

# Network modelling of Tuberculosis dynamics: transmission hotspots and Welsh pubs!

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see [http://www2.warwick.ac.uk/fac/cross\\_fac/wider/](http://www2.warwick.ac.uk/fac/cross_fac/wider/)

## Background and motivation

Tuberculosis (TB) is an infectious disease caused by the bacteria *Mycobacterium tuberculosis* that affects human populations world wide particularly in developing countries. The disease is potentially lethal if left untreated, and is difficult to treat, requiring a long course of antibiotics. TB is currently declining globally but incidence in the UK has risen in the past decade (see Walker et al. 2013).

TB transmission is intimately dependent on the patterns of social contacts of individuals in the population. A large proportion of the transmission is thought to occur within the household, but the role of contacts in the wider community in generating and sustaining epidemics is often unclear. In this project we are motivated by a 'real world' example - a sustained outbreak of TB that is occurring in Wales and is being monitored by health authorities. As a result of monitoring by the Welsh National Health Service (NHS), social contact networks of infected individuals have been obtained. In collaboration with NHS Wales, we aim to develop a model describing transmission dynamics of TB using network modelling techniques. There is strong potential for continuing the research as part of a PhD program.

## Objectives

We will develop a network model describing the dynamics of TB transmission in a human population. The model will be used to explore how aspects of network structure, including clustering and wider community contacts, can influence the spread of the infection. Model development will be guided by data from our study site, and we will compare the results to real epidemic trajectories associated with the Welsh outbreak. The models will aim to incorporate important aspects of the biology of TB infections including latency, reinfection and immunity.

## What the student will do:

A network model will be constructed based on principles of network theory and tailored to the community in our study region. The student will have the opportunity to interact with our collaborators from the NHS and gain valuable experience in applying mathematics to real epidemiological problems. The network model will be combined with a disease transmission model that reflects important aspects of the biology of TB infection. This will involve a combination of programming, simulation and analysis of theoretical disease transmission models. Regular interaction with our research group with our research group WIDER (Warwick Infectious Disease Epidemiology Research) will also be possible at weekly group meetings - see [http://www2.warwick.ac.uk/fac/cross\\_fac/wider/](http://www2.warwick.ac.uk/fac/cross_fac/wider/)

## Skills and techniques

The project is ideally suited to a student with strong numerical/computational skills and an interest in applied modelling and epidemiology. The student will have the opportunity to experience interdisciplinary research in the epidemiology of infectious disease, a highly mathematical field of study. The project provides the opportunity to interact with public health professionals.

## References

Cohen et al. 2007, Exogenous re-infection and the dynamics of tuberculosis epidemics: local effects in a network model of transmission, *Journal of the Royal Society Interface*, 4, 523-531.

Walker et al. 2013, Whole-genome sequencing to delineate *Mycobacterium tuberculosis* outbreaks: a retrospective observational study, *The Lancet*, 13(2), 137-146.

