Causal Inference (6.S059/15.C08/17.C08)

Recitation, Week 9.

Topic: Causal Machine Learning

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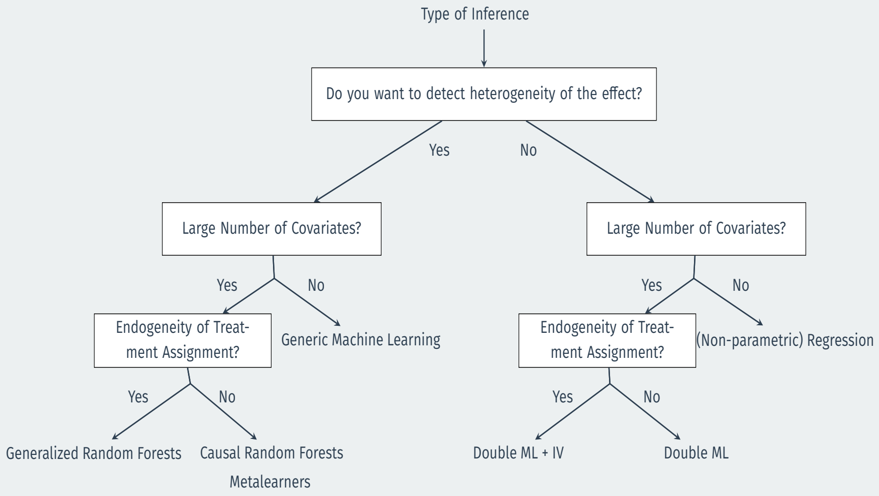
1/ Theoretical Roadmap

Causal Machine Learning



Type of Inference
Do you want to detect heterogeneity of the effect?
Yes
No
Large Number of Covariates?
Yes
No
Endogeneity of Treat-ment Assignment?
Generic Machine Learning
Yes
No
Generalized Random Forests
Causal Random Forests
Metalearners
Large Number of Covariates?
Yes
No
Endogeneity of Treat-ment Assignment?
(Non-parametric) Regression
Yes
No
Double ML + IV
Double ML

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 ($p >> n$). 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).

2/ High Dimensionality of X

High Dimensionality of X

- Definition: $p >> n$.
- 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 funcional 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 $\rightsquigarrow$ 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

```r
# 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:

$$
\begin{aligned}
Y &= \tau T + g(X) + \epsilon \\
T &= m(X) + \eta
\end{aligned}
$$

Double ML

- If we knew $m(\cdot)$ and $g(\cdot)$, recovering τ would be trivial.

  $\rightsquigarrow$ [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)
        Vsqrd <- 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$tau
                Vsqrd <-  Vsqrd + sum(results$v_hatˆ2)
                VTimesEpsilon <- VTimesEpsilon + t(results$v_hatˆ2) %*% results$epsilonˆ2
        }
        tau <- mean(tau)
        sesqrd <- (Vsqrd/nrow(X))ˆ(-2)*(VTimesEpsilon/nrow(X))
        se <- sqrt(sesqrd/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)
```

3/ Heterogeneous Treatment Effects

Conditional Average Treatment Effects

- CATE: $\tau(D; X) = \mathbb{E}(Y_i^1 - Y_i^0 | X_i = x)$

1. Linear Interactive Model

$$Y = \beta_0 + \beta_1 D + \beta_2 M + \beta_3 D \times M + \gamma X + \epsilon$$

   - **Extra Assumptions:** the treatment effect varies linearly with M, and for each value of M, the treatment and control groups should have a sufficient number of overlapping cases (see **Hainmueller, Mummolo, and Xu, 2019**).

2. Machine learning tools to estimate the heterogeneous treatment effects:
   - Loss function approach: Squared Loss SVM with separate LASSO constraints (**Imai and Ratkovic, 2013**), R-learner (**Nie and Wager, 2021**).
   - Construct potential outcomes: X-learner (**Künzel et al., 2019**), Causal Forests (**Wager and Athey, 2018**).

Causal Forests

- **Tree:** method that recursively partitions the high-dimensional covariate space into smaller units.
- Prediction $\neq$ Detection of Heterogeneity.
    - Minimization of within-leaf variance of Y (all the cases belonging to the same leaf should be homogeneous in terms of the outcome) $\rightsquigarrow$ Minimization of the within-leaf variance of the estimated treatment effects (inter-leaf variation should be large).
    - New Splitting Rule:

$$-\widehat{\mathrm{EMSE}}_{\tau}(\mathrm{S}^{\mathrm{Tr}}, \mathrm{N}^{\mathrm{est}}, \sqcap) = \underbrace{\frac{1}{N^{Tr}} \sum_{i \in S^{Tr}} \hat{\tau}^2(X_i | S^{Tr}, \sqcap)}_{\substack{\text{Variance of Treatment Effects} \\ \text{across Leaves} \\ \text{Prefer leaves with} \\ \text{Heterogeneous Effects}}} \underbrace{- \left(\frac{1}{N^{Tr}} + \frac{1}{N^{Est}}\right) \sum_{l \in \sqcap} \left(\frac{S^2_{S^{Tr}_{Treat}}(l)}{p} + \frac{S^2_{S^{Tr}_{Control}}(l)}{1-p}\right)}_{\substack{\text{Uncertainty about Leaf} \\ \text{Treatment Effects} \\ \text{Prefer leaves with Good Fit} \\ \text{(Leaf-Specific Effects estimated} \\ \text{Precisely)}}}$$

Causal Forests

- **Honest Procedure:** not use the same information for selecting the model structure as for estimation given a model structure.
    - One (independent) split of the data is used to learn the tree structure/-partition, and the second split of the data is used to conduct inference (estimation of treatment effects).

R Code

```r
# Run Causal Forests (Basic Algorithm)
library(grf)

# Estimate Causal Forest
cf <- causal_forest(X = X, Y = Y, W = W, num.trees = 10000,
                    honesty = TRUE, honesty.fraction = 0.5,
                    tune.parameters = "all", seed = 17806)

# Estimate Predicted Values (CATEs)
pred <- predict(object = cf, newdata = newX,
                estimate.variance = TRUE)$predictions

# Use expanded algorithm for Problem 3.
```

Metalearners

- Meta-algorithms decompose estimating the CATE into several subregression problems that can be solved with any supervised ML method.
- Combination of **base learners** in a specific manner while allowing the base learners to take any form.

1. **S-Learner** (Single) $\rightsquigarrow$ using all of the features and the treatment indicator (without giving to D a special role).

$$\mu(x) = \mathbb{E}[Y|X = x, D = d]$$
$$\hat{\tau}(x) = \hat{\mu}(x, D = 1) - \hat{\mu}(x, D = 0)$$

   - Risk of dropping the treatment.
   - Low statistical efficiency.

Metalearners

2. **T-Learner** (Two) $\rightsquigarrow$ use base learners to estimate the conditional expectations of the outcomes separately for control and treatment groups.

$$\mu_0(x) = \mathbb{E}[Y|D = 0, X = x]$$
$$\mu_1(x) = \mathbb{E}[Y|D = 1, X = x]$$
$$\hat{\tau}(x) = \hat{\mu}_1(x) - \hat{\mu}_0(x)$$

- Ignore group size.
- Prediction $\neq$ Heterogeneity.

Metalearners

3. **X-Learner** $\rightsquigarrow$ uses each observation in the training set in an X-like shape (Sample Splitting for Fundamental Problem of Causal Inference).

   3.1 Estimate the response functions:

$$\mu_0(x) = \mathbb{E}[Y|D = 0, X = x]$$
$$\mu_1(x) = \mathbb{E}[Y|D = 1, X = x]$$

   3.2 Impute the individual treatment effects (for the Treated group with the control-outcome estimator and for the Control group with the treatment-outcome estimator):

$$\tilde{D}_i^1 = Y_i^1 - \hat{\mu}_0(X_i^1)$$
$$\tilde{D}_i^0 = \hat{\mu}_1(X_i^0) - Y_i^0$$

Metalearners

3.3 Use any learner to estimate/predict the imputed treatment effects for each group:

$$\hat{\tau}_1(x) = \mathbb{E}[\tilde{D}_i^1 | D = 1, X = x]$$
$$\hat{\tau}_0(x) = \mathbb{E}[\tilde{D}_i^0 | D = 0, X = x]$$

3.4 Define the CATE estimate by the weighted average of the two estimates in 3.3:

$$\hat{\tau}(x) = g(x)\hat{\tau}_0(x) + (1 - g(x))\hat{\tau}_1(x)$$

- $g(x) \in [0, 1]$. Good option =Propensity Score.
- Efficient use of unbalanced design.