

Bayesian Markov models for the cost-effectiveness analysis of HPV vaccination

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June 12th, 2014

- ① Aim of the research
- ② Literature review
- ③ General introduction
 - Bayesian Markov models
- ④ Model assumptions
 - Reference population and follow-up
 - Cervical screening and HPV vaccination
 - Model structure
 - The process of sexual mixing
 - Herd immunity
 - Distributional assumptions and sources of prior information
 - Transition probabilities
- ⑤ Preliminary results
 - Convergence and autocorrelation
 - Cost-effectiveness analysis

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Identifying the most cost-effective vaccination strategy against human papillomavirus (HPV)

- 1 Incorporating the effects of herd immunity into the Bayesian Markov model
- 2 Including boys in a quadrivalent HPV vaccination scheme
- 3 Considering a great variety of HPV-induced diseases



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- Mainly sexually transmitted virus
- Infects both mucous membrane and skin
- In rare cases transmission through:
 - Shared towels
 - Public saunas
 - Digital-genital contact
- Around 40 identified genotypes, including 13 high-risk types
 - HPV 16 and 18: 79.1% of all cervical cancers
 - HPV 6 and 11: anogenital warts and recurrent respiratory papillomatosis (RRP)
 - HPV 1 and 2: benign skin warts
- Contributory cause of anal, vaginal, vulvar, penile and head/neck cancers

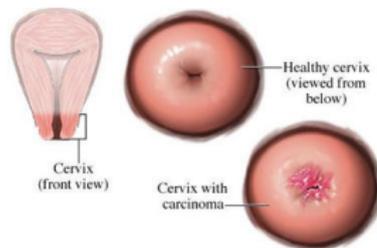
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HPV prevalence

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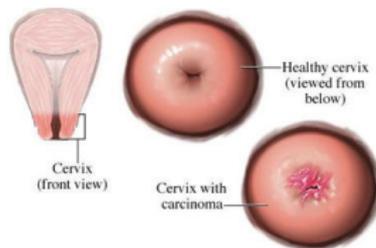


Cervical cancer

- Yearly 2,890 new cervical cancer diagnoses
- Cervical cancer 11th most frequent cancer in females

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Genital warts prevalence

- 4.7% in females
- 2.2% in males



Yearly costs borne by the NHS

- £17 million for genital warts treatment
- £157 million for cervical cancer treatment



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European public health insurance systems

- National Health Service (NHS) in the UK
- Servizio Sanitario Nazionale (SSN) in Italy
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Country-specific information

- Data on costs and utilities specific for Italy
- Cost-effectiveness analysis in an Italian context

- 5 databases searched with variety of search word combinations
- Altogether 116 publications reviewed and summarized
- Hybrid models for HPV vaccination
 - ① Simulate the process of sexual mixing
 - ② Calculate age-and gender-specific HPV prevalence by means of
 - Difference equations
 - ODEs
 - ③ Integrate those probabilities into natural disease history models afterwards

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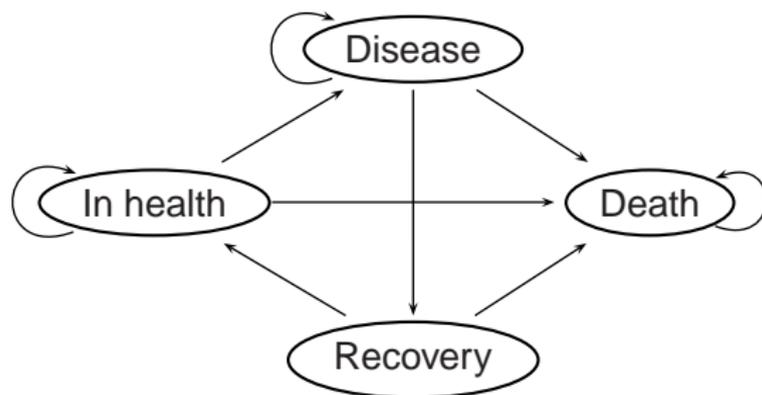
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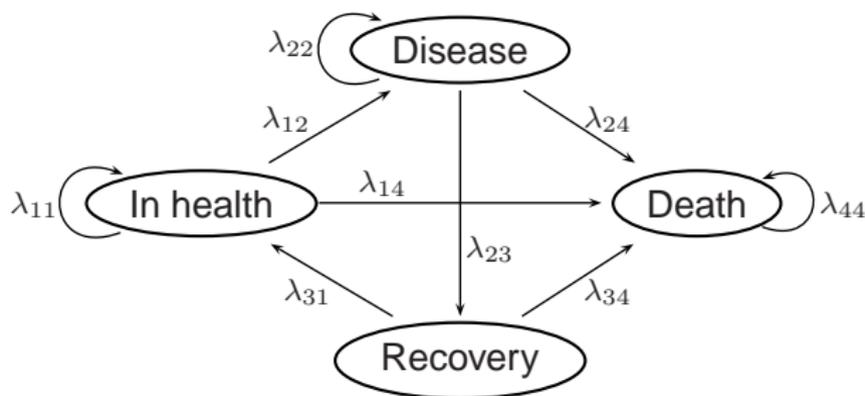
To the best of our knowledge, our methodology of including dynamic interactions between individuals directly into a static Bayesian Markov model is unique in the field of HPV transmission and disease progression modelling.

1. Define a structure



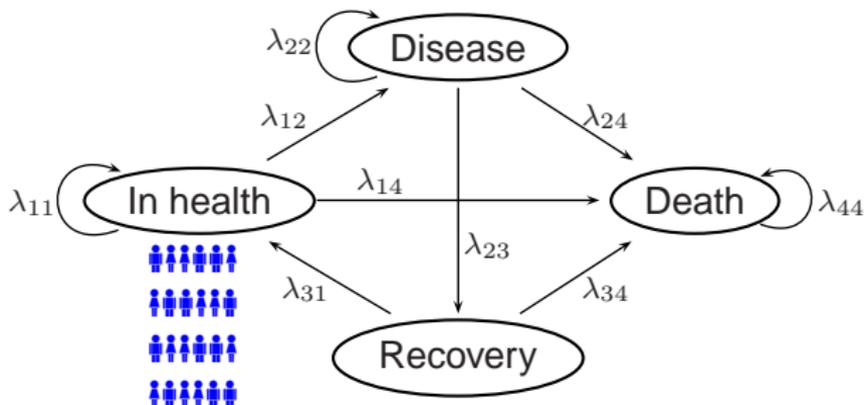
- Exhaustive and mutually exclusive health states

2. Estimate the transition probabilities



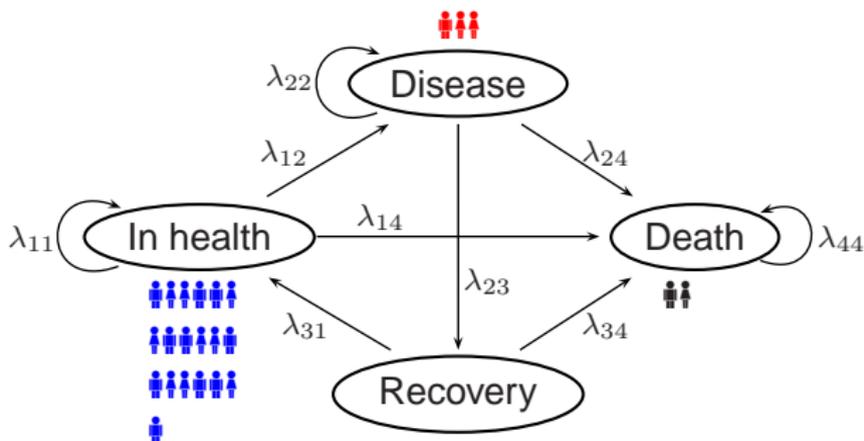
- Transition probabilities λ are functions of θ
- Assigning flat and informative distributions to parameters θ

3. Run the simulation: $t = 0$



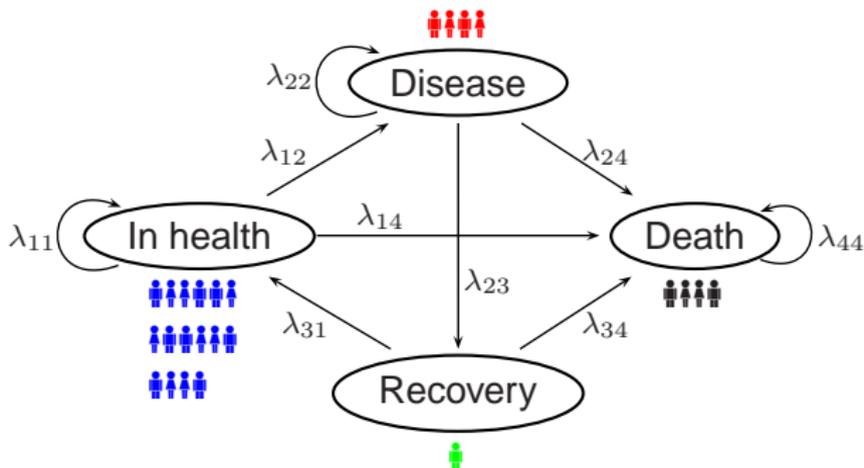
- Each health state is assigned a value of utility
- Ranging between 0 (death) and 1 (perfect health)

3. Run the simulation: $t = 1$

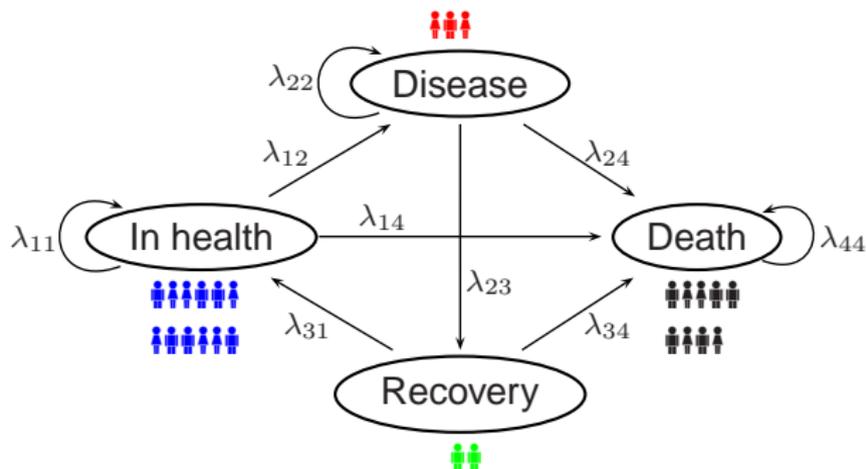


- Markov cycle length of 1 year

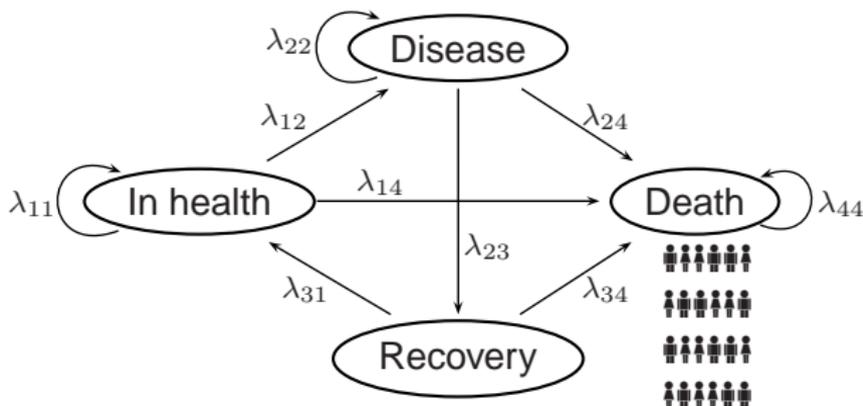
3. Run the simulation: $t = 2$



3. Run the simulation: $t = 3$



3. Run the simulation: $t = T$



- Health economic analysis of multi cohort vaccination strategy

Reference population and follow-up

- 24 cohorts of females and males aged 12-35 years
- Follow-up period of 55 years
- Population dynamics: Entering of healthy 12 year old individuals during first 10 years of observation

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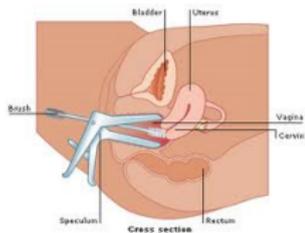
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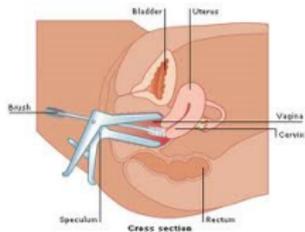
Interventions i

- 1 *Screening-only*: Screening in females, no intervention in males
- 2 *Female-only vaccination*: Screening and vaccination in 12 year old females, no intervention in males
- 3 *Universal vaccination*: Screening and vaccination in 12 year old females, vaccination in 12 year old males
 - Sensitivity analyses to male vaccination age
- 4 *Catch-up vaccination*: Screening and vaccination in 12 year old females with a catch-up at 15 years and no intervention for males
 - Sensitivity analysis to catch-up coverage rate



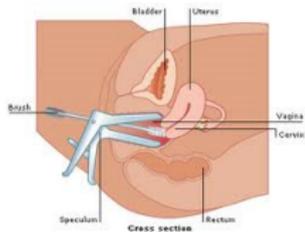
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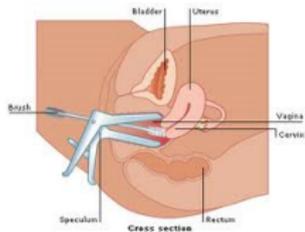
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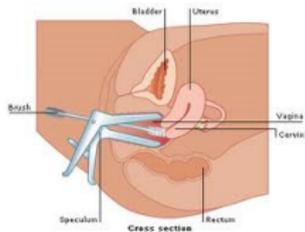
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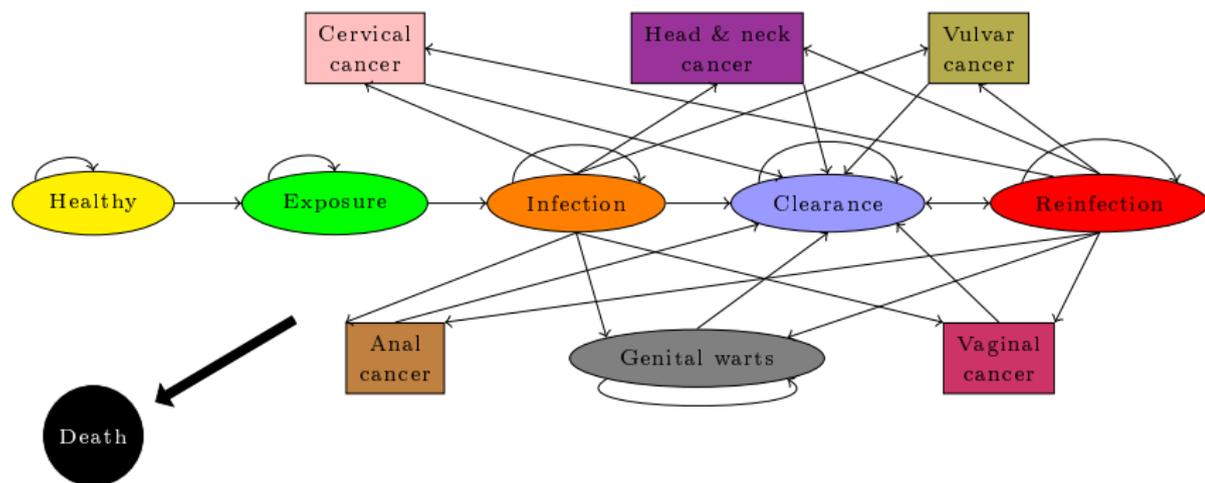


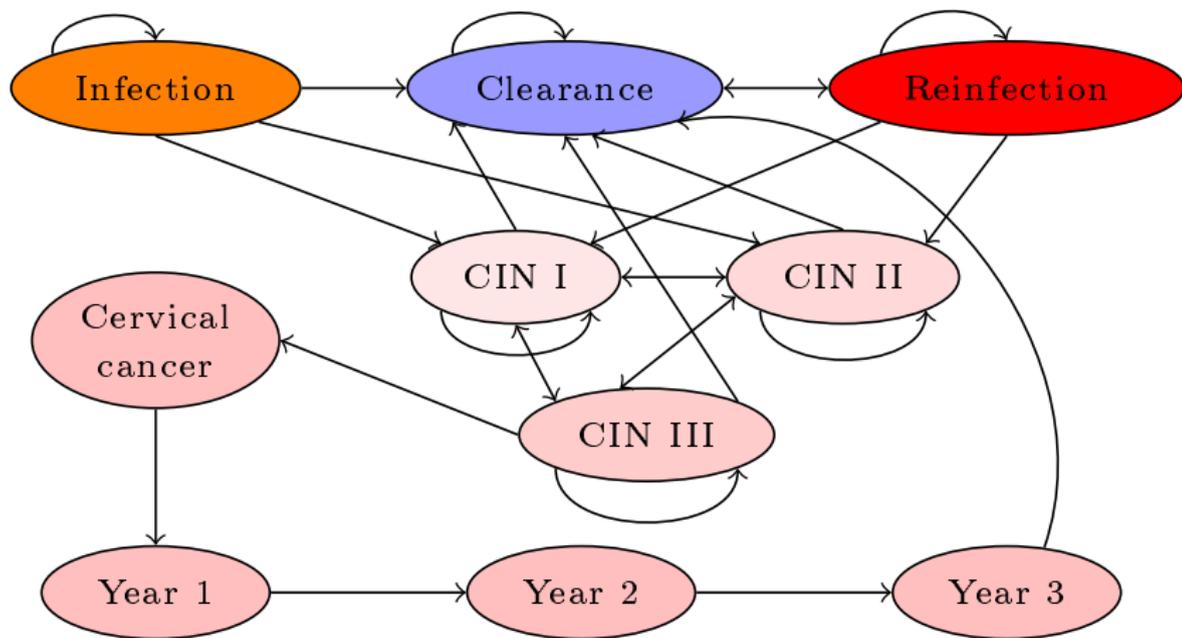
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$S_f = 36$ health states







- Most important aspect of our research
- Transforms the Bayesian MM into a hybrid model
- Accounting for herd immunity
 - unvaccinated individuals are indirectly protected
 - females and males benefit from male HPV vaccination by
 - 1 decrease in prevalence of HPV and induced diseases
 - 2 reduction of HPV transmission between the sexes
 - vaccine benefits are no longer underestimated in CE-analyses



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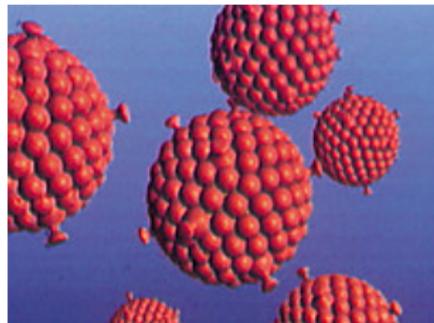
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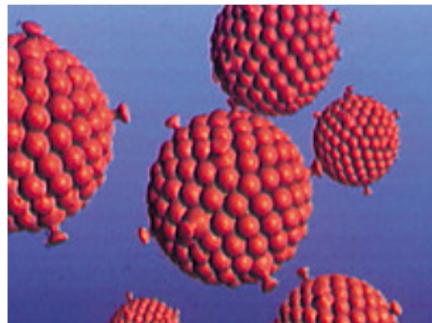
Average-risk sexual activity

- 80% of the population
- 2-10 lifetime sex partners



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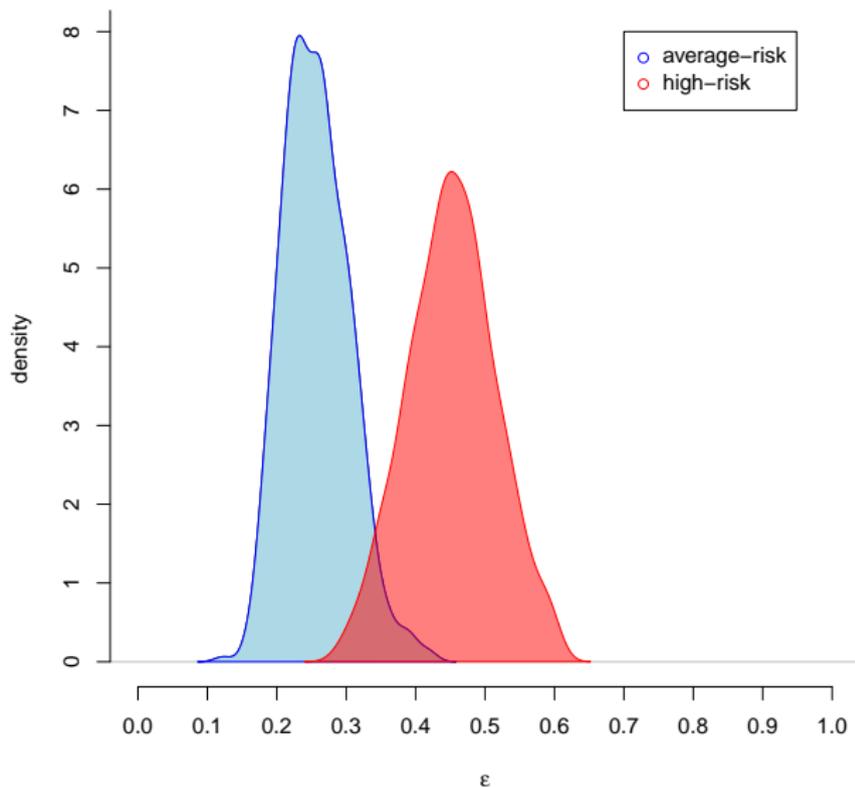
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High-risk sexual activity

- 20% of the population
- 11 or more lifetime sex partners
- Promiscuity correlates with
 - smoking
 - a low education level
 - early first sexual intercourse before the age of 18

Distributions of HPV transmission probabilities ϵ



Sexual partnership matrix for female (average-risk group)

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

Age	Females			Males		
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Sexual partnership matrix for female (average-risk group)

Age	12	15	20	25	30	35	40	45	50	55	60	65
	-14	-19	-24	-29	-34	-39	-44	-49	-54	-59	-64	-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%
...
65-80	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	14%	86%

Annual max, average and mean partner acquisition rate for females

Age	Females			Males		
	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
...
60-	0.05	0.10	0.15	0.04	0.11	0.18

- Consider a 20 year old female in the average-risk group and assume the maximum partner acquisition rate
- Then the sexual mixing matrices are defined as
 - $m_{g,s,s',a,a'} = 36\% \times 1.38 = 0.4968$, for $a' = 20-24$;
 - $m_{g,s,s',a,a'} = 49\% \times 1.38 = 0.6762$, for $a' = 25-29$;
 - $m_{g,s,s',a,a'} = 12\% \times 1.38 = 0.1656$, for $a' = 30-34$;
 - $m_{g,s,s',a,a'} = 2\% \times 1.38 = 0.0276$, for $a' = 35-39$;
 - $m_{g,s,s',a,a'} = 0$, for any other age group a' .

Equation introduced by Korostil et al.

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

- ϵ represents the HPV transmission probability per partnership
- $m_{g,s,s',a,a'}$ represents the sexual mixing matrix
- $I_{g',s',a'}$ indicates the number of infected individuals of gender g' , sexual activity s' and age a'
- $N_{g',s',a'}$ indicates the total number of individuals of gender g' , sexual activity s' and age a' .

At each time point t , the probability of HPV infection depends on the pool of opposite sex partners

- a) available for mating, depending on age and sexual activity
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Equation introduced by Cooper et al.

$$\lambda_{g,s,a} = 1 - \exp^{-\kappa_{g,s,a}}$$

- The HPV infection rates $\kappa_{g,s,a}$ have to be transformed into probabilities $\lambda_{g,s,a}$
- Cooper et al.'s formula is based on the assumption of constant transition probabilities over the whole observation period
- $\lambda_{g,s,a}$ are the transition probabilities from the health states *Exposure to Infection*
- These are directly integrated into the health state allocation algorithm of the MM
- → Health economic analysis by means of output of MM

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- 5 Calculating overall costs and utilities, resulting in the cost-effectiveness analysis

- **Just Another Gibbs Sampler (JAGS)**
- Integrated into R by means of package R2jags
- 2 parallel chains ($n_{chains} = 2$)
- $n_{iter} = 40,000$ simulations
- burn-in of $n_{burn} = 4,000$
- thinning step of $n_{thin} = 360$

$$n_{sims} = n_{chains} \frac{(n_{iter} - n_{burn})}{n_{thin}} = 2 \frac{(40,000 - 4,000)}{360} = 200$$

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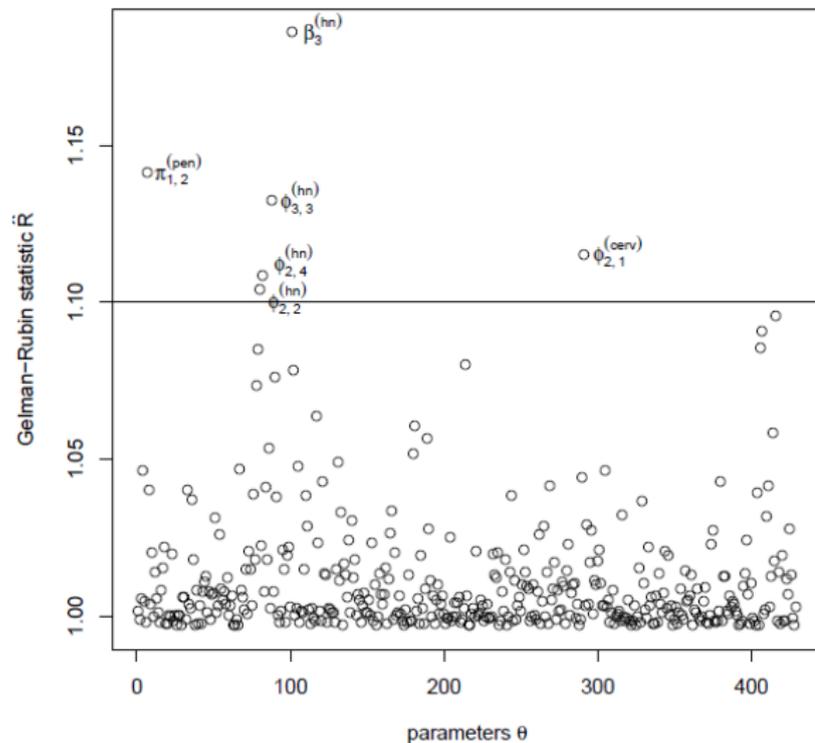
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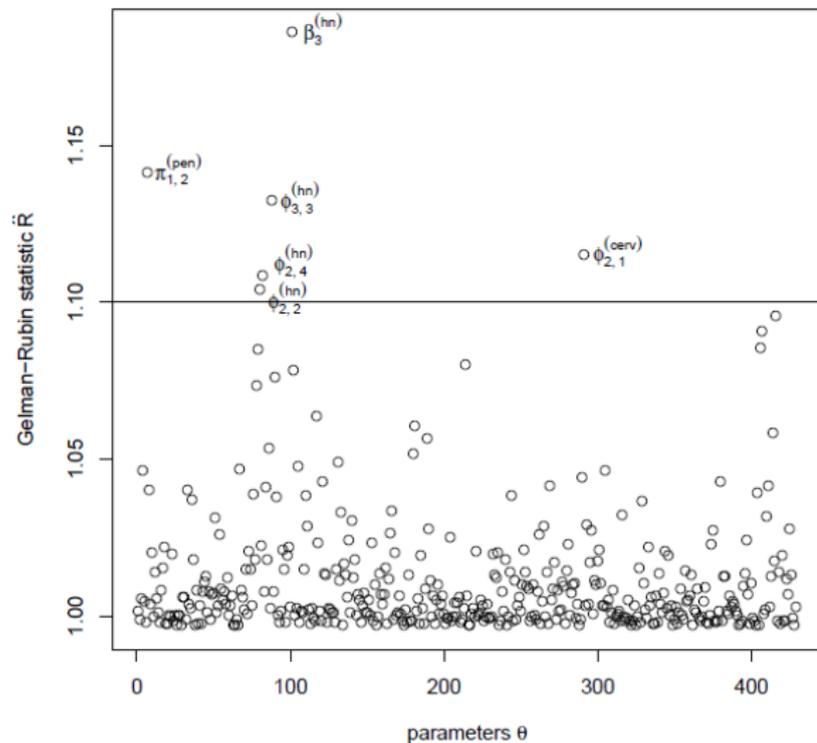
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Gelman-Rubin statistics \hat{R} for θ

Convergence evaluation with \hat{R} for all model parameters θ



Convergence evaluation with \hat{R} for all model parameters θ



$$\hat{R} = \sqrt{\frac{\widehat{Var}(\theta_k|y)}{W(\theta_k)}}$$

The PVC

- Sum of overall costs in intervention i for time $t = 1$ to $t = 55$
- Commonly discounted by $\nu_c = 0.03$

$$\text{PVC}_i = \sum_{t=1}^{t=55} \frac{C_{i,t}}{(1 + \nu_c)^{t-1}}$$

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The PVU

- Sum of overall utilities in intervention i for time $t = 1$ to $t = 55$
- Commonly discounted by $\nu_u = 0.015$

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Comparison of universal to female-only vaccination

- $\Delta_c = \text{PVC}_3 - \text{PVC}_2$
- $\Delta_e = \text{PVU}_3 - \text{PVU}_2$

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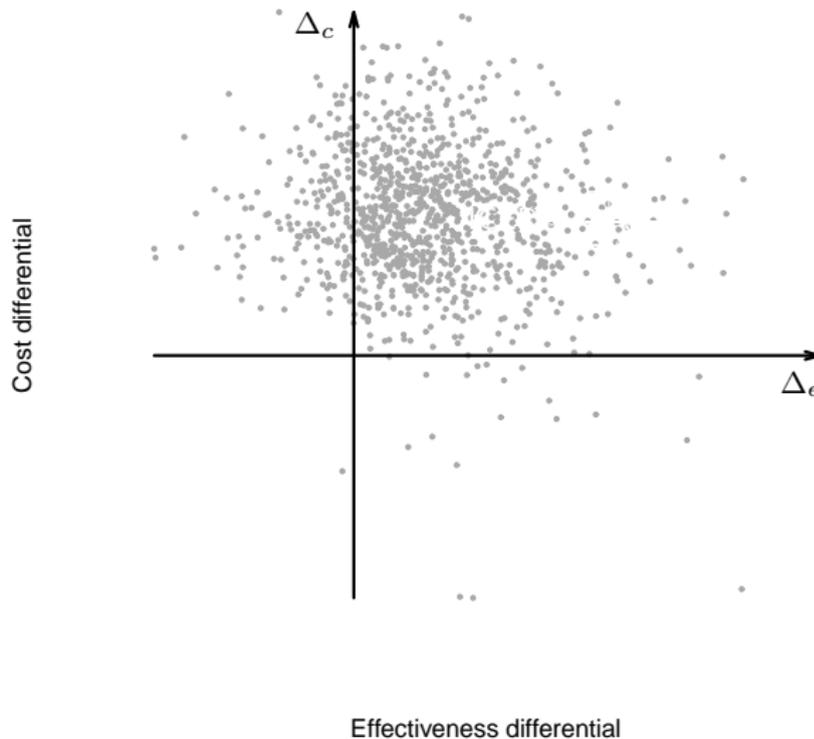
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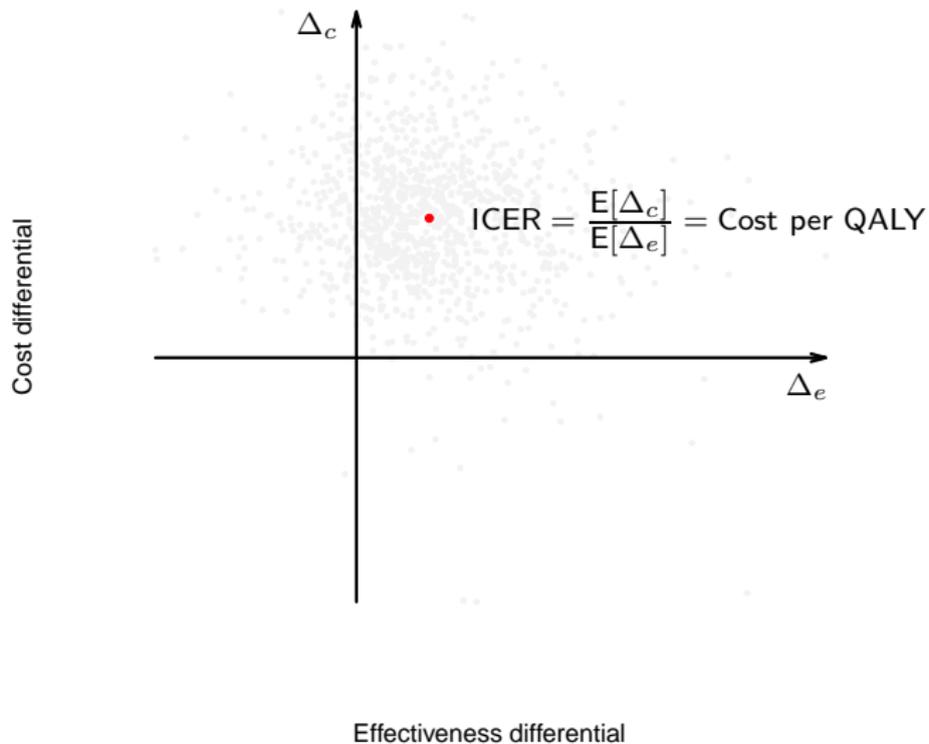
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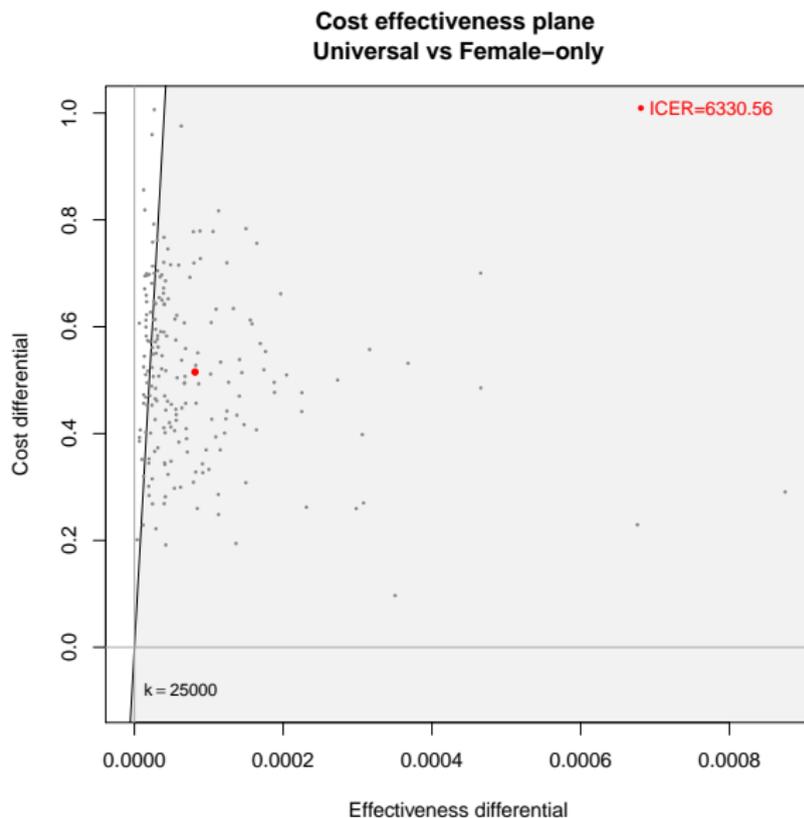
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Cost-effectiveness plane

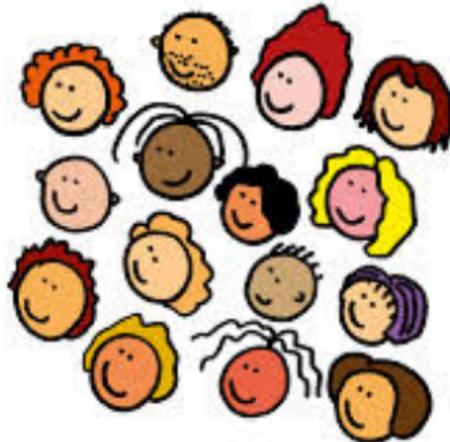


Cost-effectiveness plane





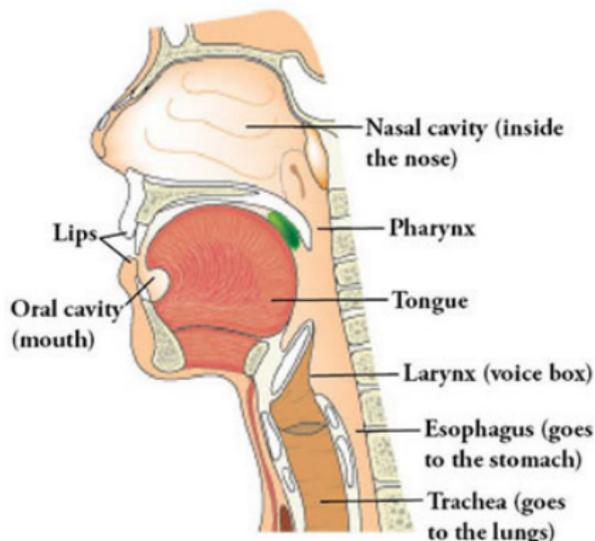
Thank you very much for your attention.



Appendix

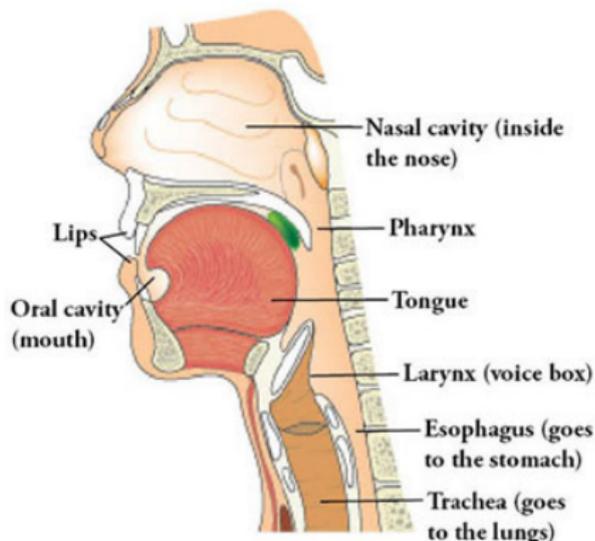
Anal, head/neck, vaginal, vulvar, and penile cancer

- Multifactorial diseases
- HPV-induced:
 - more than 90% of anal cancers
 - more than 50% of vaginal, vulvar and penile cancers
 - 60–70% of oropharyngeal cancers
- Other head/neck cancers mainly attributed to tobacco and alcohol



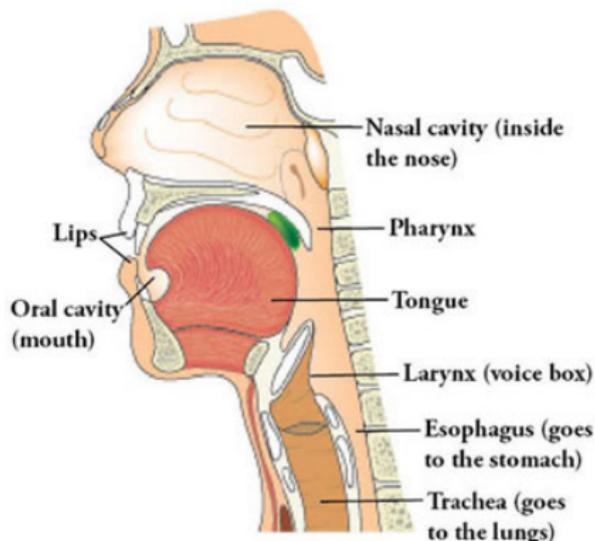
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Databases



- Scopus
- Pubmed
- Cochrane Library
- Web of Science
- Centre for Review and Dissemination (CRD)
 - Database of Abstracts of Reviews of Effects (DARE)
 - NHS Economic Evaluation Database (EED)
 - Health Technology Assessment (HTA)

Search word combinations

((cost-effectiveness) OR (cost-utility) OR (cost-benefit))
AND ((HPV vaccine) OR (human papillomavirus vaccine) OR
HPV or (human papillomavirus))

For universal vaccination extended by

AND (boys OR male)



Methodology

- Static vs. dynamic
- Deterministic vs. stochastic
- Ordinary differential equation (ODE) vs. Markov model vs. hybrid model
- Population-based vs. individual-based vs. microsimulation model

Model assumptions

- Country of investigation
- HPV types involved
- HPV-induced diseases
- Vaccine coverage rate
- Vaccine efficacy
- Vaccination age
- Male vaccination
- Duration of immunity
- Application of booster
- Levels of sexual activity
- Sexual mixing strategy
- Cervical screening strategy
- Duration of follow-up
- Time step of follow-up

Research outcome

- Cost-effectiveness analysis
- HPV-prevalence reduction

Universal HPV vaccination: 26 publications

- 8 reuse methodology
- 8 ordinary differential equation (ODE) models
- 1 static Markov model
- 2 network models
- 3 difference equation models
- 3 hybrid models
- 1 prevalence-based model

Female-only HPV vaccination: 90 publications

- $\approx 50\%$ reuse methodology
- 25 static Markov models
- 4 microsimulation models
- 3 cohort models
- 1 prevalence-based model
- 2 difference equation models
- 1 network model
- 10 ODE models
- 8 hybrid models

Universal vaccination

- 8 publications: cost-effective results
- 7 publications: non-cost-effective results
- 11 publications: only HPV prevalence reductions

Female-only vaccination

- 75 publications: cost-effective results
- 1 publication: non-cost-effective results
- 10 publications: only HPV prevalence reductions
- 4 publications: no research outcomes

Universal vaccination

- Taira et al.
 - Difference equation model for HPV transmission
 - Static Markov disease progression model
- Kim et al.
 - ODE model for HPV transmission
 - Microsimulation disease progression model
- Horn et al.
 - ODE model for HPV transmission
 - Static Markov disease progression model

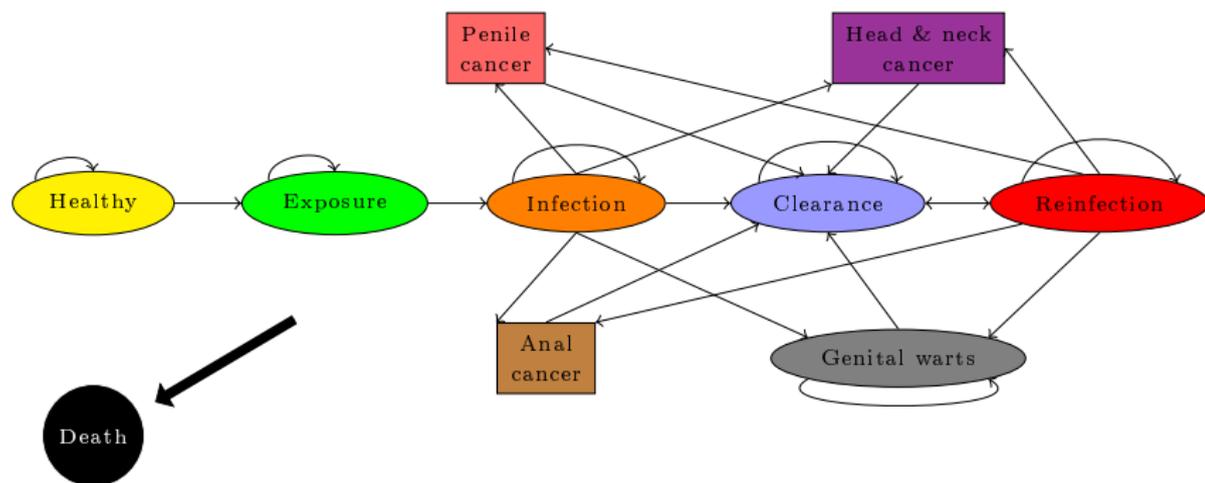
- Probabilistic nature
- Exhaustive and mutually exclusive health states
- Moving between health states according to specified transition probabilities
 - Assigning flat and informative distributions with suitable ranges
 - Prior information out of the literature or from expert opinion
 - Updating posterior distributions with available data
 - Propagating parameter uncertainty by Markov Chain Monte Carlo estimations (MCMC)
- Model calibration with age- and gender-specific data on prevalence of HPV infection and induced diseases
- Each health state is assigned a value of utility
 - Ranging between 0 and 1
 - 0 represents death, 1 perfect health
 - Specified with Time Trade-Off (TTO) method
- Health economic analysis of multi cohort HPV vaccination strategy

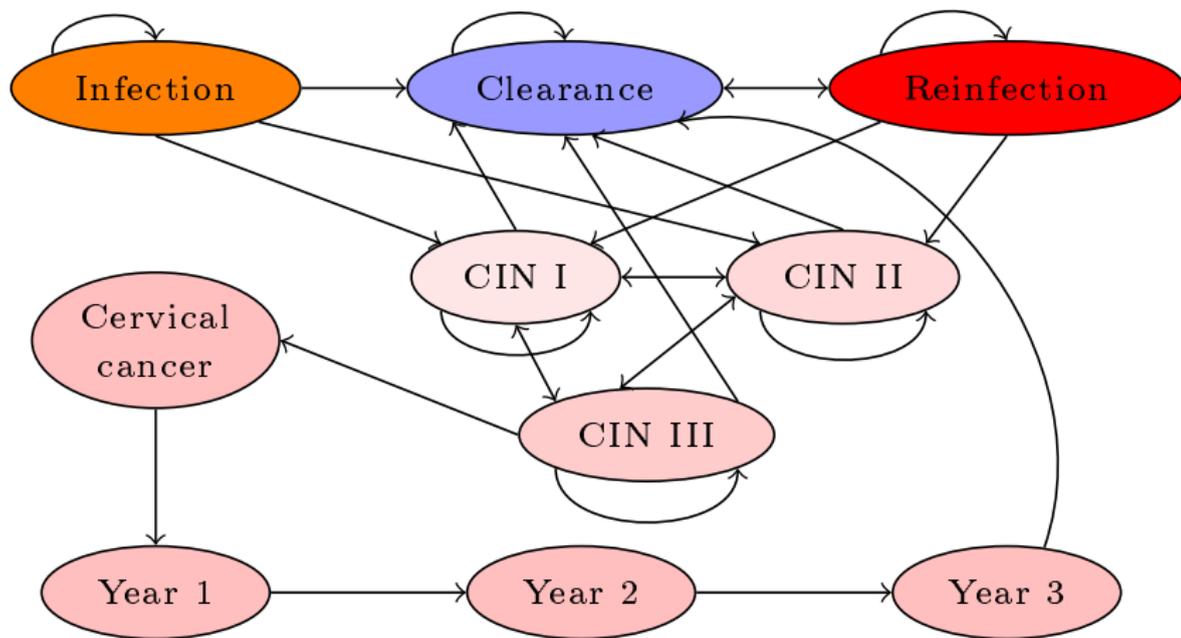
- **Combination of**
 - natural history of disease infection and progression models
 - dynamic sexual disease transmission models
- **Age- and gender-specific HPV prevalence can be calculated beforehand**
 - by means of discrete or continuous time models
 - these probabilities inform the disease progression model afterwards
- **Alternative: the process of sexual mixing can be integrated directly into the static disease progression model**

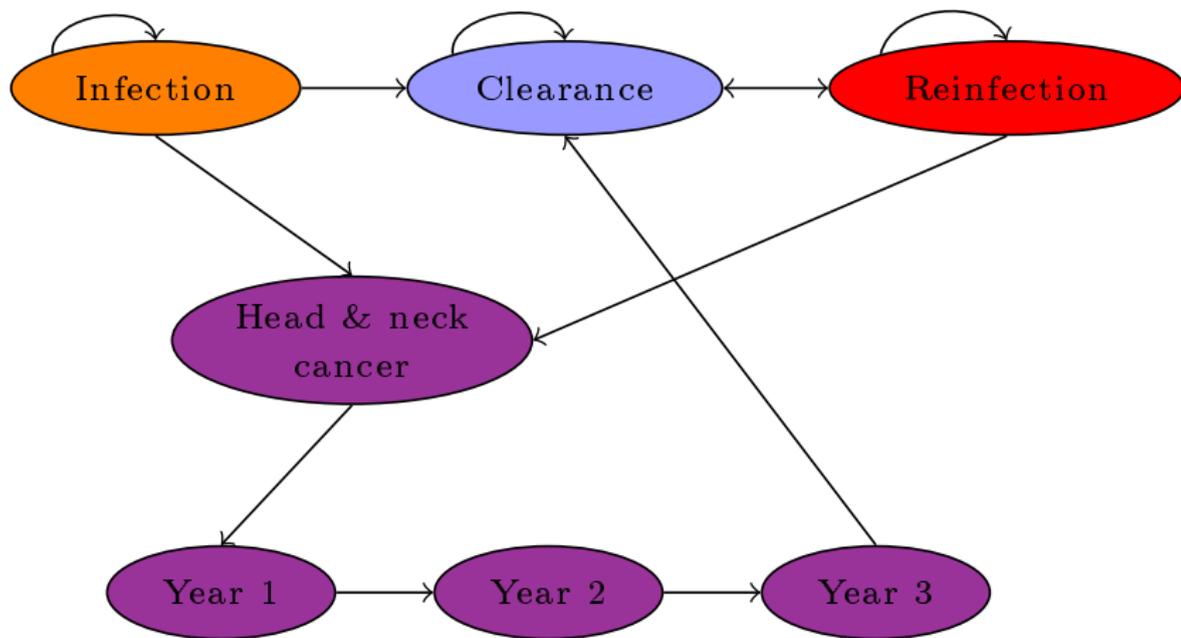
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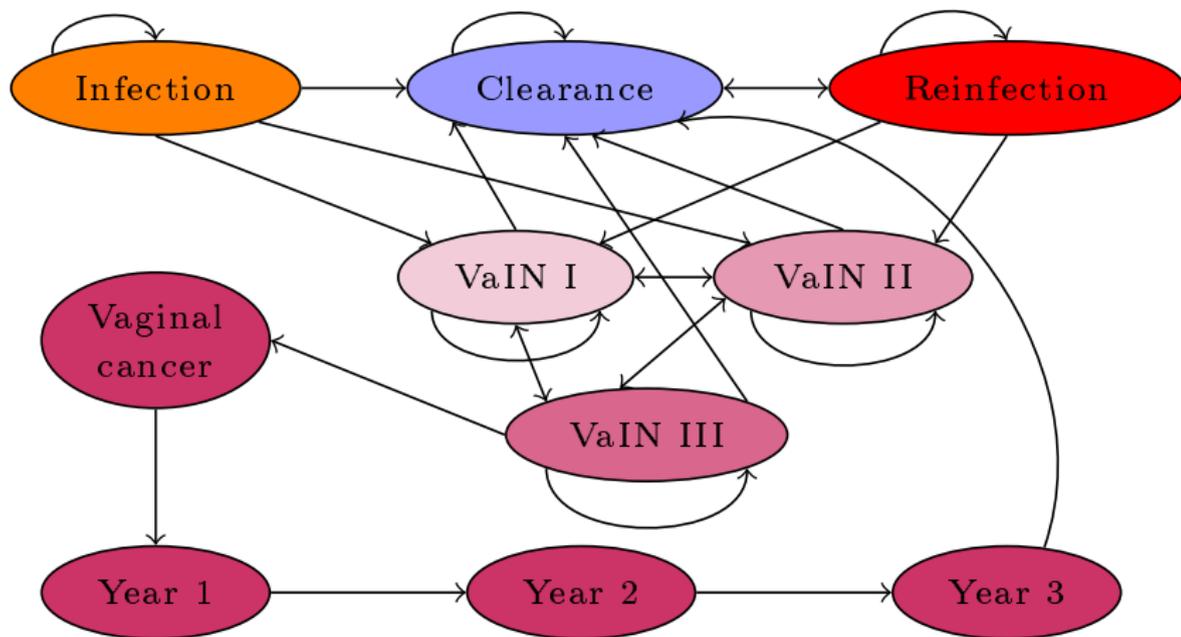
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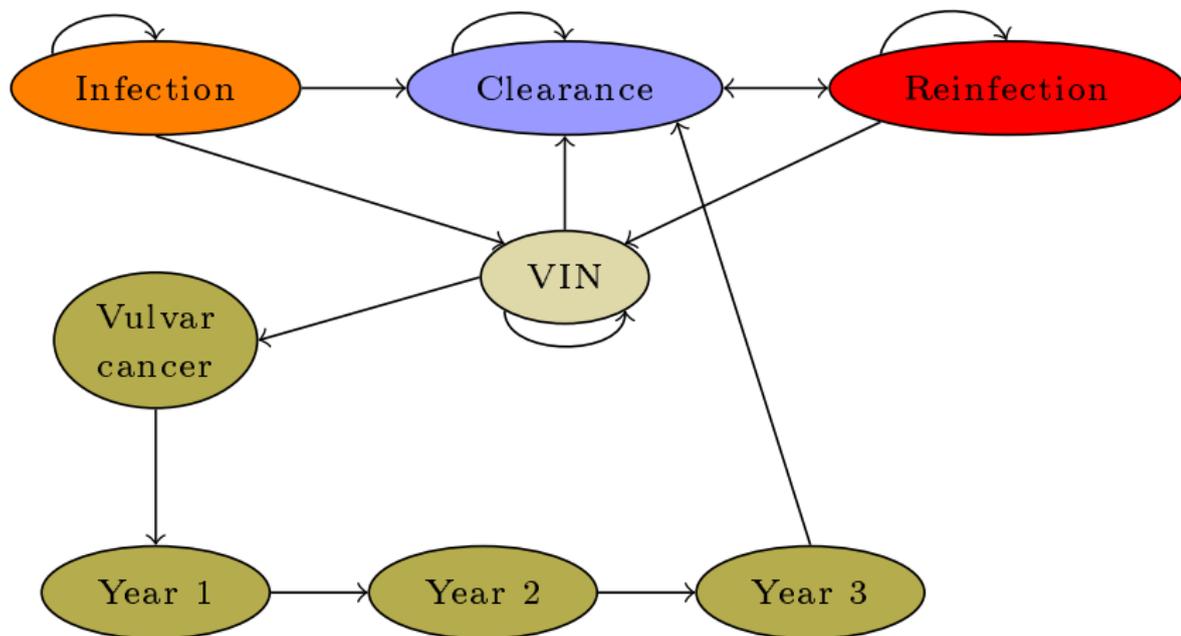
$S_m = 22$ health states

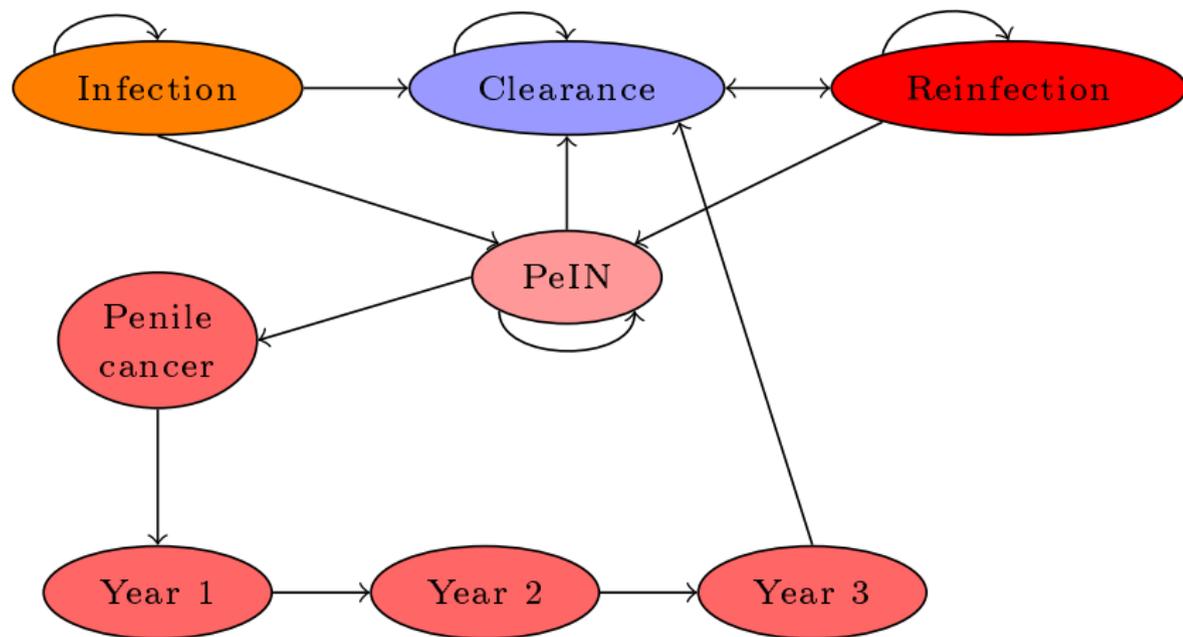












- Individuals move across health states according to $p_{i,a,j,h}$, where
 - i indexes the respective health intervention;
 - a indexes the individual's age;
 - j indexes the original health state;
 - h indexes the target health state.
- All transitions from one health state have to sum up to 1 (constraint of probabilities)
- Transitions to the set of health states \mathcal{H} are possible
- Transitions to health states outside of \mathcal{H} are set to 0
- Remaining in respective state is induced by $1 - \sum p_{i,a,j,h} \forall h \in \mathcal{H}$
- Different transition probabilities for females and males as a consequence of different numbers of health states and gender-specific parameters
- Gender-specific parameters with the index $g = 0$ represent females

- Individuals can have sex (indicated by s_a) and move to $h = 2$
- Individuals can die (indicated by $d_{a,0}$) and move to $h = 9$
- Individuals can remain in perfect health ($h = 1$)

$$p_{i,a,1,h} = 0 \forall h \notin \{1, 2, 9\}$$

$$p_{i,a,1,2} = s_a$$

$$p_{i,a,1,9} = d_{a,0}$$

$$p_{i,a,1,1} = 1 - \sum_{h \neq 1} p_{i,a,1,h}$$

- Individuals in $j = 2$ can have acquire HPV infection (indicated by $\lambda_{0,s,a}$) and move to $h = 3$
- Individuals in $j = 2$ can die (indicated by $d_{a,0}$) and move to $h = 9$
- Individuals in $j = 2$ can remain in exposure ($h = 2$)

$$p_{1,a,2,h} = 0 \forall h \notin \{2, 3, 9\}$$

$$p_{1,a,2,3} = \lambda_{0,s,a}$$

$$p_{1,a,2,9} = d_{a,0}$$

$$p_{1,a,2,2} = 1 - \sum_{h \neq 2} p_{1,a,2,h}$$

- Individuals in $j = 2$ can have acquire HPV infection (indicated by $\lambda_{0,s,a}$) and move to $h = 3$
- Individuals in $j = 2$ can die (indicated by $d_{a,0}$) and move to $h = 9$
- Individuals in $j = 2$ can remain in exposure ($h = 2$)

$$p_{2,a,2,h} = 0 \forall h \notin \{2, 3, 9\}$$

$$p_{2,a,2,3} = \alpha_1[\omega_3(1 - \gamma_1)\lambda_{0,s,a} + (1 - \omega_3)(1 - \zeta\gamma_1)\lambda_{0,s,a}] + (1 - \alpha_1)\lambda_{0,s,a}$$

$$p_{2,a,2,9} = d_{a,0}$$

$$p_{2,a,2,2} = 1 - \sum_{h \neq 2} p_{2,a,2,h}$$

- α_1 represents the vaccine coverage in female-only vaccination
- γ_1 represents the vaccine efficacy
- ω_3 represents the vaccine compliance
- ζ represents the reduction in effectiveness due to noncompliance

Cohort	Time of follow-up												
	0	1	2	3	4	5	6	7	8	9	10	...	55
1	25	26	27	28	29	30	31	32	33	34	35	...	80
2	24	25	26	27	28	29	30	31	32	33	34		79
3	23	24	25	26	27	28	29	30	31	32	33		78
4	22	23	24	25	26	27	28	29	30	31	32		77
5	21	22	23	24	25	26	27	28	29	30	31		76
6	20	21	22	23	24	25	26	27	28	29	30		75
7	19	20	21	22	23	24	25	26	27	28	29		74
8	18	19	20	21	22	23	24	25	26	27	28		73
9	17	18	19	20	21	22	23	24	25	26	27		72
10	16	17	18	19	20	21	22	23	24	25	26		71
11	15	16	17	18	19	20	21	22	23	24	25		70
12*	14	15*	16	17	18	19	20	21	22	23	24	...	69
13*	13	14	15*	16	17	18	19	20	21	22	23		68
14*	12	13	14	15*	16	17	18	19	20	21	22		67
15		12	13	14	15	16	17	18	19	20	21		66
16			12	13	14	15	16	17	18	19	20		65
17				12	13	14	15	16	17	18	19		64
18					12	13	14	15	16	17	18		63
19						12	13	14	15	16	17		62
20							12	13	14	15	16		61
21								12	13	14	15		60
22									12	13	14		59
23										12	13		58
24											12	...	57

- Running 2 chains in parallel to calculate posterior distributions of parameters $\theta = (\theta_1, \dots, \theta_k)$
- Choosing two different starting points with larger variance compared to the underlying data
- Comparing within-chain variance $W(\theta_k)$ to between-chain variance $B(\theta_k)$
- n_{sims} represents the length of the MCMC sample

$$\widehat{Var}(\theta_k|y) = \frac{n_{sims}-1}{n_{sims}}W(\theta_k) + \frac{1}{n_{sims}}B(\theta_k)$$

Convergence is monitored by assessing the *potential scale reduction*

$$\hat{R} = \sqrt{\frac{\widehat{Var}(\theta_k|y)}{W(\theta_k)}}$$

- \hat{R} is the factor by which the scale of the posterior distribution of θ_k can be further reduced
- A longer MCMC run will possibly improve convergence
- $R \leq 1.1$ represents sufficient convergence

- MCMC iterations are by definition correlated
- Current observation depends on previous one
- The higher the autocorrelation, the lower the equivalence between MCMC output and a proper *iid* sample

$$n_{eff} = \frac{n_{sims}}{1 + 2 \sum_{t=1}^{\infty} corr_t}$$

- $corr_t$ is the *lag t* autocorrelation
- $n_{eff} \approx n_{sims}$ indicates negligible autocorrelation
- In case of high autocorrelation
 - convergence can still be reached
 - extreme quantiles of the posterior distribution are typically estimated without precision

Presentation of preliminary results under baseline assumptions

- vaccination of 12 year old females and males
- high vaccine coverage rate in the catch-up vaccination

Detailed explanation of calculation process including

- overall costs and utilities
- present values of cost (PVC) and utility (PVU)
- *Incremental Cost-Effectiveness Ratio* (ICER)
- cost-effectiveness plane

Costs include

- diagnostic procedures of health states
 - 2 pap smears and 2 colposcopies in females with CIN I-III
 - 1 HPV DNA test in females with CIN III and cervical cancer
 - anoscopy, biopsy, cytology in individuals with anal LSIL and HSIL
 - diagnostic costs of other HPV-induced diseases already included in treatment costs
- treatment of HPV-induced precancerous lesions and cancers
- vaccine administration and product costs in female-only, universal and catch-up interventions

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Unit costs and utilities are multiplied by the number of individuals in intervention i at time t in the respective health state, and by the probabilities of diagnosis, to result in **overall** measures.

$$\begin{aligned}
 C_{i,t} = & C_{i,t}^{scr} + C_i^{vac} + C_{i,t}^{gw} + C_{1,i,t}^{cin} + C_{2,i,t}^{cin} + C_{3,i,t}^{cin} + C_{i,t}^{cerv} + C_{i,t}^{lsil} \\
 & + C_{i,t}^{hsil} + C_{i,t}^{an} + C_{i,t}^{hn} + C_{i,t}^{vin} + C_{i,t}^{vulv} + C_{1,i,t}^{vain} + C_{2,i,t}^{vain} + C_{3,i,t}^{vain} \\
 & + C_{i,t}^{pein} + C_{i,t}^{pen}
 \end{aligned}$$

$$\begin{aligned}
 U_{i,t} = & U_{i,t}^{health} + U_{i,t}^{inf} + U_{i,t}^{gw} + U_{1,i,t}^{cin} + U_{2,i,t}^{cin} + U_{3,i,t}^{cin} + U_{r,i,t}^{cerv} + U_{i,t}^{lsil} \\
 & + U_{i,t}^{hsil} + U_{r,i,t}^{an} + U_{r,i,t}^{hn} + U_{i,t}^{vin} + U_{r,i,t}^{vulv} + U_{1,i,t}^{vain} + U_{2,i,t}^{vain} + U_{3,i,t}^{vain} \\
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 \end{aligned}$$

- Standard measure in cost-effectiveness analyses
- Incremental cost per QALY gained
 - **Quality-Adjusted Life Year**
 - Utility of health state is multiplied with amount of time spent within
- All model parameters in vector $\theta = (\theta^3, \theta^2)$
 - θ^3 representing parameters in $i = 3$ (universal vaccination)
 - θ^2 representing parameters in $i = 2$ (female-only vaccination)
- Ratio of expectations of cost- and effectiveness-differentials
 - $\Delta_c = PVC_3 - PVC_2$
 - $\Delta_e = PVU_3 - PVU_2$

$$ICER = \frac{E[PVC|\theta^3] - E[PVC|\theta^2]}{E[PVU|\theta^3] - E[PVU|\theta^2]} = \frac{E[\Delta_c]}{E[\Delta_e]}$$

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Positive algebraic sign

- Universal vaccination both higher costs and effects than female-only vaccination
- Universal vaccination both lower costs and effects than female-only vaccination

Negative algebraic sign

- Universal vaccination higher costs and lower effects than female-only vaccination
- Universal vaccination lower costs and higher effects than female-only vaccination → cost-saving ICER

ICER values between €30,000 and €45,000 are deemed to be cost-effective according to the Italian Health Economics Association (AEIS). In contrast, the NHS in the UK define ICERs under £25,000 to be cost-effective.

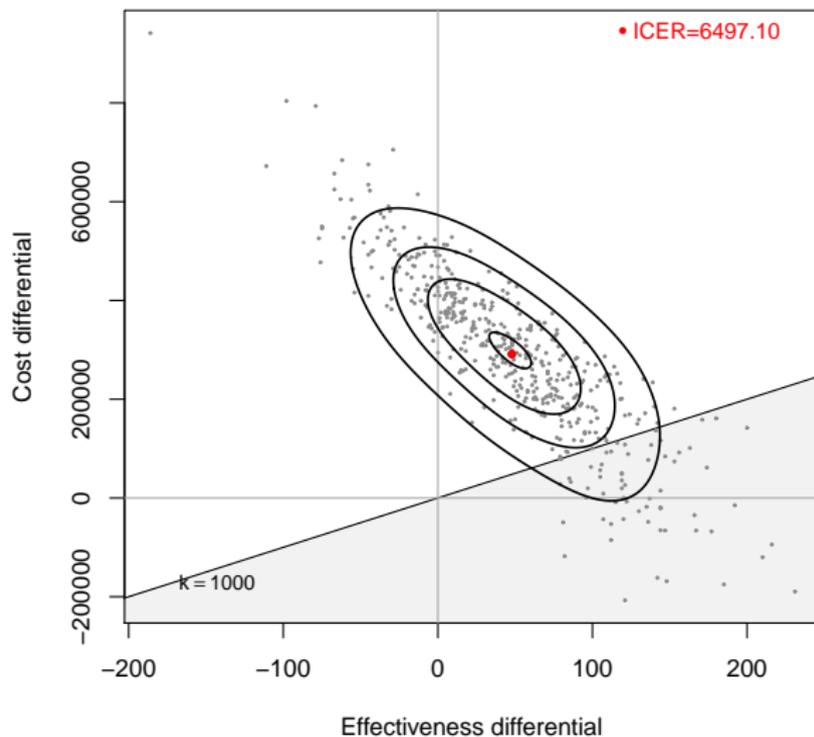
Description of the graph

- The x-axis is the effectiveness differential Δ_e
- The y-axis is the cost differential Δ_c
- Each point represents a possible future in terms of the expected measures of differential cost and benefit
- The spread of the distribution of points accounts for uncertainty
- The shaded part of the plane indicates the sustainability area (ICERs below the threshold of cost-effectiveness)
- The ICER is displayed as a red dot with its corresponding value

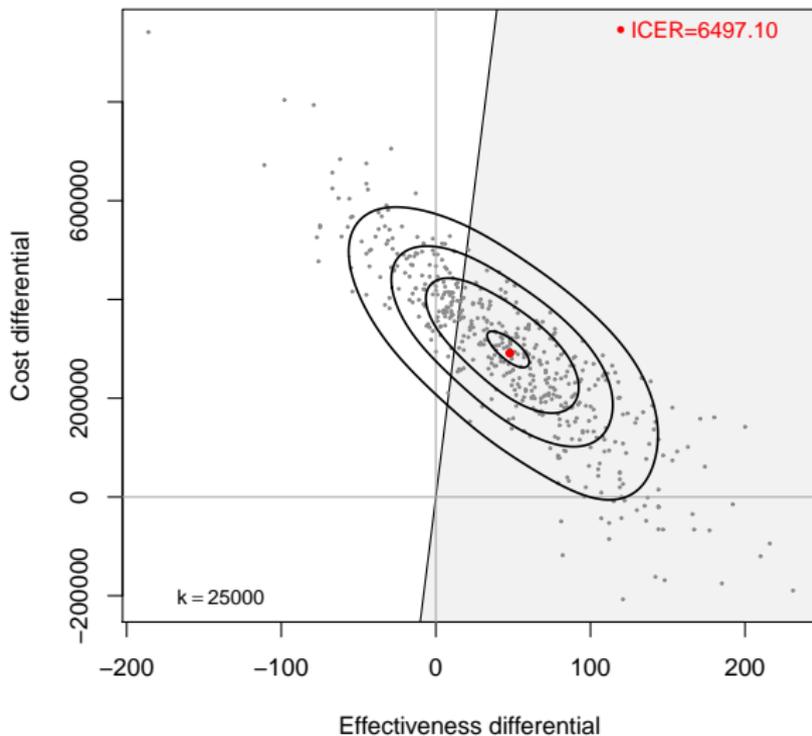
Interpretation of the graph

- Points lying in the north-eastern quadrant (i.e. when $\Delta_e > 0$ and $\Delta_c > 0$) suggest that universal vaccination proves more effective as well as more expensive than female-only vaccination.
- Points lying in the north-western quadrant (i.e. when $\Delta_e < 0$ and $\Delta_c > 0$) suggest that universal vaccination proves less effective and more expensive than female-only vaccination.
- Points lying in the south-western quadrant (i.e. when $\Delta_e < 0$ and $\Delta_c < 0$) suggest that universal vaccination proves less effective as well as less expensive than the reference intervention.
- Finally, points lying in the south-eastern quadrant (i.e. when $\Delta_e > 0$ and $\Delta_c < 0$) suggest that universal vaccination proves more effective and less expensive than female-only vaccination.

Cost effectiveness plane New Chemotherapy vs Old Chemotherapy



Cost effectiveness plane New Chemotherapy vs Old Chemotherapy



- **Programming tasks**

- Including layers of uncertainty in the deterministic age- and gender-specific mixing matrices and partner acquisition rates
- Implying the necessity of a booster application
- Generalizing the R code to enable an easier calculation of scenarios next to the baseline
- Conducting a full cost-effectiveness analysis

- **Reading literature** on standard methodology in infectious disease transmission modelling

- **Writing tasks**

- Publishing the cost-effectiveness analysis results, focusing especially on the finding of staggered male vaccination age
- Publishing the methodology of the hybrid Bayesian Markov model
- Writing up the final PhD thesis

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