Bayesian health economic modelling of different human papillomavirus (HPV) vaccination strategies in a static and pseudo-dynamic setting: the BEST II study

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(Thanks to Katrin Haussler, UCL & the BEST II team)

10th World Congress Health Economics in the Age of Longevity: a Joint iHEA & ECHE Congress

Dublin, Wednesday 16 July 2014

Background

- BEST I (2010-2012): model for the cost-effectiveness of HPV quadrivalent vaccine
 - Sanofi Pasteur MSD full financial support international collaboration (includes UCL, University of Zürich, Stockholm SE, University of York, University of Rome)
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- Both originated from applied perspective, but characterised by challenging methodological aspects
 - Focus on the methodology

Two words on HPV...

- Human Papillomavirus (HPV) is the *primum movens* both in the aetio-pathogenesis of invasive cervical cancer and in other malignant and benign neoplastic lesions
- Mainly sexually transmitted
 - But: large variability in the mode and force of infection
 - $\sim\!40$ identified genotypes, including 13 high-risk types
- HPV has a relatively large prevalence
 - ${\sim}21\%$ in females and ${\sim}17\%$ in males
- Impacts quite heavily on health-care systems
 - In the UK, annually: $\pounds 17$ million to treat genital warts $^1;\,\pounds 157$ million to treat cervical cancer 2
- Screening programmes established to detect and treat early instances of infection-related diseases
- Vaccination suggested as an effective addition
 - Disease process is complicated, so cost-effectiveness is uncertain

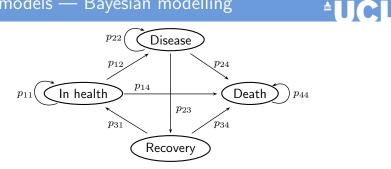
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<sup>1</sup> Health Protection Agency (2011)
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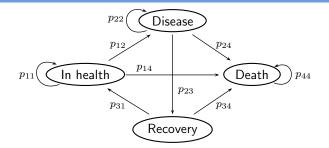
² NHS (2012)



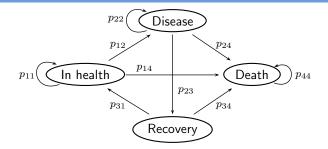
- HPV has a heavy **indirect** impact on patients utility & health-care costs infected patients are at higher risk of developing
 - Genital warts
 - Several types of cancer (especially cervical)
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 - Markov (multi-state) models particularly helpful to deal with this kind of situations
- At the same time, because the most likely mode of infection is sexual, need to consider
 - Effect of herd immunity
 - Differential impact of infection and outcomes, eg by age & sex
 - Dynamic population effects may be more important for future patients at risk





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- For example, under treatment t, we may assume $p_{12} = \pi \rho$
 - π = population prevalence of the disease
 - $\rho={\rm reduction}$ in prevalence due to treatment, estimated by (meta-analysis of) published studies
- NB: Bayesian modelling particularly effective for this
 - Flexibile/modular structure
 - Propagates uncertainty throughout



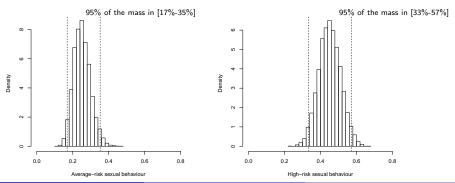
Example: HPV Transmission rate

- Crucial parameter, but limited/inconclusive evidence available
 - Uniform distribution in [0;1] (Korostil et al, 2012)?
 - Per sex act: \sim 40% with a range of 5-100% (Dunne et al, 2006)?
 - Per partnership: \sim 42% with a range of 36-47% (Burchell et al, 2011)?
 - Affected by external factors (eg average- vs high-risk sexual behaviour)?

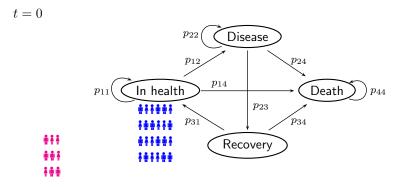
UCL

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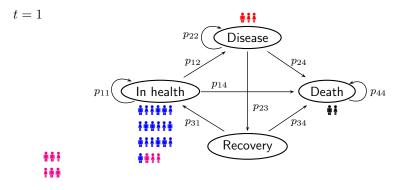
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 - Affected by external factors (eg average- vs high-risk sexual behaviour)?
- Bayesian modelling useful to include expert opinion and relatively straightforward for (probabilistic) sensitivity analysis



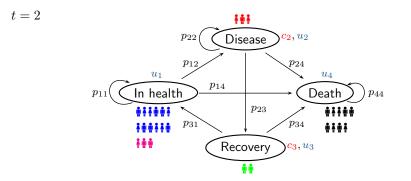
Gianluca Baio (UCL)



• 14 cohorts of males & females populate the model at time t = 0



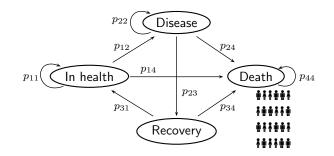
- 10 cohorts of new 12 year old enter the model sequentially
- The whole dynamic population is followed up over time



• Costs and utilities attached to each status and added over time

- Discounting is an important issue results potentially sensitive to rates
- In the base-case model, costs discounted @ 3% and utilities discounted @ 1.5%
 - + sensitivity analysis performed to these choices

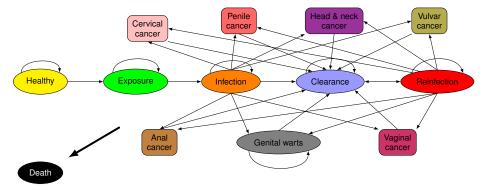
t = T



• In the base-case model, the follow up is set to 55 years — long enough to capture some of the long-term effects

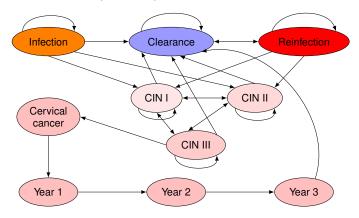
Markov models — structure

Females compartment model: $S_f = 36$ health states Males compartment model: $S_m = 22$ health states





Cervical cancer module (blown up)



Rate of HPV infection (Korostil et al, 2012):

$$\rho_{g,s,a} = \beta_s \sum_{s',a'} m_{g,s,s',a,a'} \left(\frac{I_{g',s',a'}}{N_{g',s',a'}} \right)$$

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- At each time point in the virtual follow up, $I_{g',s',a'}$ indicates the number of infected individuals of gender g', sexual activity level s' and age group a'
- Similarly, $N_{g',s',a'}$ indicates the total number of individuals of gender g', sexual activity level s' and age group a'



Sexual partnership matrix for female (average-risk group)

Age	12-14	15-19	20-24	25-29	30-34	35-39	40-44	45-49	50-54	55-59	60-64	65-80
12-19	1%	26%	58%	15%	1%	0%	0%	0%	0%	0%	0%	0%
20-24	0%	0%	36%	49%	12%	2%	0%	0%	0%	0%	0%	0%
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Annual min, average and max partner acquisition rate for females

		Females			Males		
Age	Min	Mean	Max	Min	Mean	Max	
12-19	0.74	1.26	1.78	0.90	1.92	2.94	
20-24	0.54	0.96	1.38	0.68	1.38	2.09	
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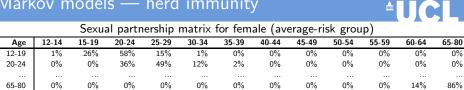
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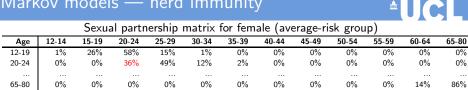
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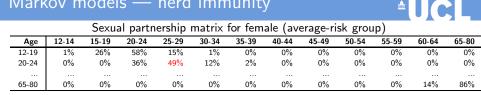


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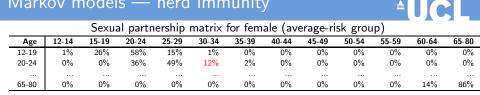
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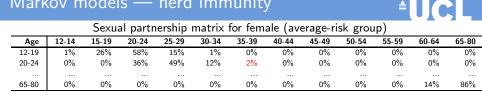
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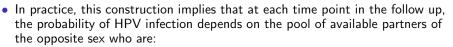
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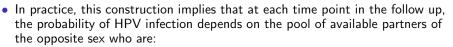
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- $m_{g,s,s',a,a'} = 2\% \times 1.38 = 0.0276$, for a' = 35-39;
- $m_{g,s,s',a,a'} = 0$, for any other age group a'.

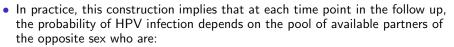


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- b) currently infected by HPV; as vaccination is likely to reduce the number of people who originally become infected by the vaccine, because of this element, the probability of HPV infection will become smaller and will be affected by the impact of vaccination, thus mimicking the mechanism underlying herd immunity

- In practice, this construction implies that at each time point in the follow up, the probability of HPV infection depends on the pool of available partners of the opposite sex who are:
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- **NB**: The HPV infection rates $\rho_{q,s,a}$ can be transformed into probabilities

 $p_{g,s,a} = 1 - \exp^{-\rho_{g,s,a}}$

(assuming constant rates over the entire cycle)

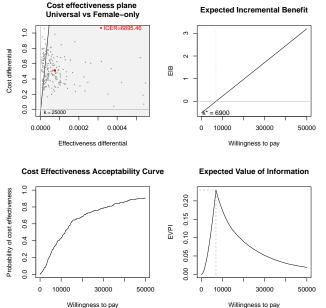
Technical issues

Complex model specification, so helpful to break down for computational efficiency

- **1** Run the Bayesian model to estimate the parameters performed in JAGS
 - Pre- and post-processing directly in R, but JAGS called to run the MCMC estimation
 - Relatively quick and easy convergence
- Onstruct the transition probabilities as functions of the parameters performed in R
 - Not too complex only needs to write down a set of relationships among the parameters
- 3 Generate the "virtual follow up" performed in R
 - Most computationally intensive part
 - Generates large arrays (dimension = number of states × number of MCMC simulations × number of cohorts × number of interventions)
- 4 Make the economic analysis performed in R
 - Straightforward, using the BCEA (Bayesian Cost-Effectiveness Analysis) package — more details at www.statistica.it/gianluca/BCEA
 - Automatically obtain CEAC, CE plane, EVPI, EVPPI, ...

A glimpse at results...





Bayesian pseudo-dynamic MMs for HPV vaccination

Limitations & potential extensions

- The dynamic Markov model is capable of dealing with much of the complexity of the problem
 - Fundamental characteristics can be taken into account
 - Can use a full Bayesian approach good thing!



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 - Fundamental characteristics can be taken into account
 - Can use a full Bayesian approach good thing!
- The sexual partnership matrices and the partnership acquisition rates are considered as fixed (for now!)
- This is not ideal, as they are likely to be subject to uncertainty that should be further propagated through the model
 - Dirichlet priors for the entries of the sexual partnership matrices, to account for uncertainty
 - Gamma priors for the partner acquisition rates, to encode information about their range
- Speed up the computation process
 - Parallel computing



Thank you!