ESRC National Centre for Research Methods

BIAS

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Session 52. Combining Data: Quantitative Methods and Applications

Bayesian Graphical Models for Combining Multiple Data Sources

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http://www.bias-project.org.uk

Outline

Motivation
- Why?
- Case study

Graphical Models
- Introduction to graphical models
- Graphical model for application

Results

Why combine multiple datasets?

- Data for the social and health sciences typically come from observational studies
- Due to the complex nature of the research question, a single data set may not provide sufficient information for valid inference
- Some data sources, such as routinely collected administrative data, have a limited number of variables for a large population
- Others, such as surveys or cohort studies, contain detailed information on a small sample of individuals
- Problems such as bias and small sample size can be mitigated by combining multiple sources of data

Case study:
water disinfection by-products and low birth weight

Objective: to estimate the association between trihalomethane (THM) concentrations, a by-product of chlorine water disinfection potentially harmful for reproductive outcomes, and risk of full term low birthweight (<2.5kg).

- Use information on births between 2000 and 2001 in North West England, serviced by the United Utilities Water Company
- Link birth records to estimated trihalomethane water concentrations using
  - residence at birth
  - a model to estimate THM concentration from the water company monitored samples
- First analysis in Molitor et al (2009)

The primary data: HES

- 8969 birth records were obtained from the Hospital Episode Statistics (HES) data base
- Advantage:
  - captures information on all hospital births in the population under study ⇒ increased power, fully representative
- Disadvantage:
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- HES contains data on
  - mother's age
  - baby gender
  - gestational age
  - an index of deprivation
- But no data on other characteristics which impact birth weight
  - maternal smoking
  - ethnicity

A naive analysis using HES data only

- denote low birthweight by Y (binary indicator)
- fit a logistic regression model using the
  - exposure of interest, X=THM
  - measured confounders,
    C={mother's age, baby gender, deprivation index}
- ignore the unmeasured confounders,
  U={maternal smoking, ethnicity}

Naive Analysis Model

$$Y_i \sim Bernoulli(p_i)$$
$$logit(p_i) = \beta_0 + \beta_X X_i + \beta_C^T \boldsymbol{C}_i$$

Analysis results using HES data only (n=8969)

no adjustment for mother’s smoking and ethnicity status

	Odds ratio (95% interval estimate)
Trihalomethanes	
$> 60\mu g/L$	1.39 (1.10,1.76)
Mother’s age	
≤ 25	1.14 (0.86,1.52)
$25-29^{\star}$	1
$30-34$	0.81 (0.57,1.15)
≥ 35	1.10 (0.73,1.65)
Male baby	0.76 (0.60,0.96)
Deprivation index	1.37 (1.20,1.56)

* Reference group

Biased from unmeasured confounders?

The supplementary data: MCS

- The Millennium Cohort Study (MCS)
  - contains survey information on mothers and infants born during 2000-2001
  - includes detailed information on ethnicity and smoking
  - is a stratified sample (advantaged/disadvantage/ethnic minority)
- For our study region, 824 cohort births can be matched to the hospital data (HES)

MCS Analysis Model

$$Y_i \sim Bernoulli(p_i)$$

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add $\boldsymbol{U}$={smoking, ethnicity}

Analysis results using MCS data only (n=824)

	Odds ratio (95% interval estimate)		
	HES only (excludes ***U***)	MCS only (excludes ***U***)	MCS only (includes ***U***)
Trihalomethanes			
$> 60\mu g/L$	1.39 (1.10,1.76)	2.06 (0.85,4.98)	1.87 (0.76, 4.62)
Mother's age			
≤ 25	1.14 (0.86,1.52)	0.65 (0.23,1.79)	0.57 (0.20, 1.61)
$25-29^\star$	1	1	1
$30-34$	0.81 (0.57,1.15)	0.13 (0.02,1.11)	0.13 (0.02, 1.11)
≥ 35	1.10 (0.73,1.65)	1.57 (0.49,5.08)	1.82 (0.55, 5.99)
Male baby	0.76 (0.60,0.96)	0.59 (0.25,1.43)	0.62 (0.25, 1.49)
Deprivation index	1.37 (1.20,1.56)	1.54 (0.78,3.02)	1.44 (0.73, 2.85)
Smoking			3.39 (1.26, 9.12)
Non-white ethnicity			2.66 (0.69,10.31)

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Lacks power to detect an association

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Some evidence of confounding

Combining the HES and MCS data

- The objective is to estimate the association between X and Y while controlling for $(\boldsymbol{C}, \boldsymbol{U})$
- Combining HES and MCS data
  - $\boldsymbol{U}$ becomes a vector of partially measured confounders
  - all the observed values of $\boldsymbol{U}$ come from the MCS
  - converts the missing confounder problem into a missing data problem
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  - an analysis sub-model (to answer question of interest)
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We will now look at how Bayesian graphical models can help with this process

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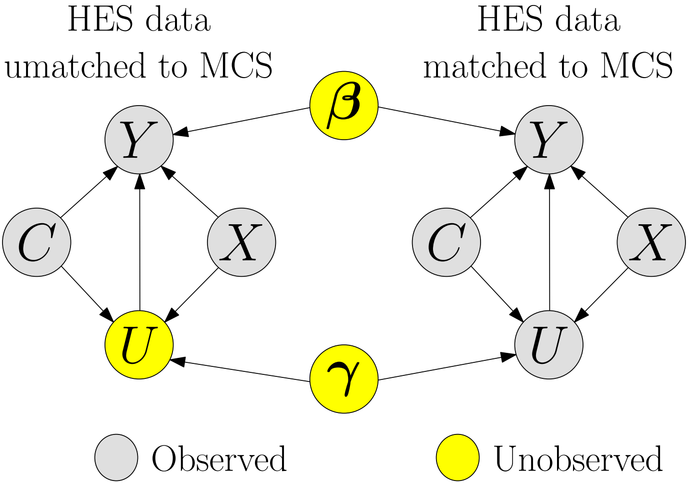

What is a graphical model?

- Diagrams can be used to provide a pictorial representation of
  - the assumed relationships between variables
  - some of the features of the model structure
- Graphical models are formal diagrams that provide a powerful tool for building and communicating complex statistical models
- Formally, a graph, G, consists of
  - finite set of nodes N
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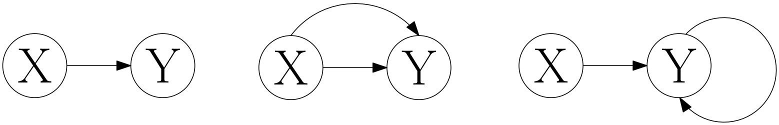

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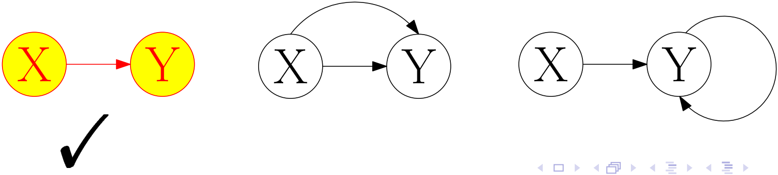

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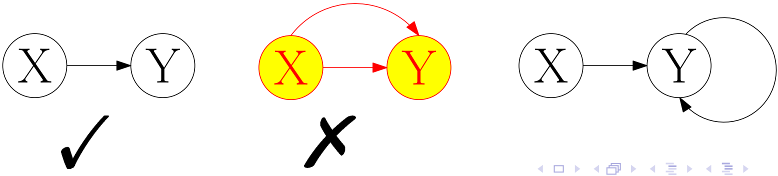

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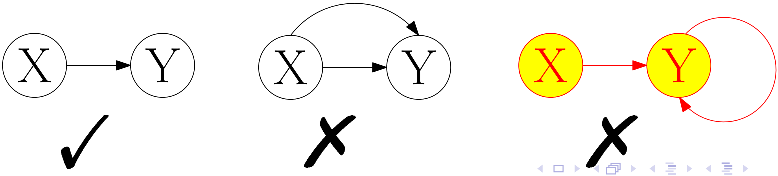

Introducing the Directed Acyclic Graph

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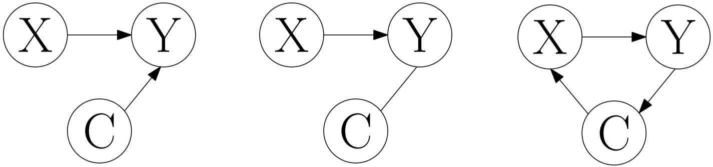

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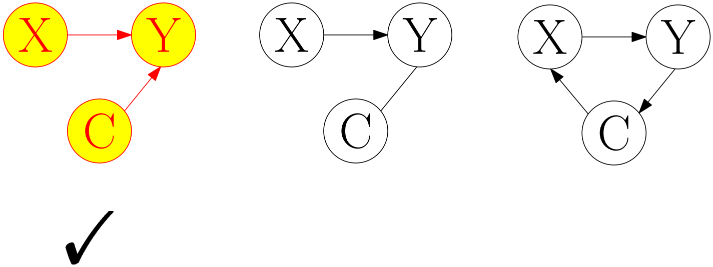

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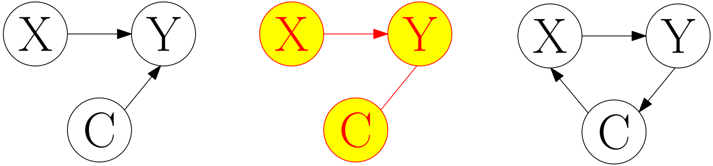

✓ ✗

undirected link

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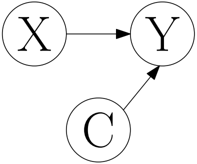

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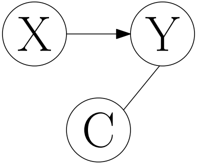

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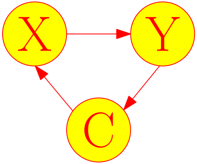

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cycle

How to represent a statistical model using a DAG

- Each element of the statistical model (variables, parameters, etc.) is represented by a node
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- The direction of the links reflects the dependence implied by the equations
- However, the arrows have no intrinsic meaning - they should NOT be interpreted as meaning causal inference unless extra assumptions are made

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We now provide examples using our application

DAG for analysis sub-model

Naive Analysis Model

$$Y_i \sim Bernoulli(p_i)$$

$$logit(p_i) = \beta_0 + \beta_X X_i + \beta_C^T \boldsymbol{C}_i$$

$nodes = \{\beta, X_i, \boldsymbol{C}_i, Y_i, p_i\}$

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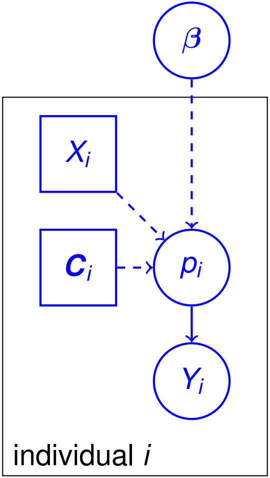
circular nodes denote random variables

square nodes denote constant quantities

probabilistic links indicated by solid arrows ("$\sim$")

deterministic links indicated by dashed arrows ("=")

repeated structure indicated by a rectangle, "plate"



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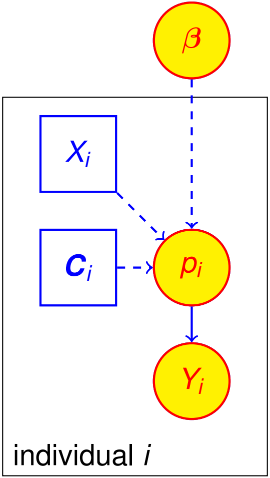

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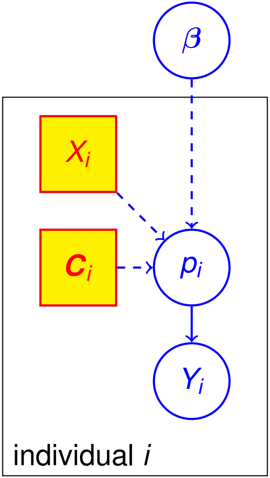

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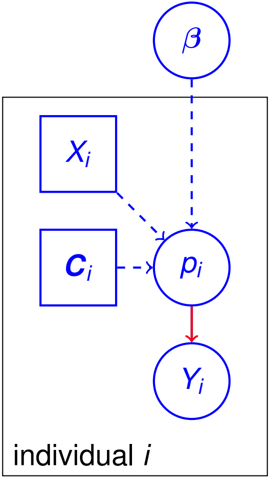

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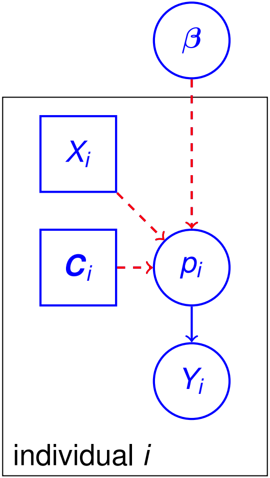

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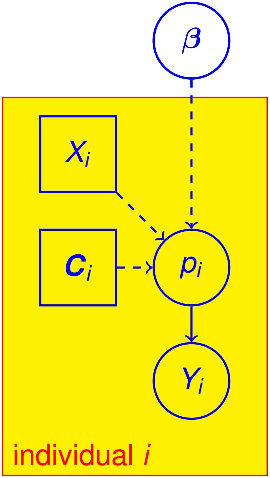

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Analysis sub-model

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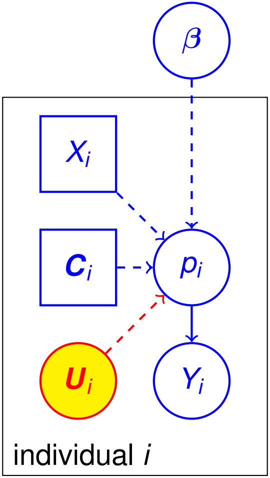

Accounting for sampling bias

Now turning to the imputation sub-model

- The supplementary data (MCS) is not a random sample from the primary data (HES)
- The MCS cohort sampling was stratified in order to oversample low socio-economic and ethnic categories
- To account for the sampling bias, include the stratum in the imputation model as stratum specific intercepts, $\alpha_{s(i)}$

Imputation sub-model

- Missing values of U (smoking and ethnicity) imputed using latent variables, $U^{\star}$
- Allows for correlation between U
- Multivariate probit model is defined as follows:

$$\boldsymbol{U}_i^{\star} \sim MVN(\boldsymbol{\mu}_i, \Sigma)$$

$$\boldsymbol{\mu}_i = \alpha_{s(i)} + \gamma_X X_i + \gamma_C^T \boldsymbol{C_i}$$

$$U_{ij} = I(U_{ij}^{\star} > 0),\ j = 1,2$$

$$\boldsymbol{U}_i^{\star} = \begin{pmatrix} U_{i1}^{\star} \\ U_{i2}^{\star} \end{pmatrix},\ \boldsymbol{\mu}_i = \begin{pmatrix} \mu_{i1} \\ \mu_{i2} \end{pmatrix},\ \Sigma = \begin{pmatrix} 1 & \kappa \\ \kappa & 1 \end{pmatrix}$$

DAG for imputation sub-model

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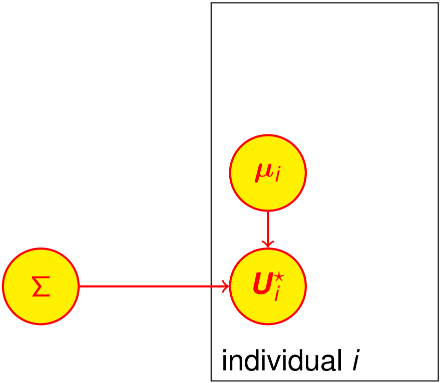

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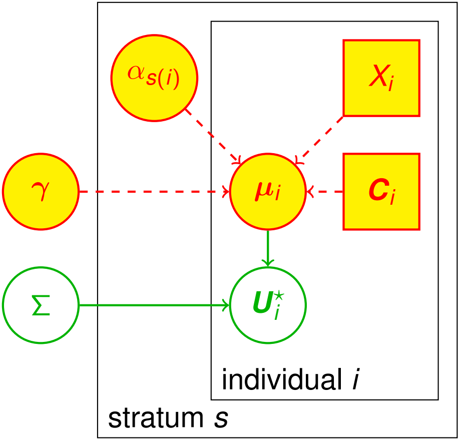

DAG for imputation sub-model

Imputation sub-model

$\boldsymbol{U}_i^\star \sim MVN(\boldsymbol{\mu}_i, \Sigma)$

$\boldsymbol{\mu}_i = \alpha_{s(i)} + \gamma_X X_i + \gamma_C^T \boldsymbol{C}_i$

$U_{ij} = I(U_{ij}^\star > 0)\ j = 1, 2$

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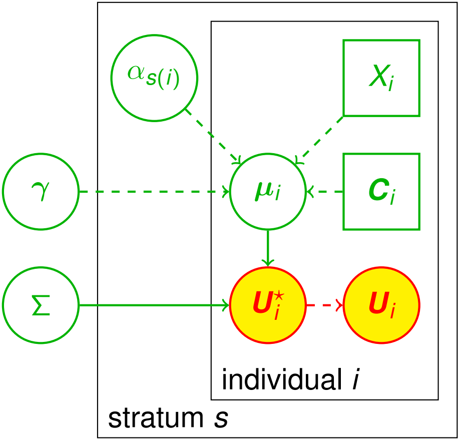

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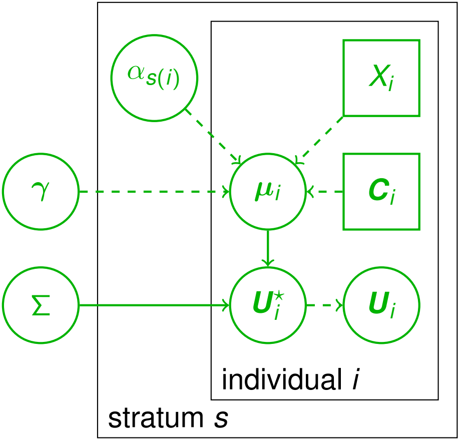
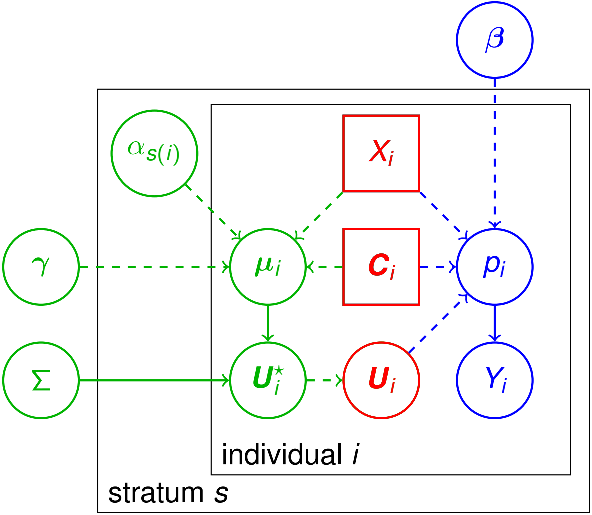


DAG for joint model



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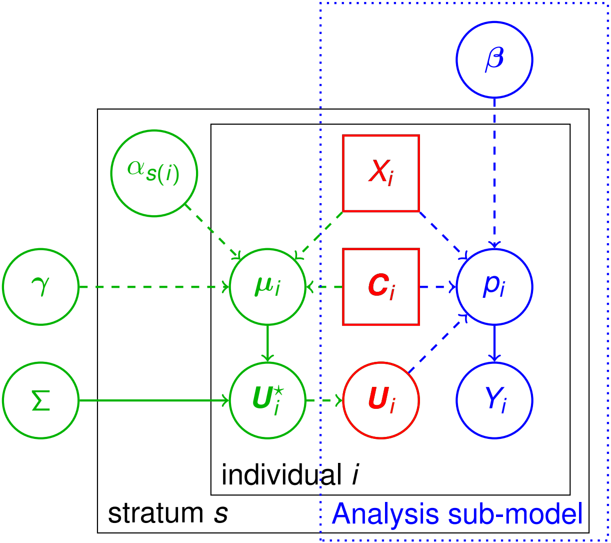

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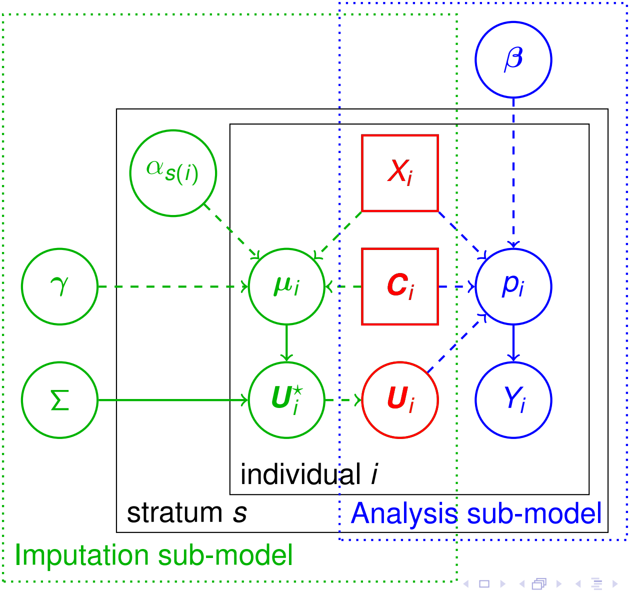

The power of graphical models

- DAGs show how sub-models fit together to form an overall model
- But, there is far more to a DAG than visual representation
- DAGs encode conditional independence statements, which
  - allow a joint distribution to be decomposed into a product of conditional distributions (factorisation theorem)
  - is very useful for implementing Markov chain Monte Carlo (MCMC) methods for Bayesian inference (e.g. exploited by WinBUGS software)
  - ensures joint model is consistent

Comparison with conventional Multiple Imputation by Chained Equations (MICE)

- Specify a separate conditional distribution for each variable with missing data: U_1 = smoking; U_2 = ethnicity
- No longer uses latent variables

MICE imputation model

$$
\begin{aligned}
U_{1i} &\sim Bernoulli(q_i) \\
logit(q_i) &= \theta_{s(i)} + \lambda_X X_i + \boldsymbol{\lambda}_C^T \boldsymbol{C_i} + \lambda_U U_{2i} + \lambda_Y Y_i \\
U_{2i} &\sim Bernoulli(r_i) \\
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include other U

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How can we represent this model graphically?

Graphical representation for MICE approach

$U_{1i} \sim Bernoulli(q_i)$

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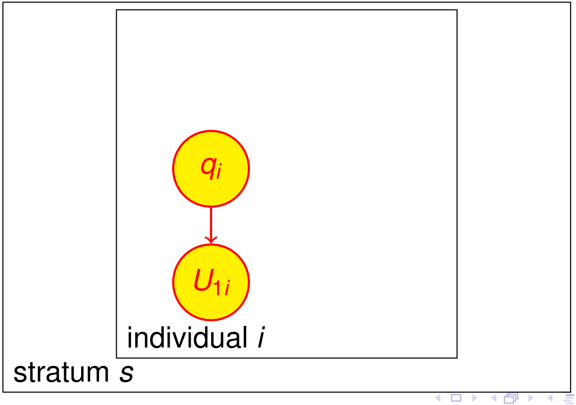

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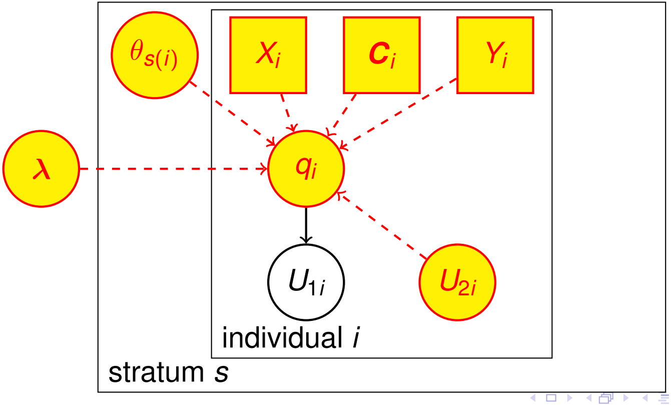

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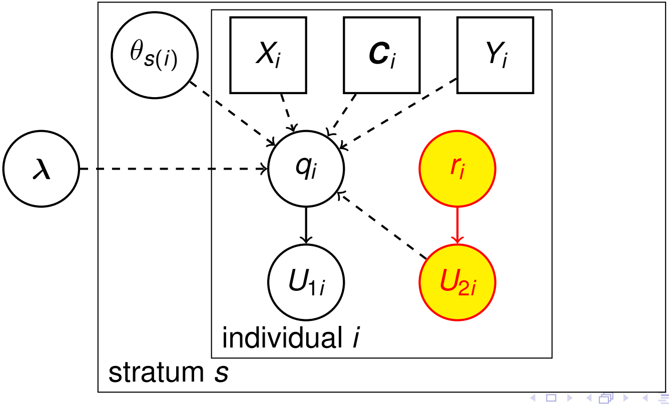

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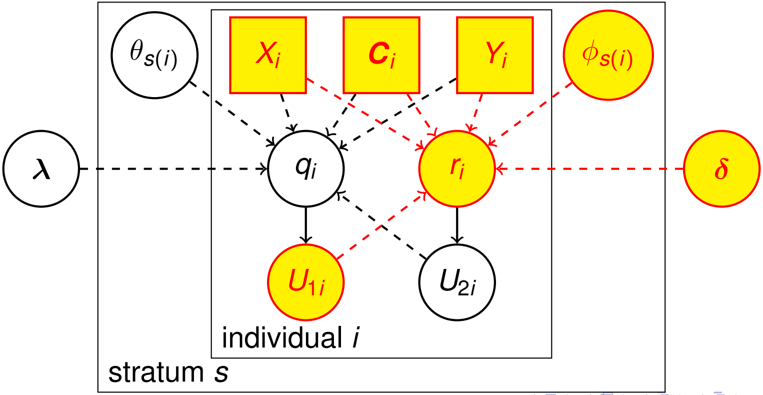

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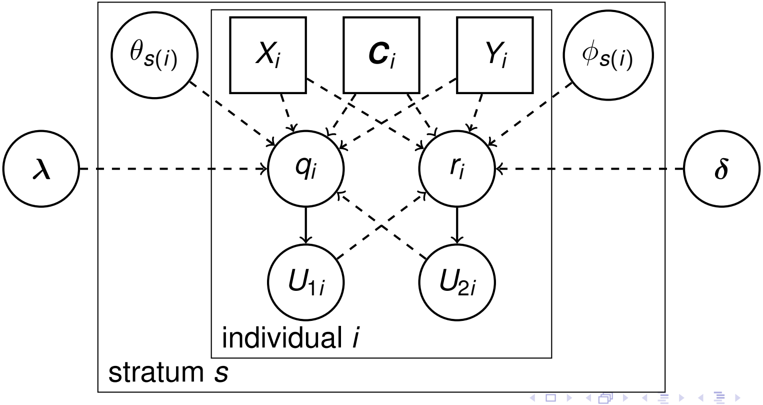

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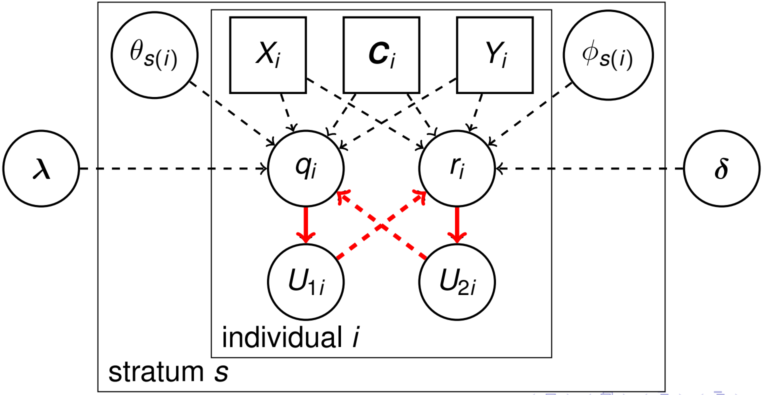

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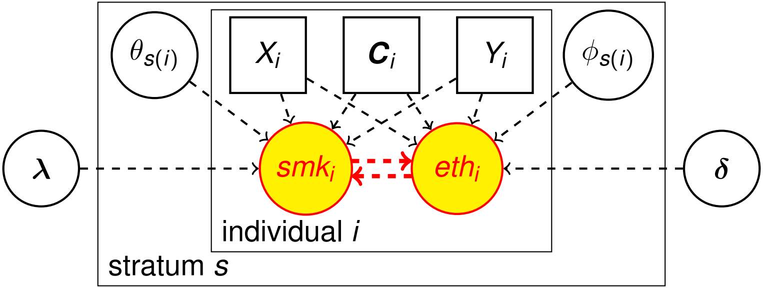

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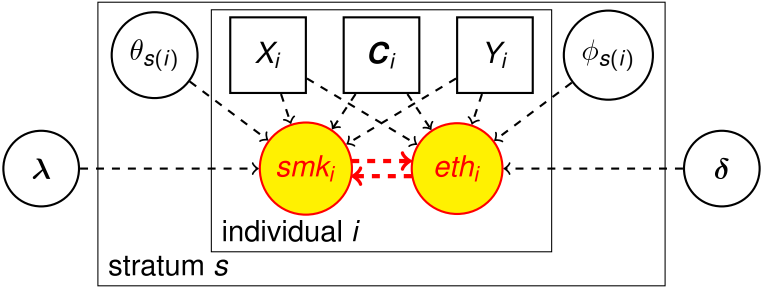

It is not even a graphical model

We iterate between 2 parts of imputation model, then fit analysis model

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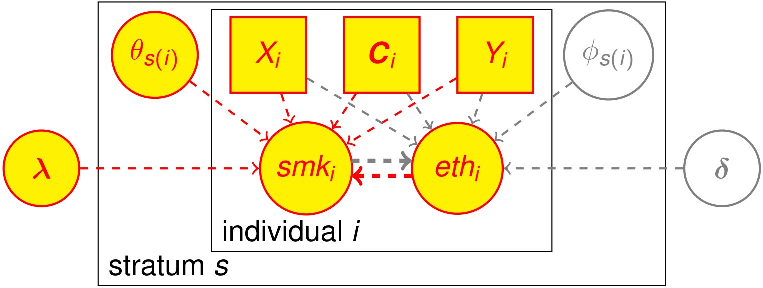

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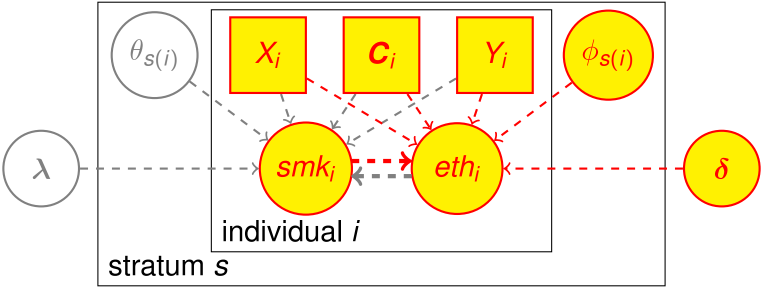

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Outline

Motivation

- Why?
- Case study

Graphical Models

- Introduction to graphical models
- Graphical model for application

Results

Comparison of results

	Odds ratio (95% interval estimate)		
	HES only	MCS only	HES+MCS
Trihalomethanes			
$> 60\mu g/L$	1.39 (1.10,1.76)	1.87 (0.76, 4.62)	1.17 (0.88,1.53)
Mother's age			
≤ 25	1.14 (0.86,1.52)	0.57 (0.20, 1.61)	1.02 (0.71,1.38)
$25 - 29^\star$	1	1	1
$30 - 34$	0.81 (0.57,1.15)	0.13 (0.02, 1.11)	0.85 (0.57,1.21)
≥ 35	1.10 (0.73,1.65)	1.82 (0.55, 5.99)	1.43 (0.88,2.21)
Male baby	0.76 (0.60,0.96)	0.62 (0.25, 1.49)	0.76 (0.59,0.97)
Deprivation index	1.37 (1.20,1.56)	1.44 (0.73, 2.85)	1.19 (1.01,1.38)
Smoking		3.39 (1.26, 9.12)	3.91 (1.35,9.92)
Non-white ethnicity		2.66 (0.69,10.31)	3.56 (1.75,6.82)

* Reference group

Accounting for missing confounders has reduced OR of THM

Comparison of results II

	Odds ratio (95% interval estimate)		
	HES only	HES+MCS (joint model)	HES+MCS (MICE: 5 imputations)
Trihalomethanes			
$> 60 \mu g/L$	1.39 (1.10,1.76)	1.17 (0.88,1.53)	1.22 (0.91, 1.62)
Mother's age			
≤ 25	1.14 (0.86,1.52)	1.02 (0.71,1.38)	0.98 (0.69, 1.38)
$25 - 29^{\star}$	1	1	1
$30 - 34$	0.81 (0.57,1.15)	0.85 (0.57,1.21)	0.84 (0.58, 1.22)
≥ 35	1.10 (0.73,1.65)	1.43 (0.88,2.21)	1.32 (0.86, 2.03)
Male baby	0.76 (0.60,0.96)	0.76 (0.59,0.97)	0.73 (0.58, 0.93)
Deprivation index	1.37 (1.20,1.56)	1.19 (1.01,1.38)	1.23 (1.05, 1.44)
Smoking		3.91 (1.35,9.92)	4.01 (1.32,12.15)
Non-white ethnicity		3.56 (1.75,6.82)	2.73 (1.83, 4.09)

* Reference group

MICE also reduces OR of THM, but greater uncertainty

Concluding remarks

- Bayesian graphical models are a powerful and flexible tool for building realistic models for complex problems
- Bayesian graphical models
    - allow complex models to be built from smaller comprehensible pieces
    - allow formal combining of multiple data sources
    - result in principled inference
    - ensure all sources of uncertainty are automatically propagated

Further Information

- Coming soon:
  - paper on comparisons of different imputation strategies
    see BIAS web site (www.bias-project.org.uk)
  - introduction to graphical models training materials
    see LEMMA multilevel modelling on-line learning course (www.cmm.bristol.ac.uk/research/Lemma)

▶ Molitor, N.-T., Best, N., Jackson, C., and Richardson, S. (2009).
Using Bayesian graphical models to model biases in observational studies and to combine multiple data sources: Application to low birth-weight and water disinfection by-products.
Journal of the Royal Statistical Society, Series A (Statistics in Society), **172**, (3), 615–37.

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- For papers and technical reports, see our web site www.bias-project.org.uk