

Request for comments

RFC-20070313SD: Replacing the algorithm for airborne spread

1st draft, Seth Dunipace, 13 March, 2007

2nd draft, Anthony "Drew" Schwickerath and Aaron Reeves, 16 April, 2009

3rd draft, Aaron Reeves, 8 May 2009

Applies to: Model description 1.1.1. Proposed for model description 2.0.0.

Summary: This RFC proposes to alter the current formula used for airborne spread, and separates local-area spread and airborne spread into two distinct mechanisms. These changes are proposed for *NAADSM* 4.0.

Justification:

The current formula allows the largest farm in a parameterized model run to be twice as infectious as the median sized farm and it allows for the smallest farm in a parameterized model run to take a near zero value. This is true regardless of the size of the largest and smallest farms. Thus, in a population with farms ranging in size from 400-600 animals and a median size of 500 animals, those farms at 600 will be twice as infectious as the median farm size and those at 400 will be hardly infectious at all. By contrast, in a population with farms ranging in size from 1 to 1000 animals, the difference in infectiousness between a farm of 400 and a farm of 600 would be dramatically less.

The proposed algorithm still accounts for farm size and distance between farms, but only the source and destination farm influence the calculation: unlike in the current method, the rest of the population has no effect on the result.

The existing airborne spread mechanism is almost always used to represent local-area spread. These two mechanisms for the dissemination of disease are probably distinct from one another: "local-area spread" refers to the non-directional spread of disease in the area surrounding an infected premises, while airborne spread is a potentially more complex phenomenon that might occur over considerable distances depending upon climatic and environmental conditions. This RFC proposes the separation of these two mechanisms. Although this RFC still treats local-area and airborne spread a similar computational ways, it would allow users to separately assign more appropriate parameters for these two mechanisms, if desired. The separation of these two mechanisms will also make it possible in the future to introduce more sophisticated approaches for modeling long-distance aerosol dissemination of disease.

The footnote shown below clarifies existing model behavior, as well as behavior of the proposed new algorithm.

A new version of *NAADSM*, tentatively called "*NAADSM* 4" is proposed for the incorporation of these changes. Like *NAADSM* 3, "*NAADSM* 4" will be a herd-based model. Because the proposed changes are not backward-compatible with existing versions of *NAADSM*, a new major version number is required. Similarly, the major version number of the model description would be incremented to 2.0.0.

Conceptual change: The formula to be used for both local-area and airborne spread to determine the daily probability of spread between a source and a recipient premises (P) would be changed to the following:

$$P = 1 - \exp(-k((n_A \times p_A) \times n_B)/d_{AB})$$

Where:

k is a constant related to the infectiousness of the disease being modeled
 n_A is the herd size of infectious farm A
 p_A is the prevalence of infectious animals on farm A
 n_B is the herd size of susceptible farm B
 d_{AB} is the distance between farms A and B

The only required parameter for this algorithm is the constant k . It will likely be easier, however, for the user to enter several values that can be used to compute k , rather than enter it directly.

In order for the model to calculate k , the user would need to enter the following parameters (the user interface might suggest reasonable starting values for these):

n_i is the number of infectious animals in source herd i

n_j is the number of susceptible animals in recipient herd j

d_{ij} is the distance between herds i and j

P is the probability that, on any given day, herd i will infect unit j by local-area spread

From this point, k would be calculated with

$$k = -1 \times [\ln(1-P) \times d_{ij}]/(n_i \times n_j)$$

This calculated value k could then be used as a constant in the formula as the sizes and distances between farms vary over the course of the model run

Notes: k would be determined once for each possible production type combination (*i.e.*, beef to dairy transmission, dairy to beef transmission, beef to beef transmission).

This correction would allow for a more consistent distribution of infectious values and probabilities across farm sizes than the current population-dependent approach.

This correction would also make it impossible to have a value greater than 1 for the probability of local-area spread from one farm to another.

Typical calculations using this formula are shown below. (Note that a direct comparison to values generated existing algorithms is not possible, because of the population dependency of the existing algorithms):

Changes to specification:

Change 1: Section 4.3 of the model specification would be altered as shown below. New text is highlighted, old text is struck out. (The changes are applied to existing text for the linearly declining probability of local-area spread. The text related to exponentially declining probability of local-area spread would be rendered obsolete, and removed entirely.)

4.3. Airborne Local area spread

The simulation of local-area 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 recipient target of an infection: that is, is it Susceptible? ~~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. ~~If using linear dropoff, Compute the probability of infection~~

$$P = 1 - \exp(-k((n_A \times p_A) \times n_B)/d_{AB})$$

$$P = \text{probability of infection at 1 km} \times \text{DistanceFactor}(A,B) \times \text{HerdSizeFactor}(A) \times \text{HerdSizeFactor}(B)$$
 If using exponential dropoff,

$$P = (\text{prevalence in } A) \times \text{HerdSizeFactor}(A) \times (\text{probability of infection at 1 km})^{\text{distance from } A \text{ to } B} \times \text{HerdSizeFactor}(B)$$
 If a within-unit infectious prevalence chart has not been specified for the source unit production type, ~~that~~ **the prevalence** term is dropped from the calculation.

 If using linear dropoff,

$$\text{DistanceFactor}(A,B) = (\text{maximum distance of spread} - \text{distance from } A \text{ to } B) / (\text{maximum distance of spread} - 1)$$

$$\text{HerdSizeFactor}(A) = (\text{area under histogram of unit sizes from 0 to size of } A) \times 2$$
 - iv. Generate a random number r in $[0,1)$.
 - v. If $r < P$, turn B Latent after a delay.

Where

- k is a constant calculated as shown below
- n_A is the herd size of infectious farm A
- p_A is the prevalence of infectious animals on farm A
- n_B is the herd size of susceptible farm B
- d_{AB} is the distance between farms A and B

$$\text{DistanceFactor}(A,B) = (\text{maximum distance of spread} - \text{distance from } A \text{ to } B) / (\text{maximum distance of spread} - 1)$$

$$\text{HerdSizeFactor}(A) = (\text{area under histogram of unit sizes from 0 to size of } A) \times 2$$

The distance between lat_1, lon_1 and lat_2, lon_2 premises 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 .¹

For each combination of source and recipient production types, the constant k is calculated from the following input parameters:

d_{ij} , the distance between two arbitrary herds i and j
 n_i , the number of infectious animals in source herd i
 n_j , the size of a susceptible recipient herd j
 P_{fixed} , the probability that, on any given day, unit i will infect unit j by local-area spread

k is then calculated as:


$$k = -1 \times [\ln(1 - P_{fixed}) \times d_{ij}] / (n_i \times n_j)$$

~~Airborne~~ Local-area spread can occur from and to quarantined units.

~~Airborne~~ Local-area exposure cannot be traced.

Parameters for ~~airborne~~ local-area spread

Parameters for each pair of production types:

- d_{ij} , the distance between two arbitrary herds i and j
- n_i , the number of infectious animals in source herd i
- n_j , the size of a susceptible recipient herd j
- P_{fixed} , the probability that, on any given day, unit i will infect unit j by local-area spread
- ~~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)~~ 

The parameters are given separately for spread in each direction between each pair of production types between each combination of potential source and recipient 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.

¹ Mathematically, the formula for local-area spread allows the possibility of infection over an infinite distance. For computational purposes, the maximum distance over which local-area spread can occur is estimated by the distance at which the largest herd in the study area would have a 1 in 1 million chance of becoming infected by the local-area spread mechanism.

Change 2: The existing figure 4.5 would be moved to a new section describing airborne spread (see below).

Change 3: The existing figure 4.6 will be replaced with the following:

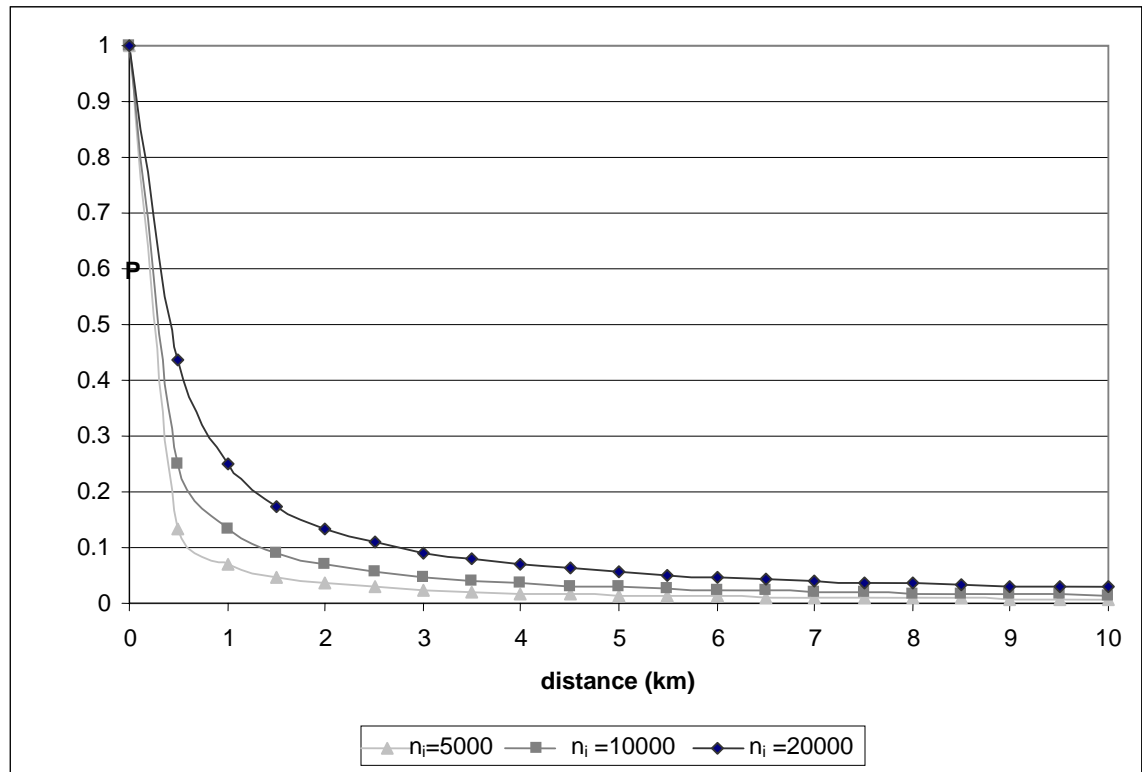


Figure 4.5. Probabilities of local-area spread from a premises with 20,000 infectious animals to premises of various sizes. Parameters used to generate these curves were $P = 0.25$; $n_i = 5,000, 10,000, \text{ or } 20,000$ animals as shown; $n_j = 20,000$ animals; $d_{ij} = 1$ kilometer. From these parameters, k is calculated as $7.19205E-10$.

Change 4: A new section 4.4 will be added to describe airborne spread.

4.4. Airborne spread

Spread of disease by airborne dissemination is simulated in the same manner as local area spread, except that disease spread by airborne dissemination may be restricted based on direction from source to recipient units (see Figure 4.6). The parameters and formula used for airborne spread are the same as those for local area spread, but are provided independently.

The distance between premises is approximated as before. The direction from source premises to recipient premises is approximated with the inverse tangent


using the same x and y coordinates for each premises as used in the distance calculation.

Parameters for airborne spread

Global parameters (applied to all combinations of production types):

- wind direction, given as a range (*start* and *end*) in degrees

Parameters specified separately for each combination of source production type and recipient production type:

- d_{ij} , the distance between two arbitrary herds i and j
- n_i , the number of infectious animals in source herd i
- n_j , the size of a susceptible recipient herd j
- P_{fixed} , the probability that, on any given day, unit i will infect unit j by local-area spread
- airborne transport delay (days) 

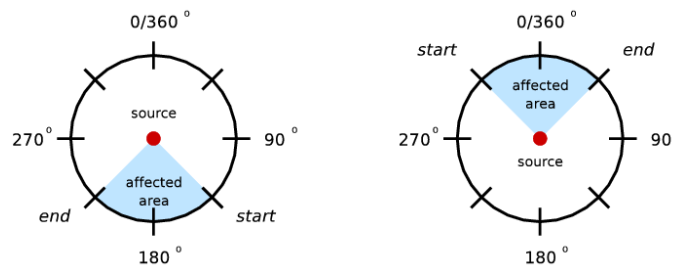


Figure A4-6. Example parameters for north winds (left) and south winds (right).

End of changes