12. Mathematical modelling: a key to control of infectious
diseases in man and animals

McLean AR, Anderson RM. Epidemiol Infect 1988; 100: 419–442

AN APPRECIATION BY PETER MORGAN-CAPNER
Crow Trees, Melling, Carnforth, Lancashire, UK
(pete.m-c@breathe.com)

Predicting the impact of infectious diseases on the
well-being of the community is a cornerstone of
identifying effective prevention, control and support.
One only has to reflect on the last few years in the
United Kingdom to see the impact mathematical
modelling has had on public and government, with
controversy around the likely numbers of sufferers
from new-variant Creutzfeld–Jakob disease, human
immunodeficiency virus, and continuing debate as to
whether to use vaccine to support control of foot-
and-mouth disease. Over the last 20–25 years,
Epidemiology and Infection, and before it the
Journal of Hygiene, have published many of the sentinel
papers in the mathematical modelling of infectious
disease, both in humans and animals. The discipline
has advanced from relatively simple analyses to the
most complex assessments whose underlying math-
ematics and statistics almost certainly exceed the
comprehension of all but a few microbiologists and
public health specialists. The depth of the analysis
does not obscure the key messages, however, for the
epidemiology of infectious disease and its control, and
a Special Article in the journal in 1988 overviewed its
contribution [1].

In 1988, McLean and Anderson published their
prediction of the impact of mass vaccination on the
transmission dynamics of measles in developing
countries [2]. Uncontrolled measles has a devastating
effect on the health of children, with even now some
one million deaths a year in developing countries. Yet
we have had effective live attenuated vaccines avail-
able since the early 1960s, and successful eradication
in much of the developed world. Predicting how to
use vaccine optimally to eradicate measles in the
developing world presents problems not seen with
such modelling in the developed world. For instance,
the high mortality rates and high population growth
have a significant impact on virus transmission.
McLean and Anderson concluded from their analyses
that there was no single optimum age to immunize
children in developing countries, that a temporary
phase of low incidence would follow mass vacci-
nation, but recurrent epidemics will appear later, and
that a one-stage programme aimed at young children
is of greater benefit than two-stage programmes. A
key parameter to be calculated in such analyses is the
basic reproductive rate of infection \( (R_0) \) – ‘the average
number of new cases that would be generated if one
infectious individual were introduced into a wholly
susceptible population’ [3]. If a vaccination strategy
were to ensure \( R_0 \) is less than 1, eradication is
achievable. Calculating \( R_0 \) is dependent on having the
appropriate data. To provide the basic data to enable
mathematical modelling to be meaningful requires
information on the epidemiology of the infection in
the community being studied. In a previous paper,
McLean and Anderson reviewed available informa-
tion on measles in developing countries [4]. Data
included duration of protection from maternally
derived antibodies, age distribution of infection, age-
stratified serological profiles, measles fatality rates,
and fertility/mortality age profile.

It is not only in developing countries that mathe-
matical modelling has led to major vaccine initiatives.
In 1994, the United Kingdom had a mass measles/
rubella vaccine campaign aimed at children aged 5–16
years. This campaign was carried out to avert an anti-
cipated epidemic in older children and younger adults.
This was presaged by modelling the age-stratified
measles antibody profile (‘seroepidemiology’) of the
population, and deducing that susceptibility was building
in the target population as a consequence of failure to
achieve the necessary high levels of immunization
with mumps, measles and rubella vaccine since its
introduction in the United Kingdom in 1988, whilst
demic measles had been reduced to the levels where
exposure was unlikely [5, 6]. This build-up of suscep-
tibles was becoming sufficient to support a major
demic, as indeed happened in Scotland in 1993.

These studies have confirmed the importance in
having high-quality seroepidemiology information
available: robust age-stratified serological infor-
mation on exposure and immunity of the community
based on validated techniques. Such information, and
the resultant conclusions on epidemiology and con-
trol, have now been presented in the journal for a wide
range of human viral infections, but particularly
measles, rubella, mumps and varicella-zoster [7–18],
bacterial infections such as whooping cough [19–23],
and parasitic infections [24, 25]. Studies also include
infections in animals [26–28], including prion diseases
[29], and from many parts of the world. International
collaborative studies have been performed [30], and
are now being reported which compare the efficacy of
the different strategies for vaccine use in Europe and
beyond [9, 12, 14, 23]. Mathematical modelling is an
essential part of understanding the epidemiology of
infectious disease, and hence its control.

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