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ScienceDirect
Journal of Health Economics 27 (2008) 405–426
JOURNAL OF HEALTH ECONOMICS
www.elsevier.com/locate/econbase

# Modelling geographic variation in the cost-effectiveness of control policies for infectious vector diseases: The example of Chagas disease☆

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Received 23 January 2006; received in revised form 24 April 2007; accepted 30 April 2007
Available online 5 December 2007

**Abstract**

Few cost-effectiveness analysis (CEA) models have accounted for geographic variation in input parameters. This paper describes a deterministic discrete-time multi-state model to estimate the cost-effectiveness of vector control policies for Chagas disease, where implementation varies according to village characteristics. The model outputs include the total number of new infections, disability adjusted life years (DALYs) incurred, costs of associated healthcare, and total costs of the Ministry of Health's control policy for house surveillance and spraying. Incremental net benefits were estimated to determine Colombian villages in which it is cost-effective to implement the control policy. The robustness of these conclusions was evaluated by deterministic sensitivity analyses. The model should help provide a decision-support system to compare control policies and to allocate resources geographically.


*JEL classification:* C6-Mathematical Methods and Programming

*Keywords:* Mathematical modelling; Cost-effectiveness analysis; Infectious vector diseases; Incremental net benefit analysis; Geographical information system (GIS)

## 1. Introduction

Whilst economic evaluation has been transformed in recent years by increasingly sophisticated approaches to the analyses of uncertainty (Claxton, 1999; Coyle et al., 2003) less attention has been paid to explaining the geographical variability of incremental cost-effectiveness ratios (ICERs) or net benefit statistics, despite concerns about the transferability of evidence (Walker and Fox-Rushby, 2000; Drummond and Pang, 2001). Where modelling or trial-based

☆ This research was funded by the Wellcome Trust.
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doi:10.1016/j.jhealeco.2007.04.005

economic evaluations have considered variation, most research has concentrated on costs (Sculpher et al., 2004) and on transferring cost-effectiveness ratios across national boundaries (Willke et al., 1998; Mulligan et al., 2003; Tan-Torres et al., 2003).

One possible reason for the paucity of modelling focussed on geographic variation within countries is the concern that specific locations will or will not be funded for an intervention, which Sculpher et al. (2004) imply can be a politically unpopular basis for decision-making. Nevertheless, there are occasions where location already influences funding and provision of health services, therefore providing a realistic decision context for studying the potential variation of ICERs. An alternative reason for the lack of explanatory evidence on variation in ICERs could be availability of relevant data. However, a potentially useful link could be made to geographic information systems (GIS) which have rarely been linked to costs of health interventions (e.g. Claborn et al., 2002) despite examples of its use in cost-benefit analysis within environmental and transport economics (Bateman et al., 2003) and others highlighting its potential for evaluating public health interventions (Mullner et al., 2004).

Control of the infectious, vector-borne, Chagas disease presents an opportunity to link newly available GIS data to a real decision context to determine how best to use limited funds to target insecticide spraying. In practice, decisions about the use of insecticide spraying are often applied uniformly across a whole country or at district level within a country. This approach may not represent the best use of limited resources where the regional aim is vector control (as for the control of native triatomine bug species such as *Triatoma dimidiata* in Central America) rather than total elimination (as for the control of introduced species such as *T. infestans* in South America), as there is geographic variation in disease incidence. Targeting limited resources on those interventions, and those areas, where they will do most good would improve efficiency.

Our paper constructs a discrete-time model to reflect Chagas disease transmission in a geographically disaggregated manner using data on villages, households and individuals. The model simulates the dynamics of house infestation and human infection in different villages, which is crucial to decisions about the time and scale of control activities. A rational approach to decision-making should set these dynamics in the context of the costs and effects of each competing policy option for detection and spraying.

The model is driven by the information that could be operationally available to policy makers and practitioners. From a practical perspective, the model can be used for two purposes: (i) to determine more cost-effective strategies for vector control and (ii) to prioritise municipalities or villages for interventions (given a budget constraint). In this paper, for illustrative purposes, we focus on vector control decisions made in two endemic departments in Colombia: Boyacá and Antioquia. However, the model is generic enough for application to other settings with a similar organisational structure for surveillance and control of vectors.

The paper sets out some background details about Chagas disease prior to describing the mathematical structure of the model and sources of data in Section 3. Section 4 presents the simulation results obtained for villages in two departments of Colombia and the final section reflects on the contribution and constraints of the model.

## 2. Chagas disease

Chagas disease is an infectious disease, caused by the protozoan parasite *Trypanosoma cruzi*, which is exclusive to the American continent. WHO previously estimated that around 90 million people lived in high risk areas and approximately 18 million are infected; however, over the last decade the number of infected individuals has decreased due to the success of the Southern Cone Programme (WHO, 2002). The most common mode of transmission to humans is by blood-sucking triatomine bug vectors, as transmission via blood transfusion is relatively rare since endemic countries introduced screening of blood banks for the parasite. The vectors are mainly found in rural areas living in the cracks of poorly constructed houses with un-plastered mud walls and floors or in roofs made of thatch or palm.

Chagas disease aetiology progresses in three phases (WHO, 2002). Following infection via a bug, 1–2% of infected people (mostly children) experience acute Chagas disease. Generally, symptoms are similar to flu and last 6–8 weeks, but very rarely patients experience acute myocarditis or severe neurological complications. The second phase is an indeterminate form, which 70–90% of infected people will maintain throughout their lives—with persistent seropositivity but no further symptoms. About 10–30% of infected people will enter a chronic phase after 15 or more