Epidemic monitoring using synthesis of information from multiple sources

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Outline



1 Motivation for the work

- 2 General problem
- 3 A few examples

4 Results

5 Methodological issues

6 Final comments

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Motivation



Planning, implementation and evaluation of public health policies in the UK e.g.

- Department of Health (DoH) National Strategy for Sexual Health
- DoH Action Plan for Hepatitis C
- Pandemic influenza Preparedness Strategy

rely on the monitoring of fundamental aspects of the disease of interest, such as

- prevalence (undiagnosed prevalence)
- incidence
- by age groups and locations
- at regular intervals (real time!)

Problem



- These characteristics are typically not easily directly measurable (if at all) with little *direct* information available on them
- There is plenty of *indirect* information on functions of these quantities from diverse sources (surveillance, ad hoc surveys etc)
- Estimated from the synthesis of both *direct* and *indirect* information
- This has been common problem underlying most of the work I have been recently involved with

[Goubar *et al*, 2008], [Presanis *et al*, 2008], [Sweeting *et al*, 2008], [De Angelis *et al*, 2009], [Sweeting *et al*, 2009], [Presanis *et al*, 2010, 2011], [Birrell *et al*, 2011].

Evidence synthesis - a long-established idea



Methods for combining evidence are *not* new:

- The *Bayesian* paradigm
 - combining prior knowledge with new evidence
- Meta-analysis
 - combining studies of same type
- Confidence Profile Method [Eddy et al (1992)]
 - combining information of different types/study designs (medical-decision making literature)
- *Multi-parameter evidence synthesis* [Spiegelhalter *et al* (2004), Ades & Sutton (2006)]
 - epidemiology



- Hepatitis C Virus (HCV)
- HIV
- A/H1N1
 - type of challenges posed by the data
 - how tackled by the proposed approach
 - methodological/epidemiological considerations and open questions

HCV

Infection with the Hepatitis C virus (HCV): how many are infected?



- Acquired through exchange of blood with infected individual (e.g. injecting drug use)
- Disease with long incubation; progressive fibrosis of the liver to cirrhosis, hepatocellular carcinoma and death
- Antiviral therapy very effective
- Planning for prevention and treatment implementation needs reliable estimates of the number currently infected

Problem: HCV prevalence estimation



No prevalence study/surveillance representatively covering the general population exists

- Estimates of proportion of infected derived in specific (opportunistic) groups
- Resulting estimates are either not interpretable or heavily biased

Widely different figures have been suggested



Hepatitis timebomb is threatening the capital

Evening standard, 24th May 2006

Daily Mail, 23rd March 2006

Daily Express, 24th May 2006

Hepatitis C may have infected a million

400,000 Britons don't know they have a deadly disease

Proposed Approach



- Information from any available study expressed in terms of 3 main risk groups g: current injecting drug users (CUR); Ex-injecting drug users (EX); Non-IDUs (NON - IDU)
- Parameters of interest
 - $\rho_{\rm CURrsa},\,\rho_{\rm EXrsa},\,\rho_{\rm NON-IDUrsa}$

prevalence (*i.e.* the proportion) of current, EX, and NON-IDU in the population for region r, gender s, and age-group a.

-
$$\rho_{\rm NONrsa} = 1 - \rho_{\rm CURrsa} - \rho_{\rm EXrsa}$$

- $\rho_{\rm IDUrsa} = \rho_{\rm CURrsa} + \rho_{\rm EXrsa}$
- $\bullet \ \pi_{\rm CURrsa}, \pi_{\rm EXrsa}, \pi_{\rm NON-IDUrsa}$

corresponding prevalence of HCV. Any other quantities can be derived from these e.g. π .

Data on $\rho_{\rm grsa}$

- Capture re-capture study in 15-44 years old in London estimate of number of current IDUs
- Household surveys:
 - British Crime Survey (HO)
 - Survey of Psychiatric Morbidity (ONS)
 - Offending Crime and Justice Survey (HO)
 - National Survey of Sexual Attitudes and Lifestyles (NATSAL)
 - use of non-prescribed IDU drugs ever past year

Data on π_{grsa}

- UA programme in STI clinics
 - HCV prevalence in ever IDUs and non-IDUs
- UA programme in current IDUs attending specialist clinics
- UA programme in antenatal clinics and neonatal samples
- Studies in blood donors
 - HCV prevalence in low risk population
- Sentinel laboratory surveillance
 - HCV prevalence in populations testing for HCV

Challenges



- data structure simple as mostly of the form $\{r_{grsa}, n_{grsa}\}$
- But the observed proportions are typically
 - biased estimates of the true proportions of interest (*e.g.* size of the populations)
 - only interpretable as mixtures of proportions
- lack of direct information on specific proportions of interest (*e.g.* the size of the ex-IDU population)



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Household studies

 i^{th} study provides information on ρ_{grsa} in the form of $\{r^i_{grsa}, n^i_{grsa}\}$. We assume that

 $r_{grsa}^{i} \sim \text{Binomial}(n_{grsa}^{i}, \rho_{grsa}^{i})$

and

 $logit(\rho_{grsa}^{i}) = logit(\rho_{grsa}) + b$

where b is a bias parameter.



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Challenges: example (2)



• Mixture of proportions the HCV prevalence in STI clinic attendees who have ever injected π_{IDUrsa}^{STI} estimated using $\{r_{IDUrsa}^{STI}, n_{IDUrsa}^{STI}\}$ can only be interpreted as being

$$\pi^{\textit{STI}}_{\textit{IDUrsa}} = \psi \pi^{\textit{STI}}_{\textit{CURrsa}} + (1 - \psi) \pi^{\textit{STI}}_{\textit{EXrsa}}$$

where the mixture coefficient ψ is informed by the NATSAL survey. Thus we assume that

$$r_{IDUrsa}^{STI} \sim \operatorname{Binomial}(n_{IDUrsa}^{STI}, \pi_{IDUrsa}^{STI})$$



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HIV

A few examples

Infection with HIV: what are trends in prevalence of undiagnosed infections?



- HIV is a long, asymptomatic disease with many infections undiagnosed
- Undiagnosed infections contribute to transmission lack of access to treatment
- Reliable estimates of the number infected, particularly those still undiagnosed, over time are required for public health policy

Parameters of interest



- ρ_{gtr} prevalence (*i.e.* the proportion in the population) of risk-group g in the population at time t for region r
- π_{gtr} corresponding prevalence of HIV
- δ_{gtr} proportion of infections diagnosed in risk-group g, region r

Any other quantities can be derived from these *e.g.* $\pi_{gtr}(1 - \delta_{gtr})$.

A few examples

Availability of data: 13 risk groups, 3 regions, over time



	Risk group	Ν	ρ	π	δ	$\pi(1-\delta)$	$f(ho,\pi,\delta)$
Men	MSM		~			✓	
	IDUs		\checkmark	\checkmark	\checkmark		\checkmark
	Born sub-Saharan Africa		\checkmark				\checkmark
	STI clinic attendees		\checkmark			\checkmark	
	Lower risk						
	ALL	\checkmark					\checkmark
Women	IDUs		\checkmark	\checkmark	\checkmark		\checkmark
	Born sub-Saharan Africa		\checkmark	\checkmark	\checkmark		\checkmark
	STI clinic attendees		\checkmark			\checkmark	
	Lower risk						
	Born UK/elsewhere			\checkmark	\checkmark		
	ALL	\checkmark		\checkmark			\checkmark

Note: multiplicity of data for some parameters

A few examples

Graphical model: MSM





A/H1N1

A few examples

A/H1N1 2009 in England: is it possible to inform policy in the midst of an epidemic?



Monitoring the epidemic through the (real time) estimation and prediction of

- the number of infections
- the number of symptomatic cases
- the number of severe cases (hospitalisations, ICU admissions, deaths)

by age group and region

Ideally



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In reality



- Q-Surveillance Daily counts of individuals reporting symptoms of influenza-like illness (ILI) at general practices (GPs).
- RMN + RCGP Sentinel GP surveillance schemes, swabbing ILI patients. Provides data on swab positivity for A/H1N1.
- HPA returns service Cross-sectional seroepidemiological surveys.
- Virologically confirmed cases.

All data stratified by age class (< 1, 1 – 4, 5 – 14, 15 – 24, 25 – 44, 45 - 64, and 65 + years) from the 1st May until 31st December.



A few examples

(a)



(a) Weekly consultations by region (Greater London, West Midlands, Rest of England) and (b) by age group

(b)

A few examples



GP consultations for ILI and virological positivity for the presence of ANY flu, by week from end-2005 to week 50, 2009

Common statistical formulation



- Interest: estimation of θ = (θ₁, θ₂..., θ_k) on the basis of a collection of data y = (y₁, y₂..., y_n)
- Each y_i provides information on
 - a *single* component of θ , or
 - a *function* of one or more components, *i.e.* on a quantity $\psi_i = f(\theta)$

Thus inference is conducted on the basis of both **direct** and **indirect** information.

- Maximum likelihood: $L(\theta) = \prod_{i=1}^{n} L_i(y_i; \theta)$
- Bayesian: $p(\theta \mid \mathbf{y}) \propto p(\theta) \times L(\theta)$







Number with HCV antibodies (thousands)

Posterior distributions for the proportion of undiagnosed HIV infections in MSM

Results





Results

London: Infections, Cases, Attack Rate





End August

Infections

Symptomatic cases IAR 672000 (544000, 826000) 217000 (133000, 324000) 9% (7%, 11%)

End December

Infections Symptomatic Cases

IAR

r 1441000 (1229000, 1681000) 469000 (298000, 676000) 19% (16%, 22%)

Methodological issues



Powerful approach that allows use of all available information inevitably leading to complex probabilistic models

- How do we assess these complex models?
 - appropriateness compared to alternative models
 - detection of conflicts between data items
 - influence of particular data items on the resulting inference

Model assessment: instruments



Deviance

$$D(\boldsymbol{\theta}) = -2[\log\{p(\mathbf{y} \mid \boldsymbol{\theta})\} - \log\{p(\mathbf{y} \mid \hat{\boldsymbol{\theta}})\}]$$



 $\bar{D} = E_{\theta|\mathbf{y}}[D(\theta)]$

• Deviance Information Criteria (DIC)

 $DIC = \bar{D} + p_D$

[Spiegelhalter et al, 2002]

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Model assessment: model choice. HCV



Model	DIC	ρ _{CUR} (%)	ρ _{ΕΧ} (%)	π _{CUR} (%)	π _{EX} (%)	π _{NON} (%)	π (%)	
No bias b = 0	1022	0.26 (0.22, 0.30)	0.73 (0.65, 0.81)	33.7 (30.3, 37.3)	19.9 (17.2, 22.8)	0.094 (0.048, 0.152)	0.32 (0.27, 0.39)	
Common bias, surveys & risk-groups b = b	976	0.67 (0.49, 0.93)	<mark>2.69</mark> (1.83, 4.04)	32.7 (29.2, 36.5)	18.9 (16.3, 21.7)	0.098 (0.048, 0.157)	<mark>0.82</mark> (0.60, 1.16)	
Risk-group specific bias $b = b_g$	978	0.68 (0.49, 0.96)	1.41 (0.58, 3.19)	33.0 (29.3, 37.2)	19.7 (16.8, 22.7)	0.091 (0.046, 0.150)	<mark>0.60</mark> (0.39, 0.97)	
Survey specific bias $b = b^i$	981	0.70 (0.50, 1.01)	2.79 (1.84, 4.27)	32.6 (29.2, 36.5)	18.8 (16.2, 21.6)	0.098 (0.049, 0.158)	0.85 (0.60, 1.21)	
Survey & risk-group specific bias $b = b_g^i$	986	0.69 (0.49, 0.96)	1.45 (0.61, 3.31)	33.2 (29.4, 37.3)	19.6 (16.7, 22.7)	0.091 (0.046, 0.151)	0.61 (0.39, 0.99)	

Methodological issues

Model assessment: conflict between data

sources





assuming independence between the n data sources becomes the sum of the item specific deviance contributions

• can be usefully employed to identify conflict between data sources

Availability of data: 13 risk groups, 3 regions, over time



	Risk group	Ν	ρ	π	δ	$\pi(1-\delta)$	$f(ho,\pi,\delta)$
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	STI clinic attendees		\checkmark			\checkmark	
	Lower risk						
	Born UK/elsewhere			\checkmark	\checkmark		
	ALL	\checkmark		\checkmark			\checkmark

Note: multiplicity of data for some parameters

Model assessment: conflict. HIV





 $\pi_{ALL_{f},r} = \pi_{SSA_{f},r}\rho_{SSA_{f},r} + \pi_{NSSA_{f},r}(1-\rho_{SSA_{f},r})$

Model assessment: influence. A/H1N1



What is the role of serological studies?





Model assessment: influence. A/H1N1

Sequential analyses with serology based on 83, 143, 192 and 245 days of epidemic surveillance data



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In a world without serology...



Other data sources unable to overcome prior information



Discussion



- Example of estimation relevant to problems of public health
- Use of multiple sources of evidence leads to complex probabilistic models
- Increasingly expert at formulating and estimating models
- The establishment of a well-defined iterative process of model criticism lags behind this expertise
- Model criticism becomes more crucial but harder as the number of data sources increases and the model becomes more complex
- Work on approaches to conflict detection, model choice and assessment needed

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