The impact of directly observed therapy on the efficacy of Tuberculosis treatment: A Bayesian multilevel approach

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- Let Y be an outcome of interest, Z be a binary exposure, and X be a set of covariates
- A dataset is a single realization of the joint process that generates the triple (Y, Z, X)
- ► Associational Inference ⇒ Relationships among observed quantities
- Causal Inference
 → Manipulation of the mechanism that generates
 the data regarding answering a causal question

- What if we intervene by changing an individual exposure status? how much would the outcome change?
- What if we intervene by changing an individual medication? how much would the outcome change?
- ⇒ When answering causal questions via observed data we aim to create a "bridge" between the observed setting and some hypothetical (or experimental) setting

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- A causal effect is a contrast between Y(0) and Y(1) (or E(Y(0)) and E(Y(1)))

 A first step when investigating a causal question is to specify conditions necessary to answer it

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- Why should we care about that?

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- A first step when investigating a causal question is to specify conditions necessary to answer it
- Why should we care about that? See Simpson's paradox!

Causal Effect of interest: Average Treatment Effect (ATE)

$$\begin{aligned} \tau &= E(Y(1)) - E(Y(0)) \\ &= \int y f_{\varepsilon_1}(y) dy - \int y f_{\varepsilon_0}(y) dy \\ &= \int y \frac{f_{\varepsilon_1}(y)}{f_O(y)} f_O(y) dy - \int y \frac{f_{\varepsilon_0}(y)}{f_O(y)} f_O(y) dy \end{aligned}$$

• If $\frac{f_{\epsilon_1}(y)}{f_O(y)}$ and $\frac{f_{\epsilon_0}(y)}{f_O(y)}$ are equal to one, then τ can be computed based on f_O (randomized experiments)

Basics of Causal Inference

- We focus on the problem of confounding, which is a phenomenon that occurs when, in the data generating process, covariates affect both simultaneously, outcome and exposure of interest
- Under no unmeasured confounding (and other mild assumptions), it can be shown that

$$\tau = E(Y(1)) - E(Y(0)) = E(Y|Z = 1, e(X)) - E(Y|Z = 0, e(X)),$$

where e(X) = P(Z = 1|X) is the (correct) propensity score

While relaxing the no unmeasured confounding assumption, we investigate the need to include random effects in propensity score and outcome regressions to account for unmeasured confounding

- Cases of Tuberculosis in the state of São Paulo, Brazil in 2016
- ⇒ Infectious disease caused by the *Mycobacterium tuberculosis* bacteria
- \Rightarrow In Brazil, the treatment against Tuberculosis is given by the public health system and lasts for at least six months
- One of the main challenges with the treatment of Tuberculosis is the drug resistance acquired by patients, which is usually due to mismanagement of medications

- In the early 1990s, in order to reduce the odds of treatment failure, the World Health Organization (WHO) introduced the directly observed therapy (DOT)
- ⇒ A health professional must watch the ingestion of medications during the entire treatment process

Multilevel structured observations: individual into municipalities

▶ Binary treatment, Z_{ji} , such that $Z_{ji}|\delta_{ji} \sim Bernoulli(\delta_{ji})$ with

$$\operatorname{logit}(\delta_{ji}) = \log\left(\frac{\delta_{ji}}{1-\delta_{ji}}\right) = \sum_{k=1}^{q} \gamma_k X_{kji} + \nu_j, \tag{1}$$

▶ Binary outcome, such that $Y_{ji}|Z_{ji} \sim Bernoulli(\mu_{ji})$ with

$$logit(\mu_{ji}) = \beta_0 + \beta_Z Z_{ji} + B_{ji} + \eta_j.$$
(2)

Proposed method

- Literature Review: Proposed methods for modeling (1) and (2)
 - 1. Joint likelihood \Rightarrow Incorrect inference because of a feedback of the outcome into the propensity score model
 - 2. Cutting Feedback ⇒ Incorrect inference because of a measurement error-like problem on the outcome model
 - 3. Two-step \Rightarrow Provide correct inference and has a fully Bayesian argument
- We follow the two-step procedure and discuss the need to include random effects in propensity score and outcome models to account for unmeasured confounders

Simulation Studies

Two settings:

- 1. We consider both Z and Y to be normally distributed yielding a scenario in which bias calculations are analytically tractable
- 2. We consider both *Z* and *Y* to be binary as this is commonly found in epidemiological studies and is representative of our motivating example

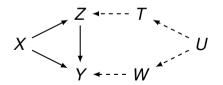


Figure 1: DAG of the data generation mechanism for the simulation studies.

An Analytically Tractable Example: The Linear Case

Data Generating Mechanism

- Let X_{ji} be an individual-level covariate generated from a standard normal distribution for j = 1, ..., m and $i = 1, ..., n_i$, and assume that

$$Z_{ji} = \alpha_0 + \alpha_X X_{ji} + T_j + \varepsilon_{ji}, \ \varepsilon_{ji} \sim \mathcal{N}(0, \rho^2)$$
(3)

$$Y_{ji} = \beta_Z Z_{ji} + \beta_X X_{ji} + W_j + \varepsilon_{ji}, \ \varepsilon_{ji} \sim \mathcal{N}(0, \kappa^2), \tag{4}$$

- Let $\mathbf{T} = (T_1, \dots, T_m)^\top$ and $\mathbf{W} = (W_1, \dots, W_m)^\top$ be two cluster-level covariates whose joint distribution is given by

$$\left(\begin{array}{c} \mathbf{T} \\ \mathbf{W} \end{array}\right) \sim \mathcal{N}\left[\left(\begin{array}{c} \mu_T \mathbf{1}_m \\ \mu_W \mathbf{1}_m \end{array}\right), \left(\begin{array}{c} \sigma_T^2 \mathbf{I}_m & \rho_{T,W} \sigma_T \sigma_W \mathbf{I}_m \\ \cdot & \sigma_W^2 \mathbf{I}_m \end{array}\right)\right],$$

where $\rho_{T,W}$ is the correlation between **T** and **W**. The quantities ρ in (3), κ in (4), and σ_T and σ_W in (13) are assumed to be known.

An Analytically Tractable Example: The Linear Case

- Model Adjustment
- Exposure model: For Z_{ji}'s generated according to Equation (3), the following model was fitted

$$Z_{ji} = lpha_0 + lpha_X X_{ji} +
u_j + arepsilon_{ji},$$

- Outcome Model: for Y_{ji} generated according to Equation (4), the following model was fitted

$$Y_{ji} = \beta_0 + \beta_Z Z_{ji} + B_{ji} + \eta_j + \varepsilon_{ji},$$

where B_{ji} indicates how the adjustment for confounding is implemented in the model.

Table 1: Continuous outcome simulation: fitted models. Data generated as in (3)-(4). The quantities $\widehat{\textbf{BS}}$ and $\widetilde{\textbf{BS}}$ are the balancing scores estimated from models described in column E(Z|X). The cluster-level random effects \boldsymbol{v} and $\boldsymbol{\eta}$ are such that $\boldsymbol{v} \sim \mathcal{N}(0, \sigma_T^2 \textbf{I}_m)$ and $\boldsymbol{\eta} \sim \mathcal{N}(0, \sigma_W^2 \textbf{I}_m)$.

Model	$E(\mathbf{Z} \mathbf{X})$	$E(\mathbf{Y} \mathbf{Z},\mathbf{X})$
MD1	$\alpha_0 1 + lpha_X \mathbf{X}$	$eta_0 1_N + eta_Z \mathbf{Z} + eta_b \widehat{\mathbf{BS}}$
MD2	$\alpha_0 1 + \alpha_X \mathbf{X} + \mathbf{A} \mathbf{v}$	$eta_0 1_N \!+\! eta_Z \mathbf{Z} \!+\! eta_b \widetilde{BS}$
MD3	$lpha_0$ 1 + $lpha_X$ X	$eta_0 1_N \!+\! eta_Z \mathbf{Z} \!+\! eta_b \widehat{\mathbf{BS}} \!+\! \mathbf{A} m{\eta}$
MD4	$\alpha_0 1 + \alpha_X \mathbf{X} + \mathbf{A} \mathbf{v}$	$\beta_0 1_N + \beta_Z \mathbf{Z} + \beta_b \widetilde{\mathbf{BS}} + \mathbf{A} \boldsymbol{\eta}$

Focusing on model MD2, it can be shown that

$$\operatorname{Bias}(\widehat{\beta}_{Z}) = \left[(\mathbf{H}^{\top}\mathbf{H})^{-1}\mathbf{H}^{\top} \left(\beta_{X}\mathbf{X} + \rho_{T,W}\sigma_{T}\sigma_{W}\mathbf{A}\mathbf{A}^{\top}\Sigma_{\mathbf{Z}|\mathbf{X}}^{-1}(\mathbf{Z} - (\alpha_{0} + \mu_{T})\mathbf{1}_{N} - \alpha_{X}\mathbf{X}) \right) \right]_{(2)},$$

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where $\mathbf{H} = \begin{bmatrix} \mathbf{Z} \mid \widetilde{\mathbf{BS}} \end{bmatrix}$ and $[\cdot]_{(2)}$ indicates the second element of the vector, and $\Sigma_{\mathbf{Z}|\mathbf{X}} = \operatorname{Var}(\mathbf{Z}|\mathbf{X})$.

An Analytically Tractable Example: The Linear Case

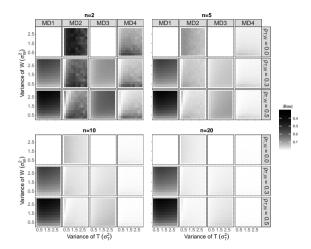


Figure 2: Absolute bias of $\hat{\beta}_Z$ under the models described in Table 1. These results are averaged over 1000 Monte Carlo replicates.

A Simulation Study with Binary Exposure and Outcome

- Data Generating Mechamism
- Confounders X_1 and X_2

Scenario 1: $v_{ji} \sim \mathcal{N}(0, 0.1^2)$ and $\zeta_j \sim \mathcal{N}(0, 0.4^2)$; Scenario 2: $v_{ji} \sim \mathcal{N}(0, 0.25^2)$ and $\zeta_j \sim \mathcal{N}(0, 1)$.

- Exposure $Z_{ji}|\delta_{ji}\sim Bernoulli(\delta_{ji})$

$$\operatorname{logit}(\delta_{ji}) = \alpha_0 + X_{1ji}\alpha_1 + X_{2ji}\alpha_2 + T_j.$$

- Outcome $Y_{ji}|\mu_{ji} \sim Bernoulli(\mu_{ji})$

$$logit(\mu_{ji}) = \beta_0 + X_{1ji}\beta_1 + X_{2ji}\beta_2 + X_{1ji}X_{2ji}\beta_3 + W_{ji}$$

Model Adjustment

Table 2: Binary outcome simulation: fitted models. Data generated as in (??)-(??). The quantities \widehat{PS}_{ji} and \widetilde{PS}_{ji} are the propensity scores estimated from models described in column logit(δ_{ji}). The cluster-level random effects v_j and η_j are such that $v_j \sim \mathcal{N}(0, \varphi^2)$ and $\eta_j \sim \mathcal{N}(0, \varphi^2)$, for j = 1, ..., m.

Model	$\operatorname{logit}(\delta_{ji})$	$logit(\mu_{ji})$
MD1	$\gamma_0 + \gamma_1 X_{1ji} + \gamma_2 X_{2ji}$	$eta+eta_{Z}Z_{ji}+eta_{b}\widehat{PS}_{ji}$
MD2	$\gamma_0 + \gamma_1 X_{1ji} + \gamma_2 X_{2ji} + v_j$	$eta+eta_Z Z_{ji}+eta_b \widetilde{PS}_{ji}$
MD3	$\gamma_0 + \gamma_1 X_{1ji} + \gamma_2 X_{2ji}$	$eta+eta_Z Z_{ji}+eta_b \widehat{PS}_{ji}+\eta_j$
MD4	$\gamma_0 + \gamma_1 X_{1ji} + \gamma_2 X_{2ji} + v_j$	$\beta + \beta_Z Z_{ji} + \beta_b \widetilde{PS}_{ji} + \eta_j$

A Simulation Study with Binary Exposure and Outcome

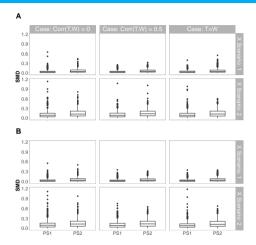
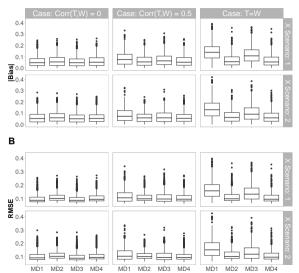


Figure 3: Boxplots of the weighted SMD of X_1 (Panel A) and X_2 (Panel B) under propensity scores estimated from models PS1 : logit(δ_{ji}) = $\gamma_0 + \gamma_1 X_{1ji} + \gamma_2 X_{2ji}$ and PS2 : logit(δ_{ji}) = $\gamma_0 + \gamma_1 X_{1ji} + \gamma_2 X_{2ji} + v_j$, over 1000 Monte Carlo data replicates.

A Simulation Study with Binary Exposure and Outcome

Α



- Z_{ij} denotes a binary exposure that indicates if individual i in the jth city received the DOT
- Y_{ij} denotes the outcome of interest that indicates if individual *i* in the *j*th city had a diagnosis of cure at the end of the treatment
- Let X_{ij} = (X_{1ij}, ··· , X_{pij}) be a p-dimensional vector of predictors for individual i in the jth city. The vector X_{ij} comprises both, individual and cluster characteristics

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- ⇒ Individual-level characteristics: indicator variables for diagnosis of Acquired Immunodeficiency Syndrome (AIDS), diagnosis of diabetes, reporting (illicit) drug use, diagnosis of alcoholism, being homeless, gender, whether currently a prisoner, diagnosis of a mental illness, and current smoking status. Additionally, type of TB, and age (in years) are available.
- \Rightarrow At the cluster-level, only the Human Development Index (HDI) is available.

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TB Data analysis: Exposure model specification

We assume $Z_{ji} | \delta_{ji} \sim Bernoulli(\delta_{ji})$, with

$$\operatorname{logit}(\delta_{ji}) = \log\left(\frac{\delta_{ji}}{1-\delta_{ji}}\right) = \sum_{k=1}^{q} \gamma_k X_{kji} + v_j,$$

▶ PS1:
$$v_j = 0$$
, for all j ;

▶ PS2:
$$v_j \sim \mathcal{N}(0, \varphi^2)$$
, for all *j*; and

PS3: v ~ N(0, φ²R(λ)), where R_{ij} = Corr(v_i, v_j) = exp(-λ||s_i - s_j||), with s_j denoting the centroid of city *j* (a two-dimensional vector of coordinates) and ||·|| denoting the Euclidean distance.

Table 3: Exposure model comparison.

	elpd (WAIC)	pWAIC	WAIC	elpd (LOO)	pLOO	LOO
PS1	-8136.17	14.10	16272.35	-8136.23	14.16	16272.45
PS2	-6884.15	242.63	13768.30	-6893.51	251.99	13787.02
PS3	-6877.74	235.82	13755.49	-6885.21	243.28	13770.42

TB Data analysis: Exposure

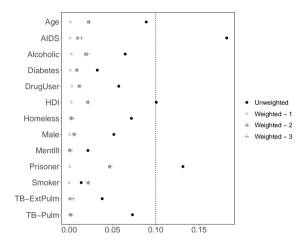


Figure 5: Standardized mean difference (SMD) for the observed baseline covariates between treated and control subjects.

Model	Outcome Model	Distribution of the random effect
M1	$logit{\mu_{ij}} = \beta + Z_{ij}\beta_Z$	_
M2	$logit{\mu_{ij}} = \beta + Z_{ij}\beta_Z + \eta_j$	$\eta \phi \sim \mathscr{N}(0, \phi^2 \mathbf{I}_{\mathcal{N}})$
M3	$logit{\mu_{ij}} = \beta + Z_{ij}\beta_Z + \eta_j$	$\eta \phi, \lambda_{m{y}} \sim \mathscr{N}(m{0}, \phi^2 m{R}(\lambda_{m{y}}))$
M4	$\operatorname{logit}\{\mu_{ij}\} = \beta + Z_{ij}\beta_Z + \mathbf{X}_{ij}^T\beta_X$	_
M5	$\operatorname{logit}\{\mu_{ij}\} = \beta + Z_{ij}\beta_{Z} + \mathbf{X}_{ij}^{T}\beta_{X} + \eta_{j}$	$\eta \phi \sim \mathscr{N}(0, \phi^2 \mathbf{I}_N)$
M6	$\operatorname{logit}\{\mu_{ij}\} = \beta + Z_{ij}\beta_Z + \mathbf{X}_{ij}^{T}\beta_X + \eta_j$	$\eta \phi, \lambda_{y} \sim \mathscr{N}(oldsymbol{0}, \phi^{2} oldsymbol{R}(\lambda_{y}))$
M7	$logit{\mu_{ij}} = \beta + Z_{ij}\beta_Z + PS1_{ij}\beta_{ps}$	_
M8	$logit{\mu_{ij}} = \beta + Z_{ij}\beta_Z + PS1_{ij}\beta_{ps} + \eta_j$	$\eta \phi \sim \mathscr{N}(0, \phi^2 \mathbf{I}_{\mathcal{N}})$
M9	$logit{\mu_{ij}} = \beta + Z_{ij}\beta_Z + PS1_{ij}\beta_{ps} + \eta_j$	$\eta \phi, \lambda_{y} \sim \mathscr{N}(0, \phi^{2} \mathbf{R}(\lambda_{y}))$
M10	$logit{\mu_{ij}} = \beta + Z_{ij}\beta_Z + PS2_{ij}\beta_{ps}$	_
M11	$logit{\mu_{ij}} = \beta + Z_{ij}\beta_Z + PS2_{ij}\beta_{ps} + \eta_j$	$\eta \phi \sim \mathscr{N}(0, \phi^2 \mathbf{I}_N)$
M12	$logit{\mu_{ij}} = \beta + Z_{ij}\beta_Z + PS2_{ij}\beta_{ps} + \eta_j$	$\eta \phi, \lambda_{m{y}} \sim \mathscr{N}(m{0}, \phi^2 m{R}(\lambda_{m{y}}))$
M13	$logit{\mu_{ij}} = \beta + Z_{ij}\beta_Z + PS3_{ij}\beta_{ps}$	_
M14	$logit{\mu_{ij}} = \beta + Z_{ij}\beta_Z + PS3_{ij}\beta_{ps} + \eta_j$	$\eta \phi \sim \mathscr{N}(0, \phi^2 \mathbf{I}_N)$
M15	$logit{\mu_{ij}} = \beta + Z_{ij}\beta_Z + PS3_{ij}\beta_{ps} + \eta_j$	$\eta \phi, \lambda_y \sim \mathscr{N}(0, \phi^2 \mathbf{R}(\lambda_y))$

	elpd (WAIC)	pWAIC	WAIC	elpd (LOO)	pLOO	LOO
M1	-3788.84	1.99	7577.67	-3788.84	2.00	7577.69
M2	-3622.66	120.45	7245.32	-3623.69	121.48	7247.38
MЗ	-3622.60	116.19	7245.20	-3623.55	117.15	7247.10
M4	-3538.21	15.07	7076.42	-3538.27	15.13	7076.54
M5	-3435.76	115.90	6871.52	-3436.61	116.74	6873.21
M6	-3436.19	111.72	6872.37	-3436.94	112.47	6873.88
M7	-3649.03	2.88	7298.06	-3649.04	2.89	7298.07
M8	-3535.18	104.18	7070.36	-3535.90	104.90	7071.81
M9	-3535.41	101.62	7070.82	-3536.10	102.31	7072.19
M10	-3734.95	2.90	7469.90	-3734.96	2.91	7469.92
M11	-3612.22	138.22	7224.45	-3613.87	139.87	7227.74
M12	-3613.57	131.75	7227.15	-3615.02	133.20	7230.05
M13	-3735.10	2.99	7470.21	-3735.11	3.00	7470.23
M14	-3613.55	137.26	7227.09	-3615.14	138.86	7230.28
M15	-3614.23	131.34	7228.47	-3615.66	132.77	7231.32

Table 4: Outcome model comparison.

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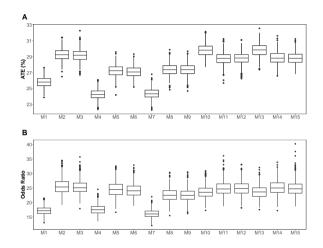


Figure 6: Posterior distributions of the ATE (Panel A) and Odds Ratio (Panel B) of the models above.

We investigate the inclusion of a random effect in the propensity score and outcome models for multilevel models

(Non-collapsibility×Causal Inference) and Spatial Confounding

- Should we advocate for the inclusion of a random effect in the propensity score model? and what about the outcome model?
- \Rightarrow If we have strong indication of potential for unmeasured confounders, and balancing diagnostics for observed confounders are not penalized, the answer might be yes for both



Muito Obrigado!!!

Bayesian theory: semi- and non-parametric methods

- Spatial statistics
- Spatio-temporal analysis
- Causal inference