# Supervised Machine Learning II: Heterogeneous Treatment Effects

Paul Goldsmith-Pinkham

April 28, 2022

# Machine Learning + Causality

- Today, focusing on how to tie machine learning methods into estimation of causal effects
- Most of our ideas revolve around how to think about estimating CATEs – conditional average treatment effects
  - Why is this interesting? Why is knowing CATEs preferable to ATEs?
- Recall that with exhaustively defined CATEs, we can estimate our ATE
  - But, crucially, we could *target* appropriately
  - Well-estimated CATEs help identify better decisions based on decision rules
  - Also good for economic theory!
- But, can be hard to do in a disciplined way

# Why can ML be powerful in this space?

- A serious concern in empirical work is specification hunting – looking for significant effects in subgroups, and then telling a story about it
- One solution is pre-analysis plans – tying our hands before the fact about what we will look at
- However, sometimes we would like to let the "data speak"
  - What if we could automate the process for estimating signficant CATEs?
- Machine learning could allow us to estimate these approaches in a standardized way, while using out-of-sample testing to ensure that we are not data mining

# The literatures with Machine learning and CATEs

- Today, will talk about two papers/lits:
  - Causal Trees (From Athey and Imbens (2016)
    - More generally in the space of causal partitioning
    - Causal “Forests” by Wager and Athey (2019) as well
  - GATES and CLAN from Chernozhukov et al. (2020)
    - GATES = Sorted Group Average Treatment Effects
    - CLAN = Classification Analysis

- These approaches are similarly focusing on CATEs, but solving a crucial statistical problem in two distinct ways

# Machine learning and CATEs

- What is the statistical problem? There are two (related) issues:
  1. Inference: even if we predict or show the effect of a treatment is higher in one subgroup than another, can we say whether this is just due to random variation, or a meaningful difference?
  2. Testing causal inference out-of-sample: Evaluating how "accurate" you are requires knowing your target outcome. E.g. $Y_i - \hat{Y}_i$. But, $\tau_i = Y_i(1) - Y_i(0)$ is fundamentally unknown.

- These issues are in large part solved by additional sample splitting

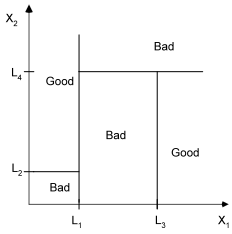
- Importantly: these approaches do *not* solve the issue of exogeneous variation
  - In most settings, this should be viewed as a setting where we have a randomly varying treatment (e.g. an RCT) and we want to study CATEs
  - However, if we have a good IV, we could study the reduced form quite sensibly!

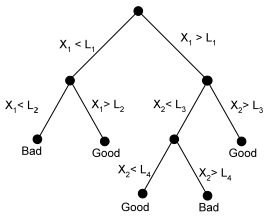
# Causal trees (Athey and Imbens (2016)

- Necessary notation: Binary treatment, $D_i$, and covariates (potentially high dimensional) $X_i$. Outcome $Y_i$.

- In our discussion, we'll assume completely random assignment of $D_i$, but it is possible to account for conditioning variables as well using a p-score method

- The key approach will be following the tree-based approach from last class, but with some essential modifications
  - Recall that trees worked by splitting up observations at a given node based on a given characteristic



# Causal trees (Athey and Imbens (2016)

- Key insight of this paper: when you choose what to split on, you are picking something that is "unusual" relative to the underlying data generating process
  - This induces bias!

- To see this, first focus on estimation of means, and consider a simple example where $X$ is a simple dummy variable. You can either split on it, or not split on it.
  - Imagine you split on it if $\bar{Y}_1 - \bar{Y}_0 > c$, some cutoff

- On average, while each one is consistent, if you split only when the difference is large, you'll be selecting on a subset that will be biased relative to the population

- Key idea: split the sample into a training and test sample
  - Use the training sample to decide on where to split
  - Use the test to calculate means and evaluate the fit

# Causal trees (Athey and Imbens (2016)

- Algorithmically, the approach trades off between the following issues:
  - Tree / Forest approaches overfit within sample
    - Shows up in depth
    - Shows up in means of splits
  - The algorithm focuses just on splitting within a leaf
    - Ignores the fact that making many splits will create a lot of overall variance (that may not be meaningful)

- Sample splitting will address these issues
  - Sample split to get consistent estimates
  - Sample split to penalize too much depth and overall variance

- Key payout: results will be pointwise consistent!
  - In Wager and Athey's Causal Forests, will also have asymptotically normal distributions as well

# Causal trees (Athey and Imbens (2016)

- How to implement? In `R`, there's a very nice package that includes the Random Forest (see Wager and Athey (2019)) approach as well: `https://grf-labs.github.io/grf/`

## The GRF Algorithm

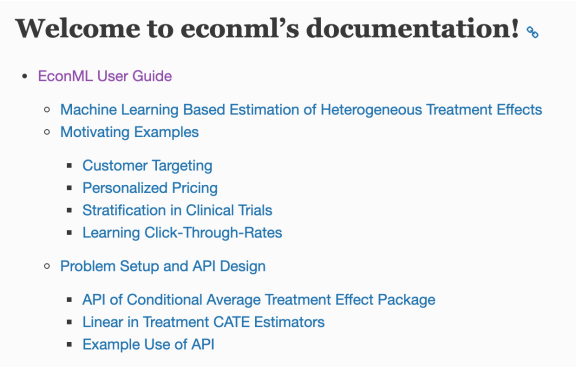
The following guide gives an introduction to the generalized random forests algorithm as implemented in the `grf` package. It aims to give a complete description of the training and prediction procedures, as well as the options available for tuning. This guide is intended as an informal and practical reference; for a theoretical treatment of GRF, please consult the 'Generalized Random Forests' paper.

GRF extends the idea of a classic random forest to allow for estimating other statistical quantities besides the expected outcome. Each forest type, for example `quantile_forest`, trains a random forest targeted at a particular problem, like quantile estimation. The most common use of GRF is in estimating treatment effects through the function `causal_forest`.

# Causal trees (Athey and Imbens (2016)

- How to implement? In `R`, there's a very nice package that includes the Random Forest (see Wager and Athey (2019)) approach as well: `https://grf-labs.github.io/grf/`

- For `Python`, the `econml` package can do this as well (as well as many other approaches): `https://econml.azurewebsites.net/spec/spec.html`



**Welcome to econml's documentation!**

- EconML User Guide
  - Machine Learning Based Estimation of Heterogeneous Treatment Effects
  - Motivating Examples
    - Customer Targeting
    - Personalized Pricing
    - Stratification in Clinical Trials
    - Learning Click-Through-Rates
  - Problem Setup and API Design
    - API of Conditional Average Treatment Effect Package
    - Linear in Treatment CATE Estimators
    - Example Use of API

# Causal trees (Athey and Imbens (2016)

- How to implement? In `R`, there's a very nice package that includes the Random Forest (see Wager and Athey (2019)) approach as well: `https://grf-labs.github.io/grf/`

- For `Python`, the `econml` package can do this as well (as well as many other approaches): `https://econml.azurewebsites.net/spec/spec.html`

- Nothing in Stata, sorry

# GATES and CLAN (Chernozhukov et al. (2020)

- The causal tree approach is a beautiful approach in solving the bias and infernece issues

- However, the general inference solution does not account for the uncertainty in the binning of the covariates
  - Recall how the method works – by using a split sample to choose the bins, the CATEs within those bins work just as well as any standard regression approach
  - But this fails to account for the fact that these bins may change in different samples
  - Consider how much your CATE changes if the cutoff point had changed slightly

- Chernozhukov et al. (2020) highlight this issue, and propose a much more general approach
  - This approach has more limitations, but at the benefit of being even more general

# GATES and CLAN (Chernozhukov et al. (2020)

- The key concept is that instead of trying to identify the CATEs directly, identify the key features of the CATEs instead
  - More precisely, identify how much heterogeneity there is in the underlying estimates
  - Then, figure out the characteristics of those groups with heterogeneous effects

- The key approach starts with the following concept:
  - Randomly split the sample into a main and auxiliary sample
  - In the auxiliary sample, estimate the control mean, $B(X)$, and the treatment effect $S(X)$ (note that $S(X)$ will just be the treatment mean minus the control mean)

- This really just entails prediction of the control and treatment means for each group using an ML method

- Hence, we estimate $\hat{B}(X)$ and $\hat{S}(X)$ using a training sample, and then use the test sample to predict the actual values

# BLP (Chernozhukov et al. (2020)

- Crucially, the punchline is that $\hat{B}(X)$ and $\hat{S}(X)$ will be biased, the inputs from the training sample are uncorrelated with the estimation error
- This implies that for a given observation in the training sample, $\hat{B}(X_i)$ and $\hat{S}(X_i)$ are useful summary statistics (projections) for that observation.
- What the paper shows is that if you take these measures and run the following regression, you can identify whether there is meaningful heterogeneity

A consequence is our first main identification result, namely that

$$\beta_1 + \beta_2(S(Z) - \mathrm{E}S) = \mathrm{BLP}[s_0(Z) \mid S(Z)],$$

in particular $\beta_1 = \mathrm{E}s_0(Z)$ and $\beta_2 = \mathrm{Cov}(s_0(Z), S(Z))/\mathrm{Var}(S(Z))$.

**Theorem 3.1** (BLP 1). *Consider $z \mapsto S(z)$ and $z \mapsto B(z)$ as fixed maps. Assume that $Y$ and $X$ have finite second moments, $\mathrm{E}XX'$ is full rank, and $\mathrm{Var}(S(Z)) > 0$. Then, $(\beta_1, \beta_2)$ defined in (3.1) also solves the best linear predictor/approximation problem for the target $s_0(Z)$:*

$$(\beta_1, \beta_2)' = \arg\min_{b_1, b_2} \mathrm{E}[s_0(Z) - b_1 - b_2(S(Z) - \mathrm{E}S(Z))]^2,$$

*in particular $\beta_1 = \mathrm{E}s_0(Z)$ and $\beta_2 = \mathrm{Cov}(s_0(Z), S(Z))/\mathrm{Var}(S(Z))$.*

The identification result is constructive. We can base the corresponding estimation strategy on the empirical analog:

$$Y_i = \widehat{\alpha}' X_{1i} + \widehat{\beta}_1(D_i - p(Z_i)) + \widehat{\beta}_2(D_i - p(Z_i))(S_i - \mathbb{E}_{N,M} S_i) + \widehat{\epsilon}_i, \quad i \in M,$$

$$\mathbb{E}_{N,M}[w(Z_i)\widehat{\epsilon}_i X_i] = 0,$$

# BLP (Chernozhukov et al. (2020)

- Crucially, the punchline is that $\hat{B}(X)$ and $\hat{S}(X)$ will be biased, the inputs from the training sample are uncorrelated with the estimation error

- This implies that for a given observation in the training sample, $\hat{B}(X_i)$ and $\hat{S}(X_i)$ are useful summary statistics (projections) for that observation.

- What the paper shows is that if you take these measures and run the following regression, you can identify whether there is meaningful heterogeneity

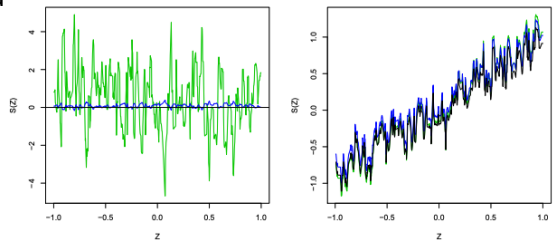
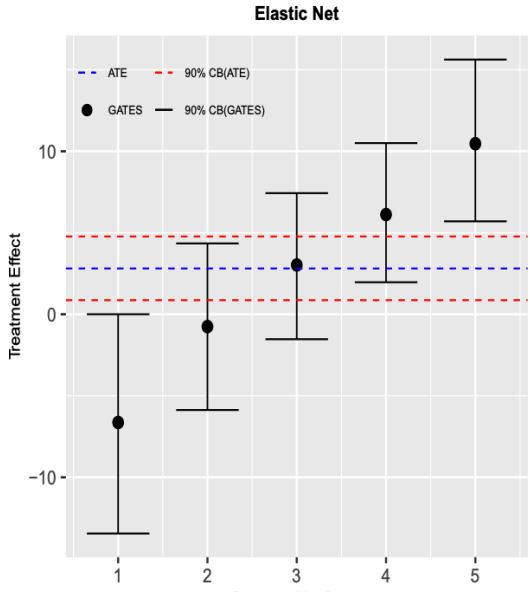



FIGURE 1. Example. In the left panel we have a homogeneous CATE $s_0(Z) = 0$; in the right panel we have heterogeneous CATE $s_0(Z) = Z$. The proxy predictor $S(Z)$ is produced by the Random Forest, shown by green line, the true BLP of CATE is shown by black line, and the estimated BLP of CATE is shown by blue line. The true and estimated BLP of CATE are more attenuated towards zero than the proxy predictor.

# GATES and CLAN

- If we identify heterogeneity, we'd like to know which $X$ drive it. The problem is that $\tau(X)$ is very high-dimensional
- The GATES approach says – what if we grouped the effects into bins $G$, increasing in effect size.
  - We can talk about the property of these GROUPED average treamtent effects, which average of the high dimensional properties
  - In turns out we can say a lot about that, statistically
- Moreover, we can test for whether these are all the same
  - Harkens back to binscatter and testing for monotonicity!



# GATES and CLAN

- The issue is that we still haven't solved for what these groups are
  - Knowledge of heterogeneity doesn't get us very far
- The CLAN approach asks how important characteristics vary by these binned groups
- We can use this to identify bins worth targetting

TABLE 5. CLAN of Immunization Incentives

| | Elastic Net | | |
|---|---|---|---|
| | 20% Most ($\delta_5$) | 20% Least ($\delta_1$) | Difference ($\delta_5 - \delta_1$) |
| Number of vaccines to pregnant mother | 2.161 (2.110,2.212) - | 2.288 (2.237,2.337) - | -0.128 (-0.200,-0.055) [0.001] |
| Number of vaccines to child since birth | 4.230 (4.100,4.369) - | 4.714 (4.573,4.860) - | -0.513 (-0.710,-0.311) [0.000] |
| Fraction of children received polio drops | 1.000 (1.000,1.000) - | 1.000 (1.000,1.000) - | 0.000 (0.000,0.000) [0.000] |
| Number of polio drops to child | 2.964 (2.954,2.975) - | 2.998 (2.987,3.007) - | -0.033 (-0.047,-0.019) [0.000] |
| Fraction of children received immunization card | 0.899 (0.878,0.922) - | 0.932 (0.908,0.956) - | -0.036 (-0.065,-0.004) [0.000] |
| Fraction of children received Measles vaccine by 15 months of age | 0.127 (0.100,0.155) - | 0.255 (0.230,0.282) - | -0.131 (-0.167,-0.094) [0.052] |
| Fraction of children received Measles at credible locations | 0.290 (0.252,0.327) - | 0.435 (0.400,0.470) - | -0.152 (-0.198,-0.097) [0.000] |

Notes: Medians over 100 splits. 90% confidence interval in parenthesis.
Notes: P-values for the hypothesis that the parameter is equal to zero in brackets.

# Implementation in practice

- Chernozhukov et al. (2020) outline the algorithm in detail in the paper
- Code is available here from Mert Demirer (`https://github.com/demirermert/MLInference/blob/master/Heterogeneity/EL1.R`)
- We will be implementing this for the homework
- Important note – still need conditional exogeneity / strict ignorability!