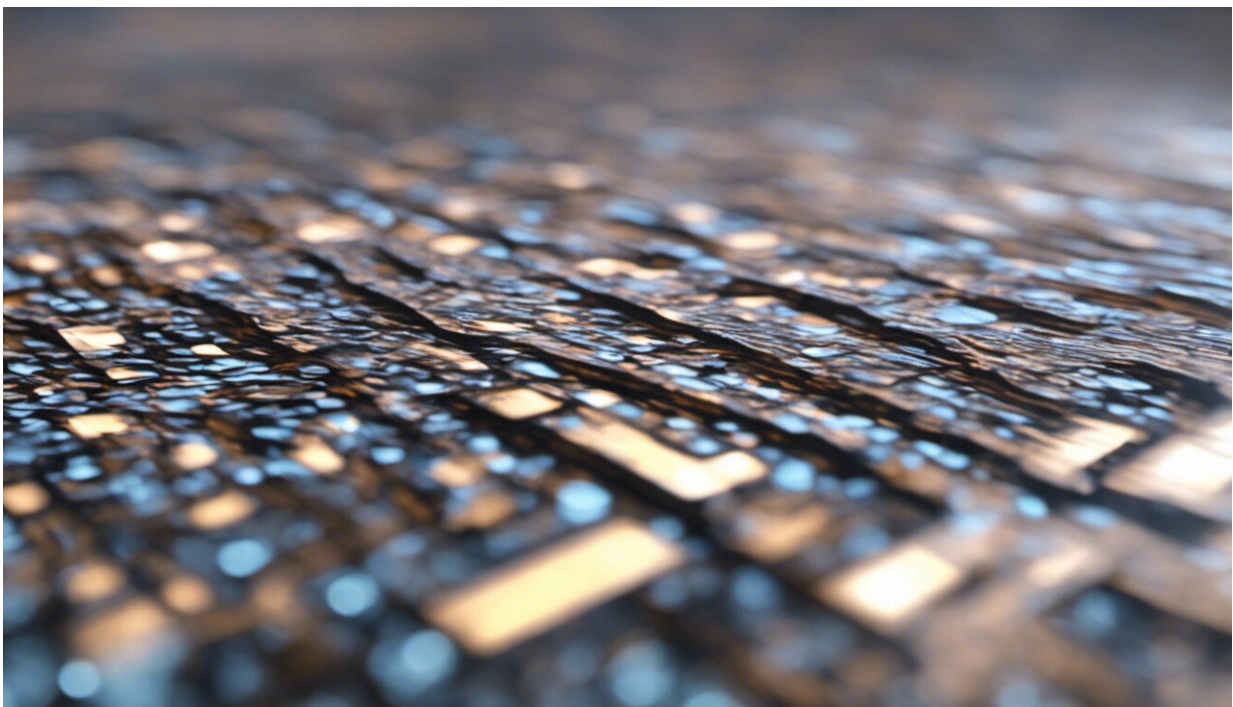


Computing helps the study of infections on a global and local scale

June 6 2016, by Jodie Mcvernon, Joshua Ross, Kathryn Glass, Lewis Mitchell, Nicholas Geard And Rob Moss



Credit: AI-generated image ([disclaimer](#))

Millions of people suffer each year from infectious diseases which are responsible for about [a quarter of all deaths worldwide](#). But tracking the cause of such illness and trying to avoid their spread is always a challenge.

For example, more than [15,000 Indigenous Australian children](#) suffer from [skin sores \(impetigo\)](#) at any one time.

The majority of these infections are caused by a bug called Group A streptococcus ([GAS](#)). This can trigger abnormal immune reactions that result in chronic heart and kidney disease.

Penicillin is a highly effective treatment for this condition, but the number of children infected hasn't changed in 20 years. To find solutions to this apparently intractable problem, we clearly need a fresh approach.

Crunch the data

This is where computers can help. With funding support from the National Health and Medical Research Council, we aim to revisit 20 years' worth of study data generated by the Menzies Research Institute, in Darwin.

Using mathematical models, we hope to develop a better understanding of the drivers of high skin sore rates.

We also need to collect detailed data on the rich social connections within and between remote communities in the Northern Territory that could spread infection. We will develop computer simulation models that represent these linkages and their likely contribution to infection risk.

The findings of these models will hopefully inform consultation with communities about prevention and treatment approaches to keep children healthy.

So why hasn't this approach been used before?

Better computing power

Mathematical and computational models of infection are not new. But their capacity to deal with multiple data sources, and represent detailed human interactions and differences, has dramatically increased in recent years due to advances in technology.

Increased [computing power](#) lets us combine diverse and complementary information to provide a richness that is difficult to capture with a single study. We can combine data from disease surveillance systems, observational studies and clinical trials.

With such data from many countries and regions we can then estimate the global number of [infections and associated deaths](#).

This process is particularly helpful for diseases of poverty, such as skin sores, as the greatest burden is usually experienced in settings where resources are constrained and health information systems are often limited.

Using computer models we can fill the gaps in incomplete, uncertain and variable data. We can also reflect data uncertainty through best-case and worst-case estimates.

On the move

New methods for collecting data on human movements, and the social interactions responsible for the spread of infections, have led to fresh opportunities for incorporating behavioural aspects into models. Mobile phone data allows for high-resolution patterns of [social behaviour and mobility](#).

Wearable sensor devices that monitor movement, closeness to others and speech patterns can be used to collect data on [short and long-range social connections](#), even in remote and hard to reach areas.

Insights into attitudes that underpin health-related behaviours, such as choosing whether to immunise, may be studied using social media. But given the vast amounts of [data](#) available through these sources, separating signal from noise remains a significant challenge.

Faced with such diverse sources of information, the next step is to make sense of it all.

Simulations of disease spread

Computers have made it possible to simulate populations and the [disease transmission](#) process in very fine levels of detail.

Individual-based models (IBMs, not to be confused with the computer tech company [IBM](#)) can explicitly represent each member of a population, and their demographic and health characteristics (think of [The Sims](#) computer game, but with more sneezing). We can then simulate how interactions between people lead to the spread of disease.

Prior to the advent of modern computing, the calculations required for this type of model would have been prohibitive. IBMs were first used to model disease transmission in the 1970s to [simulate the spread of influenza](#) in a population of 1,000 people. Each person was represented by a single punch card!

Distributed computing now makes it possible to simulate populations containing [millions of people](#).

IBMs are an important tool for understanding how complex patterns of

geographic distribution, transport and mobility and social behaviour underlie the emergence and spread of epidemic diseases such as [pandemic influenza](#) and [Ebola](#).

Obviously, the behaviour of individuals and their impact on disease transmission, cannot be determined exactly. But, once again, advances in computing have allowed us to accommodate this variability by incorporating an element of chance in models.

Rather than running a single "what if" scenario, we can produce millions of alternatives, representing many possible pathways of [infection spread](#). These simulations help us understand the variation observed in patterns of disease in different populations, and explore the full range of outcomes that might be witnessed in the future.

This process helps [assess risks](#) and develop locally applicable public health management plans for efficient and effective disease prevention and control.

Optimising intervention strategies in this way is particularly useful when health sector resources are [thinly stretched](#).

We won't eradicate [infectious diseases](#), but computers provide us with new tools and approaches to reduce health inequalities and their associated long-term disease burden.

This article was originally published on [The Conversation](#). Read the [original article](#).

Source: The Conversation

Citation: Computing helps the study of infections on a global and local scale (2016, June 6)

retrieved 5 May 2024 from

<https://medicalxpress.com/news/2016-06-infections-global-local-scale.html>

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