Markov chain and state transition models

Aaron Reeves, Animal Population Health Institute
College of Veterinary Medicine and Biomedical Sciences
Colorado State University, Fort Collins, Colorado

Moving between disease states in a Reed-Frost model

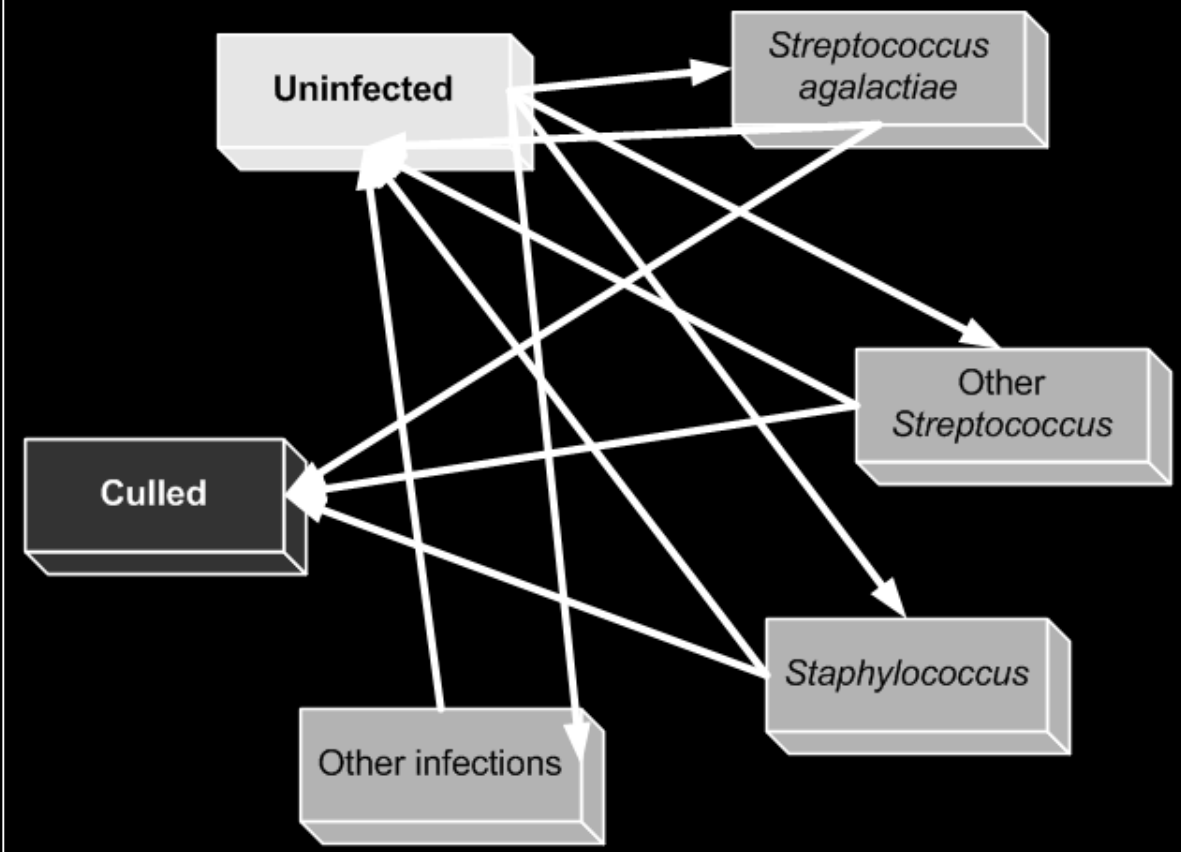
- The transition from one disease state to another is a linear process:

- The number of individuals in each state during a particular time period is dependent only on the number of individuals in each state during the previous time period
- “Lags” can be introduced to alter the timing, but this basic principle still applies

Moving between disease states in life

- In more complex (*e.g.*, real) systems, the transition between disease states is not necessarily linear
  - Chronic conditions
- The Reed-Frost framework does not account for the effects of interventions
  - Culling
  - Vaccination

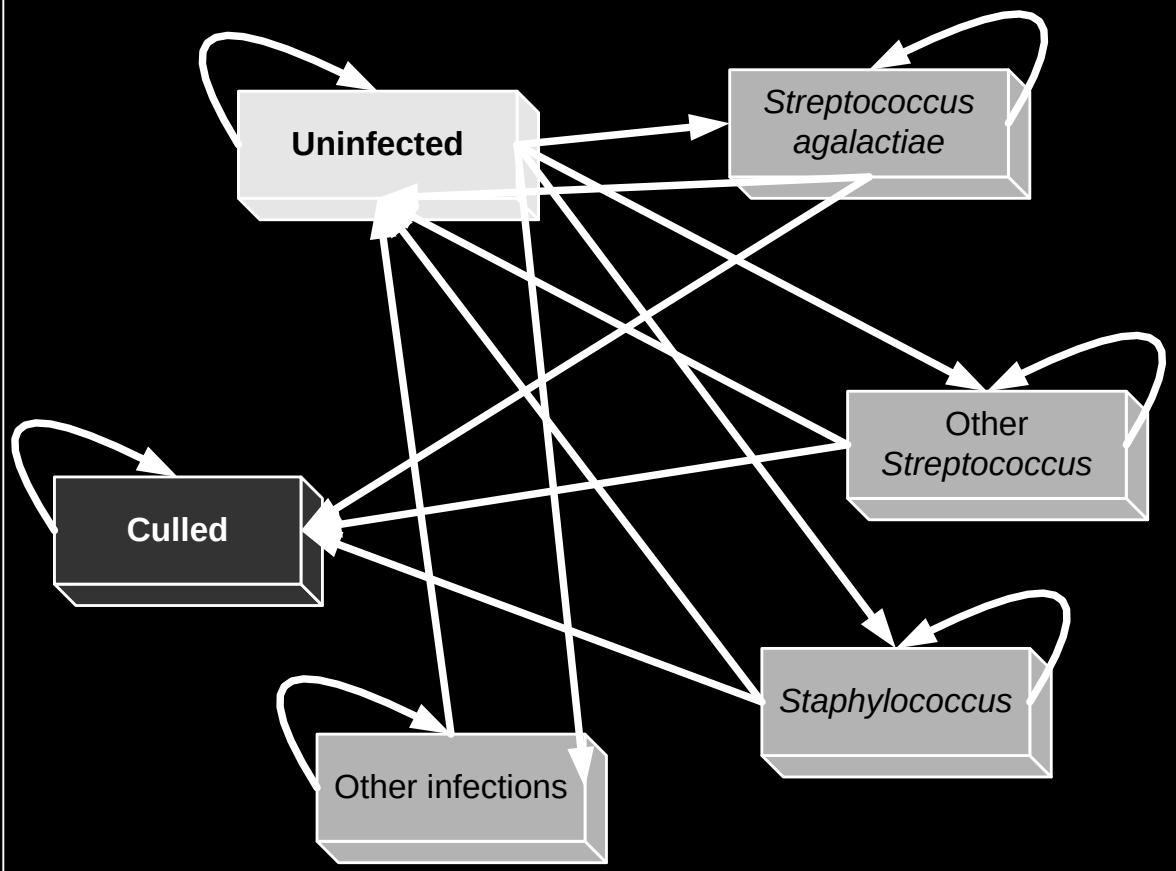
Example: A state transition diagram for a model of mastitis in cattle (I)



- The arrows represent all of the possible (or at least all of the important) transitions between states
- As in Reed-Frost and the differential calculus models, an individual can have only one state per time period

Based on Schwabe *et al.*, 1977 and Carpenter, 1988

Example: A state transition diagram for a model of mastitis in cattle (II)



- Individuals can also remain in a state for more than one time period
- It is more convenient to illustrate a state transition model as a table, or a *matrix*

Based on Schwabe *et al.*, 1977 and Carpenter, 1988

Example: A state transition matrix for a model of foot-and-mouth disease

	TO			
FROM	*Susceptible*	*Infectious*	*Immune*	*Removed*
Susceptible	Remaining susceptible	Infection	Effective vaccination	Preemptive culling
Infectious	--	--	Natural immunity	Slaughter of affected herds
Immune	Waning immunity	--	Remaining immune	--
Removed	--	--	--	Once removed, an individual remains removed

- Each cell shows the pathway or pathways by which individuals transition between states
- These pathways can be expressed as probabilities

Modified from Miller, 1976

Example: Representing an *SLIR* model in a state transition matrix

	Susceptible	*Latent*	*Infectious*	*Recovered*
Susceptible	1 – P(infection)	P(infection)	0	0
Latent	0	0	1	0
Infectious	0	0	0	1
Recovered	0	0	0	1

- The value in each cell represents the probability that an individual will move from $State_{Row}$ to $State_{Column}$

Example: A state transition matrix for mastitis

	Uninfected	*Strep ag.*	*Strep. other*	*Staph.*	*Other*	*Culled*
Uninfected	0.52	0.03	0.02	0.12	0.02	0.29
Strep. ag.	0.7	0.01	0	0	0	0.29
Strep. other	0.7	0	0.01	0	0	0.29
Staph.	0.1	0	0	0.4	0	0.5
Other	0.71	0	0	0	0	0.29
Culled	0	0	0	0	0	1

- Note that the sum across each row is 1: every “possible” transition is accounted for

Carpenter, 1988

Applying a state transition matrix in a disease model: *SLIR*

	Susceptible	*Latent*	*Infectious*	*Recovered*
Susceptible	0.7	0.3	0	0
Latent	0	0	1	0
Infectious	0	0	0	1
Recovered	0	0	0	1

- Let's start with a population of 100 susceptible individuals

	Number of individuals in each state			
Time period	*Susceptible*	*Latent*	*Infectious*	*Recovered*
0	100	0	0	0

- What does the model predict for time period 1?

Susceptible individuals in time period 1 (SLIR)

	Susceptible	*Latent*	*Infectious*	*Recovered*
Susceptible	0.7	0.3	0	0
Latent	0	0	1	0
Infectious	0	0	0	1
Recovered	0	0	0	1

- $S_1 = (S_0 \times P_{SS}) + (L_0 \times P_{LS}) + (I_0 \times P_{IS}) + (R_0 \times P_{RS})$
- $S_1 = (100 \times 0.7) + (0 \times 0) + (0 \times 0) + (0 \times 0)$
- $S_1 = 70$

	Number of individuals in each state			
Time period	*Susceptible*	*Latent*	*Infectious*	*Recovered*
0	100	0	0	0
1	70			

Latent individuals in time period 1 (SLIR)

	Susceptible	*Latent*	*Infectious*	*Recovered*
Susceptible	0.7	0.3	0	0
Latent	0	0	1	0
Infectious	0	0	0	1
Recovered	0	0	0	1

- $L_1 = (S_0 \times P_{SL}) + (L_0 \times P_{LL}) + (I_0 \times P_{IL}) + (R_0 \times P_{RL})$
- $L_1 = (100 \times 0.3) + (0 \times 0) + (0 \times 0) + (0 \times 0)$
- $L_1 = 30$

	Number of individuals in each state			
Time period	*Susceptible*	*Latent*	*Infectious*	*Recovered*
0	100	0	0	0
1	70	30	0	0

Susceptible individuals in time period 2 (SLIR)

	Susceptible	*Latent*	*Infectious*	*Recovered*
Susceptible	0.7	0.3	0	0
Latent	0	0	1	0
Infectious	0	0	0	1
Recovered	0	0	0	1

- $S_2 = (S_2 \times P_{SS}) + (L_2 \times P_{LS}) + (I_2 \times P_{IS}) + (R_2 \times P_{RS})$
- $S_2 = (70 \times 0.7) + (30 \times 0) + (0 \times 0) + (0 \times 0)$
- $S_2 = 49$

	Number of individuals in each state			
Time period	*Susceptible*	*Latent*	*Infectious*	*Recovered*
0	100	0	0	0
1	70	30	0	0
2	49			

Latent individuals in time period 2 (SLIR)

	Susceptible	*Latent*	*Infectious*	*Recovered*
Susceptible	0.7	0.3	0	0
Latent	0	0	1	0
Infectious	0	0	0	1
Recovered	0	0	0	1

- $L_2 = (S_2 \times P_{SL}) + (L_2 \times P_{LL}) + (I_2 \times P_{IL}) + (R_2 \times P_{RL})$
- $L_2 = (70 \times 0.3) + (30 \times 0) + (0 \times 0) + (0 \times 0)$
- $L_2 = 21$

	Number of individuals in each state			
Time period	*Susceptible*	*Latent*	*Infectious*	*Recovered*
0	100	0	0	0
1	70	30	0	0
2	49	21		

Infectious individuals in time period 2 (SLIR)

	Susceptible	*Latent*	*Infectious*	*Recovered*
Susceptible	0.7	0.3	0	0
Latent	0	0	1	0
Infectious	0	0	0	1
Recovered	0	0	0	1

- $I_2 = (S_2 \times P_{SI}) + (L_2 \times P_{LI}) + (I_2 \times P_{II}) + (R_2 \times P_{RI})$
- $I_2 = (70 \times 0) + (30 \times 1) + (0 \times 0) + (0 \times 0)$
- $I_2 = 21$

	Number of individuals in each state			
Time period	*Susceptible*	*Latent*	*Infectious*	*Recovered*
0	100	0	0	0
1	70	30	0	0
2	49	21	30	0

A more complex state transition model: Mastitis

	Uninfected	*Strep ag.*	*Strep. other*	*Staph.*	*Other*	*Culled*
Uninfected	0.52	0.03	0.02	0.12	0.02	0.29
Strep. ag.	0.7	0.01	0	0	0	0.29
Strep. other	0.7	0	0.01	0	0	0.29
Staph.	0.1	0	0	0.4	0	0.5
Other	0.71	0	0	0	0	0.29
Culled	0	0	0	0	0	1

$U_1 = (803 \times 0.52)+(52 \times 0.7)+(52 \times 0.7)+(79 \times 0.1)+(14 \times 0.71)+(0 \times 0) = 508$

$Sa_1 = (803 \times 0.03)+(52 \times 0.01)+(52 \times 0)+(79 \times 0)+(14 \times 0)+(0 \times) = 25$

Time period	*Uninfected*	*Strep ag.*	*Strep. other*	*Staph.*	*Other*	*Culled*
0	803	52	52	79	14	0
1	508	25	17	128	16	305
etc.						

Adapted from Carpenter, 1988

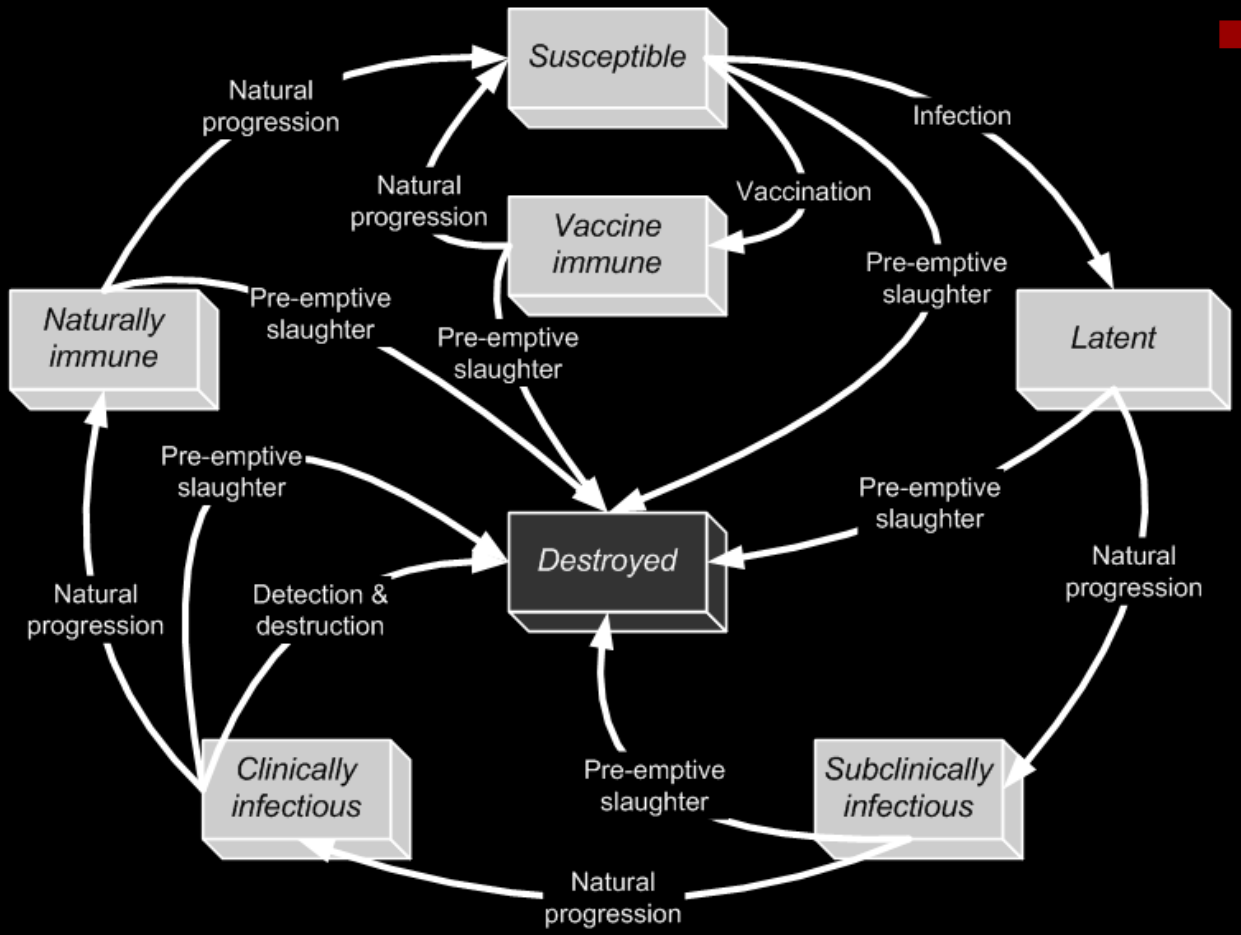
An aside: Markov chain vs. state transition models

- A Markov chain is a special case of a state transition model
  - In a Markov chain model, the transition probabilities are fixed
  - Markov chain models can be useful for modeling endemic diseases (as in the mastitis example)
- In more complex state transition models ("modified Markov chains"), the transition probabilities can change over time
  - For example, the probability of infection may depend on the number of cases in the previous time period
    - Does this look familiar?

Monte Carlo state transition models

- We've seen that Monte Carlo methods can be used to allow probabilities in a model to vary
- There are a lot of probabilities in a state transition matrix
- There is a great deal of potential for the use of Monte Carlo methods in a state transition model

Preview of coming attractions



- *NAADSM* is a framework for sophisticated state transition models which make extensive use of Monte Carlo methods

Figure modified from Harvey *et al.*, 2007

Recommended reading

- Carpenter, T.E., 1988. Microcomputer programs for Markov and modified Markov chain disease models. *Preventive Veterinary Medicine* 5: 169–179. *(A very nice demonstration of state transition modeling with a spreadsheet.)*
- Miller, W.M., 1976. A state-transition model of epidemic foot-and-mouth disease. In Ellis, P.R., Shaw, A.P.M., and Stephens, A.J., eds. New Techniques in Veterinary Epidemiology and Economics, Proceedings of a Symposium, University of Reading, England: ISVEE I. *http://www.sciquest.org.nz (An early application of a state transition model for animal disease.)*

References cited

- Carpenter, T.E., 1988. Microcomputer programs for Markov and modified Markov chain disease models. *Preventive Veterinary Medicine* 5: 169–179.
- 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., and 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*, in press.
- Miller, W.M., 1976. A state-transition model of epidemic foot-and-mouth disease. In Ellis, P.R., Shaw, A.P.M., and Stephens, A.J., eds. New Techniques in Veterinary Epidemiology and Economics, Proceedings of a Symposium, University of Reading, England: ISVEE I. *http://www.sciquest.org.nz*
- Schwabe, C.W., Riemann, H.P., and Franti, C.E., 1977. Epidemiological Models. In: Epidemiology in Veterinary Practice. Philadelphia: Lea and Febiger.