same characteristics. ECDC launches a cluster investigation.

Were the genomes of the *M. tuberculosis* strains sequenced?

NO → **Assistance and coordination**
ECDC assists the countries to have their samples analysed in a European laboratory equipped to perform whole genome sequencing for *M. tuberculosis*.

YES → Submitting the results

SUBMITTING THE RESULTS

All samples are now sequenced. ECDC receives DNA sequence files for all samples

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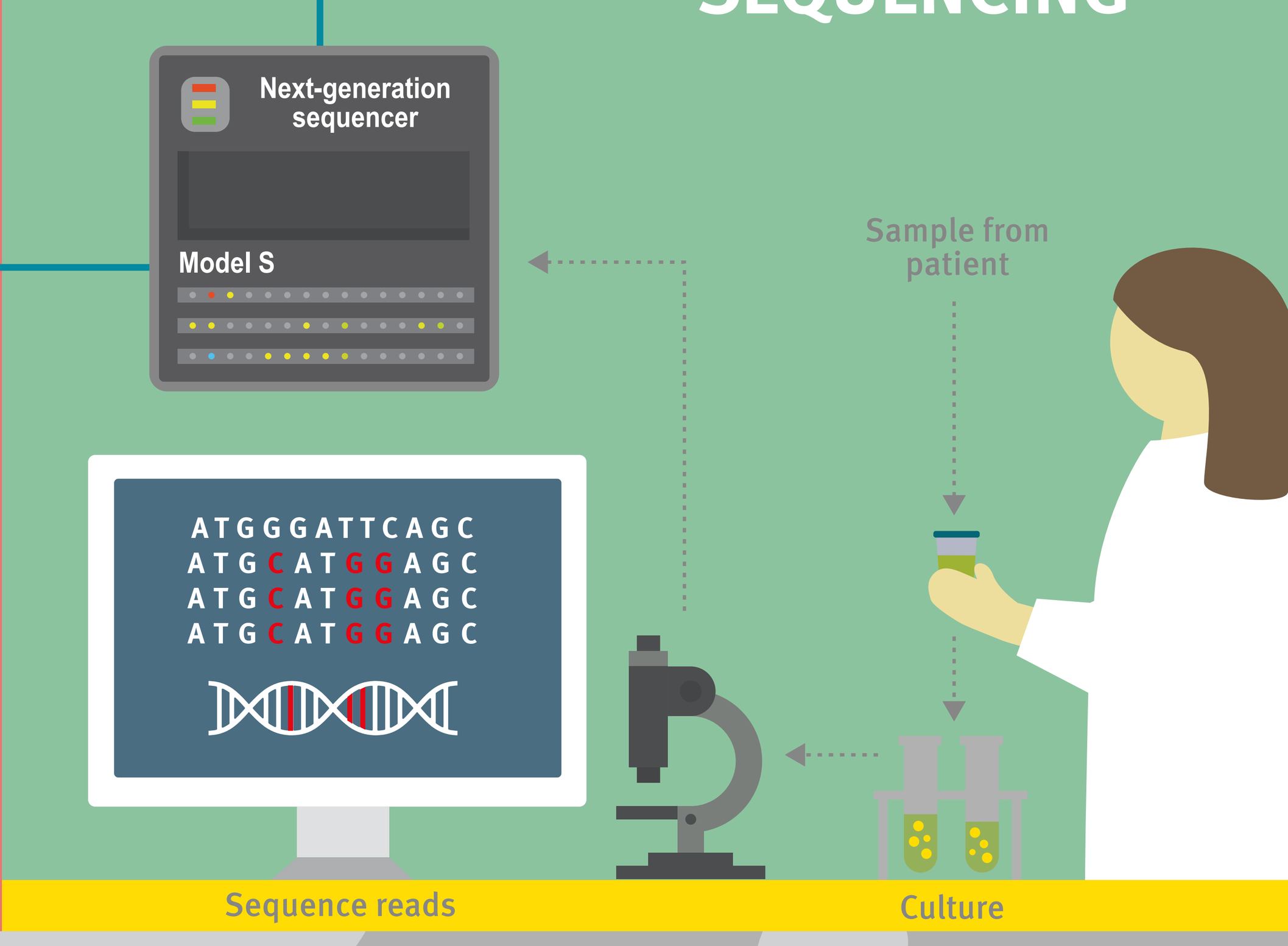
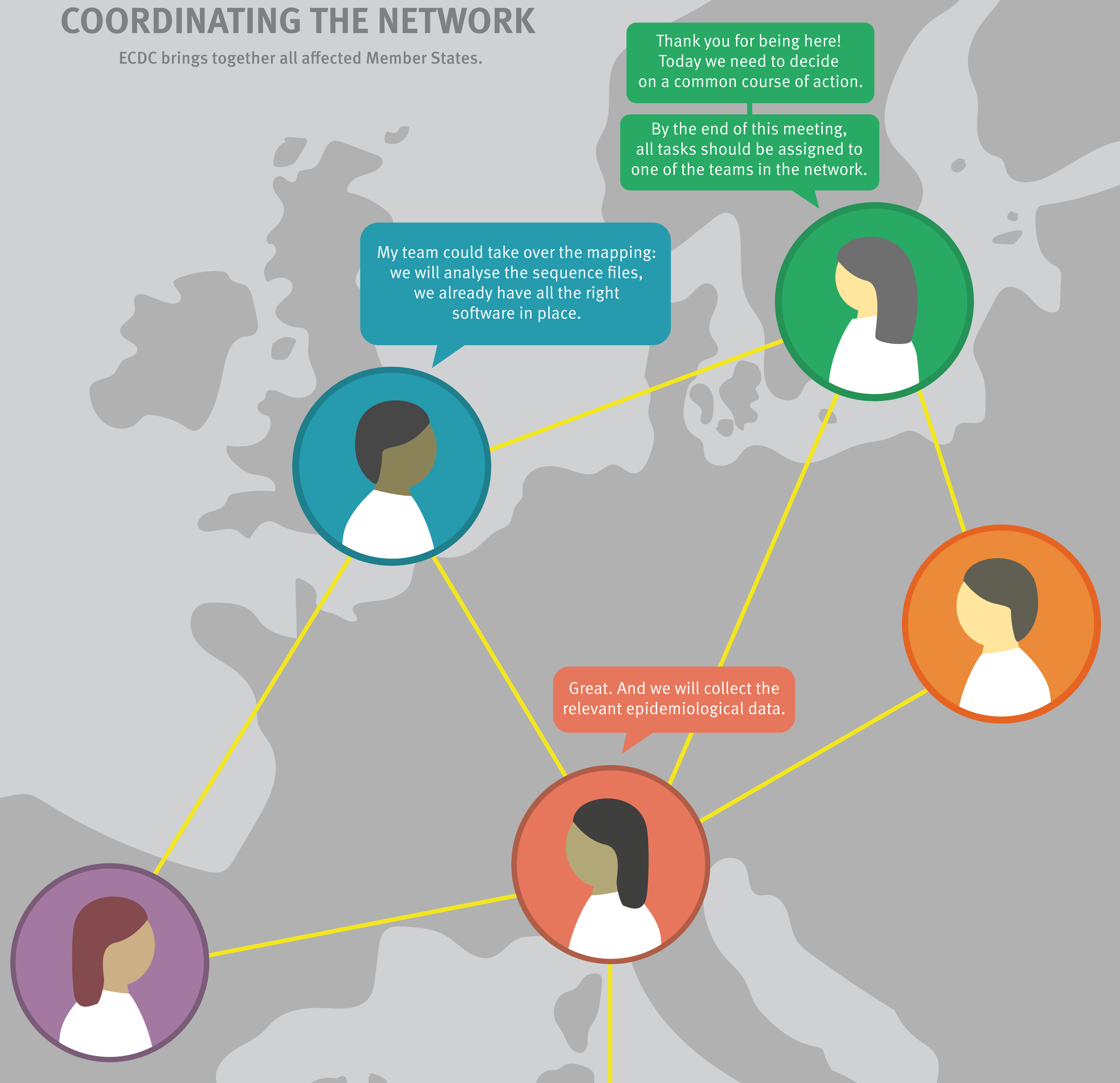
SEQUENCING



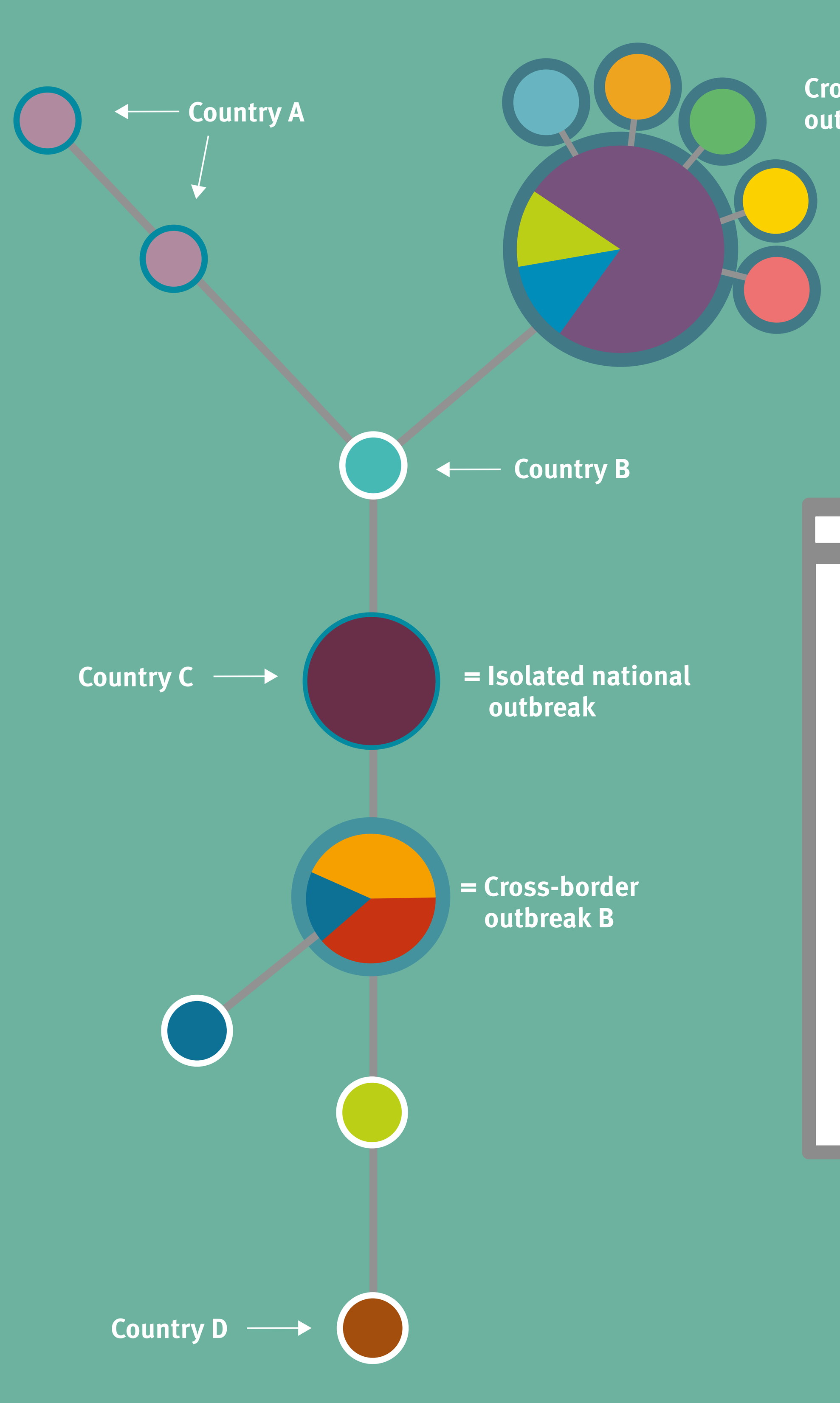
COORDINATING THE NETWORK

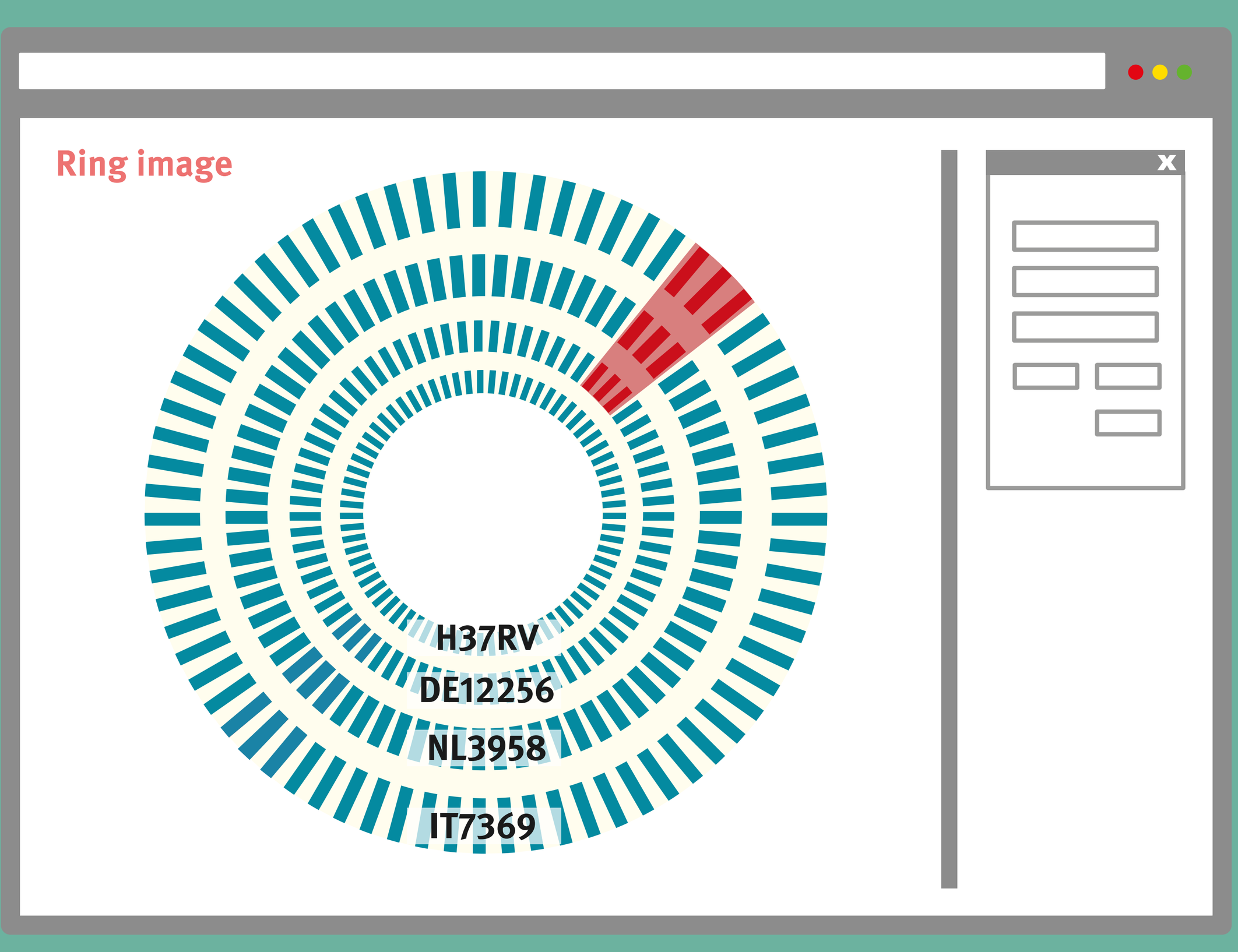
ECDC brings together all affected Member States.



DATA ANALYSIS AND INTERPRETATION

Sophisticated software is used to analyse and visualise the genomic and epidemiological data





RESULTS (FICTITIOUS SCENARIO)

Out of a total of 25 MDR TB patients, 13 patients – diagnosed in eight countries – were diagnosed with the same *M. tuberculosis* clone.

DISSEMINATION OF RESULTS

ECDC can now confirm an outbreak of MDR TB in eight countries.

Detailed information is sent to the Member States and the WHO Regional Office for Europe.

Further steps will be taken to detect additional cases linked to this outbreak and to assess what public health measures are needed.

* While the procedures illustrated here are accurate and scientifically correct, some details are fictitious.

** The ECDC pilot project on the use of whole genome sequencing for molecular typing and characterisation of *M. tuberculosis* in the EU/EEA was initiated in autumn 2017. It aims to establish common standards for WGS in the Member States and improve the understanding of strain diversity in multidrug-resistant tuberculosis, the characterisation of emerging multidrug-resistant clones, the detection and tracing of outbreaks, and the mapping of transmission routes of multidrug-resistant tuberculosis.