



InterSpread Plus: a spatial and stochastic simulation model of disease in animal populations

M.A. Stevenson^{a,*}, R.L. Sanson^b, M.W. Stern^a, B.D. O'Leary^a, M. Sujau^a,
N. Moles-Benfell^a, R.S. Morris^a

^a EpiCentre, Institute of Veterinary, Animal, and Biomedical Sciences, Massey University, Private Bag 11-222, Palmerston North, New Zealand

^bASUREQuality Limited, PO Box 585, Palmerston North, New Zealand

ARTICLE INFO

Article history:

Received 16 November 2011

Received in revised form 23 August 2012

Accepted 24 August 2012

Keywords:

Simulation models

Disease control

Disease spread

Animal populations

Epidemiology

ABSTRACT

We describe the spatially explicit, stochastic simulation model of disease spread, InterSpread Plus, in terms of its epidemiological framework, operation, and mode of use. The input data required by the model, the method for simulating contact and infection spread, and methods for simulating disease control measures are described. Data and parameters that are essential for disease simulation modelling using InterSpread Plus are distinguished from those that are non-essential, and it is suggested that a rational approach to simulating disease epidemics using this tool is to start with core data and parameters, adding additional layers of complexity if and when the specific requirements of the simulation exercise require it.

We recommend that simulation models of disease are best developed as part of epidemic contingency planning so decision makers are familiar with model outputs and assumptions and are well-positioned to evaluate their strengths and weaknesses to make informed decisions in times of crisis.

© 2012 Elsevier B.V. All rights reserved.

1. Introduction

InterSpread (Sanson, 1993; Sanson et al., 1993) is a computer program designed to provide a framework for modelling the spread of infectious diseases. The 2001 epidemic of foot-and-mouth disease (FMD) in Great Britain was the first time InterSpread was used as a decision support tool during a large, multicentred epidemic as it was evolving (Morris et al., 2001, 2002). This epidemic provided a unique opportunity to evaluate the model's useability and to quantify its ability to predict the location and time of incident FMD-infected premises (Stevenson, 2003). In parallel with further modelling work that evaluated strategies to reduce the size of FMD epidemics following hypothetical incursions into Great Britain (Wilesmith et al., 2003)

InterSpread's design was rationalised with the intention of making it sufficiently flexible to simulate a range of disease conditions (for example avian influenza and classical swine fever) – not just FMD. The result is a revised version of the InterSpread model which we call 'InterSpread Plus.' In this paper we provide a description of the structure and function of InterSpread Plus in terms of its epidemiological framework, operation and use. Detailed descriptions of each of the parameter settings used within the model are provided by Stern (2003).

2. Model description

2.1. Epidemiological framework

We describe the use of InterSpread Plus for modelling disease in domestic animal populations with specific reference to FMD. Within the model the farm is the epidemiological unit of interest, with the model classifying

* Corresponding author. Tel.: +64 6 3505915; fax: +64 6 3505716.
E-mail address: m.stevenson@massey.ac.nz (M.A. Stevenson).

Table 1
Definitions of terms used when describing an InterSpread Plus model.

Item	Details
Airborne spread	Long distance transmission of infection remote from known foci, without history of contact (Donaldson, 1983)
Animals	Individuals (e.g. cattle, sheep, deer, pigs, goats) capable of becoming infected at a given farm location
Animal movement	The act of shipping animals from one farm location to another
Production type	A descriptor variable used to define sub-categories of animal species. For example the terms 'beef cattle' and 'dairy cattle' might be used as production type definitions for cattle
Clinical signs	The stage when disease can be diagnosed via one or more defined surveillance programmes. Usually refers to the appearance of observable clinical lesions, however, within a particular simulation model, it could refer to the stage when a disease-positive animal would return a positive result if testing was carried out
Dangerous contacts	A descriptor for either direct or indirect movement events indicating that the probability of disease transfer as a result of contact is high. The indiscriminate movement of animals from farms in an infected area to farms in a non-infected area would be a practice likely to produce a large number of dangerous contacts
Depopulated	A farm state referring to the situation where all animals have been removed and the farm is no longer considered to be infectious
Detected	The farm state where the presence of disease has been diagnosed in one or more individual animals present on that farm
Direct contact	Physical contact between two individual animals such that if one is infected and the other is susceptible horizontal transmission of disease can occur. Direct contact occurs when animals are transferred from one farm location to another and animals from the source farm make physical contact with animals resident on the destination farm
Farm	A physical location within an area of study capable of becoming infected. A farm may or may not contain animals, however, for a farm to become infected, animals must be present
Farm class	A descriptor variable defining the type of farm enterprise within an area of study. For example those farms that are comprised primarily of cattle might be classified as 'dairy', 'beef breeding', or 'feedlot'
Incubation period	The time interval between the date of infection and the date of onset of clinical signs
Index case	The first farm in an epidemic recognised (detected) as diseased
Indirect contact	Contact between two individual animals mediated by a vector (e.g. a person or insect) or fomite (any inanimate object or substance capable of carrying an infectious organism)
Infected	The farm location state where individual animals at the location have been exposed to an infective agent and are either incubating disease or showing clinical signs of disease
Local spread	Short distance (generally 5 km or less) spread of disease between locations when there is no clear linkage other than geographical proximity
Not at risk	The farm location state where sanitary measures have been applied to render individual animals at the location incapable of becoming infected
Primary case	The first infected farm location in an epidemic (i.e. the farm location that initiates an epidemic)
Processing	The farm location state where individual animals at the location are receiving sanitary measures such as depopulation or vaccination
Silent spread phase	The interval between the date on which the primary case farm was infected and the date on which disease was detected on the index case farm
Susceptible	The farm state where individual animals at the location are capable of becoming infected

farms as either infected or uninfected after a specified simulation period. The term 'farm' is used to refer to physical locations within an area of study and 'animals' refer to the individual units (capable of becoming infected) present at each farm location (Table 1). Details of the data required to develop a model of between-farm spread of infectious disease in InterSpread Plus are shown in Table 2. A central requirement is explicit description of the farm population at risk. This consists of a unique identifier and a set of Cartesian coordinates defining the position of each farm in Euclidean space. For each farm the number of individual animals present are specified as counts with the option to stratify this number by species (e.g. cattle, sheep, pigs, goats, and deer) or production type (e.g. dairy cattle, beef cattle).

Within the model farm location details can be specified as either discrete polygonal units or as points. To define location details in polygon format, a series of Cartesian coordinates are used to define the vertices of the boundary of each farm area. To define location details in point format a single set of coordinates are used, typically the farm centroid. Within the model these data are stored within an R-tree (Guttman, 1984) allowing spatial relationships such as neighbouring farms and farms within a given distance of an infected source farm to be identified.

In addition to defining the number of individual animals present, the model allows for descriptor variables to be associated with each farm. In an agricultural context these descriptors are used to specify farm class (e.g. 'dairy', 'beef breeding', 'beef fattening', and 'mixed'). Once defined, parameters can be associated with each descriptor, allowing the behaviours of each farm class to be characterised. For example regular, short distance movement events might be parameterised for farms with a 'dairy' descriptor whereas infrequent, longer distance movement events specified for those described as 'beef breeding'. The model also allows for non-farm locations (termed 'contact locations') to be defined allowing sites where individual animals congregate on a regular or intermittent basis to be represented. This facility is typically used to represent animal markets, fairs, or rodeos.

2.2. Set states and epidemic history

2.2.1. Set states

InterSpread Plus is a state-transition model (Isham, 1993) meaning that the epidemiological units of interest (farm locations) exist in one of several states at any time, as shown in Fig. 1. The major intrinsic states defined in InterSpread Plus are *susceptible* (individuals on a farm are

Download English Version:

<https://daneshyari.com/en/article/5793924>

Download Persian Version:

<https://daneshyari.com/article/5793924>

[Daneshyari.com](https://daneshyari.com)