



Statistical Methods for Infectious Diseases
Household Based Studies II
Lecture 11A

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Background

Pneumococcal Studies

Data structure

Models and analysis

Bayesian latent variable model

Hidden Markov model



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Studies conditioning on exposure to infection:
 VE_S (VE_{col}), VE_I , VE_T

- Households, partnerships, or other small transmission units
- → Households assuming independence of households
- → Households assumed within communities
- Data structure:
 - → final-value data
 - → time-to-event data
 - → longitudinal panel data over time (pneumococcal carriage)



Table: Parameters used for measuring various effects of vaccination*

Level Parameter choice	Comparison groups and effect			
	Susceptibility	Infectiousness	Combined change in susceptibility and infectiousness	
Conditional on exposure:				
I Transmission probability	$VE_{S,p} \dagger = 1 - \frac{p_1}{p_0}$	$VE_{I,p} = 1 - \frac{p_1}{p_0}$	$VE_{T,p} = 1 - \frac{p_{11}}{p_{00}}$	
	Study design			
	I direct	IIA indirect	IIB total	III overall
Unconditional:				
II Incidence or hazard rate, IR, λ	$VE_{S,IR} = 1 - \frac{IR_{A1}}{IR_{A0}}$ $VE_{S,\lambda} = 1 - \frac{\lambda_{A1}}{\lambda_{A0}}$	$VE_{IIA,IR} = 1 - \frac{IR_{A0}}{IR_{B0}}$ $VE_{IIA,\lambda} = 1 - \frac{\lambda_{A0}}{\lambda_{B0}}$	$VE_{IIB,IR} = 1 - \frac{IR_{A1}}{IR_{B0}}$ $VE_{IIB,\lambda} = 1 - \frac{\lambda_{A1}}{\lambda_{B0}}$	$VE_{III,IR} = 1 - \frac{IR_{A.}}{IR_{B.}}$ $VE_{III,\lambda} = 1 - \frac{\lambda_{A.}}{\lambda_{B.}}$
III Proport. hazards, PH	$VE_{S,PH} = 1 - e^{-\beta_1}$	NA	NA	NA
IV Cumulative incidence	$VE_{S,CI} = 1 - \frac{CI_{A1}}{CI_{A0}}$	$VE_{IIA,CI} = 1 - \frac{CI_{A0}}{CI_{B0}}$	$VE_{IIB,CI} = 1 - \frac{CI_{A1}}{CI_{B0}}$	$VE_{III,CI} = 1 - \frac{CI_{A.}}{CI_{B.}}$

* From Halloran, Struchiner, Longini, Am. J. Epidemiol 1997; 146:789–803.



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Longitudinal (panel) carriage data

- Collection of transmission units, such as households or schools
- Carriage data at certain time intervals
- Relevant covariates, such as age or vaccine status
- Choice of analyses



Statistical Models

- Models of transmission within units such as households or schools assumed within communities.
- Two types of parameters:
 - rate of acquisition from the community (unconditional)
 - rate of acquisition from infective within transmission unit (conditional).
- Covariate (vaccine) effects are modeled affecting these parameters.
- Vaccine effect on duration of carriage (clearance rate) can be modeled directly.



Longitudinal data on pneumococcal carriage

- Problem: neither the acquisition or clearance times are observed.
- Different approaches to statistical models can deal with this problem making a variety of assumptions.
- Other problems: combining multiple serotype data, missing data, competition, errors in diagnosis.



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- Auranen, Arjas, Leino, Takala (2000)

$$\begin{aligned}\tilde{\lambda}_i^{(s)} &= \left[\alpha(t - T_i) + \beta(t - T_i) \sum_{k=1}^n C_k^{(s)}(t) \right] \\ &\quad \times \{1 - C_i(t)\} \\ \tilde{\mu}_i(t) &= \mu C_i(t)\end{aligned}$$

- α is rate to acquire carriage of serotype s from community
- β is rate of transmission from infective in family to susceptible
- μ is the clearance rate (no serotype specific rates)
- n is size of family, $C_i^{(s)}(t)$ is 0,1 indicator if individual is carrier of serotype s at time t , $C_i(t)$ is indicator of any of the three serotypes
- Problem solved: data augmented by unobserved event times of acquiring and clearing carriage (latent variables) using MCMC methods.



Observed data : swabs ↓ ❖ Serotype: S1,..., S15; ❖ No serotype: No.	Augmented data (unobserved): — ❖ Carriage in continuous time; ❖ Compatible with the observation.
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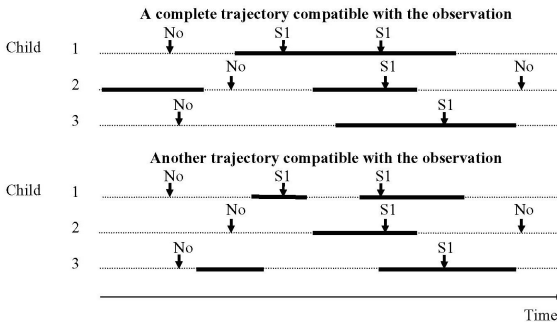


Figure 2

Data augmentation strategy to estimate transmission parameters of *S. pneumoniae* from the longitudinal follow-up of pneumococcal carriage in schools. The observed data consist of the times when swabs are collected in the school. The data are augmented with the times of colonization/decolonization. In the MCMC algorithm, augmented periods of carriage may be added/suppressed, split/combined; and the times of colonization/decolonization may change.



- Cauchemez, Temime, Valleron, Varon, Thomas, Guillemot, Boëlle (2006)
- similar approach to Auranen et al (2000), school data rather than household
- included serotype data, clustered by community acquisition of infection into two groups
- used same model for influenza household studies



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- Auranen et al (1996) (Hib), Melegaro, et al (2004), Melegaro, et al (2007)

$$\Pr_i(S \rightarrow C)_{\delta t} = \left(\alpha_i + \frac{\beta_{1i}l_1(t) + \beta_{2i}l_2(t)}{(z-1)^w} \right) \cdot \delta t$$

$$\Pr_i(C \rightarrow S)_{\delta t} = \mu_i \cdot \delta t$$

- $l_1(t)$ and $l_2(t)$ are number of infected children (< 5 yrs) and adults in household, i is age group.
- Problem solved: use a Markov model with 1 day intervals to analyze 28-day interval data assuming only one person can change in household per day.
- Vaccine parameters for susceptibility and infectiousness, also vaccine-dependent clearance rates can be added.



Intensity matrix Q

	000	001	010	011	100	101	110	111
000	q_{11}	$\alpha^{(3)}$	$\alpha^{(2)}$	0	$\alpha^{(1)}$	0	0	0
001	$\mu^{(3)}$	q_{22}	0	$\alpha^{(2)} + \beta^{(2)}$	0	$\alpha^{(1)} + \beta^{(1)}$	0	0
010	$\mu^{(2)}$	0	q_{33}	$\alpha^{(3)} + \beta^{(3)}$	0	0	$\alpha^{(1)} + \beta^{(1)}$	0
011	0	$\mu^{(2)}$	$\mu^{(3)}$	q_{44}	0	0	0	$\alpha^{(1)} + 2\beta^{(1)}$
100	$\mu^{(1)}$	0	0	0	q_{55}	$\alpha^{(3)} + 2\beta^{(3)}$	$\alpha^{(2)} + \beta^{(2)}$	0
101	0	$\mu^{(1)}$	0	0	$\mu^{(3)}$	q_{66}	0	$\alpha^{(2)} + 2\beta^{(2)}$
110	0	0	$\mu^{(1)}$	0	$\mu^{(2)}$	0	q_{77}	$\alpha^{(3)} + 2\beta^{(3)}$
111	0	0	0	$\mu^{(1)}$	0	$\mu^{(2)}$	$\mu^{(3)}$	q_{88}

- The elements on the diagonals represent the intensity of staying in the same state.
- The $q_{ii} = 1 - \sum_{j \neq i} q_{ij}$ (Karlin and Taylor 1975).
- The element (4,8) represents the transition from state 011 to state 111.



Thank You!