Causal inference using the g-formula in Stan

Leah Comment

Department of Biostatistics Harvard T.H. Chan School of Public Health

January 12, 2018

Presentation information

https://github.com/lcomm/stancon2018

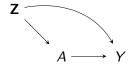
You'll find:

- ▶ These slides
- A document with more details on motivation and implementation
- ► Stan code files for all models shown here

Crash course on causal inference

- Goal: learn about causal mechanisms using observational data
- ► Why?
 - Useful for identifying targets for policy intervention
 - Can create projections for what would occur after some policy change
 - Need to make decisions even when conclusive data are not available
- Caveats:
 - Correlation still ≠ causation; more about formalizing what would be necessary for that to hold
 - Not going to be very rigorous today

The potential outcomes framework



- Some treatment or exposure A
- Outcome of interest is Y
- ▶ Under some assumptions, the **potential outcome** *Y*_a is the value *Y* would take on if *A* were set to *a*
- For binary A:
 - Average treatment effect: $\mathbb{E}\left[Y_1 Y_0\right]$
 - lacktriangle Average treatment effect on treated: $\mathbb{E}\left[Y_1-Y_0|A=1
 ight]$
- Often need to adjust for a set of baseline confounders Z

The g-formula for standardization

g-formula:
$$\mathbb{E}[Y_a] = \sum_{\mathbf{z}} \mathbb{E}[Y|A = a, \mathbf{Z} = \mathbf{z}]P(\mathbf{Z} = \mathbf{z})$$

- ▶ This requires no unmeasured confounding given **Z**: $Y_a \perp \!\!\! \perp A|\mathbf{Z}$
- ▶ Average treatment effect of changing A from a to a^* for whole population: $\mathbb{E}[Y_{a^*}] \mathbb{E}[Y_a]$
- ► Common (frequentist) approach is to adopt parametric models for $Y|A, \mathbf{Z}$ and use empirical distribution of \mathbf{Z} for $P(\mathbf{Z} = \mathbf{z})$
- Frequentist bootstrap used for inference

A Bayesian version of the g-formula

Adopting parametric models indexed by θ , the Bayesian g-formula is:

$$p(\tilde{y}_{a}|o) = \int \int p(\tilde{y}|a, \tilde{z}, \theta) p(\tilde{z}|\theta) p(\theta|o) d\theta d\tilde{z}$$

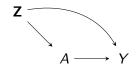
- $ightharpoonup p(\tilde{y}_a|o)$
 - ▶ Distribution of *Y* we would expect to see if *A* were set to *a* in some population with same:
 - Underlying confounder distribution (comparability)
 - Data-generating parameters (causal transportability)
- lacktriangle This integrates over uncertainty in $oldsymbol{ heta}$
- ▶ Causal estimands usually compare means of $p(\tilde{y}_1|o)$ and $p(\tilde{y}_0|o)$
- ▶ See paper by Keil et al for more details (Keil et al. 2015)

Causal inference with Stan

Two components to Bayesian causal inference with the g-formula:

- Get posterior samples of parameters θ
 - ▶ Learn from data in data block
 - ▶ Fit parametric models in model block
- Do causal inference using posterior predictive draws of potential outcomes
 - Use confounder distribution from data block (may or may not be same data used to fit the model)
 - Sample potential outcomes in the generated quantities block

A simple example



- ▶ Nothing in particular assumed about distribution of **Z**
- ▶ Binary *A*
- ▶ Binary Y

Assume Y is generated according to logistic model:

$$\operatorname{logit} \big(P\big(Y_i = 1 | A_i, Z_i \big) \big) = \alpha_0 + \alpha_A A_i + \alpha_Z' \mathbf{Z}_i$$

https://github.com/lcomm/stancon2018/simple_mc.stan

```
data {
  // number of observations
  int<lower=0> N:
  // number of columns in design matrix excluding A
  int<lower=0> P:
  // design matrix, excluding treatment A
  matrix[N. P] X:
  // observed treatment
  vector[N] A:
  // outcome
  int<lower=0,upper=1> Y[N];
```

```
https://github.com/lcomm/stancon2018/simple_mc.stan

transformed data {
   // make vector of 1/N for (classical) bootstrapping
   vector[N] boot_probs = rep_vector(1.0/N, N);
```

 $https://github.com/lcomm/stancon2018/simple_mc.stan$

```
parameters {
   // regression coefficients
   vector[P + 1] alpha;
}

transformed parameters {
  vector[P] alphaZ = head(alpha, P);
  real alphaA = alpha[P + 1];
}
```

https://github.com/lcomm/stancon2018/simple_mc.stan

```
model {
   // priors for regression coefficients
   alpha ~ normal(0, 2.5);

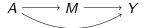
   // likelihood
   Y ~ bernoulli_logit(X * alphaZ + A * alphaA);
}
```

```
generated quantities {
  // row index to be sampled for bootstrap
  int row_i;
 // calculate ATE in the bootstrapped sample
  real ATE = 0;
  vector[N] Y a1;
  vector[N] Y a0;
  for (n in 1:N) {
   // sample baseline covariates
    row_i = categorical_rng(boot_probs);
   // sample Ya where a = 1 and a = 0
    Y a1[n] = bernoulli logit rng(X[row i] * alphaZ + alphaA);
    Y a0[n] = bernoulli_logit_rng(X[row_i] * alphaZ);
    // add contribution of this observation to the ATE
    ATE = ATE + (Y a1[n] - Y a0[n])/N;
```

Simple example: more on the ATE calculation

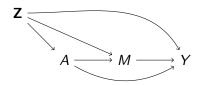
- ▶ Remember: we want $\mathbb{E}[Y_1] \mathbb{E}[Y_0]$, which marginalizes over **Z**
- ▶ Weighted average of causal effects for different **Z** values (like $P(\mathbf{Z} = \mathbf{z})$ in the frequentist g-formula)
- ▶ On average, bootstrapped data sets will have same $P(\mathbf{Z} = \mathbf{z})$ as in the main data set

Switching gears: mediation analysis



- Mediation analysis seeks to understand more about causal mechanisms of actions
- ► For every causal intermediate ("mediator") *M*, we can decompose the total effect of an exposure into two parts:
 - ▶ Part mediated by *M* (natural indirect effect; NIE)
 - ▶ Part enacted through other pathways (natural direct; NDE)
- Policymakers want to target the causal paths with biggest impact

A mediation example



- Nothing in particular assumed about distribution of Z
- Binary treatment A
- Binary mediator M
- ▶ Binary outcome Y

Mediation: models

Assume M and Y are generated according to logistic models:

$$\operatorname{logit} \big(P\big(M_i = 1 | A_i, Z_i \big) \big) = \beta_0 + \beta_Z' \mathbf{Z}_i + \beta_A A_i$$

logit
$$(P(Y_i = 1|A_i, M_i, Z_i)) = \alpha_0 + \alpha'_Z \mathbf{Z}_i + \alpha_A A_i + \alpha_M M_i$$

Mediation: code

https://github.com/lcomm/stancon2018/mediation_mc.stan

Changes to data and model blocks are the addition of a model for M

```
data {
  vector[P + 1] beta m;
  cov matrix[P + 1] beta vcv;
  . . .
model {
  M ~ bernoulli_logit(X * betaZ + A * betaA);
  Y ~ bernoulli_logit(X * alphaZ + A * alphaA + Mv * alphaM);
  . . .
```

Mediation: code

https://github.com/lcomm/stancon2018/mediation_mc.stan

Calculation of NDE is done in generated quantities block:

```
// calculate NDE in the bootstrapped sample
real NDE = 0:
. . .
for (n in 1:N) {
  . . .
  // sample Ma where a = 0
 M_a0[n] = bernoulli_logit_rng(X[row_i] * betaZ);
  // sample Y_{a=1, M=M_0} and Y_{a=0, M=M_0}
  Y_a1Ma0[n] = bernoulli_logit_rng(X[row_i] * alphaZ +
                                    M_a0[n] * alphaM + alphaA);
  Y_aOMaO[n] = bernoulli_logit_rng(X[row_i] * alphaZ +
                                    M = 0[n] * alphaM);
  // add contribution of this observation to the bootstrapped NDE
  NDE = NDE + (Y_a1Ma0[n] - Y_a0Ma0[n])/N;
}
```

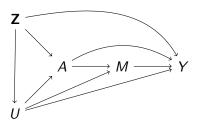
Data integration for unmeasured confounding

- Policymakers usually have to make decisions based on available data
- ▶ We rarely have the ideal data set → often lack important confounders
- ► This is problematic for causal inference
- Analysts may struggle to communicate the additional uncertainty to the decision maker

Prior information to the rescue

- Thankfully, all is not lost!
- We often have some information about the unmeasured confounder in another data source
- ▶ We can derive informative priors from the external data source

Revisiting mediation example: new structure



▶ Now we have an unmeasured binary baseline confounder *U*

Revisiting mediation example: new models

Assume the following generative models:

$$\operatorname{logit}\left(P(U_i=1|\mathbf{Z}_i,A_i)\right)=\gamma_0+\gamma_Z'\mathbf{Z}_i$$

logit
$$(P(M_i = 1|\mathbf{Z}_i, A_i, U_i)) = \beta_0 + \beta_Z' \mathbf{Z}_i + \beta_U U_i + \beta_A A_i$$

$$\operatorname{logit}(P(Y_i = 1 | A_i, Z_i, U_i, M_i)) = \alpha_0 + \alpha'_Z \mathbf{Z}_i + \alpha_U U_i + \alpha_A A_i + \alpha_M M_i$$

Marginalization over unmeasured confounder

► Full data likelihood (i.e., if *U* were measured)

$$\prod_{i=1}^n f(y_i|\alpha, \mathbf{z}_i, a_i, m_i, u_i) f(m_i|\beta, \mathbf{z}_i, a_i, u_i) f(u_i|\gamma, \mathbf{z}_i)$$

ightharpoonup Marginalizing likelihood over binary U

$$\prod_{i=1}^n \left[\sum_{u=0}^1 f(y_i | \boldsymbol{\alpha}, \mathbf{z}_i, a_i, m_i, u_i = u) f(m_i | \boldsymbol{\beta}, \mathbf{z}_i, a_i, u_i = u) P(U_i = u | \boldsymbol{\gamma}, \mathbf{z}_i) \right]$$

Incorporation of prior information

Obviously, parameters involving U are unidentifiable in the original data set

- Fit maximum likelihood models in supplemental
- Use MLE from external data as priors in main analysis
 - ▶ Point estimates as prior means
 - Variance-covariance matrices as prior variances on parameter vectors
- ▶ Other data integration possibilities exist, but this one:
 - Sidesteps data privacy concerns that hinder data sharing
 - Keeps interpretability of confounder distribution

Unmeasured confounding in mediation: code

https://github.com/lcomm/stancon2018/mediation_unmeasured_mc.stan

Likelihood in model block becomes a mixture:

```
// likelihood
for (n in 1:N) {
    // contribution if U = 0
    ll_0 = ...;

    // contribution if U = 1
    ll_1 = ...;

    // contribution is summation over U possibilities
    target += log_sum_exp(ll_0, ll_1);
}
```

Unmeasured confounding in mediation: code

Informative priors (based on R model fits) are passed in as data

```
model {
    ...
    // informative priors
    alpha ~ multi_normal(alpha_m, alpha_vcv);
    beta ~ multi_normal(beta_m, beta_vcv);
    gamma ~ multi_normal(gamma_m, gamma_vcv);
    ...
}
```

Unmeasured confounding in mediation: code

Recreating the data-generating sequence $\mathbf{Z} \to U \to A \to M \to Y$

```
for (n in 1:N) {
 // sample U
 U[n] = bernoulli logit rng(pU1[n]);
  // sample M_a where a = 0
 M_a0[n] = bernoulli_logit_rng(X[n] * betaZ + U[n] * betaU);
  // sample Y (a=0, M=M 0) and Y (a=1, M=M 0)
  Y_aOMaO[n] = bernoulli_logit_rng(X[n] * alphaZ + M_aO[n] * alphaM +
                                   U[n] * alphaU);
 Y_a1Ma0[n] = bernoulli_logit_rng(X[n] * alphaZ + M_a0[n] * alphaM +
                                   alphaA + U[n] * alphaU);
```

Summary

- Bayesian causal inference with the parametric g-formula is a powerful tool
- The generated quantities block allows us to sample potential outcomes for new observations based on model for data
- Prior information is a nice way to integrate data sources and perform informed sensitivity analyses

Acknowledgments

- Collaborators Brent Coull and Linda Valeri
- ▶ NIH grants T32ES007142 and T32CA009337
- StanCon reviewers for helpful comments

References

Imbens, G.W., and D.B. Rubin. 2015. *Causal Inference in Statistics, Social, and Biomedical Sciences*. Causal Inference for Statistics, Social, and Biomedical Sciences: An Introduction. Cambridge University Press.

Keil, Alexander P, Eric J Daza, Stephanie M Engel, Jessie P Buckley, and Jessie K Edwards. 2015. "A Bayesian Approach to the G-Formula." *Statistical Methods in Medical Research*. SAGE Publications Sage UK: London, England.

VanderWeele, T. 2015. Explanation in Causal Inference: Methods for Mediation and Interaction. Oxford University Press. https://books.google.com/books?id=K6cgBgAAQBAJ.