



Modelling immune responses to COVID-19 vaccination with a Bayesian three-level hierarchical model

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Acknowledgements

- PICOBOO Team
 - Investigators, site staff, participants,...
- Coauthors:
 - **Charlie McLeod**
 - Tom Snelling
 - Peter Richmond
 - **Julie Marsh**





Overview

- PICOBOO Recap
 - Design
 - Decision rules
- Bayesian model
 - Multivariate responses
 - Hierarchical prior structure
- Simulations
- First scheduled analysis



PICOB00 Recap

- COVID-19 vaccinations in immunocompetent participants
- Participants randomised to receive a booster dose and *may* be rerandomised
- Strata: Primary schedule and age group
- Interventions: Pfizer, Moderna, Novavax, ...
- Primary estimand: log₁₀ ancestral SARS-CoV2 anti-spike IgG at 28 days
- Decision rules: Stop recruitment if adequate precision



Notation

- Participant: $i \in I = \{1, 2, \dots, N\}$
- Primary Schedule: $j \in J = \{AZ, Pf, \text{Mod}\}$
- Age Group: $l \in L = \{12 - < 18, 18 - < 50, 50 - < 70, \geq 70\}$
- Intervention: $k \in K = \{Pf, Mod, Nvx, \text{Pf BA. 1}, \text{Mod BA. 1}, \text{Pf BA. 4/5}, \text{Mod BA. 4/5}\}$
- Booster Number: $m \in M_i \subseteq M = \{1, 2, 3\}$
- Covariates: $\mathbf{x}_{im} = \{x_{im1}, x_{im2}, \dots, x_{imP}\}$
- Outcome: $\mathbf{y}_{ijk^*l} \in \mathbb{R}^{|M_i|} \subseteq \mathbb{R}^3$ ($y_{ijklm} \in \mathbb{R}, \mathbf{k}^* \subseteq K$)



Model

$$Y_{ijk^*l} \sim N \left([\mu_{jklm} + \mathbf{x}_{im}\boldsymbol{\beta}]^{|M_i|}, [\boldsymbol{\Sigma}_l]^{|M_i| \times |M_i|} \right)$$



Model

$$Y_{ijk^*l} \sim N \left([\mu_{jklm} + x_{im}\beta]^{M_i}, [\Sigma_l]^{M_i \times M_i} \right)$$



Multivariate outcome



Model

Mean response conditional on covariates



$$Y_{ijk^*l} \sim N \left([\mu_{jklm} + x_{im}\beta]^{M_i}, [\Sigma_l]^{M_i \times M_i} \right)$$



Multivariate outcome



Model

Mean response conditional on covariates



$$Y_{ijk^*l} \sim N \left([\mu_{jklm} + x_{im}\beta]^{M_i}, [\Sigma_l]^{M_i \times M_i} \right)$$



Multivariate outcome



Covariate effects



Model

Mean response conditional on covariates

Vector is length $|M_i|$

$$Y_{ijk^*l} \sim N \left([\mu_{jklm} + x_{im}\beta]^{M_i}, [\Sigma_l]^{M_i \times M_i} \right)$$

Multivariate outcome

Covariate effects



Model

Mean response conditional on covariates

Vector is length $|M_i|$

$$Y_{ijk^*l} \sim N \left([\mu_{jklm} + x_{im}\beta]^{M_i}, [\Sigma_l]^{M_i \times M_i} \right)$$

Multivariate outcome

Covariate effects

3x3 variance-covariance matrix



Model

Mean response conditional on covariates

Vector is length $|M_i|$

Matrix has dimension $|M_i| \times |M_i|$

$$Y_{ijk^*l} \sim N \left([\mu_{jklm} + x_{im}\beta]^{M_i}, [\Sigma_l]^{M_i \times M_i} \right)$$

Multivariate outcome

Covariate effects

3x3 variance-covariance matrix



Example: Participant has outcomes for 4th and 5th dose

$$\begin{bmatrix} Y_{ijkl2} \\ Y_{ijk'l3} \end{bmatrix} \sim N \left(\begin{bmatrix} \mu_{jkl2} + \mathbf{x}_{i2}\boldsymbol{\beta} \\ \mu_{jk'l3} + \mathbf{x}_{i3}\boldsymbol{\beta} \end{bmatrix}, \begin{bmatrix} \sigma_l^2 & r_{l23}\sigma_l^2 \\ r_{l32}\sigma_l^2 & \sigma_l^2 \end{bmatrix} \right)$$



Hierarchical prior structure (μ_{jklm})

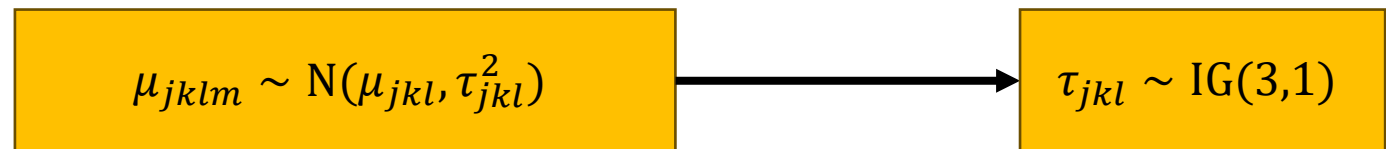
First level: share between booster doses

$$\mu_{jklm} \sim N(\mu_{jkl}, \tau_{jkl}^2)$$



Hierarchical prior structure (μ_{jklm})

First level: share between booster doses





Hierarchical prior structure (μ_{jklm})

Second level: share between age groups

$$\mu_{jkl} \sim N(\mu_{jk}, \tau_{jk}^2)$$

First level: share between booster doses

$$\mu_{jklm} \sim N(\mu_{jkl}, \tau_{jkl}^2)$$

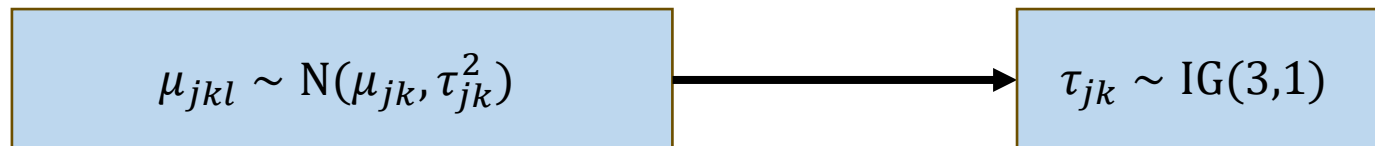
$$\tau_{jkl} \sim \text{IG}(3, 1)$$



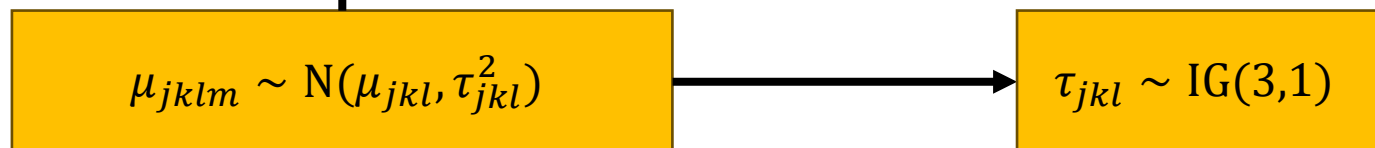


Hierarchical prior structure (μ_{jklm})

Second level: share between age groups



First level: share between booster doses





Hierarchical prior structure (μ_{jklm})

Third level: share between mRNA interventions

$$\mu_{jk} \sim N(\mu_j, \tau_j^2), k \in \{\text{mRNA}\}$$

Second level: share between age groups

$$\mu_{jkl} \sim N(\mu_{jk}, \tau_{jk}^2)$$

$$\tau_{jk} \sim \text{IG}(3,1)$$

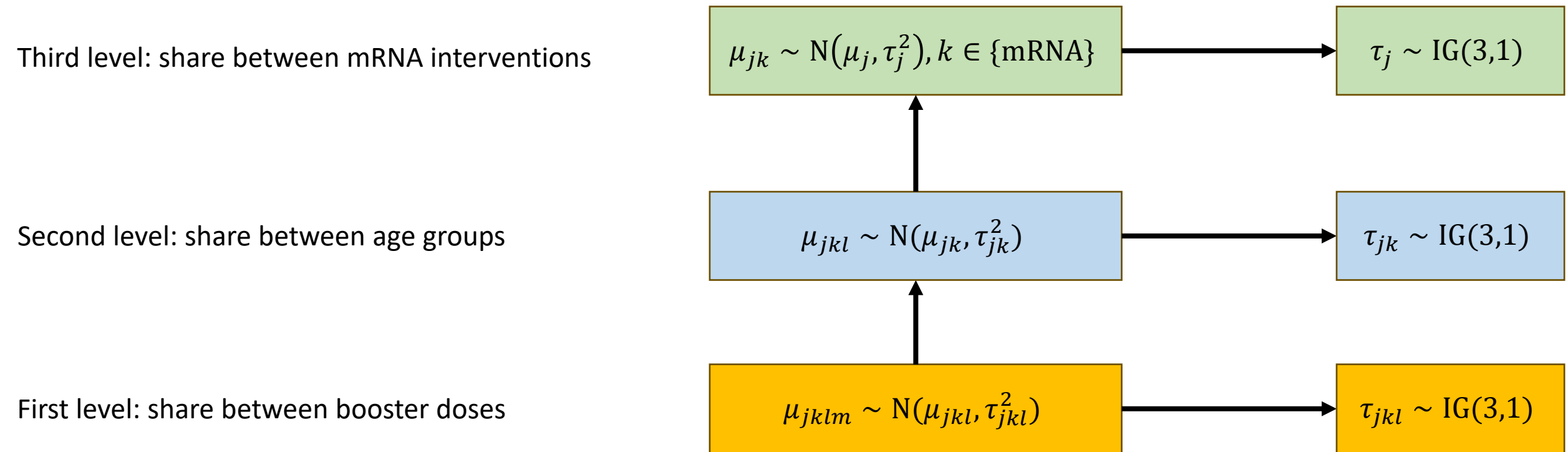
First level: share between booster doses

$$\mu_{jklm} \sim N(\mu_{jkl}, \tau_{jkl}^2)$$

$$\tau_{jkl} \sim \text{IG}(3,1)$$




Hierarchical prior structure (μ_{jklm})



Hierarchical prior structure (μ_{jklm})

$$\mu_{jk} \sim N(\log_{10}(8,347), 0.5^2), k = \text{NvX}$$

Third level: share between mRNA interventions

$$\mu_{jk} \sim N(\mu_j, \tau_j^2), k \in \{\text{mRNA}\}$$

$$\tau_j \sim \text{IG}(3,1)$$

Second level: share between age groups

$$\mu_{jkl} \sim N(\mu_{jk}, \tau_{jk}^2)$$

$$\tau_{jk} \sim \text{IG}(3,1)$$

First level: share between booster doses

$$\mu_{jklm} \sim N(\mu_{jkl}, \tau_{jkl}^2)$$

$$\tau_{jkl} \sim \text{IG}(3,1)$$





Hierarchical prior structure (μ_{jklm})

$$\mu_{jk} \sim N(\log_{10}(8,347), 0.5^2), k = \text{NvX}$$

$$\mu_j \sim N(\log_{10}(20,517), 0.5^2)$$

$$\mu_{jk} \sim N(\mu_j, \tau_j^2), k \in \{\text{mRNA}\}$$

$$\tau_j \sim \text{IG}(3,1)$$

$$\mu_{jkl} \sim N(\mu_{jk}, \tau_{jk}^2)$$

$$\tau_{jk} \sim \text{IG}(3,1)$$

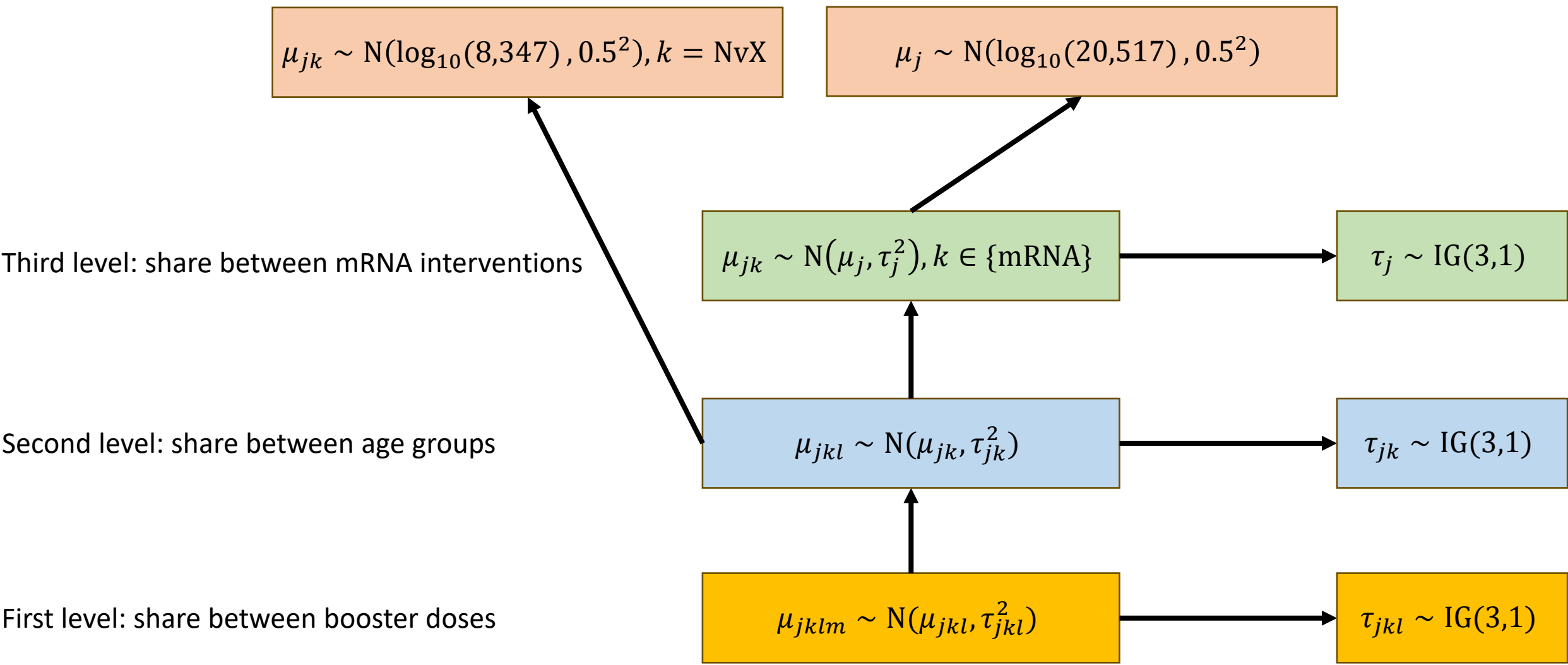
$$\mu_{jklm} \sim N(\mu_{jkl}, \tau_{jkl}^2)$$

$$\tau_{jkl} \sim \text{IG}(3,1)$$

Third level: share between mRNA interventions

Second level: share between age groups

First level: share between booster doses





Other prior distributions

$$\beta_p \sim N(0,1)$$

$$\Sigma_l = \mathbf{Q}_l \mathbf{R}_l \mathbf{Q}_l$$

$$\mathbf{Q}_l = \sigma_l \mathbf{I}_3$$

$$\mathbf{R}_l = \begin{pmatrix} 1 & r_{l12} & r_{l13} \\ r_{l21} & 1 & r_{l23} \\ r_{l31} & r_{l32} & 1 \end{pmatrix}$$

$$\sigma_l \sim \text{Exponential}(0.5)$$

$$\mathbf{R}_l \sim \text{LKJcorr}^1(2)$$

¹Lewandowski, et. al. (2009) – Cholesky decomposition



Simulated example

Assume:

$$i \in I = \{1, 2, \dots, 300\}$$

$$j \in J = \{\text{Pf}\}$$

$$l \in L = \{12 - < 18, 18 - < 50, 50 - < 70, \geq 70\}$$

$$k \in K = \{\text{Pf}, \text{Mod}, \text{Nvx}\}$$

$$m \in M_i = M = \{2, 3\}$$

Scenarios:

1) SD = 0.2

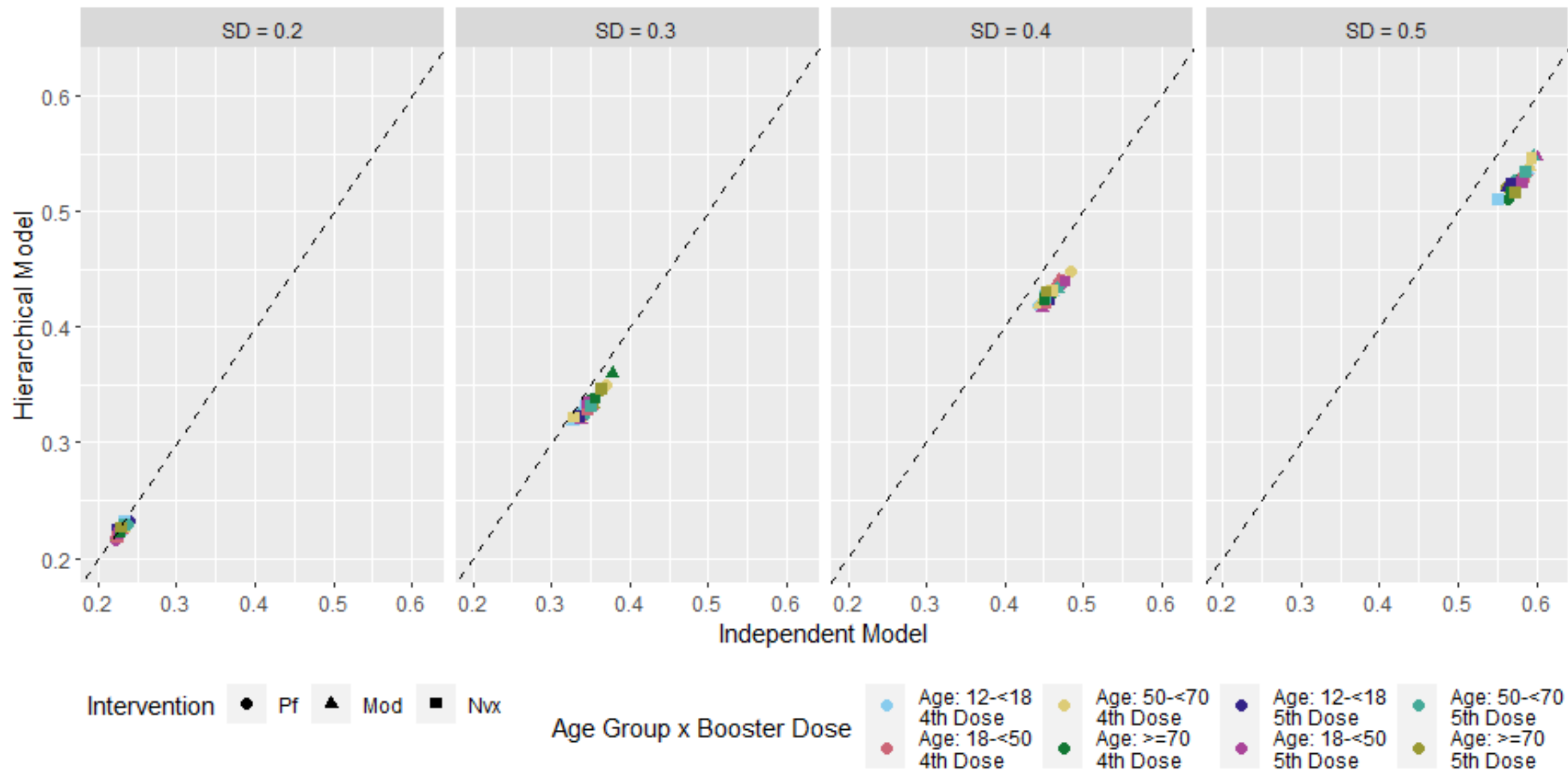
2) SD = 0.3

3) SD = 0.4

4) SD = 0.5

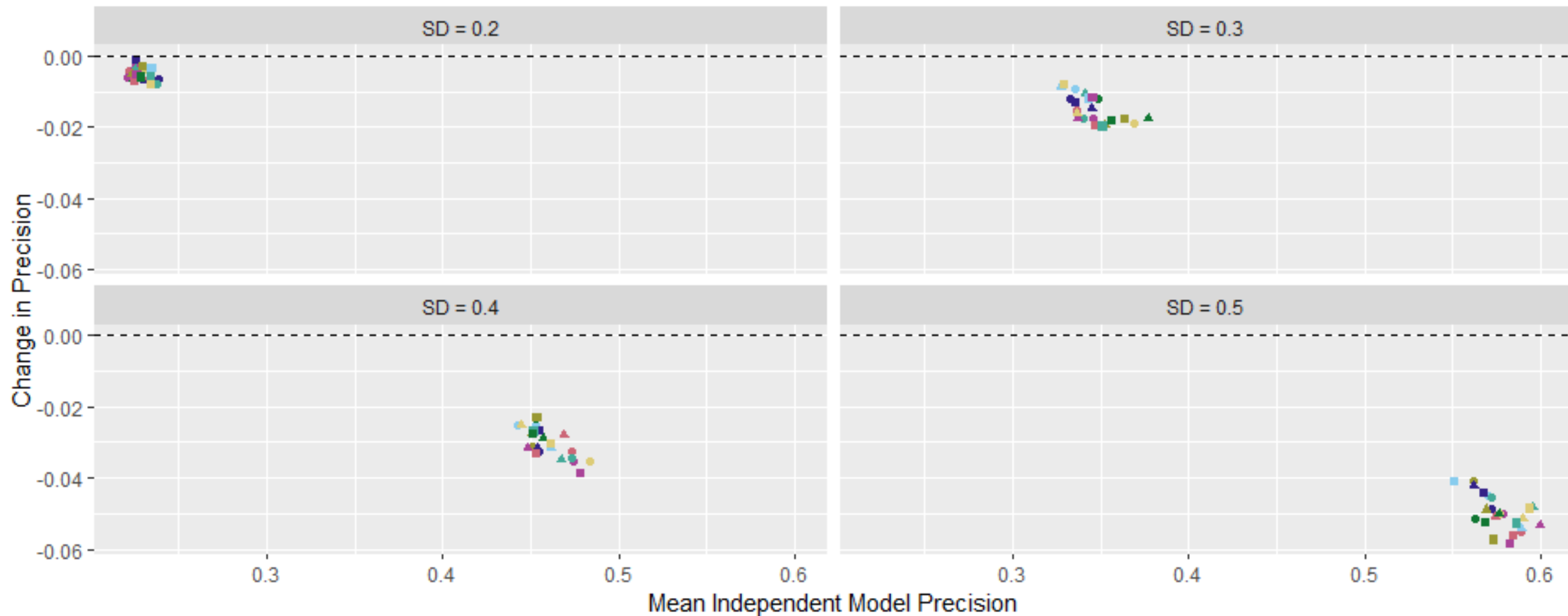


Precision comparison





Change in precision



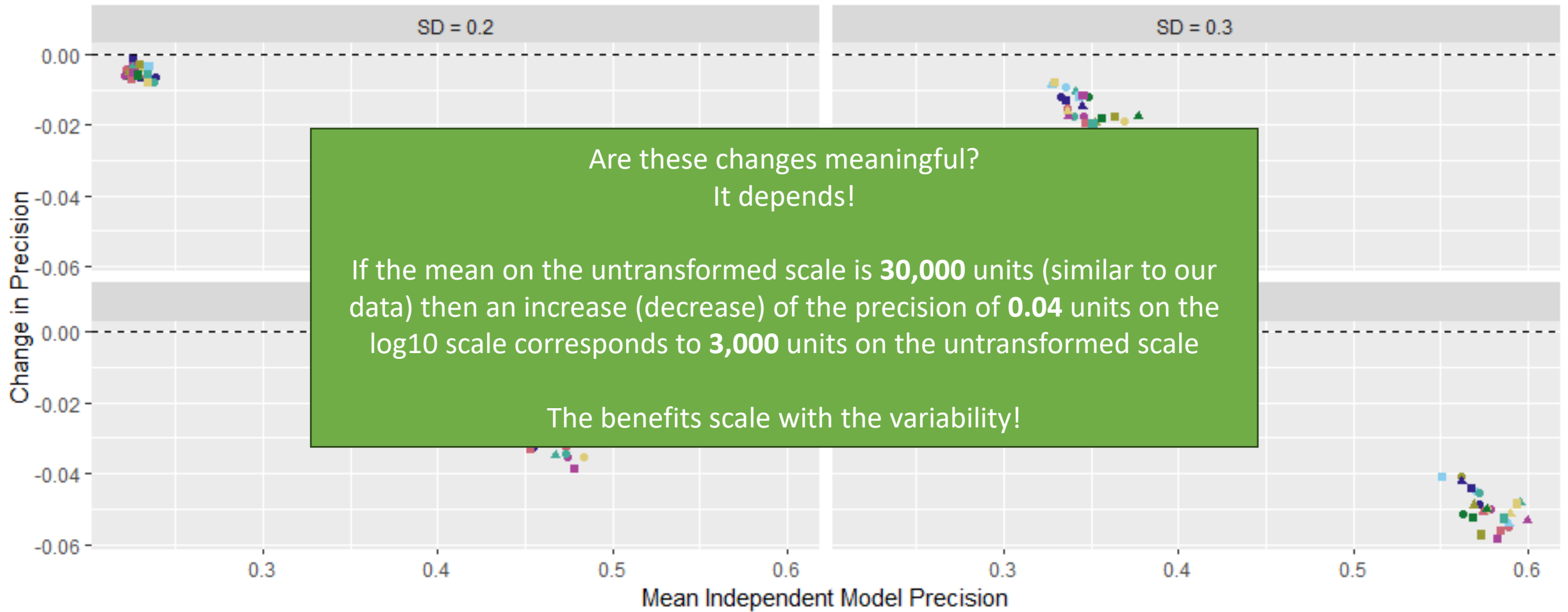
Intervention ● Pf ▲ Mod ■ Nvx

Age Group x Booster Dose

● Age: 12-<18 4th Dose	● Age: 50-<70 4th Dose	● Age: 12-<18 5th Dose	● Age: 50-<70 5th Dose
● Age: 18-<50 4th Dose	● Age: >=70 4th Dose	● Age: 18-<50 5th Dose	● Age: >=70 5th Dose



Change in precision



Intervention ● Pf ▲ Mod ■ Nvx

Age Group x Booster Dose

● Age: 12-<18 4th Dose	● Age: 50-<70 4th Dose	● Age: 12-<18 5th Dose	● Age: 50-<70 5th Dose
● Age: 18-<50 4th Dose	● Age: >=70 4th Dose	● Age: 18-<50 5th Dose	● Age: >=70 5th Dose



First Scheduled Analysis

$$i \in I = \{1, 2, \dots, 266^*\}$$

$$j \in J = \{\text{AZ}, \text{Pf}\}$$

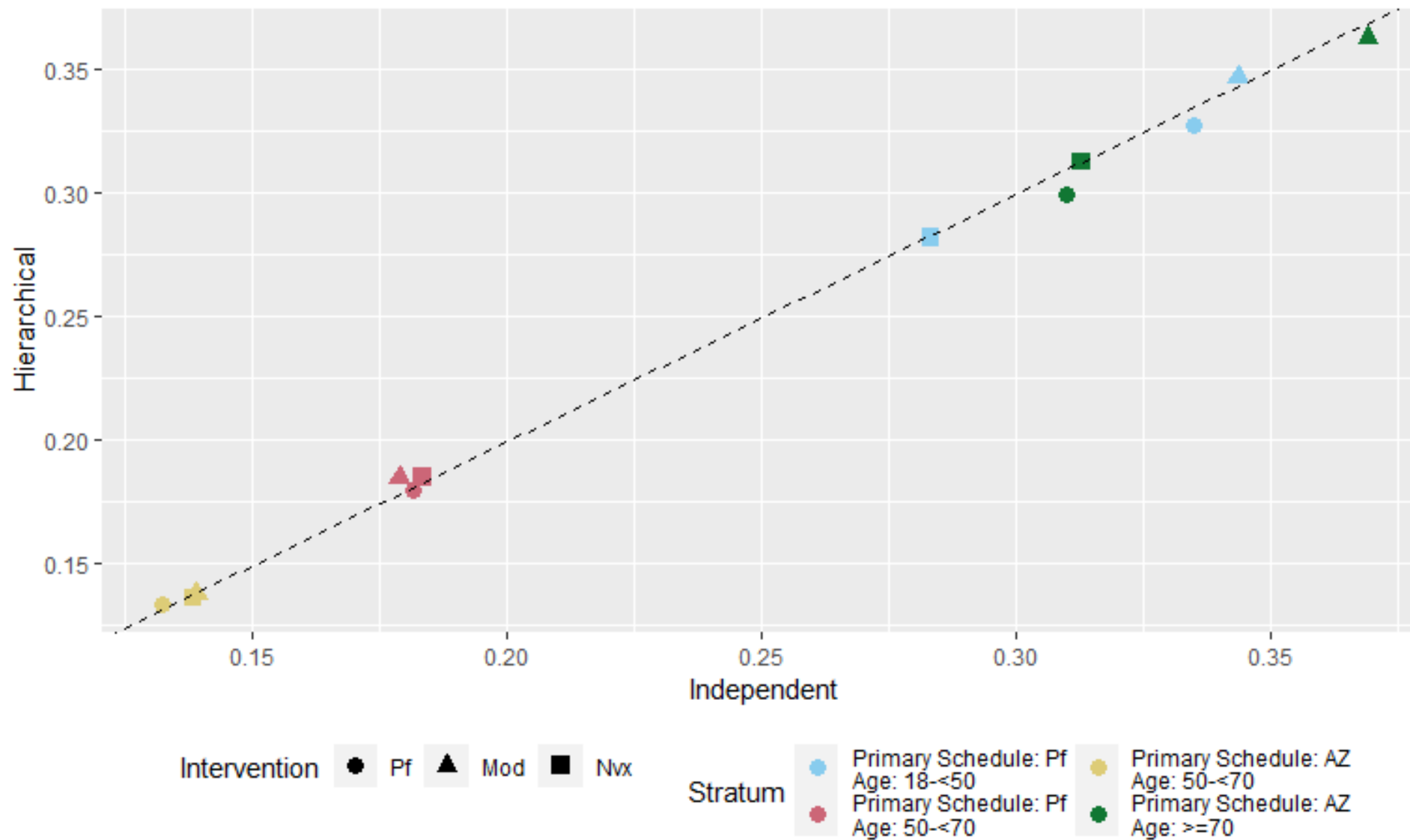
$$l \in L = \{12 - < 18, 18 - < 50, 50 - < 70, \geq 70\}$$

$$m \in M = \{1, 2\} \text{ **but no rerandomised participants**}$$

*Analysis scheduled for 300 but only 266 “eligible” samples due to missed visit windows, exclusion due to COVID-19 infection, etc.



First Scheduled Analysis – Precision Comparison





Discussion

- Bayesian hierarchical model efficiently estimates parameters by allowing for *information borrowing* between subgroups
- Gains in precision scale with data variability (perhaps not surprisingly)
- Is the additional statistical machinery worthwhile?
- Will the gains (or lack of gains) in precision vary as PICOBOO progresses?