

Quantitative Research Methods IV - 17.806

Recitation, Week 6.

Topic: Causal Machine Learning I.

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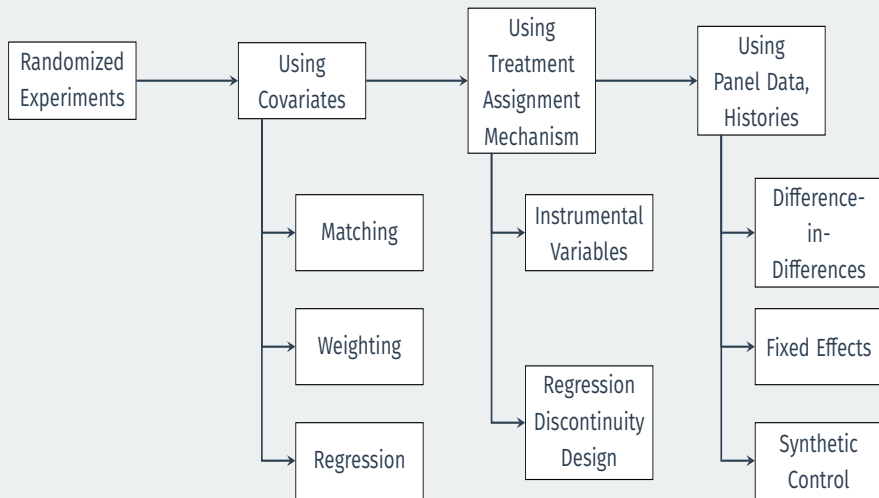
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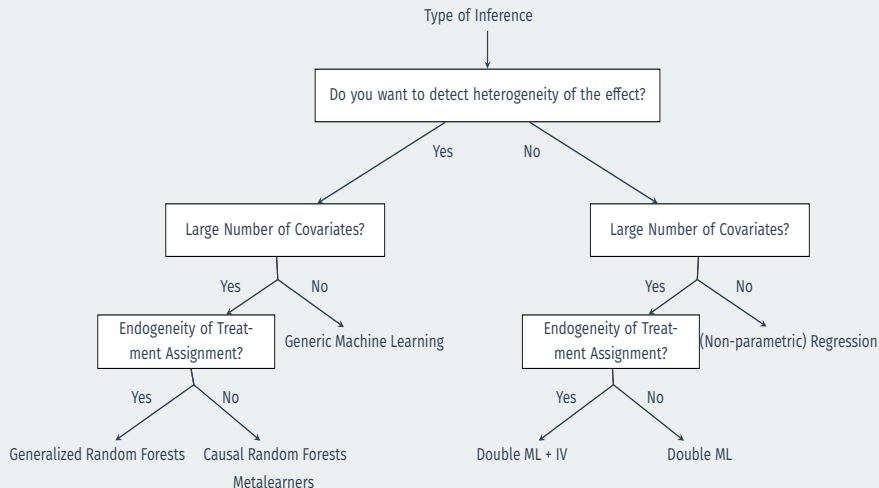
1. Theoretical Roadmap
2. Causal Inference Review
3. High Dimensionality of X

1/ Theoretical Roadmap

Identification Strategies Quant II



Causal Machine Learning



What Type of Problems Can Machine Learning Solve?

- Machine Learning techniques cannot solve causal identification problems.
 - How much can we learn about parameters from infinite amount of data? (Manski, 2007).
- The predictive power of ML tools can indeed solve some inferential issues.
 - : How much can we learn about parameters from infinite amount of data? (Manski, 2007).
 - However, these techniques create potential new problems, which must be taken into consideration (efficiency, bias, etc.).

What kind of problems will we try to solve?

1. High Dimensionality of \mathbf{X} :

- I have a large number of covariates ($p \gg n$). How can I use them to justify my identification strategy (Selection on Observables)?

2. Heterogeneous Treatment Effects:

- The typical Quantity of Interest is the Conditional Average Treatment Effect. But what if I want a different QoI? (Fundamental Problem of Causal Inference).
- A typical strategy is to use a linear interactive model. But these models impose strong assumptions (see Hainmueller, Mummolo, and Xu, 2019).
- The best practice is to pre-register my study. But usually, we don't. So how can we protect against the problem of multiple tests?

2/ Causal Inference Review

Design Trumps Analysis

- Ignorability \leadsto Ideal setup (e.g, experiment)

$$D_i \perp \{Y_i^0, Y_i^1\}$$

- At least we want conditional ignorability

$$D_i \perp \{Y_i^0, Y_i^1\} \mid X$$

- Additional Assumption: Common Support

$$0 < P(D_i = 1 | X_i = x) < 1 \forall x \in \mathcal{X}$$

Design Trumps Analysis

- **Regression:** Two extra assumptions:
 - Constant Treatment Effect ($\tau = Y_i^1 - Y_i^0$ for all i).
 - Linearity ($Y_{di} = \beta_0 + d\beta_1 + \gamma^T \mathbf{X} + \epsilon_i$).
- OLS approach: modeling $E(Y|X)$ correctly.
- **Matching:** nonparametric method of adjustment for treatment assignment patterns.
- Propensity score approach: modeling $E(T|X)$ correctly.
- We'll need to specify at least one of two models correctly:

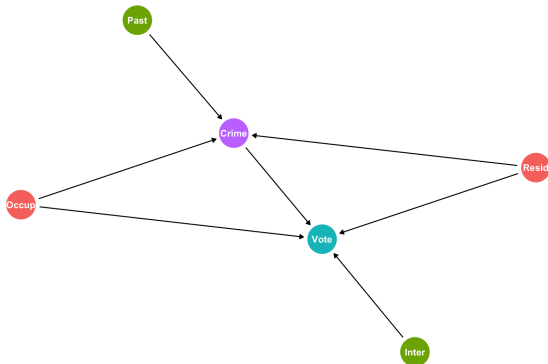
Outcome model: $E(Y|X) = f(X)$

Treatment assignment mechanism: $E(T|X) = g(X)$

Design Trumps Analysis

- DAG Perspective – Can Block Either Backdoor path.

Figure 1: Confounding Paths in DAG



Typology Confounder Other Outcome Treatment

Regression Estimation

- Bias and Variance Tradeoff.
- The analyst has to correctly specify the model fairly precisely.
- Including irrelevant variables is ok, but only if there aren't too many.
 \leadsto too many variables lead to less precise estimate (high variance).

3/ High Dimensionality of X

High Dimensionality of X

- Definition: $p \gg n$.
- Parametric Asymptotics: p is fixed as $n \rightarrow \infty$. Nonparametric regression $p \rightarrow \infty$ but at a much slower rate than n .
- Typical Regression Setting: if $p > n$, then $\widehat{\beta}_{OLS}$ is not uniquely defined. For $p < n$ but *large*, $\widehat{\beta}_{OLS}$ can be unstable and have high variance.
- ML based approach can:
 - deal with arbitrary interactions or flexible specification.
 - regularize irrelevant terms.
- **Sparsity**: only a subset of the elements of β are nonzero.
- **Approximate Sparsity**: generalization of Sparsity.
 - Recasts the High-Dimensional problem in a variable selection framework.

High Dimensionality of X

- Algorithms
 1. **Post-LASSO:** Choose correct variables for outcome model (naive-Lasso).
 2. **Double Selection:** Choose correct variables for treatment and outcome model.
 3. **Double/Debiased ML:** Choose correct variables for treatment and outcome model and allow for flexible functional form.
- Model Selection and Estimation cannot be achieved optimally at the same time.
 - Chances of mistakes in selection step = Contamination of estimation+inference step. Regularization Bias

Post Lasso (Naïve LASSO)

- One (naive) approach is to focus on just the outcome model.
- Instead of specifying a small set of covariates that almost all matter, analyst specifies a large number of covariates that mostly do not.
- Use a Lasso model to choose the ones that are significant (non-zero covariates).
- Coverage probability of standard confidence intervals can be far from the nominal level (downward bias). Affected by (and increasing in) the correlation between D and X Omitted-Variable Bias (Zero if $\beta = 0$ or $\rho = 0$).

Post Lasso (Naïve LASSO)

R Code

```
#Load package
library(glmnet)

# CV is not how chernozhukov et al choose

# Run the Outcome model
lasso <- cv.glmnet(x = X, y = y)

# Choose which variables to keep
keep <- as.matrix(coef(lasso, s = "lambda.min")[-1]) != 0

# Run OLS
lm(y ~ T + X[, keep])
```

Double Selection

- Concern with post Lasso: it might miss weak predictors of the outcome that are strong predictors of the treatment.
- This is particularly a concern if the outcome model is non-sparse or if covariates are highly correlated.
- Want to have the covariates and functional form suitable for outcome and treatment models.
- Solution is to select covariates that predict both the treatment and the outcome \leadsto Double Selection.
- You can put many covariates as you want as well as their interactions.
- Under approximate sparsity, asymptotic normality
- **Post-Regularization LASSO** (Partialling Out LASSO): Gains in efficiency. Uses only the relevant components of X to separately demean Y and D , leading to a greater parsimony,

Double Selection

R Code

```
# CV is not how chernozhukov et al choose
# the penalty term. decide outcome model
outcome_model <- cv.glmnet(x = X, y = y)

# Choose covariates whose coefficients are not zero
keep_outcome_model <- as.matrix(coef(outcome_model, s = "lambda.min")[-1]) != 0

# Decide treatment model
treat_model <- cv.glmnet(x = X, y = T, family = "binomial")

# Choose covariates whose coefficients are not zero
keep_treat_model <- as.matrix(coef(treat_model, s = "lambda.min")[-1]) != 0

# Run regression on chosen variables
lm(y ~ T + X[, keep_outcome_model|keep_treat_model])

### Alternative Code
library(hdm)

#### Implement Double Selection with LASSO
dsl <- rlassoEffect(x = X, d = T, y = Y, method = "double selection", post = TRUE)
summary(dsl)
```

Double ML

- In principle, double selection can be used to protect us from many forms of model misspecification.
- For example, a high order polynomial can fit most response functions very flexibly.
- However, no guarantees that this function is sparse or efficiently estimated.
- Double ML – tries to overcome this by using flexible ML methods to model the covariates.
- Suppose true model is:

$$Y = \tau T + g(X) + \epsilon$$

$$T = m(X) + \eta$$

Double ML

- If we knew $m(\cdot)$ and $g(\cdot)$, recovering τ would be trivial.
 \leadsto [FWL Theorem] Just regress $u = Y - g(X)$ on $e = T - m(X)$.
- Immunization/Orthogonalization Procedure.
- **Intuition:** remove a part of T and Y that can be explained by X (i.e., partialing out, obtain residual), and then run a regression of them.
- Instead, we will use machine learning to flexibly model \hat{g} and \hat{f} .
- The problem with this is overfitting – that we'll capture noise or the effect of the treatment in our estimates.
- The solution is **cross fitting** – fit $m(X)$ and $g(X)$ within one part of the sample and estimate the residuals on the other.
- Sample Splitting reduces the dependency between the estimation stages and can improve performance.

Double ML Implementation

R Code

```
# also check slide 11
# for each fold k,
#get_resids <- function(X,y,treat, fold, folds) {
  d <- data.frame(y = y[fold != folds], X = X[fold != folds,])
  outcome_model <- ranger(y ~ ., data = d)
  d <- data.frame(treat = treat[fold != folds], X = X[fold != folds,])
  treat_model <- ranger(treat ~ ., data = d)
  V_hat <- treat[fold == folds] - predict(treat_model, newx = X[fold == folds,])
  W_hat <- y[fold == folds] - predict(outcome_model, newx=X[fold == folds,])
  mod <- lm(W_hat~V_hat)
  tau <- coef(mod)[2]
  epsilon <- resid(mod)
  return(list(tau = tau, epsilon = epsilon, v_hat = V_hat))
}
# naive approach to conduct k-fold cross validation
folds <- sample(1:k, nrow(X), replace = TRUE)
Vsqr <- 0 VTimesEpsilon <- 0 tau <- rep(NA, k) for(i in 1:k) {
  results <- get_resids(X, y, treat = treat, fold = i, folds = folds)
  tau[i] <- results$tau
  Vsqr <- Vsqr + sum(results$v_hat^2)
  VTimesEpsilon <- VTimesEpsilon + t(results$v_hat^2) %*% results$epsilon^2
}
tau <- mean(tau)
sesqr <- (Vsqr/nrow(X))^(2)*(VTimesEpsilon/nrow(X))
se <- sqrt(sesqr/nrow(X))
```

Double ML Implementation

R Code

```
### Alternative Code
library(DoubleML)
library(mlr3)
library(mlr3learners)

#### Define data for DDML
dml_data_sim <- double_ml_data_from_matrix(X = X, y= Y, d = T)

#### Select LASSO learner
learner <- lrn("regr.cv_glmnet", s="lambda.min")
ml_l_sim <- learner$clone()
ml_m_sim <- learner$clone()

#### Execute DDML
obj_dml_plr_sim <- DoubleMLPLR$new(dml_data_sim, ml_l=ml_l_sim, ml_m=ml_m_sim)
obj_dml_plr_sim$fit()
print(obj_dml_plr_sim)
```