# Causal Interaction Trees: Finding Subgroups with Heterogeneous Treatment Effects in Observational Data 

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CFAR Symposium on Statistics and Data Science

## Collaborators

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- Joseph W. Hogan
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- Rami Kantor
- Issa J. Dahabreh
- Allison Delong
- Monicah Nyambura


## Introduction

- Concept of heterogeneous treatment effects is at the centre of comparative effectiveness research and precision medicine
* Treatment effects vary across patients
* Aim to determine which treatment works best, for whom and under what circumstances


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* People belong to multiple subgroups.
* Type I and type II errors.


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- Heterogeneous treatment effect estimation usually done using pre-specified subgroup estimation:
* People belong to multiple subgroups.
* Type I and type II errors.
- Develop Data-driven tree-based algorithms for identification of subgroups with differential treatment effects.


## Motivating problem

Identify HIV patients that are more or less likely to gain weight while on dolutegravir based ARTs using data from electronic health records on HIV patients in Western Kenya.

- Some statistical challanges:
* repeated measures over time, not temporally aligned, number and timing of the measurements often being informative about outcomes
$\star$ time-varying confounding
* potentially informative dropout


## Subset of related work

- Tree-based algorithms for subgroup identification in observational data include:
* Su et al. (2012) and Kang et al. (2014) proposed likelihood-based splitting statistic and AIC type pruning criteria in tree-based algorithms


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- Tree-based algorithms for subgroup identification in observational data include:
* Su et al. (2012) and Kang et al. (2014) proposed likelihood-based splitting statistic and AIC type pruning criteria in tree-based algorithms
* Causal Tree algorithm of Athey and Imbens (2016) minimizes an estimator of the mean squared error of subgroup-specific treatment effect in splitting statistic


## CART Algorithm for Outcome Prediction

1. Grow a maximum sized tree until pre-determined stopping criterion is met


## CART Algorithm for Outcome Prediction

2. Prune to create a set of candidate trees for final prediction


## CART Algorithm for Outcome Prediction

3. Cross-validate to select final tree from candidate trees generated in pruning step


## Generalized Interaction Trees (GIT): Splitting

## CART: 1) Grow a maximum sized tree until pre-determined stopping criterion is met

- Grow a maximum sized tree using splitting statistic that maximizes standardized treatment effect differences between child nodes

$$
\left(\frac{\left(\hat{\mu}_{1}(I)-\hat{\mu}_{0}(I)\right)-\left(\hat{\mu}_{1}(r)-\hat{\mu}_{0}(r)\right)}{\sqrt{\widehat{\operatorname{Var}}\left[\left(\hat{\mu}_{1}(I)-\hat{\mu}_{0}(I)\right)-\left(\hat{\mu}_{1}(r)-\hat{\mu}_{0}(r)\right)\right]}}\right)^{2}
$$

where

* $\hat{\mu}_{a}(w)$ : Subgroup-specific treatment effect estimator
* $I$, $r$ : left and right subgroups


## Generalized Interaction Trees (GIT): Pruning

CART: 2) Prune to create a set of candidate trees for final prediction

- For a penalization parameter $\lambda \in \mathbb{R}_{+}$, define the split complexity for a tree $\psi$ as

$$
G^{(\lambda)}(\psi)=\underbrace{\sum_{i \in I_{\psi}} G_{i}(\psi)}_{\text {Sum of splitting statistics }}-\underbrace{\lambda\left|I_{\psi}\right|}_{\text {Size penalty }}
$$

where
$\star I_{\psi}$ : The set of internal nodes of $\psi$

* $\left|I_{\psi}\right|$ : Number of internal nodes
* $G_{i}(\psi)$ : Splitting statistic for internal node $i$


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where

* $I_{\psi}$ : The set of internal nodes of $\psi$
* $\left|I_{\psi}\right|$ : Number of internal nodes
* $G_{i}(\psi)$ : Splitting statistic for internal node $i$
- Varying $\lambda$ creates a sequence of candidate trees that maximize the split complexity for different values of $\lambda$
* $\lambda=0$ : maximum sized tree
* $\lambda \rightarrow \infty$ : root-only tree


## Generalized Interaction Trees (GIT): Final Tree Selection

CART: 3) Select final tree from candidate trees generated in pruning step

- Complication: True treatment effects are not observed on individual participants


## Generalized Interaction Trees (GIT): Final Tree Selection

CART: 3) Select final tree from candidate trees generated in pruning step

- Complication: True treatment effects are not observed on individual participants
- Loosely speaking, select the final tree that maximizes the cross-validated split complexity for a fixed penalization parameter $\lambda$
* Select $\lambda$ at quantile of asymptotic distribution of splitting statistic


## Inference

- Likely overestimation of treatment effect differences.
- Data splitting: Fit tree on one part of data and estimate treatment effects using the other part.


## Back to EHR data: Data structure

Assume we have longitudinal data

$$
\boldsymbol{O}=\left(\boldsymbol{L}_{0}, A_{0}, C_{0}, \boldsymbol{L}_{1}, A_{1}, C_{1}, \ldots, \boldsymbol{L}_{K}, A_{K}, C_{K}, Y_{K+1}\right) .
$$

Where

- $\boldsymbol{L}_{k}$ are covariates
- $C_{k}$ censoring indicator
- $A_{k}$ treatment indicator
- $Y_{K+1}$ outcome


## Back to EHR data: Target parameter and estimator

Want to estimate a contrast between always on DTG-containing ART vs never on DTG-containing ART if censoring abolished.

$$
\delta(w)=\mathrm{E}\left[Y_{K+1}^{1, \boldsymbol{c}=\mathbf{0}} \mid \boldsymbol{L}_{0} \in w\right]-\mathrm{E}\left[Y_{K+1}^{0, c=0} \mid \boldsymbol{L}_{0} \in w\right]
$$

We propose to use longitutional TMLE to estimate $\delta(w)$

## Subgroup Discovery for Longitudtional Data Algorithm

Use longitutional TMLE in combintion with the causal interaction tree algorithm for subgroup discovery with longitudional data.

## Analysis of EHRs

Data from Academic Model Providing Access to Healthcare that focuses on prevention and treatment of HIV in western Kenya. Data split into 200 day
intervals.

- Time 0 defined as maximum time of first database entry or July 1, 2016.
- Outcome $\left(Y_{K+1}\right)$ : weight (kg).
- Treatment $\left(A_{k}\right)$ : Whether on DTG-containing ART
- Ten time-dependent covariates and five additional baseline covariates.
- Sample size 62, 073, always on DTG 424, never on DTG 30, 307.


## Estimated average weight gain



## Final tree



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## NextGen scholars: Advertisement

Scholarship that fully funds participation in the masters program at Brown University that is restricted to graduated from HBCUs.

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## Questions

Thank you!

## Subgroup Identification Using Tree-Based Algorithms

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* Data driven
* Partition data directly into identifiable subgroups


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## Identifiability of $\mu_{a}(w)$

- Consistency of potential outcomes: For binary $A$,

$$
Y=Y^{1} A+Y^{0}(1-A)
$$

- Mean exchangeability:

$$
\mathrm{E}\left[Y^{a} \mid \boldsymbol{A}=a, \boldsymbol{X}=\boldsymbol{x}\right]=\mathrm{E}\left[Y^{a} \mid \boldsymbol{X}=\boldsymbol{x}\right]
$$

for all covariate patterns $\boldsymbol{x} \in w$ that have a positive density.

- Positivity:

$$
0<\mathrm{P}(A=1 \mid X=x)<1
$$

for all covariate patterns $\boldsymbol{x} \in W$ that have a positive density.

## Inference from CIT Algorithm

- Data-splitting for consistent terminal node estimator
* First part of dataset for fitting CIT algorithm
* Second part of dataset for treatment effect estimation
- Under certain conditions, data adaptive CITs are consistent


## Simulation

- 1000 observations in training, and 1000 in test data:
* $\boldsymbol{X} 6$-dimensional multivariate normal, $\mathrm{E}\left(X^{(j)}\right)=0, \operatorname{Var}\left(X^{(j)}\right)=1$, $\operatorname{cov}\left(X^{(j)}, X^{(k)}\right)=0.3$ when $j \neq k$


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$$
e(\boldsymbol{X}, \boldsymbol{\beta})=\operatorname{expit}\left(0.6 X^{(1)}-0.6 X^{(2)}+0.6 X^{(3)}\right)
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* Outcome with heterogeneous treatment effect:

$$
Y=2+2 A+2 I\left(X^{(1)}<0\right)+e^{X^{(2)}}+3 A \cdot I\left(X^{(4)}>0\right)+\left(X^{(5)}\right)^{3}+\epsilon
$$

* Outcome with homogeneous treatment effect:

$$
Y=2+2 A+2 I\left(X^{(1)}<0\right)+e^{X^{(2)}}+3 I\left(X^{(4)}>0\right)+\left(X^{(5)}\right)^{3}+\epsilon
$$

where $\epsilon \sim N(0,1)$.

## Implementation

- Causal Interaction Trees:
* Generalized Interaction Trees implemented with IPW, g-formula, DR estimators (IPW-CIT, g-CIT, DR-CIT)
* Use rpart's ability to incorporate user written splitting functions


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* Generalized Interaction Trees implemented with IPW, g-formula, DR estimators (IPW-CIT, g-CIT, DR-CIT)
* Use rpart's ability to incorporate user written splitting functions
- Evaluated performance against Causal Trees (causalTree):
* Original CT: default splitting rule and cross-validation method
* Optimized CT: oracle version with optimal splitting rule and cross-validation method


## Implementation

- Terms in GLM for estimating nuisance parameters:

| Model | Probability of treatment | Outcome |
| :--- | :---: | :---: |
| Correct model specification | $X^{(1)}, X^{(2)}, X^{(3)}$ | $A, I\left(X^{(1)}<0\right), e^{X^{(2)}}$ |
| Functional form misspecification | $e^{X^{(1)}}, \ldots, e^{X^{(6)}}$ | $A I\left(X^{(4)}>0\right)$ or $I\left(X^{(4)}>0\right),\left(X^{(5)}\right)^{3}$ |
| Unmeasured covariate* | $X^{(1)}, X^{(3)}$ <br> $X^{(4)}, X^{(5)}, X^{(6)}$ | Main effects and all two-way interactions effects and all two-way interactions <br> between $\boldsymbol{X}$ and $A$ <br> between $\boldsymbol{X}$ and $A$ except for terms involving $X^{(2)}$ |

*: Remove $X^{(2)}$ from dataset when fitting CITs

## Simulation Result - Test Dataset MSE



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## Simulation Result

- Performance in terms of other measures also shows similar trend
* Proportion of simulations identifying correct tree structure
* Average number of noise variables
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- Performance in terms of other measures also shows similar trend
* Proportion of simulations identifying correct tree structure
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* Proportion of simulations identifying correct first split in heterogeneous setting
- CTs are sensitive to chosen splitting rule and cross-validation method
* Original CTs overfit by splitting on noise variables
* Best CTs underfit by not making any splits


## Simulation Result

- Performance in terms of other measures also shows similar trend
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| Algorithm | Model | Homogeneous Effect |  | Heterogeneous Effect |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Correct Trees | Number Noise | Correct Trees | Number Noise | Correct First Split |
| Original CT | Unmeasured Cov | 0.00 | 28.34 | 0.00 | 21.49 | 0.63 |
|  | Mis Func | 0.00 | 25.28 | 0.00 | 19.87 | 0.30 |
|  | True | 0.02 | 25.75 | 0.02 | 19.31 | 0.58 |
| Optimized CT | Unmeasured Cov | 0.99 | 0.03 | 0.52 | 0.15 | 0.87 |
|  | Mis Func | 0.99 | 0.01 | 0.27 | 0.27 | 0.47 |
|  | True | 0.99 | 0.01 | 0.59 | 0.19 | 0.84 |
| DR-CIT | Both Unmeasured Cov | 0.89 | 0.65 | 0.54 | 0.60 | 0.97 |
|  | Both Mis Func | 0.90 | 0.56 | 0.67 | 0.65 | 0.99 |
|  | True Treat Mis Func Out | 0.91 | 0.58 | 0.71 | 0.58 | 1.00 |
|  | True Out Mis Func Treat | 0.95 | 0.14 | 0.93 | 0.14 | 1.00 |
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## Analysis of SUPPORT Study - Result

- All CITs found no subgroups
* Fully grown tree by DR-CIT first splits on if estimate of 2-month survival probability at study entry is greater than or equal to 0.85 or not
* Data-splitting based treatment effect and confidence interval

| $\mathrm{P}($ Survival $) \geq 0.85$ | $\mathrm{P}($ Survival $)<0.85$ |
| :---: | :---: |
| $-0.007(-0 .-091,0.081)$ | $0.066(0.022,0.108)$ |

* Previous predetermined subgroup analysis on this covariate not significant
- CTs are sensitive to chosen splitting rule and cross-validation method
* Original CT produced a tree with 232 terminal nodes
* Optimized CT found no subgroups
* Performance consistent with simulations where Original CT build large trees and Optimized CT build small trees
- Important feature of CITs: find no subgroups when there is no signal


## Future Work - GIT Algorithm in Longitudinal Data

- Motivating dataset from AMPATH project
* Collaborative project with the goal of providing HIV care in Kenya
* Examine heterogeneous treatment effect of Dolutegravir (DTG) based therapy on weight gain and viral load response
* 88,366 participants with $1,193,340$ visits met eligibility criteria from database


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* Examine heterogeneous treatment effect of Dolutegravir (DTG) based therapy on weight gain and viral load response
* 88,366 participants with $1,193,340$ visits met eligibility criteria from database
- Estimate conditional expectation of potential outcome at end of study had participant received treatment pattern of interest and remained in study
* Treatment pattern of interest: Always or never on DTG
* Conditional on baseline covariates including demographic variables, lab measures, baseline clinic visit information


## Analysis of EHRs

## Covariates

- Time-dependent covariates: HIV viral load, systolic blood pressure, diastolic blood pressure, weight, height, whether the individual had active tuberculosis, was being treated for tuberculosis, was married or living with partner, and whether the individual was covered by the National Health Insurance Fund.
- Additional baseline covariates: Gender, age when starting ART, age at time 0 , time on ART at time 0, whether the individual was enrolled on or after July 1, 2016 and whether the individual was newly initiating ART or had been on ART 200 days before time 0

