Model Description v. 1.0.1
SpreadModel v3.0 / SHARCSpread v1.0

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Document history

Version 1.0 (19 May 2004) – Initial specification
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1. Introduction

This document is intended to be a plain-language description of the simulation model implemented by SpreadModel v3.0 and SHARCSpread v1.0. Its purpose is to facilitate agreement among current team members on details of the model, to provide a basis for functional testing, and to provide the validation committee and future team members with a complete but accessible description of the model.

The description is based on the paper *Modeling alternative mitigation strategies for a hypothetical outbreak of foot-and-mouth disease in the United States* by Mark A. Schoenbaum and W. Terry Disney, the document *SpreadModel Version 3.0 Diagrams and pseudocoding* by Mark A. Schoenbaum and Francisco Zagmutt-Vergara, observations of SpreadModel v2.14 and beta versions of 3.0, and discussions with the project team.

Keywords: herd-level stochastic spatial state-transition simulation

2. Basics

A collection of animals, called a “unit,” is the basis of the simulation. A unit has a production type, size, location, and disease state. The production type may be a single kind of livestock (e.g., “dairy cattle”) or a mixed type (e.g., “sheep and poultry”). Figure 1 shows the states a unit may be in and possible transitions among them.

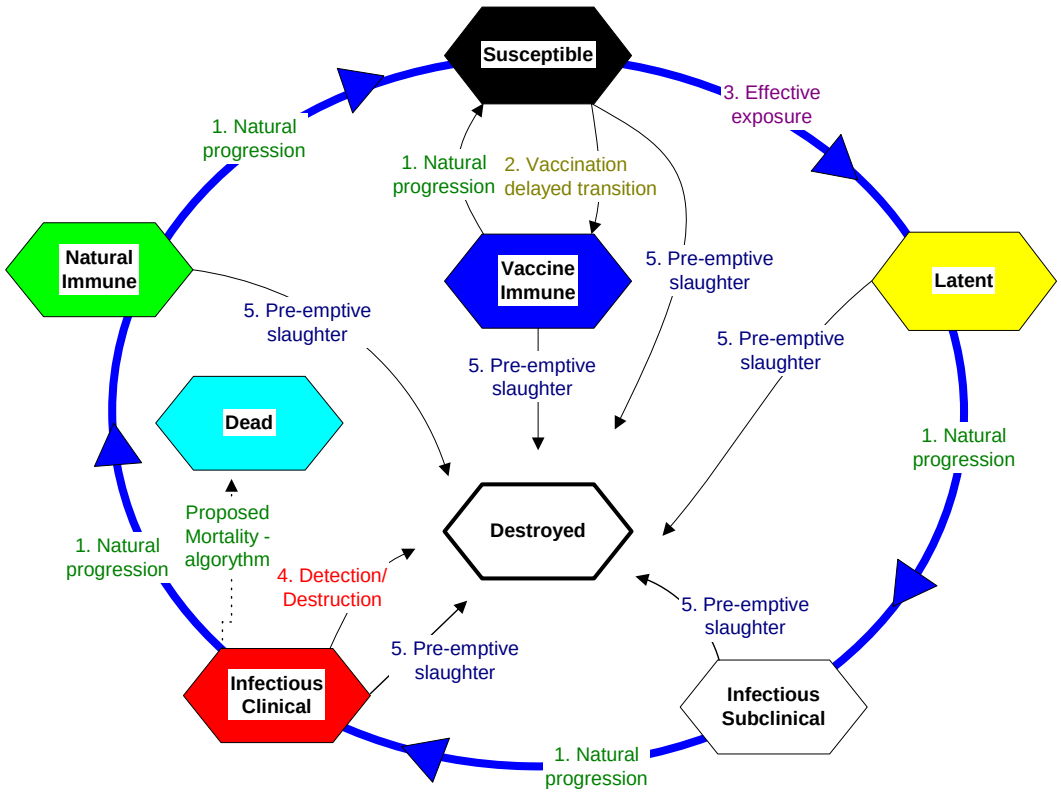

Figure 1. States and transitions

The simulation proceeds in time steps of one day. Each day units may be affected by biological processes happening in the animals (e.g., the natural progress of the disease), processes happening in the environment (e.g., airborne spread), and/or human actions (e.g., detection, vaccination, and destruction). The "model" is the sum of these processes and actions.

3. Disease

When a Susceptible unit is infected, it becomes Latent. The infection progresses in the unit from Latent to Infectious Subclinical (shedding agent without visible signs of disease), to Infectious Clinical (shedding agent with visible signs of disease), to Natural Immune, and back to the Susceptible state. Probability functions characterize the length of the periods and this length is determined stochastically for each new infection. The disease is never fatal, that is, all infected units will eventually return to Susceptible unless destroyed. If time-frames for simulations are long, a particular unit may progress through the infected states more than once.

A unit can spend zero time in a state. For example, the parameter for time spent as Infectious Subclinical can be zero. In that case, units will change directly from Latent to Infectious Clinical.

Attempting to infect a unit that is not Susceptible has no effect.

If two units are at the same location, infecting one does not automatically infect the other.

Parameters:

- latent period (days) [1]
- infectious subclinical period (days)
- infectious clinical period (days)
- natural immune period (days)

The parameters are given separately for each production type. That is, the duration of the disease stages can be different for cattle, pigs, etc.

4. Spread

4.1. Direct contact spread

The simulation of direct contact – movement of animals among units – works as follows:

On each day,

1. Look up a multiplier to adjust the rate of movement of animals based on the number of days since the first detection of the disease. Use this multiplier to scale the movement rate. This approximates applying movement-controls over the course of an infection spreading through the population of units.
2. For each unit *A*,
   (a) Check whether *A* can be the source of an infection. That is, is it Latent, Infectious Subclinical, or Infectious Clinical, and not quarantined?[2] (Infectious Clinical is always a source. Latent and Infectious Subclinical are optionally a source.)
   (b) If *A* cannot be a source, go on to the next unit.
   (c) Sample a number *N* from a Poisson distribution whose mean is the movement rate (adjusted by 1 above).
   (d) Create *N* shipments from *A*.
3. For each shipment,
   (a) Sample a number, *distance*, from the movement distance distribution.
   (b) From all units that can be the target of disease-exposure (that is, those that are not Destroyed or are the source), choose the unit *B* whose distance from the source is closest to *distance*. If several possible targets are the same distance from the source, choose one randomly, giving preference to larger units (a unit with twice as many animals is twice as likely to be chosen).

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[1] indicates a parameter that is given as a probability function.
[2] see section 6. Control measures for a description of quarantine.

(c) If *B* is not Susceptible, the shipment has no effect on the disease state but is recorded as an exposure; go on to the next shipment.
(d) Generate a random number *r* in [0,1), that is, from 0 up to but not including 1.
(e) If $r < P$, the probability of infection given exposure, turn *B* Latent after a shipping delay.

The progress of the disease in the receiving unit starts at Latent, with the duration of each stage of the disease chosen stochastically, regardless of whether the shipping unit was Latent, Infectious Subclinical, or Infectious Clinical. A unit that receives Infectious Clinical animals could technically be regarded as immediately Infectious Clinical (able to infect other units by airborne spread and indirect contact, and detectable by a farmer or attending veterinarian) but starting the receiving herd at Latent reflects the fact that *most* of the animals in the receiving unit have to progress through the earlier disease-stages. The disease-state is an attribute of the unit as a whole rather than a direct reflection of the state of a particular animal in the unit.

Direct contacts (even ones that do not result in a new infection) are recorded and can be discovered later during trace-investigations.

The size of a shipment is not considered, and the number of animals in each unit does not change during the simulation.

The distance between lat_1, lon_1 and lat_2, lon_2 is approximated as:

$$y = lat_2 - lat_1$$
$$x = (lon_2 - lon_1) \cdot \cos(lat_1)$$
$$d = \tfrac{c}{360} \cdot \sqrt{x^2 + y^2}$$

where c = the circumference of the earth.

Parameters:

- Mean rate of movement (recipient-units for shipments per source-unit per day)
- movement distance (km) 
- shipping delay (days)  [1]
- probability of infection given exposure
- movement rate multiplier vs. days since the first detection  [2]

When more than one production-type is considered, the above parameters are specified for each pairing of one production-type with another. Consider the production-types "Beef" and "Dairy", referring to herds of beef cattle and dairy cattle. You specify the most important pairings of these production-types with regard to direct-contact parameters. For example: "Beef" to "Beef", "Beef" to "Dairy", "Dairy" to "Beef", and "Dairy" to "Dairy" are the possible pairings of these production-types. Separate

[1] fixed at 24-48 hours in SpreadModel v3.0.

[2]  indicates a parameter that is given as a relational chart.

parameters are specified for each of these pairs since the direct-contact among different production-type may vary.

Note that parameters are separate for movement in each direction between each pair of production-types. That is, the parameters for movement from "Beef" to "Dairy" can be different from the parameters for movement from "Dairy" to "Beef", and the parameters for movement from "Beef" to say "Pigs" can be different again.

If parameters are given for movements from "Beef" to "Beef" and from "Beef" to "Dairy", the number of shipments a "Beef" cattle herd *A* sends to "Beef" cattle herds on a particular day and the number of shipments *A* sends to "Dairy" cattle herds on the same day are independent.

Shipping animals from a Latent, Infectious Subclinical, or Infectious Clinical unit to a Natural Immune or Vaccine Immune unit has no effect on the disease-stage of the recipient unit. Shipping animals from a unit in a more advanced disease stage to a unit in a less advanced disease stage (e.g., from an Infectious Clinical unit to a Latent unit) also has no effect.

4.2. Indirect contact spread

Indirect contact – movement of people, materials, vehicles, equipment, animal products, etc among units – is simulated in the same manner as direct contact, except that only Infectious Subclinical and Infectious Clinical units, not Latent units, can be the source of infection. The parameters for indirect contact are similar to but independent of those for direct contact.

Indirect contacts can be discovered later during trace-investigations.

4.3. Airborne spread

The simulation of airborne spread works as follows:

On each day,

1. For each unit *A*,
    (a) Check whether *A* can be the source of an infection. That is, is it Infectious Subclinical or Infectious Clinical?
    (b) If *A* cannot be a source, go on to the next unit.
    (c) For each other unit *B*,
        i. Check whether *B* can be the target of an infection. That is, is it Suspectible, is the distance from *A* to *B* < the maximum distance of spread, and is the direction from *A* to *B* inside the wind direction range?
        ii. If *B* cannot be a target, go on to the next unit.

iii. Compute the probability of infection P = probability of infection at 1 km × *DistanceFactor*(A,B) × *HerdSizeFactor*(A) × *HerdSizeFactor*(B).
iv. Generate a random number r in [0,1).
v. If $r < P$, turn B Latent after a delay.

Where
DistanceFactor(A,B) = (maximum distance of spread - distance from A to B) / (maximum distance of spread - 1)
HerdSizeFactor(A) = (area under histogram of unit sizes from 0 to size of A) × 2

The distance between lat_1, lon_1 and lat_2, lon_2 is approximated as before. The direction from lat_1, lon_1 to lat_2, lon_2 is approximated with the inverse tangent using the same x and y.

Airborne spread can occur from and to quarantined units.[1]

Airborne exposure is not recorded since it would not be used directly by mitigation processes such as movement-controls, vaccination, and destruction.

Parameters:

- probability of infection at 1 km from source (Infectious Subclinical or Infectious Clinical unit)
- wind direction, given as a range (*start* and *end*) in degrees
- maximum distance of spread (km)
- airborne transport delay (days) [2]

The parameters are given separately for spread in each direction between each pair of production types. That is, the parameters for spread from pig herds to cattle herds can be different from the parameters for spread from cattle herds to pig herds, to account for potential differences in amount of virus produced and/or different minimum-infective-doses for animals in different production-types.

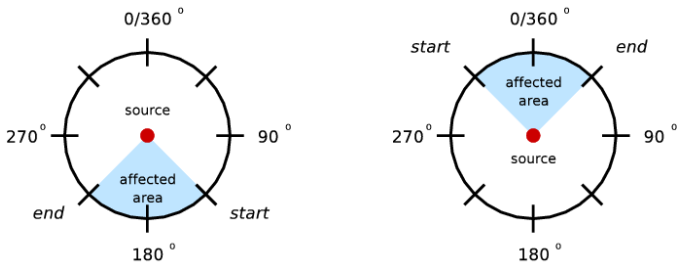

Figure 2. Example parameters for north winds (left) and south winds (right).

[1] see section 6. Control measures for a description of quarantine.
[2] fixed at 0-24 hours in SpreadModel v3.0.

5. Detection

The simulation of detection works as follows:

On each day,

1. Look up the probability that a farmer or attending veterinarian, for example, will report signs of disease to authorities based on the number of days since the first detection in the population. A static probability represents the baseline before the first detection.
2. For each Infectious Clinical unit,
    (a) Look up the probability of detecting signs of disease based on the number of days the unit has been Infectious Clinical.
    (b) Compute the probability of detection and reporting (Equation 1 X 2a).
    (c) Generate a random number r in [0,1).
    (d) If $r < P$, the disease is detected and reported.

There are no false-positive detections.

A report is immediately known to the authorities.

Parameters:

- probability of reporting vs. days since the first detection 
- probability of detection vs. days the unit has been Infectious Clinical 

The parameters are given separately for each production type, to account for the possibility that signs of disease may be more obvious in animals of certain production-types, e.g., signs may be reported more rapidly in intensive swine production systems versus cow-calf operations on pastures.

6. Control measures

6.1. Quarantine

A diseased unit is quarantined as soon as it is detected. Quarantined units cannot be involved in direct contact, but indirect contact and airborne spread may still occur to or from a quarantined unit.

6.2. Destruction

When the first detection happens in the study population, the authorities may initiate a destruction program. It can take several days before the authorities are ready to begin destroying.

All detected units are marked for destruction. Units that have had contact with diseased units within a given number of days prior to detection of the diseased unit (found through trace-investigations) and units within a given distance of diseased units may also be marked for destruction. The destruction of these units associated by trace or distance has been called pre-emptive or dangerous-contact slaughter.

Trace-investigations are immediate. Tracing goes one level forward, that is, it identifies units that have had recent contact with a diseased unit, but not units that have had contact with units that have had contact with a diseased unit, and so on (Figure 3).

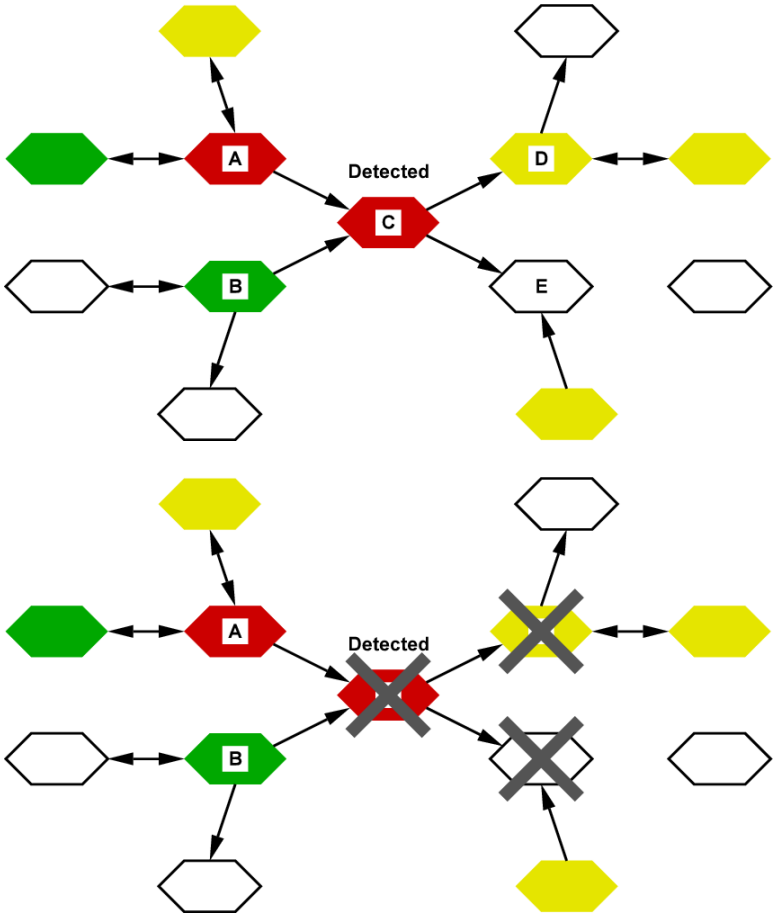

Figure 3. Trace out. When unit C is detected, units to which C has shipped animals or sent people or equipment are marked for destruction. The trace does not extend further (e.g., to units that shipped animals to C, or units that received animals from D).

There is a limit (called Capacity) on how many units can be destroyed per day. If a unit is marked for destruction but cannot be destroyed immediately, it is quarantined and goes onto a prioritized waiting list.

The priorities are set according to production-type, reason for destruction and the number of days already holding for destruction. For example, cattle herds that are marked for destruction because they were detected as diseased may have a higher priority than cattle herds that are marked for destruction because they are near a diseased unit, and pig herds

may have a higher priority still.

No two production-type/reason for destruction combinations can have the same priority. That is, cattle herds that were detected as diseased *must* have a strictly higher priority than pig herds that were detected as diseased (or vice versa), and cattle herds that were detected as diseased *must* have a strictly higher priority than cattle herds that were simply near to a detected unit (or vice versa).

On each day, the authorities destroy as many units as possible (up to the limit) from the waiting list beginning with the highest priority.

Parameters:

- delay to begin a destruction program (days)
- destruction capacity vs. days since the first detection (units per day) 
- probability of a trace-out investigation succeeding
- period of interest for trace-out investigations (days)
- radius of destruction ring (km)

The parameters are given separately for each production type.

6.3. Vaccination

When the disease is detected, authorities may also initiate a vaccination campaign. This consists of vaccinating units within a specified distance of the detected units – in circles or rings around detected units. The decision to vaccinate may be delayed until a certain trigger point is reached in terms of numbers of detected units.

Vaccination orders result in vaccination unless the herd has already been vaccinated recently.

If a unit is marked for vaccination but cannot be vaccinated immediately, it goes onto a prioritized waiting list, which is managed the same way as the waiting list for destruction.

Personnel for destruction cannot be temporarily loaned to vaccination teams, or vice versa, during a simulation run. In other words, the daily limits for destroying and vaccinating operate independently of each other and other production-types as well.

Parameters:

- number of detected units before vaccination begins
- vaccination capacity vs. days since the first detection (units per day) 
- radius of vaccination ring (km)
- minimum time between vaccinations (days)

The parameters are given separately for each production type.

7. Vaccine

When a unit is vaccinated, it remains Susceptible for a time while immunity develops, then becomes Vaccine Immune. The length of the immunity period is decided stochastically for each new vaccination. After the immunity period, the unit reverts to Susceptible.

If a unit is infected after being vaccinated but before turning Vaccine Immune, the effects of the vaccination are cancelled.

Vaccinating a unit that is not Susceptible has no effect on its disease state.

Parameters:

- delay to produce immunity (days)
- immunity period (days) 

The parameters are given separately for each production type.

8. Priorities of action

Because the events in one simulation day should be considered to happen simultaneously, and because different processes may try to make conflicting changes to a unit, there is a need to order or prioritize the processes.

The ordering is:

1. Infection, vaccination, or destruction
2. Biological processes happening inside the animals

(Note that these correspond to the transition labels in Figure 1.)

If a unit is both infected and vaccinated, infected and destroyed, vaccinated and destroyed, or all three on the same day, the order in which these happen is chosen randomly.

If two or more processes infect the same unit on the same day, one process is chosen randomly as the cause of the infection, for the purpose of reporting in simulation statistics. Similarly, if there are two or more reasons for vaccinating or destroying a unit, one reason is chosen randomly for the purpose of reporting.

Some examples illustrating the effects of this ordering:

- If unit *A* is due to change from Susceptible to Vaccine Immune on day *D*, and a shipment of infectious animals arrives on day *D*, *A* is infected. (The exposure happens “before” the natural progression to Vaccine Immune.)
- If unit *A* is due to change from Vaccine Immune to Susceptible on day *D*, and the wind carries virus from an infectious unit on day *D*, *A* is not infected. (The exposure happens “before” the natural progression to Susceptible.)

- If unit *A* is destroyed on day *D*, and the wind carries virus from an infectious unit on day *D*, *A* may be reported in simulation statistics as having been an infected unit or a healthy unit. (Whether the infection happens "before" the destruction is determined randomly.)