

# Handling missing data in meta-analysis of individual participant data with correlated mixed outcomes

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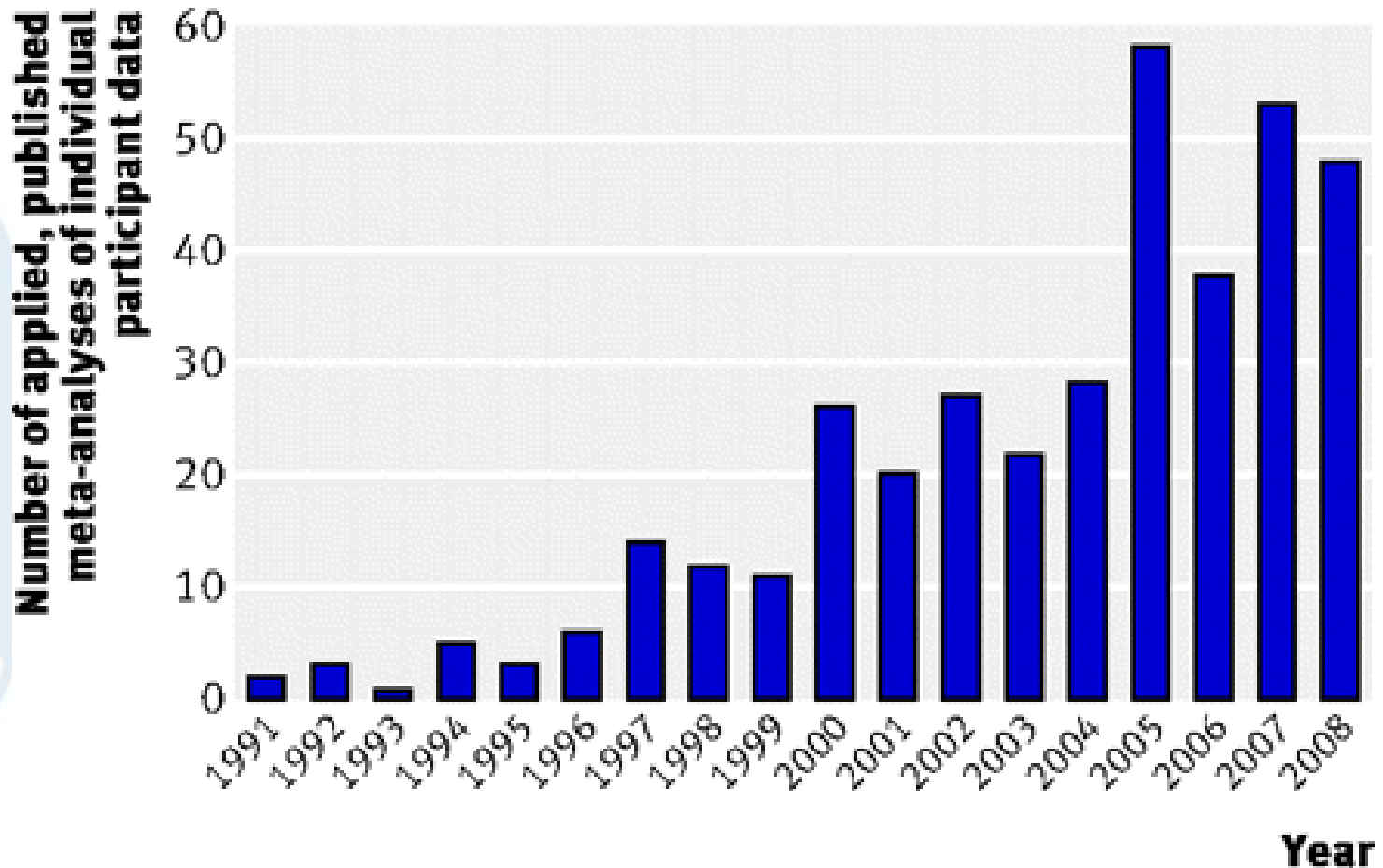
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# Acknowledgments

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- Individual Participant Data (IPD) meta-analysis
- Methodological challenges
- A full-Bayesian approach
- Motivating example
- Some simulation results
- Discussion

# IPD meta-analysis



**Source:** Riley et al 2010. Meta-analysis of individual participant data: rationale, conduct, and reporting. *BMJ* 340 (7745):4521-525.



## Key advantages of IPD meta-analysis:

- Consistent inclusion/exclusion criteria
- Analyses/modelling can be standardised across studies
- Potential for including additional confounders
- Missing data can be addressed using all available data

## IN PRACTICE:

- Subgroup analysis
- Inference based on multiple outcomes



## Challenges:

- Outcomes are partially or completely unobserved for some studies
- Multiplicity of outcomes
- Between-study heterogeneity
- Small number of studies



**A multivariate Bayesian hierarchical model  
for handling the missing data  
in IPD meta-analysis**



## Full-Bayesian analysis

- Unknown parameters and missing values are estimated simultaneously, given the observed data.

$$f(\theta, Y^{mis} | Y^{obs}) = f(Y^{mis} | Y^{obs}) f(\theta | Y^{mis}, Y^{obs})$$

- Flexible framework for addressing between-study heterogeneity, and modelling multiple mixed outcomes
- Offers additional advantages in the context of evidence synthesis when prior evidence is available
- Requires that all variables explaining missingness are included in the analysis model



# A Bayesian approach

## Bayesian hierarchical mixed model (Goldstein et al 2009)

$Y_{ij}^k$  -  $k$ th continuous outcome,  $k = 1, \dots, K$  ;  $Y_{ij}^l$  -  $l$ th binary outcome,  $l = 1, \dots, L$

$$Y_{ij}^k = \mu_{ij}^k + \varepsilon_{ij}^k$$

$$Z_{ij}^l = \mu_{ij}^l + \varepsilon_{ij}^l$$

$$P(Y_{ij}^l = 1) = P(z_{ij}^l > 0)$$

$$\mu_{ij} = \beta_0 + \beta_1 t_{ij} + \beta_2 X_{ij} + u_j$$

$\varepsilon_{ij} \sim N(\mathbf{0}, \mathbf{\Omega}_\varepsilon)$  where  $\mathbf{\Omega}_\varepsilon$  is the  $k \times l$  level-1 covariance matrix with  $\sigma_l^2$  constrained to 1

$u_j \sim N(\mathbf{0}, \mathbf{\Omega}_u)$  where  $\mathbf{\Omega}_u$  is the  $k \times l$  level-2 covariance matrix

# A Bayesian approach



**Diffuse priors** (parameters constant across studies)

- **Level-2 covariance matrix**

$$\tau_k \sim N(0, 0.001)I(0, )$$

$$\tau_l \sim N(0, 0.001)I(0, )$$

$$\phi \sim Unif(-1, 1)$$

Inverse-Wishart prior could be used but uses a single parameter to control the precision of all elements of the matrix -> informative

- **Level-1 covariance matrix**

$$\sigma_k \sim N(0, 0.001)I(0, )$$

$$\rho \sim Unif(-1, 1)$$

- **Regression Coefficients**

$$\beta \sim N(0, 1.0E - 6)$$



# Alternative methods



## Complete-case analysis (CCA)

- Patients with missing observations are dropped
- Assumes data are MCAR
- Typically leads to biased/imprecise results

## Multiple Imputation (MI)

- Each missing value is replaced by a set of plausible values drawn from the posterior distribution of missing data given the observed
  - Imputation model is estimated separately from the analysis model (allows for the inclusion of ‘auxiliary variables’)
  - Recognises the uncertainty associated with the missing data and the estimation of the imputed values
  - Implementation is relative simple and available in a wide range of software



## Multiple Imputation via fully-conditional specification

- Each incomplete variable is imputed iteratively.

Let  $y_1^{(t-1)}$  and  $y_2^{(t-1)}$  be the initial values. For each iteration  $t$ :

$$\theta_1^{(t)} \sim p(\theta_1) p(y_1^{obs} | y_2^{(t-1)}, X, \theta_1) \quad y_1^{mis(t)} \sim p(y_1^{mis} | y_2^{(t-1)}, X, \theta_1^{(t)})$$

$$\theta_2^{(t)} \sim p(\theta_2) p(y_2^{obs} | y_1^{(t-1)}, X, \theta_2) \quad y_2^{mis(t)} \sim p(y_2^{mis} | y_1^{(t-1)}, X, \theta_2^{(t)})$$

Typically after 10 to 20 iterations,  $y_1^{mis}$  and  $y_2^{mis}$  are imputed from the posterior distribution as follows:

$y_1^{mis}$  is drawn from  $p(y_1^{mis} | y_2^*, X, \theta_1^*)$

$y_2^{mis}$  is drawn from  $p(y_2^{mis} | y_1^*, X, \theta_2^*)$

# Methodological intrigue

- In standard (non-hierarchical) settings, MI via FCS approximates the posterior distribution implied by the joint model (Gelman et al 2012)
- Previous work comparing JM with MI on correlated mixed outcomes found similar performance (He and Belin 2014)
- Unclear whether this holds in hierarchical settings:
  - Correlation structure is not explicitly partitioned between patient and study-level components
  - Marginal distribution may provide information about the conditional distribution. E.g., General location model



# Motivating example







## Analysis of five randomized controlled trials (N=5273):

- **Aim:** To compare cardiac resynchronization therapy (CRT) versus CRT combined with implantable cardioverter defibrillator (CRT-D) for treating chronic heart failure
- **Outcomes:**
  - Mortality
  - Functional: NYHA Class and 6-minute walk
  - Quality-of-life: Minnesota Living with Heart Failure questionnaire
- **Key research question:**

Is the treatment effect different for males versus females?

# Case study

**Data completeness:** complete cases: 2725 (52%)

Outcome	Mortality (5% missing)	NYHA class (15% missing)	6-min walk (22% missing)	Quality of Life (44% missing)
Study 1 (N=490)	✓ x	✓ x	✓ x	✓ x
Study 2 (N=555)	✓	✓ x	✓ x	✓ x
Study 3 (N=1798)	✓	✓ x	✓ x	x
Study 4 (N=610)	✓	✓ x	✓ x	✓ x
Study 5 (N=1820)	✓ x	✓ x	✓ x	x

- ✓: fully-observed;
- ✓ x: partially missing
- x: completely missing

# Case-study: analysis model

## Multilevel mixed model (2 binary, 2 continuous)

$$Z_{ij}^{death} \sim N(\mu_{ij}^1, 1) \quad P(\text{death}_{ij} = 1) = P(Z_{ij}^{death} > 0)$$

$$Z_{ij}^{nyha} \sim N(\mu_{ij}^2, 1) \quad P(\text{nyha}_{ij} = 1) = P(Z_{ij}^{nyha} > 0)$$

$$\text{walk}_{ij} \sim N(\mu_{ij}^3, \sigma_3^2)$$

$$\text{qol}_{ij} \sim N(\mu_{ij}^4, \sigma_4^2)$$

$$\mu_{ij}^k = \beta_0^k + \beta_1^k \text{treat}_{ij} + \beta_2^k \text{sex}_{ij} + \beta_3^k \text{treat}_{ij} * \text{sex}_{ij} + u_j^k$$

$$u_j^k \sim N(0, \Omega_u) \quad k = 1, \dots, 4$$

# Case-study: results

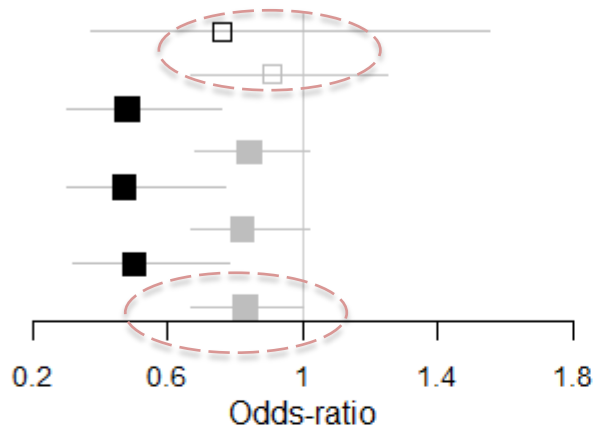
## Mortality

Complete-cases

Multiple Imputation 1

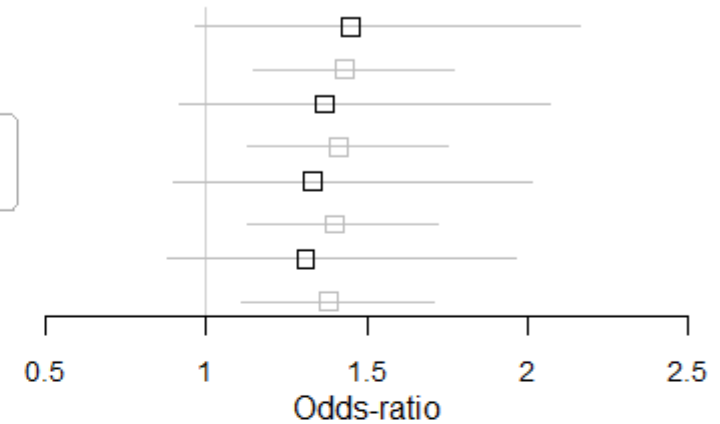
Multiple imputation 2

Full-Bayesian model



## NYHA class

Female  
Male



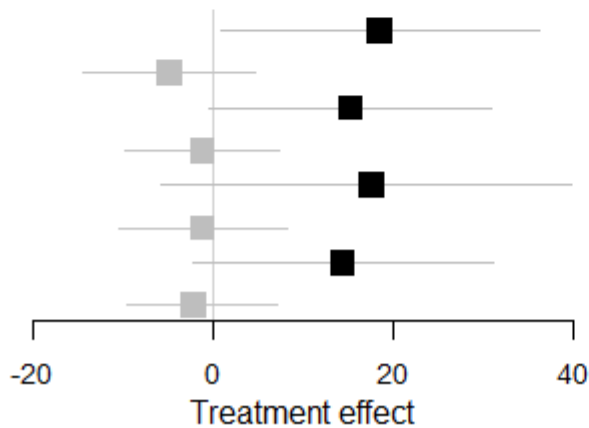
## 6-minute walk

Complete-cases

Multiple Imputation 1

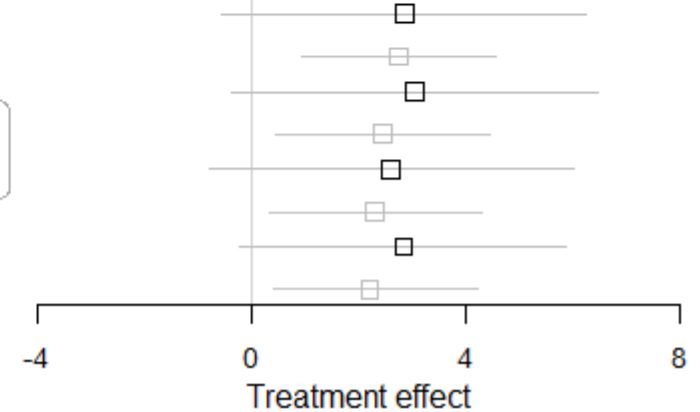
Multiple imputation 2

Full-Bayesian model



## Quality-of-life

Female  
Male





## Summary:

### 1. Unprincipled methods for handling missing data

- Complete-case analysis with multiple outcomes is inefficient and leads to different inferences on mortality
- Available-case analysis could be used, BUT
  - Inconsistent sample across outcomes
  - No correlation between outcomes accounted for
  - Still assumes MCAR

### 2. Principled methods for handling the missing data

- Led to same inferences about the differential treatment effect
- CIs somewhat narrower for joint Bayesian model



## Some simulation results



# Simulations: data generation



## Covariates

$$X_{ij}^k \sim N(0, 1) \quad k = 1, \dots, 4$$

## Outcomes

(multivariate distribution via copulas)

$$Y_{ij}^1 \sim N(\mu_{ij}, \sigma_1^2) \quad Y_{ij}^2 \sim \text{Bern}(\pi_{ij})$$

$$\mu_{ij} = 1 + 1T_{ij} + 0.5X_{1,ij} + 0.5X_{2,ij} + u_j^1$$

$$\text{logit}(\pi_{ij}) = -0.5 - 0.1T_{ij} + 0.2X_{3,ij} + 0.2X_{4,ij} + u_j^2$$

$$\begin{pmatrix} u_j^1 \\ u_j^2 \end{pmatrix} \sim N \left( \begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} 1 & 0.1 \\ 0 & 1 \end{pmatrix} \right)$$

# Simulations: implementation

## 1. Scenarios differed according to:

- **No. of studies:** 5 and 20
- **Correlation between outcomes:** 0.2 and 0.7
- **% Missing data:** 20% and 50%
- **Missingness data mechanism**
  - sporadically missing (MAR on X, MAR on X and Y)
  - systematically missing (MCAR)

## 2. Implementation

- **1000 replications**
- **Parameter of interest:** treatment effect on binary & continuous outcomes
- **Performance metrics:** bias, mean square error and joint CI coverage



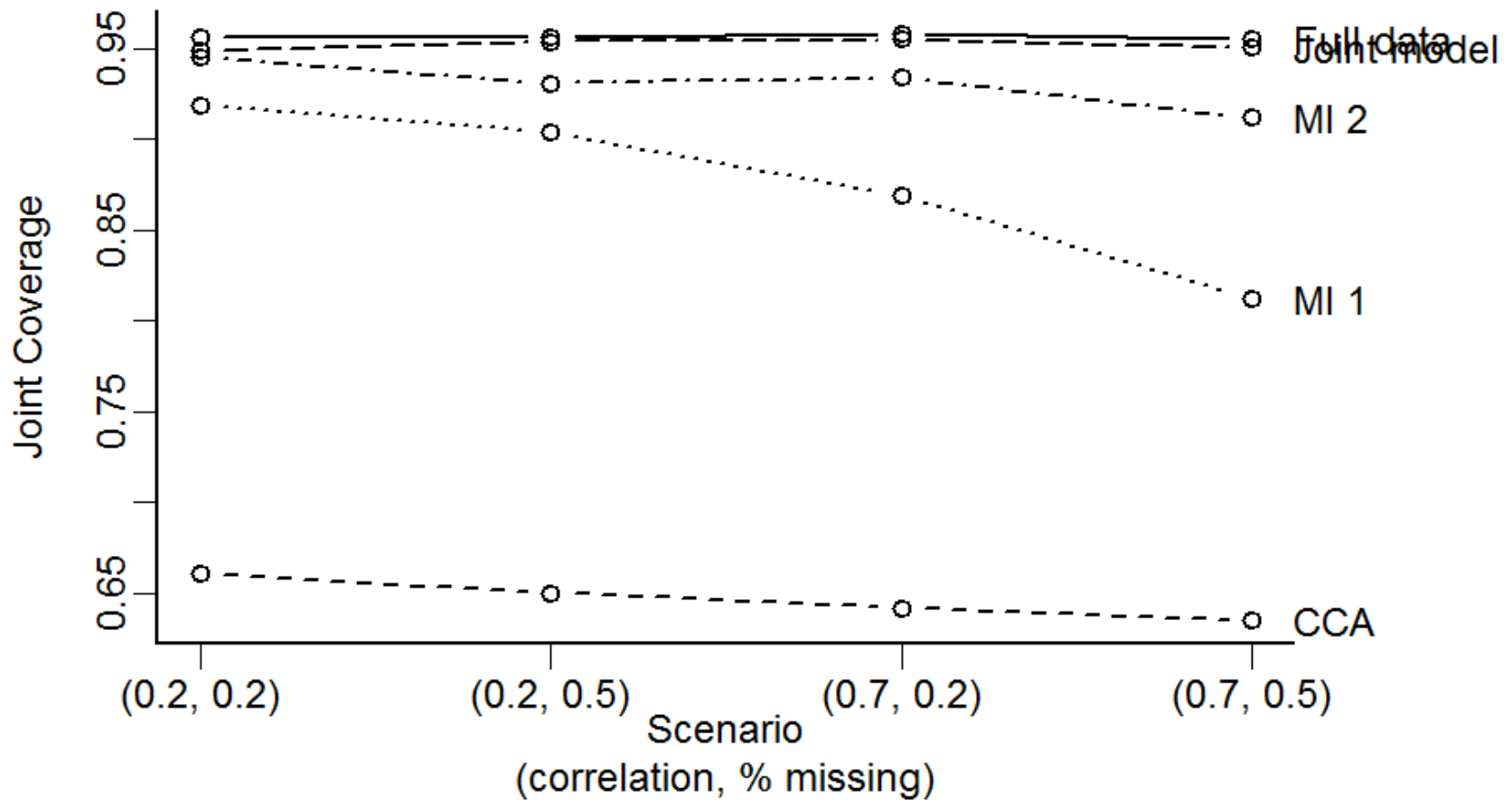
# Simulations: results 1

**Scenario:** 20 studies, corr between outcomes=0.7, % missing=0.5, MAR on X

Method	Bias (%)		Root MSE		Joint coverage
	beta.Y1	beta.Y2	beta.Y1	beta.Y2	
Full data	0.0	1.2	0.040	0.075	0.958
Complete cases	10.1	34.9	0.121	0.128	0.503
MI 1	0.1	7.4	0.054	0.103	0.944
MI 2	0.1	6.1	0.049	0.100	0.947
Joint Model	0.0	3.9	0.040	0.083	0.957

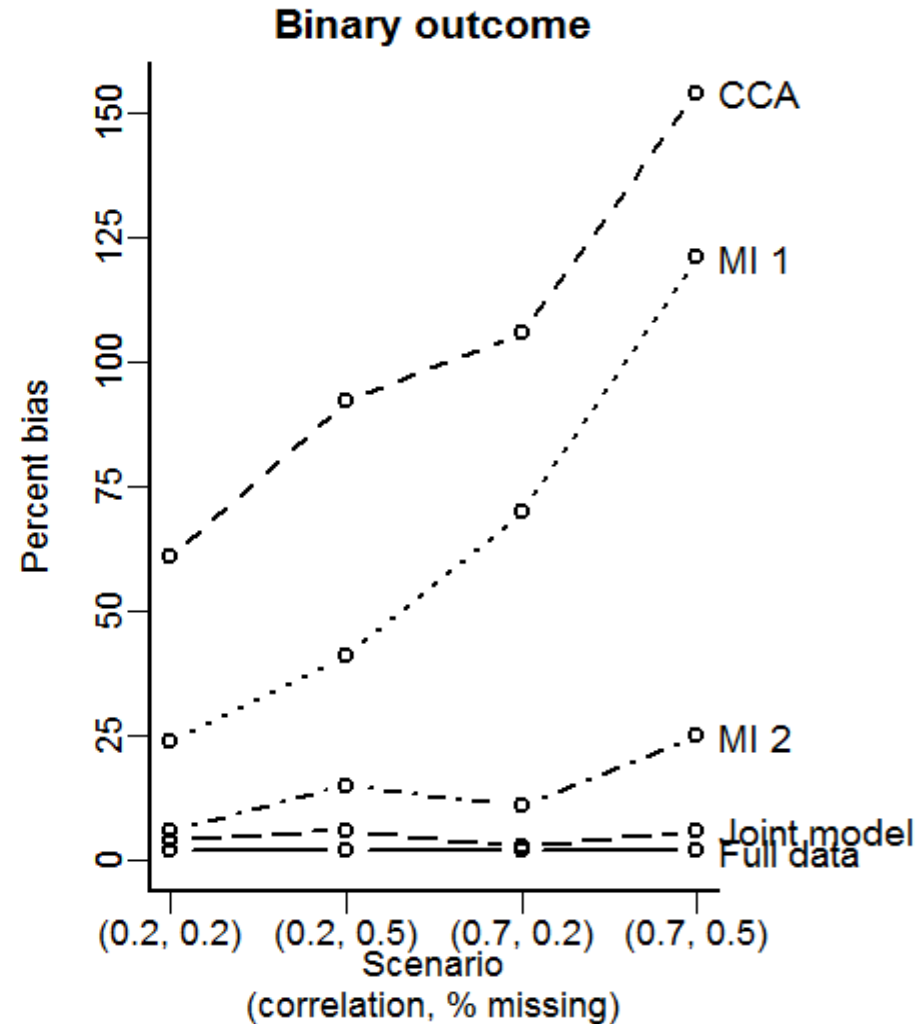
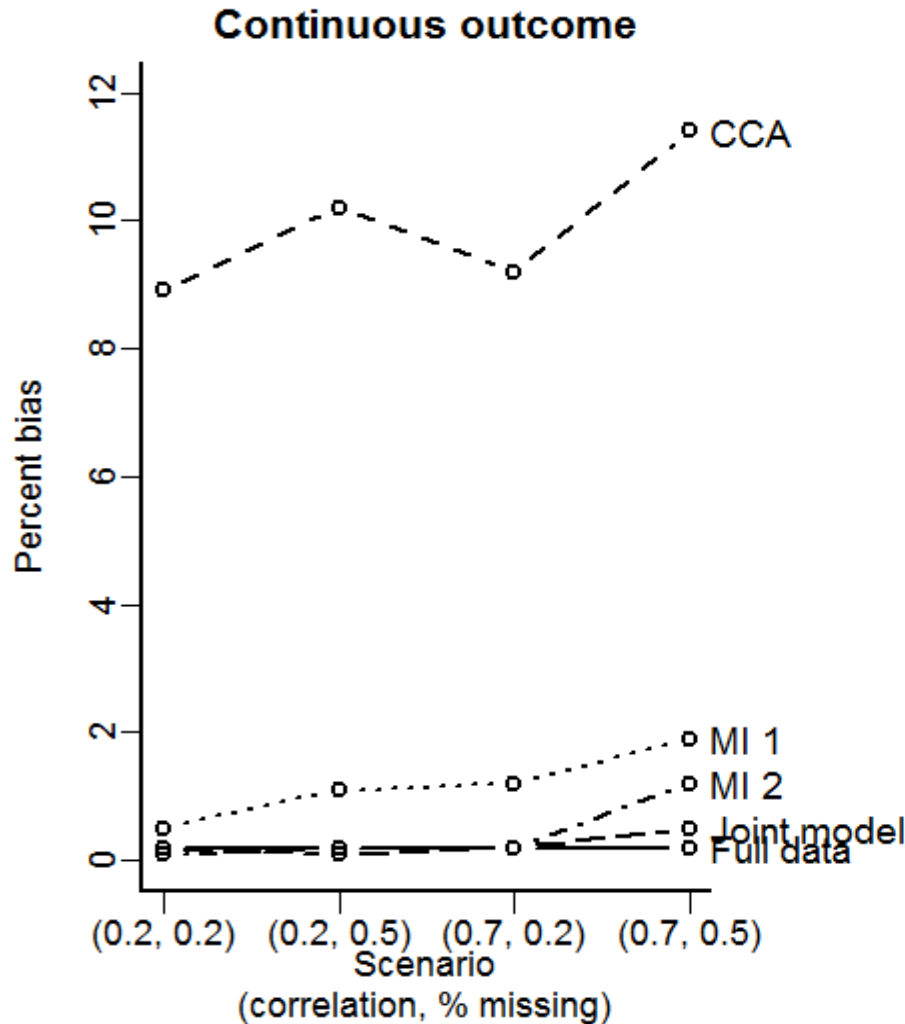
# Simulations: results 2

**Scenario:** 5 studies,  $\text{corr}=0.7$ , % missing=0.5, MAR on X and Y



# Simulations: results 2

**Scenario:** 5 studies,  $\text{corr}=0.7$ , % missing=0.5, MAR on X and Y



# Discussion 1

- Similar results for scenarios with systematically missing data
- Bayesian approach performed well across all scenarios
- MI approach provided a decent alternative for most scenarios

# Discussion 2

- Improvements to current implementation of MI via FCS
- Joint imputation model
- MI and two-stage meta-analysis with very few studies

# Limitations and further work

- No missing covariates
- Fairly simple covariance structures

## Ongoing work

- Assess the relative merits of the Bayesian approach under MNAR