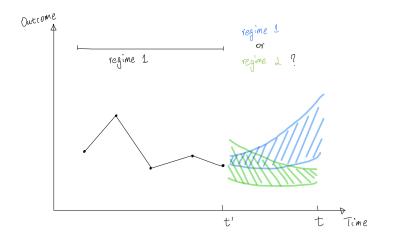
Causal Framework for Individualized Treatment Evaluation using Multivariate Generalized Mixed Effect Models with Longitudinal Data

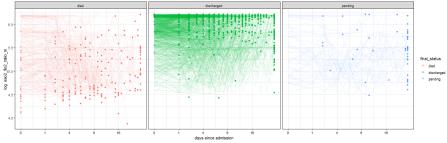
Motivation



Individualized causal effect of treatment regimes on important biomarkers and endpoints

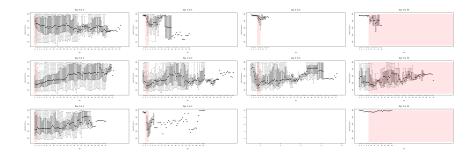


sao2_fio2_ratio_m day trajectory by status



- Data source: The Johns Hopkins Covid-19 Precision Medicine Analytics Platform (PMAP) Registry
- All patients consecutively admitted with confirmed SARS-CoV-2 infection by microbiological testing from 3/4/2020-6/25/2020





 Understand how individual's mortality and important biomarkers vary as a function of ventilation initiation

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Challenges

- Causal inference is usually about population causal effect.
 - Individual causal effect is unidentifiable in most cases.
- Informative patient heterogeneity in treatment assignment.
 - Clinician's tendency in making treatment decisions from unobserved factors; we assume the existence of unobserved time-invariant confounders.
 - With unmeasured confounding, standard approaches in longitudinal causal inference may lead to biased estimates. (*Yang and Lok, 2018*)
- Unit fixed effects regression models are widely used to adjust for unobserved time-invariant confounders
 - Drawback: trade-off between causal dynamics and time-invariant unobservables. (*Imai and Kim, 2019*)

Contributions

Propose a Bayesian framework for quantifying the individual counterfactual benefit of dynamic treatment regimes

- relaxes the no unmeasured confounders assumption
- summarizes the evidence relevant to clinical decisions of a single patient
- defines the causal effect for a specific patient at a day t as a functional of
 - observed history of that patient up to day t' (t' < t)
 - parameters estimated based on data from similar patients
 - counterfactual paths of that patient during days (t', t], accounting for unobserved time-invariant confounders

Notations

For patient *i* at day *t*,

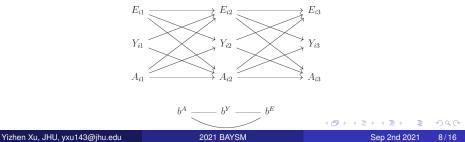
- ► Y_{it}: biomarker(s), i.e. continuous lung efficiency score
- \blacktriangleright *E_{it}*: competing risk endpoints, i.e. death and discharge
- ► *A_{it}*: indicator of first-time ventilation
- V: baseline covariates

Model Specification

Multivariate mixed model of time-varying components

$$\begin{aligned} Y_{it} &= f_{Y}(V, A_{i,t-1}; \beta^{Y}, b_{i}^{Y}, \epsilon_{it}) \\ A_{it} &= f_{A}(V, A_{i,t-1}, Y_{i,t-1}; \beta^{A}, b_{i}^{A}) \\ E_{it} &= f_{E}(V, A_{i,t-1}, Y_{i,t-1}; \beta^{E}, b_{i}^{E}) \\ (b_{i}^{Y}, b_{i}^{A}, b_{i}^{E}) &\sim MVN(0, G) \end{aligned}$$

The random effect (b_i^Y, b_i^A, b_i^E) captures a vector of unobserved time-invariant confounders in a flexible manner.

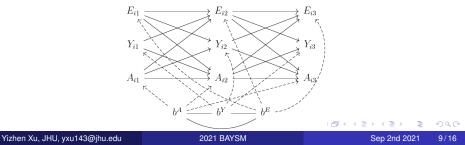


Model Specification

Multivariate mixed model of time-varying components

$$\begin{split} Y_{it} &= f_{Y}(V, A_{i,t-1}; \beta^{Y}, b_{i}^{Y}, \epsilon_{it}) \\ A_{it} &= f_{A}(V, A_{i,t-1}, Y_{i,t-1}; \beta^{A}, b_{i}^{A}) \\ E_{it} &= f_{E}(V, A_{i,t-1}, Y_{i,t-1}; \beta^{E}, b_{i}^{E}) \\ (b_{i}^{Y}, b_{i}^{A}, b_{i}^{E}) &\sim MVN(0, G) \end{split}$$

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Model Specification

Why multivariate mixed model?

- Repeated measurement makes it possible to partially inform individual heterogeneity that arises from unobserved covariates
- Connects the progression of biomarkers, events, and treatment assignments

Difficulties

- Estimation of patient heterogeneity usually uses complete history information
- Longitudinal causal estimation only uses up-to-date history information to infer on future counterfactuals

Model Estimation

Obtain posterior estimates of population level parameters ($\beta^{Y}, \beta^{A}, \beta^{E}, G$)

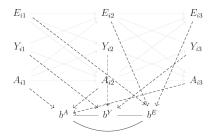


Figure: Information flow in the estimation of G

A "G-computation" Approach

Posterior sampling of individual counterfactual trajectories under a treatment regime of interest

Given history $(E_{i1}, Y_{i1}, A_{i1}, E_{i2}, Y_{i2})$, regime $(A_{i1}, A_{i2}) = (a_1, a_2) = \bar{a}$

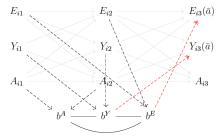


Figure: Information flow in computing potential outcomes

- Real-time update of random effect estimation
- Conditional on treatment heterogeneity b^A_i for the identifiability of individualized treatment effect based on the assumed DAG

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2021 BAYSM

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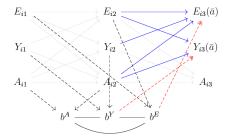


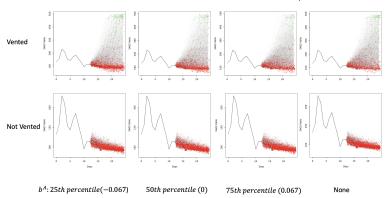
Figure: Information flow in computing potential outcomes

Causal Comparison

Compute target quantity for treatment regime comparison as a functional of the posterior counterfactual trajectories under different treatment options

 Example: Contrasts of cumulative hazards between two treatment regimes.

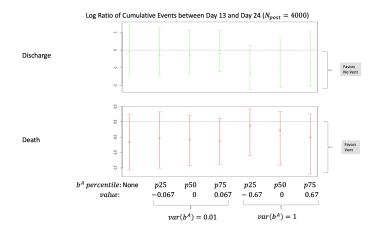
Preliminary Resuts



Simulated Trajectories and Events between Day 13 and Day 24 ($var(b^A) = 0.01$, $N_{post} = 4000$)

Figure: Venting the person on day 12 versus always no ventilation

Preliminary Resuts



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