

# Genomics and social network analysis team up to solve disease outbreaks

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Combining the cutting-edge technology of whole genome sequencing of bacteria with social networking analysis, public health officials can get a more detailed picture of disease outbreaks that will better help track and stop them, say researchers today at the 111th General Meeting of the American Society for Microbiology.

"Public health agencies are now able to harness the power of genome sequencing, which, when combined with the detailed clinical and epidemiological data we have access to, allows us to reconstruct outbreaks and really understand how a pathogen moves through a population," says Jennifer Gardy of the British Columbia Center for Disease Control, presenting a case study where she and her colleagues used this new technique to track and eventually stop a tuberculosis [outbreak](#) in the province.

An outbreak of tuberculosis occurred over a 3-year period in a medium-sized community in British Columbia. In order to stop the event, public health officials turned to traditional epidemiological methods to identify the source and other contributing factors, but the results were hazy.

The researchers combined two [new tools](#) to get a clearer picture of the outbreak: social network analysis, which has become increasingly common in tracking [infectious diseases](#) in the past decade, and whole-genome sequencing (analysis of the entire microbe's DNA), which has become cheaper and less time-consuming over the past few years.

"The complete genome sequence of a pathogen is the ultimate [DNA fingerprint](#), and now, with the costs and time associated with genome sequencing dropping almost exponentially, it is possible to sequence most or all of the bacterial isolates taken from and outbreak," says Gardy

And while it may sound like something having to do with Facebook, social network analysis takes traditional epidemiology one step further, asking patients about more than just with whom they have been in contact. In this case Gardy and her colleagues asked patients for a detailed account of their time on a daily basis including where they went and what they did at those places.

"Instead of getting a list of names, you are getting names, places and behaviors, and you can paint a much more detailed picture of the underlying structure. Key people and places and certain behaviors that might be contributing to an outbreak's spread become much more apparent and allow you to adjust your outbreak investigation in real time as this new information becomes available," says Gardy.

Using this new combinatorial technique, the researchers eventually determined that the outbreak was likely not instigated by genetic changes to the pathogen, but was instead likely due to increased usage of crack cocaine in the community. The disease was being transmitted in crack houses where people were coughing often while spending hours together in poorly ventilated rooms.

Additionally they were able to determine that a few key individuals acted as superspreaders, and these people were socially well connected and symptomatic for long periods of time. This information is being used in a current outbreak investigation where public health officials are trying to target socially popular people for screening as a priority.

"We took an outbreak that was an absolute mystery by traditional

methods and solved it using [genome sequencing](#) and social network analysis," says Gardy who calls this and other genomic epidemiological studies "a new and exciting direction for epidemiology and the study of infectious disease, particularly for public health agencies."

Provided by American Society for Microbiology

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