How to stop an epidemic

The models built by mathematicians like Professor Mick Roberts, of Massey University at Albany, have saved many people from sickness and death.

He builds and analyses models of how infectious diseases spread in populations, to determine how pathogens can be controlled or eliminated.

"In 1996, I built a model of measles in New Zealand and analysed the current vaccination policy." The measles, mumps and rubella vaccine was then scheduled at 15 months and 11 years. "I showed that that was not going to prevent recurrent epidemics of measles; as a result the Ministry of Health changed the schedule to 15 months and four years."

"With whooping cough (which is caused by a bacterium) the result was the opposite," says Roberts. "An immunisation had to be added at age 11 because the vaccine protects for up to 10 years, unlike measles which gives protection for life."

"We get new viruses every year; for example, there are three seasonal influenza viruses, H1N1 and H3N2 - which are both influenza A - as well as influenza B." These viruses are slightly different each year. "Each flu season you get a mixture of all of them in different proportions."

"We get a pandemic when there's a major shift in a virus, leaving most people with very little protection." Roberts also helped with the ministry's pandemic planning for SARS. "In 2002, SARS had a four-day period between infection to becoming infectious, so there was time to do some contact tracing."

When exotic diseases enter society, health services need to know where to focus their efforts. "For example, if it's a point of entry for a region, you need to concentrate your resources there and model those networks so the spread of infection is minimised." What interests Roberts is the methodology behind the models.

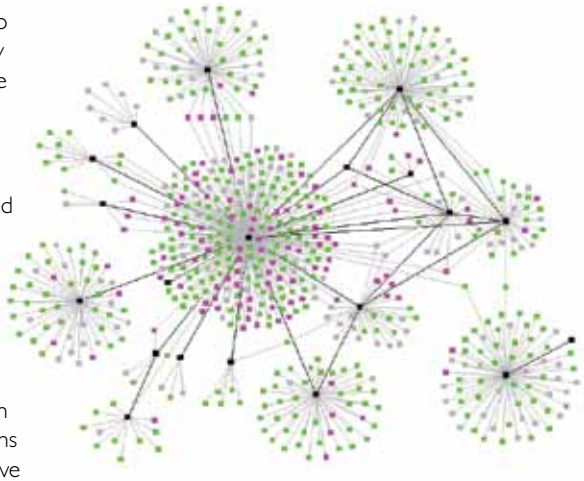
"The contact process is different for each infection – you're not going to get HIV from someone you're standing next to in a bus, whereas flu you could." Models describe how diseases spread through contact networks - based on sizes of households and workplaces and average numbers of people met in a day - and how the structure of these networks might change how infectious diseases spread.

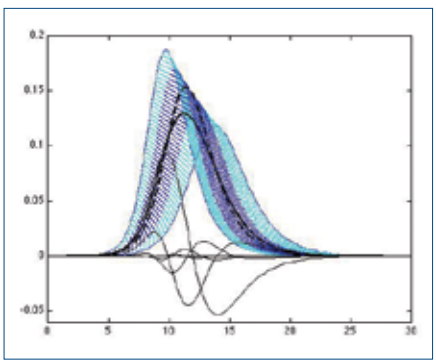
"I'm trying to improve the non-linear differential and integral equations behind the models. They're a highly complicated set of very big equations; we have to find ways to simplify them to something we can actually solve or understand. You can't always solve them but you can assess qualitatively what the solution might look like."

The crucial point is the threshold, where things change drastically. This is represented by the basic reproduction number, R_0. "If the number is greater than one, you can get an epidemic; if it's less you won't," says Roberts. Models for some diseases also have to represent contact between humans and animals; mosquito carriers in the case of dengue fever. He is working on more sophisticated and accurate predictions of the epidemic curve. "Predicting the curve tells us how many people will get sick next week or by the middle of winter. It forecasts the demand on health services."

Roberts' main collaborator for the last 20 years is Professor Hans Heesterbeek of Utrecht University in the Netherlands. Since they shared an office for six months at Cambridge University in the UK they have met almost every year, and their families have become good friends. "Our skills complement each other – we both have good intuition in different areas. The results we get are better than the sum of our individual abilities."

Below: Mapping the spread of contagion with contact tracing, © 2003 by Valdis Krobs, www.orgnet.com/contagion.html, used with permission.
Bottom: An epidemic curve.





$$R_0 + \frac{1}{p}\log\left(1 - \frac{N}{S(0)}p\right) = 0$$

Statistics and forensic evidence

Professor James Curran, of the University of Auckland, consults with forensic agencies in New Zealand, Australia and the UK, producing expert systems software to interpret crime evidence. He has also appeared as an expert witness about DNA and glass evidence in the USA and Australia.

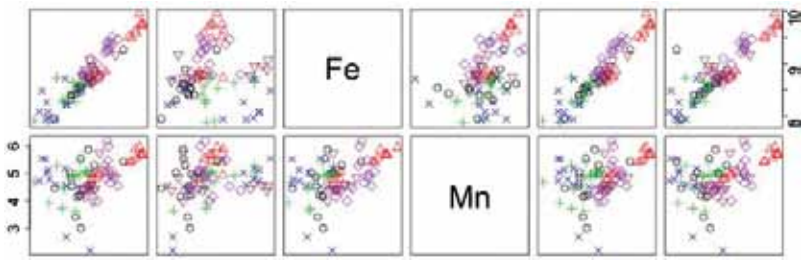
Curran's work has helped interpret evidence involving DNA, glass, mosquitoes, cellphone records and stolen pounamu. "Most law enforcement agencies spend their money on DNA, so that's the bulk of my work," he says. Globally, the number of forensic statisticians is small, as generally they need to be attached to a forensic agency to access crime scene data.

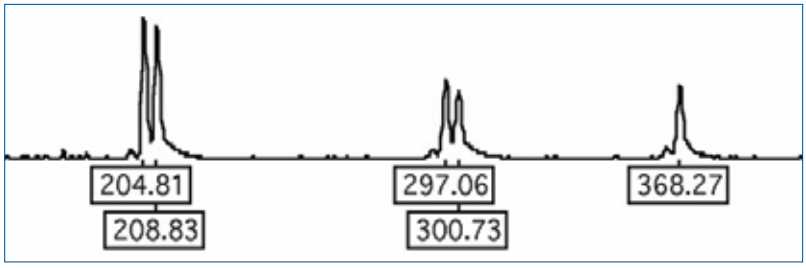
DNA evidence can be gathered from as little as ten cells, but it is often not as clear cut as juries expect from watching TV forensic shows, instead involving subjective interpretation and judgement calls. To interpret DNA, forensic scientists compare differences in the length of two alleles at standard places on the chromosome. "The position of the two peaks tell us the length variant, and their height reflects the amount of DNA in the sample," says Curran. "If it's all from one person, there should be clear spikes of the same height across the profile, but when there is small amount of DNA that may not be the case. We're trying to understand what controls this."

Forensic statisticians use standard statistical tools such as log-linear modelling and Bayesian estimation to model the stochastic behaviour of evidence. The weight of the evidence is presented in court using a likelihood ratio.

Curran gives an example of a break-in where the burglar cut himself and left a blood stain, and the suspect's DNA matches the stain. "The statistician has to calculate the likelihood of the match if the suspect left the blood at the scene, or someone unrelated left the blood. The likelihood ratio is the ratio of these two quantities. Using standard population genetic models, they can say the evidence is 3.8×10^{13} times more likely if the suspect left this blood rather than if someone unrelated left the blood."

Samples of mixed DNA from two people are common in rape cases. "The bulk of the DNA is usually from the victim and smaller peaks are from the offender," says Curran. These profiles have up to four peaks at each locus. There are six different ways that four peaks may be assigned to two people. This increase in the number of possibilities weakens the strength of the evidence.





"Many profiles have small bumps next to the peaks, called stutters. In a mixed sample, the stutter peak could be confused with the offender's allele." This confusion also weakens the strength of the evidence, and complicates the interpretation.

Glass is a common type of trace evidence, and this field is another heavy user of statistics. Fragments found on suspects are often smaller than a grain of salt; the most common technique compares their refractive index with a sample of control glass from the crime scene. The chemical composition of glass, or any biological or inorganic substance, can also be measured and used to associate evidence with a crime scene or not. One of Curran's recent projects involved a case where a cellphone call was made to a companion in the getaway car by a Dutch bank robber trying to fake an alibi.

"The evidence was a voice echo on the line," he said. "The Netherlands people estimated from their experiments that the echo was about 42 times more likely if the call was made inside a car rather than outside. But they were concerned that this statement was stronger than it should be. Our research concluded that the evidence was about 12 times more likely."

One of Curran's students used multivariate statistics to describe the elemental composition of greenstone from different locations. The research arose from Operation Roar, after which two helicopter pilots were convicted of the theft of 20 tonnes of pounamu. "Old school geologists, used to judging by shape and colour, said we couldn't differentiate between different sources of greenstone using elemental techniques," he says.

"Questions in the interpretation of evidence are primarily probabilistic; we don't know exactly what happened and have to speculate," he says. "Statistics is involved in the same way in most sciences, dealing with variation, and modelling in the face of uncertainty."

Above: Iron and manganese in different outcrops of Wakatipu pounamu.
Left: An electropherogram showing tiny DNA stutter peaks to the left of the main peaks.