Online epidemic tracking tool embraces open data and collective intelligence

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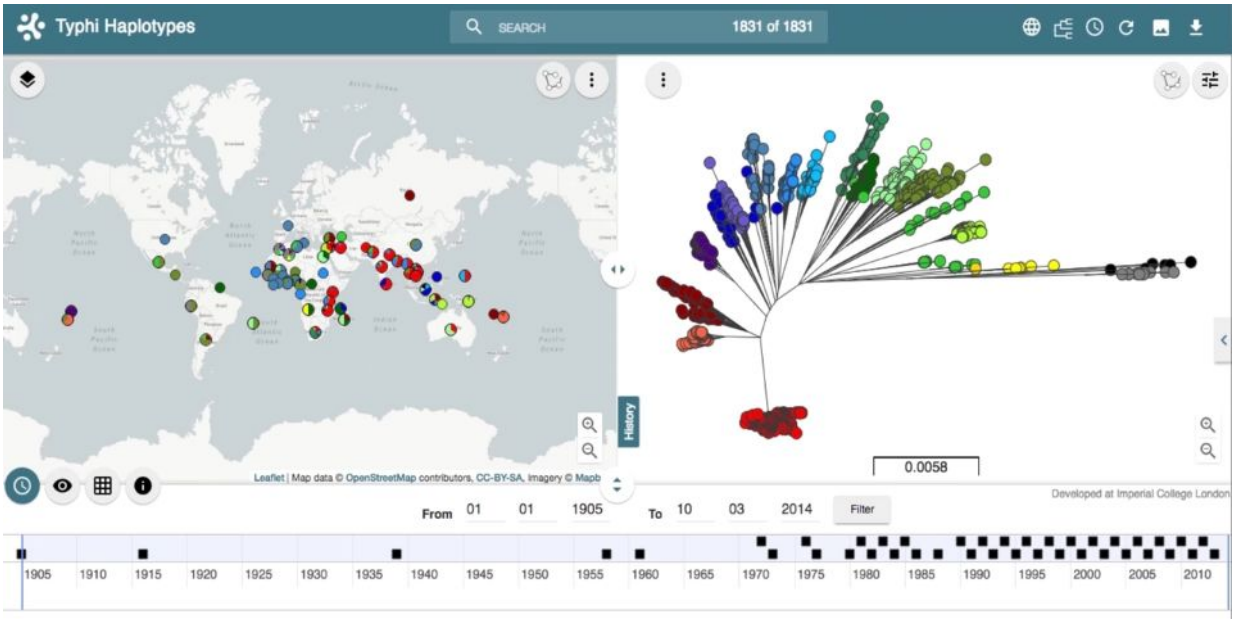

Researchers from the Wellcome Trust Sanger Institute and Imperial College London have developed Microreact, a free, real-time epidemic visualisation and tracking platform that has been used to monitor outbreaks of Ebola, Zika and antibiotic-resistant microbes. The team have collaborated with the Microbiology Society to allow any researcher around the world to share their latest information about disease outbreaks. Details of the platform are published in the journal *Microbial*

Genomics today.

Until now, disease data and geographic information about the movement of an infection or disease as it evolves and spreads has been locked up in databases that are often out of people's reach. Researchers have been left to rely on published information in research papers, which may be many months out of date, containing static visuals which show only a small part of the whole disease or infection threat.

Microreact is a cloud-based system that combines the power of open data and the web, to provide real-time global data sharing and visualisation, allowing anyone to explore and examine outbreak information with unprecedented speed and detail. This is becoming increasingly important in the race to monitor and control fast-developing outbreaks like Ebola or Zika, or the growing threat of anti-microbial resistance.

Microreact allows data and metadata sets to be uploaded via a web browser, which can then be visualised, shared and published in a research paper via a permanent web link. The partnership with *Microbial Genomics* allows the journal to make data from prospective publications available through Microreact. This promotes open availability and access while also starting to build a unique resource for global health professionals and scientists.

Dr David Aanensen, Director of the Centre for Genomic Pathogen Surveillance (a joint initiative between Imperial College London and the Sanger Institute) and one of Microreact's creators, said: "Until now, the global research community has been hamstrung because results are generally only shared in static pictures or tables in publications. Microreact allows everyone to explore the information dynamically - across both time and space - letting them see the whole picture. Using Microreact takes disease tracking out the hands of a privileged few and

gives it to everyone who wants to understand disease evolution."

One example of how Microreact can democratise genomic data and resulting insights is the work of Dr Kathryn Holt and Professor Gordon Dougan. They have recently published two papers on the global distribution of typhoid bacteria around the world, showing the epidemic spread of a multidrug resistant strain. But they also published their data to Microreact to help others build on their work.

Dr Kathryn Holt, from the University of Melbourne, said: "We gathered together data from almost 2000 samples Salmonella Typhi bacteria collected by 74 collaborators in 63 countries. By comparing the different strains and mapping them to when and where they were 'caught' we were able to show that a new drug-resistant strain emerged in Asia and has spread across that continent and into Africa. We have put all this information on Microreact and now anyone can see exactly what we saw - both scientists and those public health professionals tasked with controlling such outbreaks."

By putting this information on Microreact, the researchers have ensured that the data continues to live on - allowing others to learn from their work and to use the information as a basis of comparison or foundation for future work. Microreact also allows individual researchers to share information globally and in real-time - crowdsourcing new discoveries and insights that could have immediate impact.

Leighton Chipperfield, Director of Publishing at the Microbiology Society said: "We are delighted that our open-access, open-data journal Microbial Genomics is partnering with Microreact. All Microreact projects that appear in *Microbial Genomics* papers will be highlighted on the journal's website to increase the discoverability and accessibility of researchers' datasets."

More information: Global typhoid distribution in Microreact - microreact.org/project/styphi

Microbial Genomics, DOI: 10.1099/mgen.0.000093

Vanessa K. Wong et al. An extended genotyping framework for Salmonella enterica serovar Typhi, the cause of human typhoid, *Nature Communications* (2016). DOI: 10.1038/ncomms12827

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