Supplemental Materials

CACE for a single trial with noncompliance

According to Zhou et al. (2019), each observed n_{rto} has a corresponding probability that can be written in terms of parameters defined in $\boldsymbol{\beta} = (\pi_a, \pi_n, u_1, v_1, s_1, b_1)$. $\lambda = \Pr(R_j = 1)$ is the proportion of assigning the active treatment, which is usually known in randomized trials. Thus the vector $(n_{000}, n_{001}, n_{010}, n_{011}, n_{100}, n_{101}, n_{110}, n_{111})$ follows a multinomial distribution with parameters N and $\mathbf{p}$, where $N = \sum n_{rto}$ and the elements of $\mathbf{p}$ are listed in Table 1.

Table 1: Observed data and probabilities

Observed	Probabilities
n_{000}	$(1-\lambda)\{\pi_c(1-v_1)+\pi_n(1-s_1)\}$
n_{001}	$(1-\lambda)(\pi_c v_1+\pi_n s_1)$
n_{010}	$(1-\lambda)\pi_a(1-b_1)$
n_{011}	$(1-\lambda)\pi_a b_1$
n_{100}	$\lambda\pi_n(1-s_1)$
n_{101}	$\lambda\pi_n s_1$
n_{110}	$\lambda\{\pi_c(1-u_1)+\pi_a(1-b_1)\}$
n_{111}	$\lambda(\pi_c u_1+\pi_a b_1)$

Therefore, the log likelihood is

$$\begin{aligned}\log L(\boldsymbol{\beta}) = & n_{000}\log\{\pi_c(1-v_1)+\pi_n(1-s_1)\} + n_{001}\log(\pi_c v_1+\pi_n s_1) + n_{010}\log\{\pi_a(1-b_1)\} \\ & + n_{011}\log\{\pi_a b_1\} + n_{100}\log\{\pi_n(1-s_1)\} + n_{101}\log(\pi_n s_1) \\ & + n_{110}\log\{(\pi_c(1-u_1)+\pi_a(1-b_1)\} + n_{111}\log(\pi_c u_1+\pi_a b_1) + \text{constant}.\end{aligned} \tag{1}$$

Assigning a vague prior distribution $f(\boldsymbol{\beta})$ to the parameters $\boldsymbol{\beta} = (\pi_a, \pi_n, u_1, v_1, s_1, b_1)$, by Bayes' theorem the joint posterior distribution is proportional to $L(\boldsymbol{\beta})f(\boldsymbol{\beta})$. Functionals of the posterior distribution can be estimated by Gibbs and Metropolis–Hastings sampling algorithms using the software JAGS via the **rjags** package in R.

CACE for meta-analysis with incomplete compliance information

Table 2: Observed data and probabilities in study i

Observed	Probabilities
n_{i000}	$(1-\lambda_i)\{\pi_{ic}(1-v_{i1})+\pi_{in}(1-s_{i1})\}$
n_{i001}	$(1-\lambda_i)(\pi_{ic}v_{i1}+\pi_{in}s_{i1})$
n_{i010}	$(1-\lambda_i)\pi_{ia}(1-b_{i1})$
n_{i011}	$(1-\lambda_i)\pi_{ia}b_{i1}$
n_{i100}	$\lambda_i\pi_{in}(1-s_{i1})$
n_{i101}	$\lambda_i\pi_{in}s_{i1}$
n_{i110}	$\lambda_i\{(\pi_{ic}(1-u_{i1})+\pi_{ia}(1-b_{i1})\}$
n_{i111}	$\lambda_i(\pi_{ic}u_{i1}+\pi_{ia}b_{i1})$
n_{i0*0}	$(1-\lambda_i)\{\pi_{ic}(1-v_{i1})+\pi_{in}(1-s_{i1})+\pi_{ia}(1-b_{i1})\}$
n_{i0*1}	$(1-\lambda_i)(\pi_{ic}v_{i1}+\pi_{in}s_{i1}+\pi_{ia}b_{i1})$
n_{i1*0}	$\lambda_i\{(\pi_{ic}(1-u_{i1})+\pi_{ia}(1-b_{i1})+\pi_{in}(1-s_{i1})\}$
n_{i1*1}	$\lambda_i(\pi_{ic}u_{i1}+\pi_{ia}b_{i1}+\pi_{in}s_{i1})$

Table 2 shows the relation between each observed count and the corresponding probability, which is a function of the parameters defined in the complete-compliance CACE section of the main paper. As before, λ_i is the known allocation ratio for study i, i.e., $\lambda_i = \Pr(R_{ij} = 1)$.

The log likelihood contribution for trial i is obtained from the multinomial distribution:

$$\begin{aligned}
&\log L_i(\boldsymbol{\beta}_i)\\
=&n_{i000}\log\{\pi_{ic}(1-v_{i1})+\pi_{in}(1-s_{i1})\}+n_{i001}\log(\pi_{ic}v_{i1}+\pi_{in}s_{i1})\\
&+n_{i010}\log\{\pi_{iia}(1-b_{i1})\}+n_{i011}\log(\pi_{ia}b_{i1})+n_{i100}\log\{\pi_{in}(1-s_{i1})\}\\
&+n_{i101}\log(\pi_{in}s_{i1})+n_{i110}\log\{(\pi_{ic}(1-u_{i1})+\pi_{ia}(1-b_{i1})\}+n_{i111}\log(\pi_{ic}u_{i1}+\pi_{ia}b_{i1})\\
&+n_{i0*0}\log\{\pi_{ic}(1-v_{i1})+\pi_{in}(1-s_{i1})+\pi_{ia}(1-b_{i1})\}+n_{i0*1}\log(\pi_{ic}v_{i1}+\pi_{in}s_{i1}+\pi_{ia}b_{i1})\\
&+n_{i1*0}\log\{(\pi_{ic}(1-u_{i1})+\pi_{ia}(1-b_{i1})+\pi_{in}(1-s_{i1})\}+n_{i1*1}\log(\pi_{ic}u_{i1}+\pi_{ia}b_{i1}+\pi_{in}s_{i1})
\end{aligned}\tag{2}$$

Because the parameters $\boldsymbol{\beta}_i=(\pi_{ia},\pi_{in},s_{i1},b_{i1},u_{i1},v_{i1})$ are the same as in the complete-compliance case, the estimation process is also the same: assign distributions $f(\boldsymbol{\beta}_i|\boldsymbol{\beta}_0,\boldsymbol{\Sigma}_0)$, where $\boldsymbol{\beta}_0$ is the vector of mean hyper-parameters, and $\boldsymbol{\Sigma}_0$ is the covariance matrix; then specify prior distributions for $f(\boldsymbol{\beta}_0)$ and $f(\boldsymbol{\Sigma}_0)$, so the joint posterior is proportional to $\prod_i L_i(\boldsymbol{\beta}_i)f(\boldsymbol{\beta}_i|\boldsymbol{\beta}_0,\boldsymbol{\Sigma}_0)f(\boldsymbol{\beta}_0)f(\boldsymbol{\Sigma}_0)$. Similarly, the CACE for this meta-analysis incorporating incomplete compliance data is $\theta^{\text{CACE}}=E(\theta_i^{\text{CACE}})=E(u_{i1})-E(v_{i1})=\Phi(\frac{\alpha_u}{\sqrt{1+\sigma_u^2}})-\Phi(\frac{\alpha_v}{\sqrt{1+\sigma_v^2}})$ if the probit link function is used for u_{i1} and v_{i1}.

Bibliography

J. Zhou, J. S. Hodges, M. F. K. Suri, and H. Chu. A bayesian hierarchical model estimating cace in meta-analysis of randomized clinical trials with noncompliance. *Biometrics*, 75(3): 978–987, 2019. [p1]