

Coots/Deschler Initial Analysis

Initial results table:

	No text	Planmaking	Consequences	Combination	Overall
Appeared	181861	3459	3667	1854	190841
Failed to Appear	129249	1616	1497	719	133081
Appearance rate	0.585	0.682	0.71	0.721	0.589

Treating each treatment independently but with the same large control group, let π_{jk} be the proportion of individuals in the principal stratum where $(Y_i(0), Y_i(1)) = (j, k)$. Then, for any set of constraints on the strata, we know that the possible range of the graduation rate, G is $[\min(\pi_{11}), \max(1 - \pi_{00})]$. Additionally, we can write the possible range if we make the monotonicity assumption. Using the repro, we can then write the range of possible appearance rates under each treatment type. Additionally, we can write the possible range if we make the monotonicity assumption $Y_i(1) \geq Y_i(0)$. For various reasons with this data, we believe the monotonicity assumption is not a good one to make. There are a multitude of theoretical mechanisms by which a text message could cause individuals to *not* appear in court, thus resulting in $Y_i(0) > Y_i(1)$. These could include, but are not limited to, messages scaring individuals due to the consequential nature, TODO.

Treatment	No assumption	Monotonicity assumption
Planmaking	[.266, 1]	[.584, .682]
Consequences	[.294, 1]	[.584, .710]
Combination	[.305, 1]	[.584, .721]

Individualized Treatment Rules

The main focus of our analysis is to identify various individualized treatment rules (“ITRs”), and compare them to the experimental results using techniques from Imai and Li (2021).

- Simple ITR - by borough (what is the best we can do?)
- Simple ITR - by racial composition (what is the best we can do?)
- ITR from Imai and Strauss (2011)?
- ML ITR

Exploratory stuff

Subgroup analysis

The original dataset did not contain a variable for the race of an individual, but did contain the percentage of the population in each individual’s ZIP code that was either black or Hispanic. We can construct a approximation of an individual’s race by coding someone as, for example, black if more than 50% of the population in that ZIP code was black. We can do the same based on the percentage below the poverty line column. One could argue that we should actually be using a lower threshold than 50% given that communities of color and poor communities tend to be overpoliced, but without further data, we stick to the 50% threshold. The table below summarizes the appearance rates for various demographics in the data, using the heuristic just described.

Demo.	Group	Overall	Planmaking	Consequences	Combination
Gender	Male	0.585	0.682	0.709	0.712
	Female	0.628	0.675	0.728	0.778
Race	Black	0.556	0.621	0.663	0.675
	Hispanic	0.551	0.633	0.68	0.696
	Black or Hispanic	0.565	0.651	0.68	0.702
Poverty	Below Poverty Line	0.59	0.683	0.712	0.702

We can likewise break down the appearance rate by NYC borough:

Borough	Overall	Any Treatment	Planmaking	Consequences	Combination
The Bronx	0.568	0.666	0.647	0.673	0.689
Brooklyn	0.566	0.673	0.654	0.679	0.701
Manhattan	0.578	0.696	0.663	0.717	0.721
Queens	0.604	0.747	0.742	0.748	0.754
Staten Island	0.808	0.912	0.913	0.916	0.897

TODO interpret

For First Write-up

First Causal Forest Attempt - Binary

```
library(grf)
# covariate set, leave one borough out
# offense-based covariates
X_offense <- c("StatenIsland", "Bronx", "Brooklyn", "Queens", "Park", "Alcohol", "Marijuana",
               "DisorderlyAcvtive", "DisorderlyPassive", "Disorderly", "Bike", "Noise",
               "MotorVehicle", "Urination")
# individual-based covariates
X_perp <- c("Female", "Age", "PastFTA", "NbPastFTA", "NbSummons", "PastSummons",
            "MedianIncZip", "PctBlackZip", "PctHispZip", "PctBelowPovZip", "DOW")
# all covariates
X_full <- c(X_offense, X_other)

# fit forests
forest_bin_full<- causal_forest(df[X_full], as.vector(df$success), as.vector(df$Treatment))
forest_bin_offense<- causal_forest(df[X_offense], as.vector(df$success), as.vector(df$Treatment))
forest_bin_perp<- causal_forest(df[X_perp], as.vector(df$success), as.vector(df$Treatment))

tau_hat <- predict(forest)$predictions
pred <- predict(forest, estimate.variance = TRUE)
```

Multi-arm Causal Forest Attempt

```
# create single treatment array, 1 is planmaking, 2 is consequences, 3 is combo
treat_type <- df$planmaking + 2*df$consequences + 3*df$combination
multi_arm <- multi_arm_causal_forest(df[X_full], as.vector(df$success), factor(treat_type))
tau_hat_multi <- predict(multi_arm)$predictions
```