Using *NAADSM* 3.1

Part 4: Advanced features & planned development

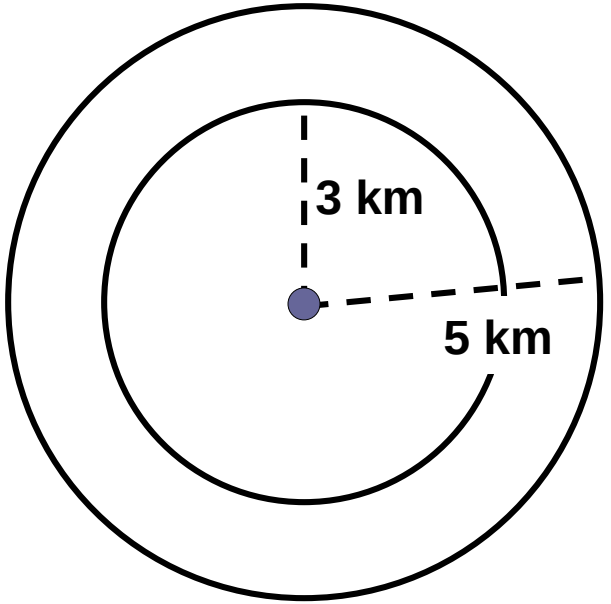
NAADSM Development Team

Zones

- Circular zones can be created to simulate:
  - Enhanced movement restriction in a control area
    - Rates of direct and/or indirect contact can be altered or reduced
  - Enhanced detection in a surveillance area
- Parameters for movement restriction and detection are specified separately for each combination of zone and production type
- Zones operate independently of destruction rings and vaccination rings

Creating zones

- Zones are specified by a user-defined name and radius
- Zone foci may be created around:
  - Infected, detected units
  - Units identified by tracing of direct or indirect contact (dangerous contacts)

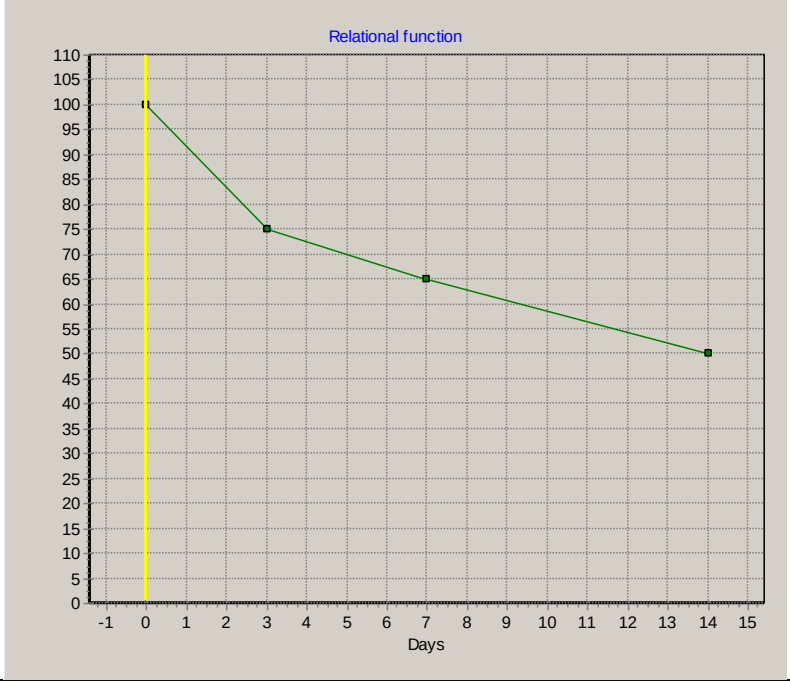


- The number of zones is not limited by *NAADSM*

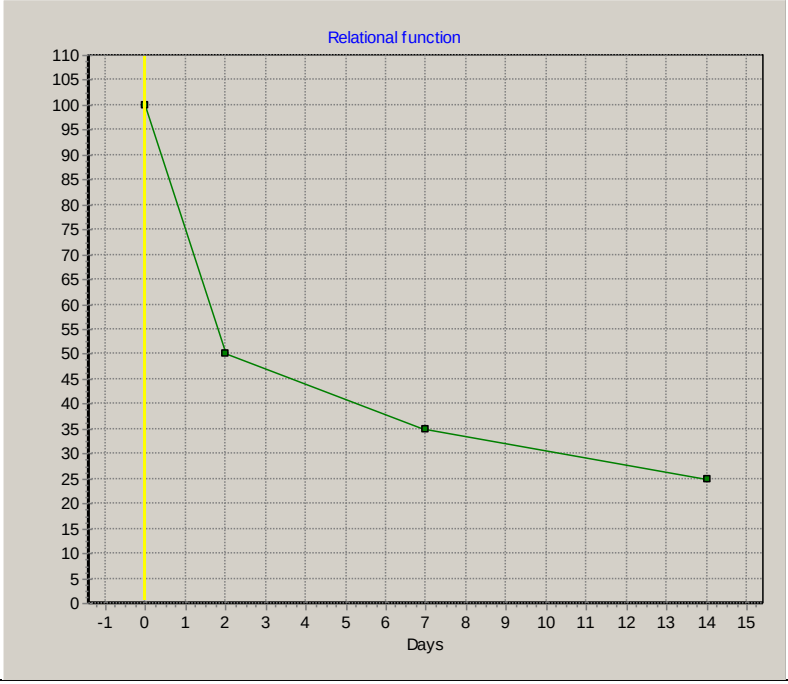
Zones for enhanced movement control

- Zone parameters for movement control override “global” movement control parameters
- Parameters for smaller zones override parameters for larger zones

Sample “global” movement control



Sample zone movement control

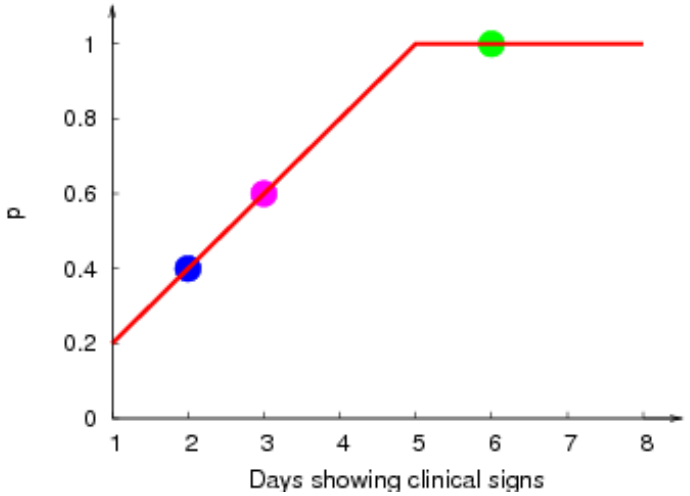


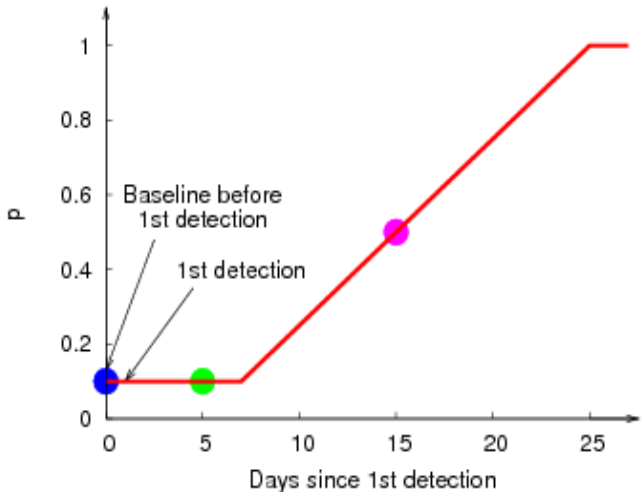
Zones for enhanced detection

- Recall that “standard” detection is modeled with two probabilities:
  - Probability of observing clinical signs
    - Can change based on the number of days that a unit has been showing clinical signs
  - Probability that a unit with clinical signs will be reported
    - Can change based on the length of time since an outbreak was first detected
- Each zone has a “multiplier” that alters the baseline probability of observing clinical signs
- Probability of reporting in a zone is assumed to be 1 (*i.e.*, reporting is guaranteed)

Zones and detection: An example

- Consider “standard” detection in the case of
  - A unit that has shown clinical signs for 3 days
  - An outbreak that has been recognized for 15 days

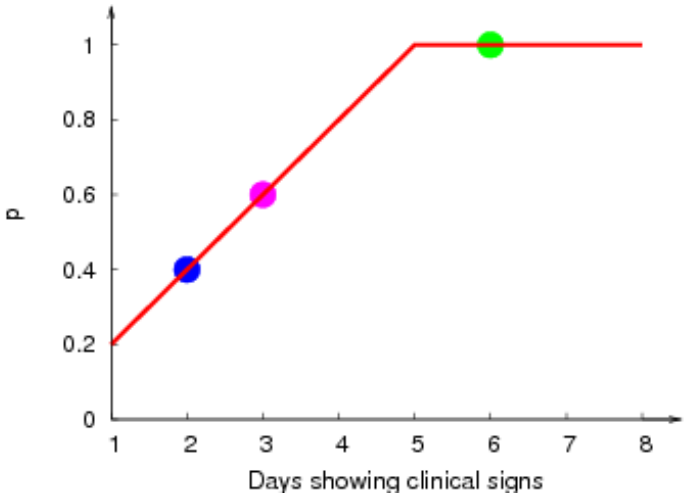


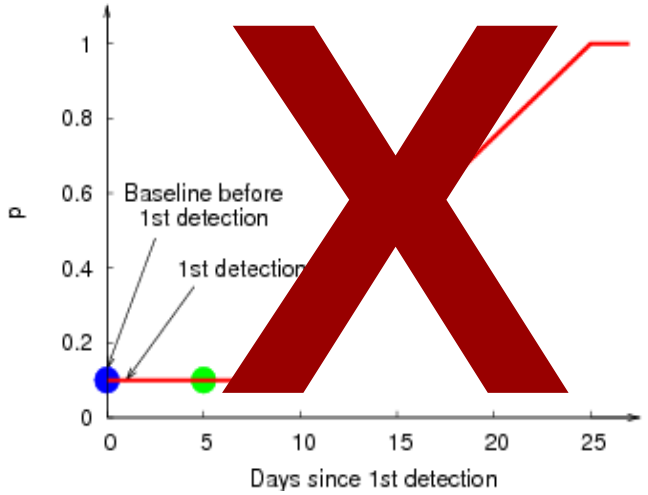


- Probability of detection is
  $0.6 \times 0.5 = 0.3$

Zones and detection: An example (cont.)

- Now consider detection in a zone with a detection multiplier of 1.25:





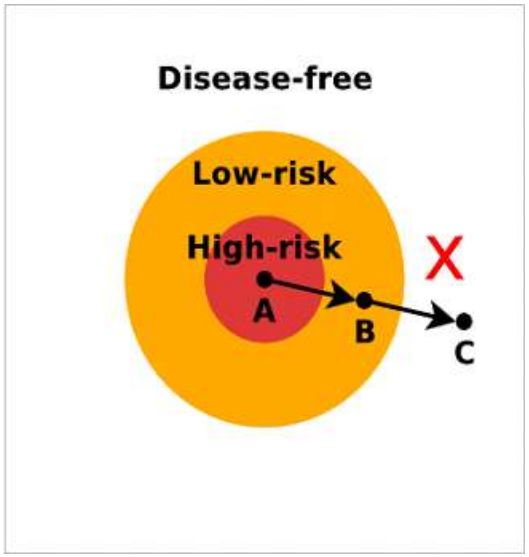
- P(Obs. signs) = 0.6 × 1.25 = 0.75
- P(Reporting) = 1
- Overall P(Detection) = 0.75 × 1 = 0.75

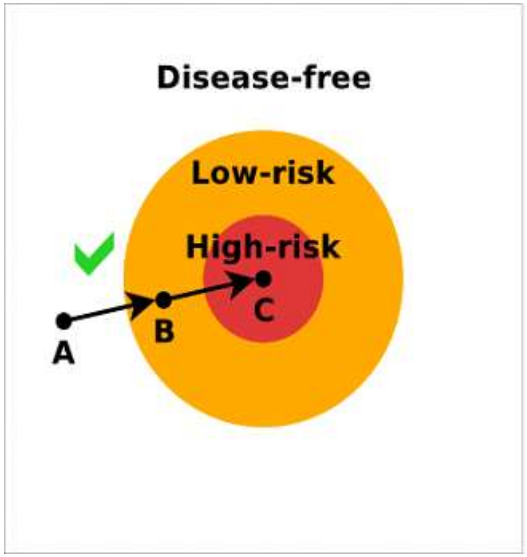
NAADSM demo (XIV): Zones

- Enabling and disabling zones with global zone options
- Creating and modifying zones
- Specifying parameters for zone/production type combinations

Additional movement rules associated with zones

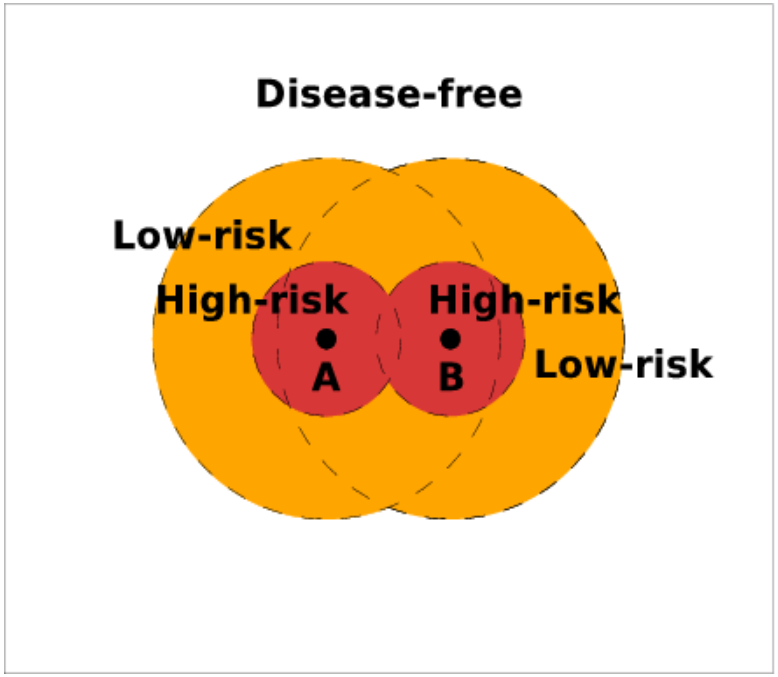
- Movement from a higher risk (smaller) zone to a lower risk (larger) zone is not allowed
- Movement from a lower risk (larger) zone to a higher risk (smaller) zone is currently allowed
  - (Is this assumption realistic?)





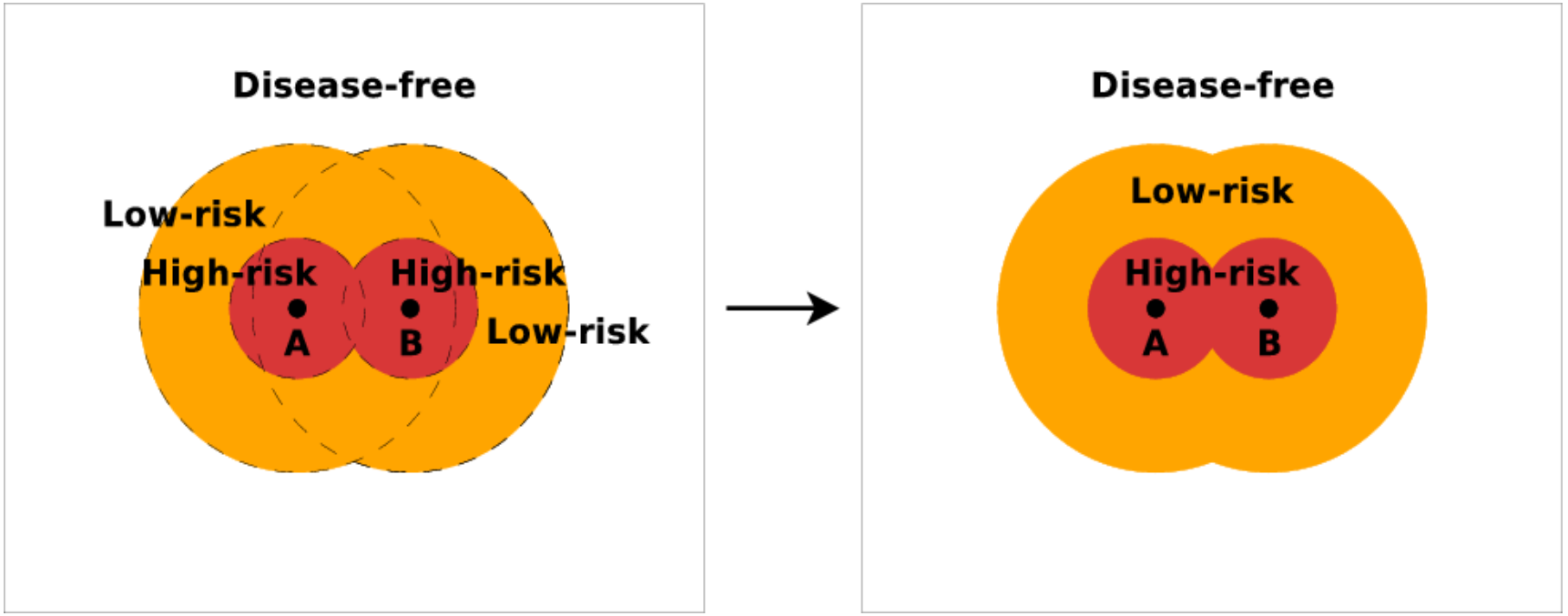
Zones are dynamic (I)

When an infected herd is newly detected in an existing zone, a new zone focus is created



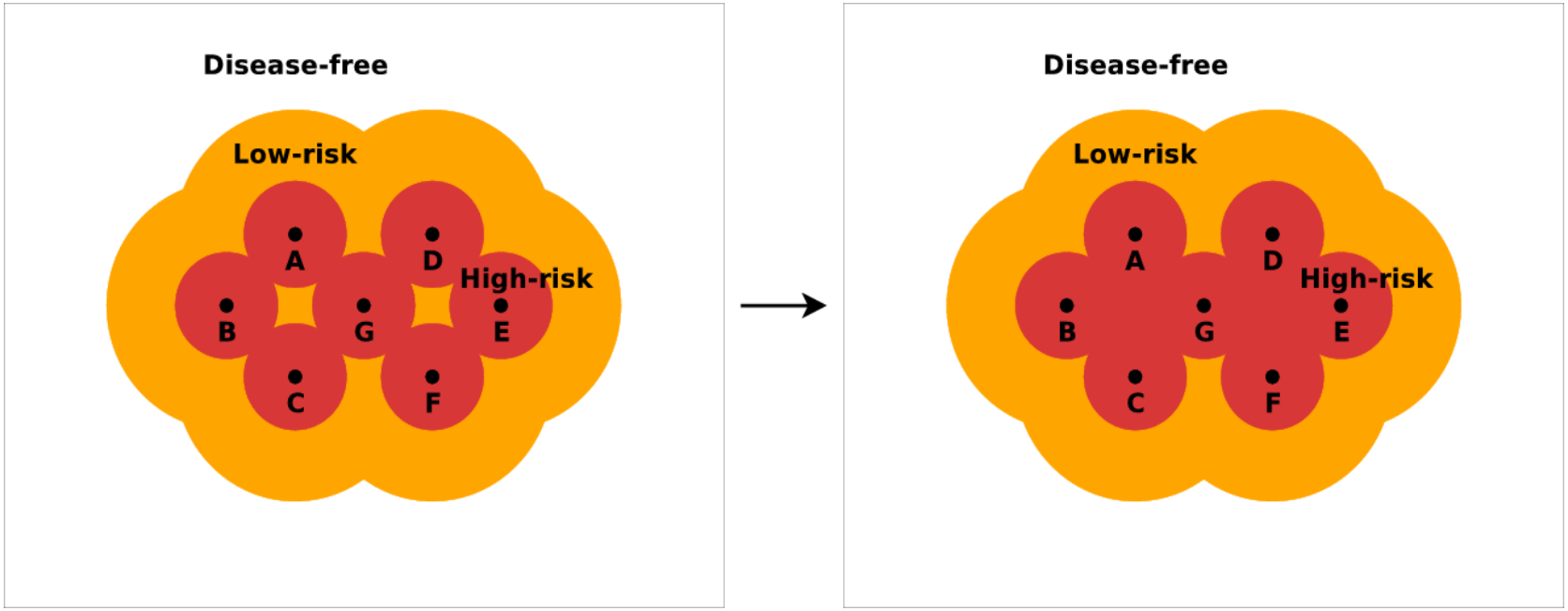
Zones are dynamic (II)

Overlapping foci of the same zone merge



Zones are dynamic (III)

- Enclosed areas of a lower surveillance level are absorbed:



- Once created, zones are permanent
  - Like quarantine, there is currently no way in *NAADSM* to lift zone restrictions once they are in place

Zones in future versions of *NAADSM*

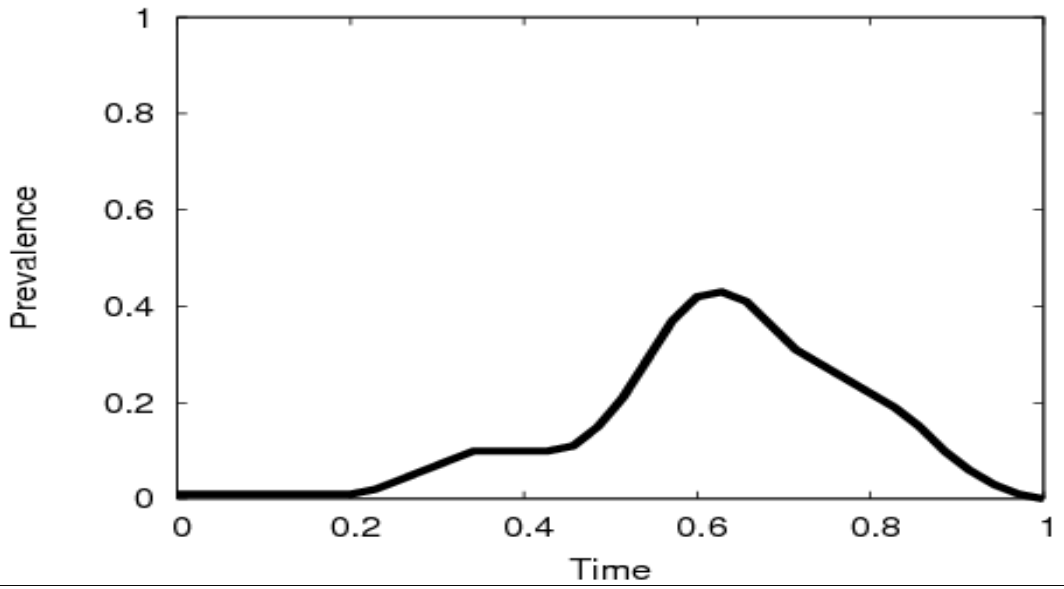
- We are considering tying vaccination and destruction to zones
  - This would allow for greater flexibility in devising and prioritizing strategies for these activities
- We are currently re-evaluating our assumptions that:
  - Movement from low-risk to high-risk zones should be allowed
  - New zone foci should be created when infected herds are detected within existing zones

Disease states in *NAADSM*: Advanced use

- Is it realistic to treat an entire herd as though it has just one disease state?
  - No.
- Do we need to consider – and model – changes in disease prevalence within a herd over time?
  - Maybe: the jury's still out.
    - See Carpenter *et al.* 2004 and Savill *et al.* 2007 for two different takes on the question.
- Can changes in disease prevalence within a herd be simulated with *NAADSM*?
  - Sort of...

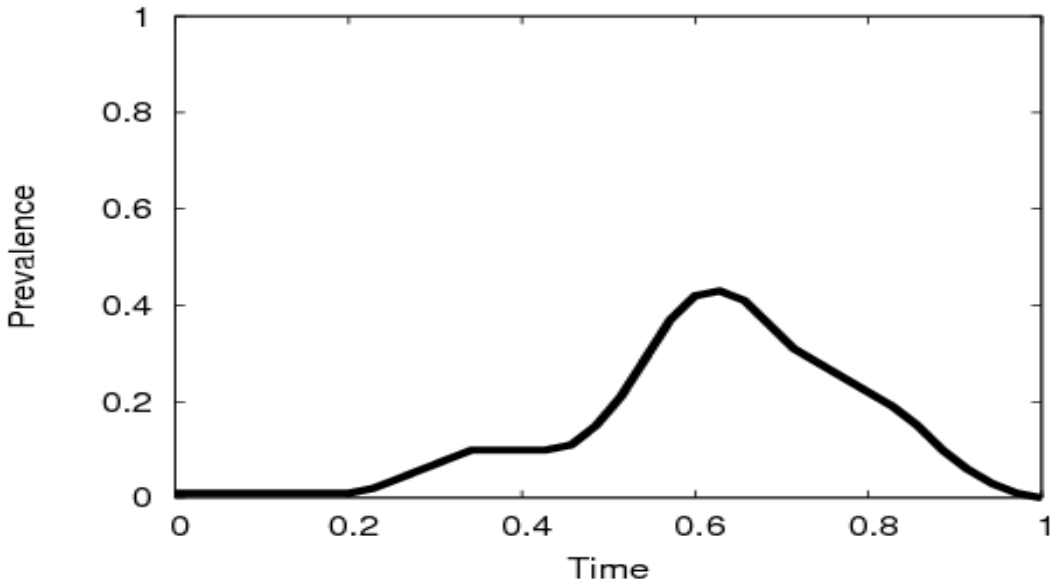
"Simulating" within-unit prevalence in *NAADSM*

- Within-herd (within-unit) prevalence may optionally be used to represent changing infectivity of an infected unit over time
  - Increasing or decreasing prevalence affects disease transmission
- Within-herd prevalence is specified in *NAADSM* as a function of time
- (How might someone develop such a function?)



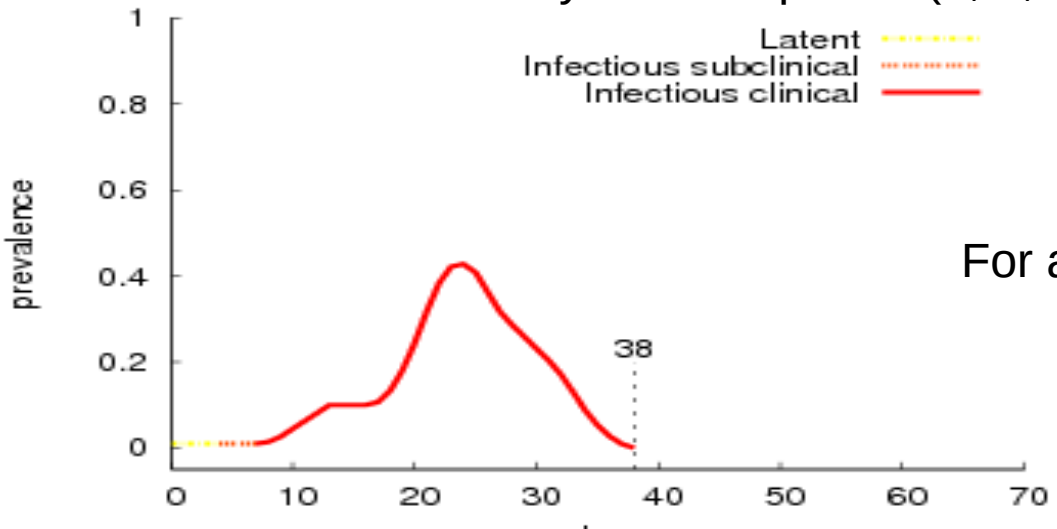
How NAADSM uses within-unit prevalence and herd-level disease states

- The time scale that the user creates for the within-unit prevalence function is *arbitrary*
  - This is the only place in *NAADSM* where the specified time scale of a relational function does not matter

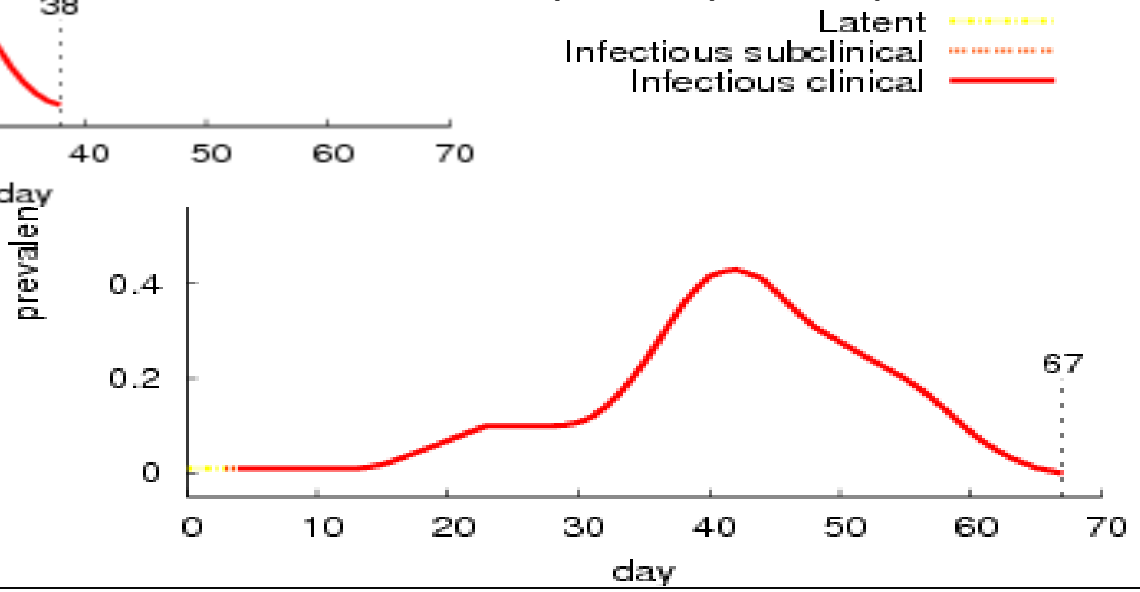


How within-unit prevalence is applied

For a unit with a 38-day infected period (4, 3, 31):

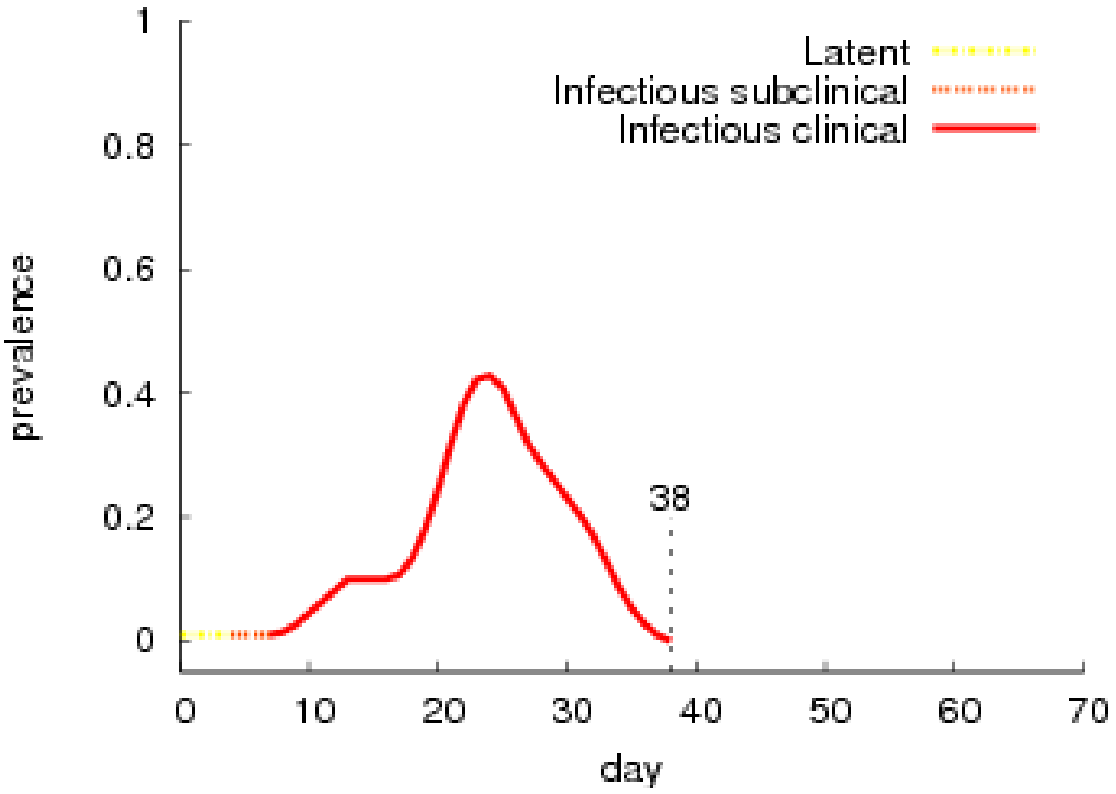


For a unit with a 67-day infected period (3, 1, 63):



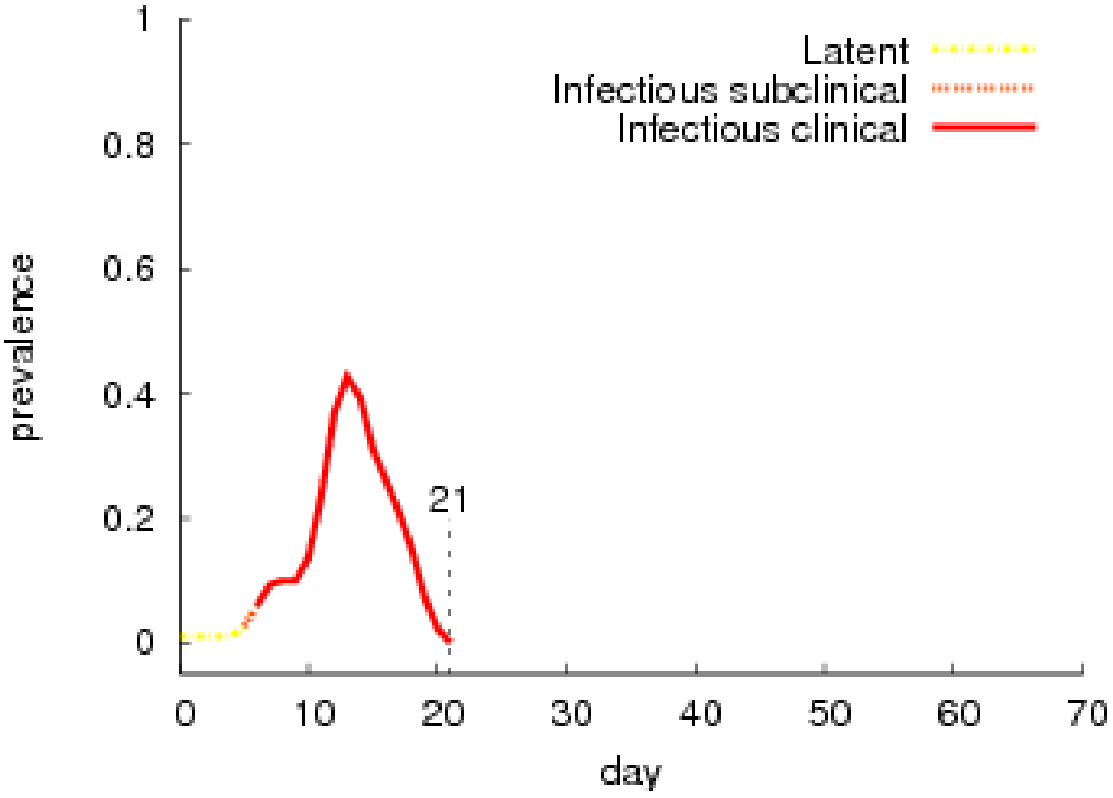
Application of the within-unit prevalence curve in *NAADSM*: An example

- Recall our unit that was latent for 4 days, subclinical for 3, and clinical for 31:



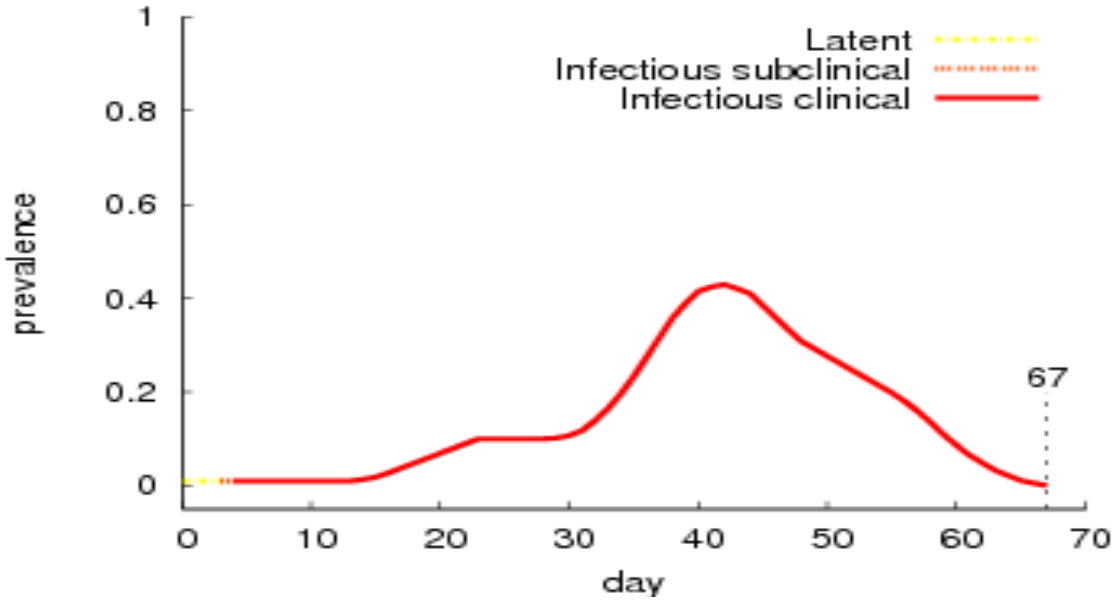
Application of the within-unit prevalence curve in *NAADSM*: Another example

- Recall our unit that was latent for 5 days, subclinical for 1, and clinical for 15:



Application of the within-unit prevalence curve in *NAADSM*: A final example

- Recall our unit that was latent for 3 days, subclinical for 1, and clinical for 63:



NAADSM demo (XV): Within-unit prevalence

- Using a within-unit prevalence function in *NAADSM*
- Creating a relational function in *NAADSM* to represent changes in within-unit prevalence over time
- If within-unit prevalence is used, the prevalence of the infecting unit is used as the probability of infection transfer

Within-unit prevalence in future versions of *NAADSM*

- We are currently designing an improved method for simulating within-unit prevalence
- This new approach will be evaluated and probably incorporated in a future release of *NAADSM*

Tracing in *NAADSM* 3.1

- Recall that tracing currently occurs as follows:
  - Only trace-forward (trace-out) investigations are attempted
  - Tracing proceeds only a single step
  - Tracing occurs immediately (there is no delay)
  - Tracing is independent of detection, i.e., a successful trace does not actually lead to detection of infected units

Tracing in *NAADSM* 3.2

- In the next version of *NAADSM*, the following improvements will be introduced:
  - Trace-back (trace-in) investigations will be possible
  - Tracing in either direction will be conducted for multiple steps
  - Diagnostic testing will be simulated so that tracing activities can result in more rapid detection
  - Delays for carrying out trace investigations can be simulated

Questions?

Recommended reading

- Harvey, N., Reeves, A., Schoenbaum, M.A., Zagmutt-Vergara, F.J., Dubé, C., Hill, A.E., Corso, B.A., McNab, W.B., Cartwright, C.I., Salman, M.D., 2007. The North American Animal Disease Spread Model: A simulation model to assist decision making in evaluating animal disease incursions. *Preventive Veterinary Medicine* 82: 176–197.
- Hill, A., and Reeves, A. 2006. User's Guide for the *North American Animal Disease Spread Model*, 2nd ed. Fort Collins, Colorado: Animal Population Health Institute, Colorado State University. Available at *http://wwww.naadsm.org*

References cited

- Carpenter, T.E., Thurmond, M.C., Bates, T.W., 2004. A simulation model of intraherd transmission of foot and mouth disease with special reference to disease spread before and after clinical diagnosis. *Journal of Veterinary Diagnostic Investigation* 16: 11–16.
- Savill, N.J., Shaw, D.J., Deardon, R., Tildesley, M.J., Keeling, M.J., Woolhouse, M.E.J., Brooks, S.P., Grenfell, B.T., 2007. Effect of data quality on estimates of farm infectiousness trends in the UK 2001 foot-and-mouth disease epidemic. *Journal of the Royal Society Interface* 4: 235–241.

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  - W. Bruce McNab
- United States Department of Agriculture
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