Estimating Optimal Treatment Regimes Using Multivariate Random Forests

Boyi Guo

Department of Biostatistics

University of Alabama at Birmingham

Ruoqing Zhu

Department of Statistics

University of Illinois at Urbana-Champaign



Outline

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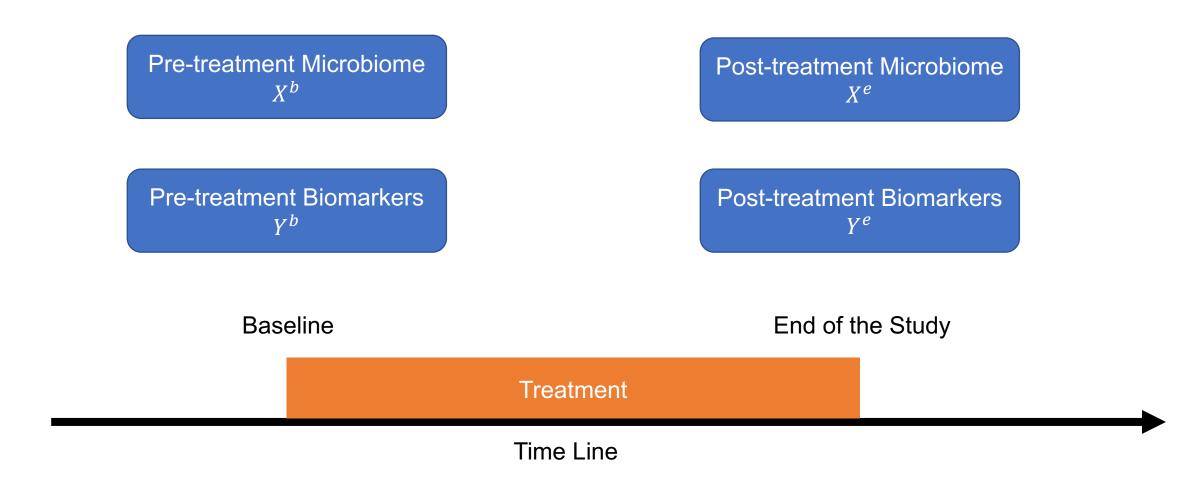
Motivation & Objectives

- A recent study (Holscher, 2018) investigated the effect of almonds on gastrointestinal microbiota and their interrelationship with human health-related biomarkers
 - Randomized controlled trial
 - Two arms of treatments
- The aim of the study is to recommend personalized almond diet, with respect to the microbiome composition, to improve the biomarkers

Challenges

- The treatment effect is not directly observable
- The microbiome and biomarkers are highly correlated
- Extra information collected in the study would not be fully utilized with any conventional models

Study Design

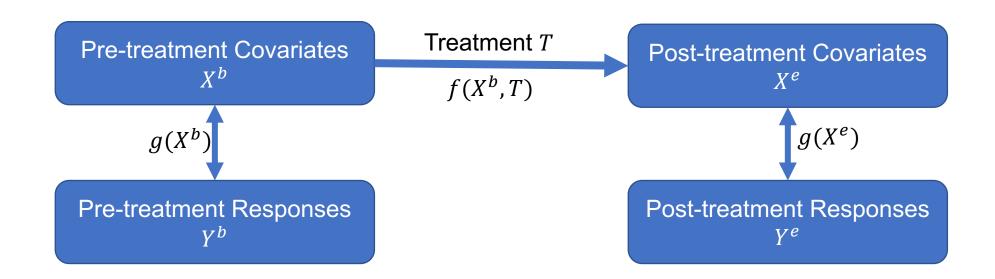


Solution

- Two-step procedure
 - Predict the post-treatment biomarkers under each arm of the treatments
 - Compare the predicted biomarkers for both treatments on a desired direction
- Predicting biomarkers conditioning on a treatment
 - A conventional solution: constructing a linear regression of the biomarkers as a function of all the interaction terms of treatment and microbiomes.
 - Multiple assumptions are not realistic: normality assumption, linear assumption, and model specification.
 - Number of variables in the model can exceed the sample size

Notation & Assumptions

- Pre- and post-treatment covariates, $X^b, X^e \in \mathbb{R}^p$
- Pre- and post-treatment responses, $Y^b, Y^e \in \mathbb{R}^q$
- Treatment, $T \in \mathcal{T} \equiv \{1, -1\}$, is independent of X^b
- Unknown treatment effect function, $f(\cdot, \cdot): \mathbb{R}^p \times \mathcal{T} \to \mathbb{R}^p$
- Unknown link function from covariates to responses, $g(\cdot)$: $\mathbb{R}^q \to \mathbb{R}^q$



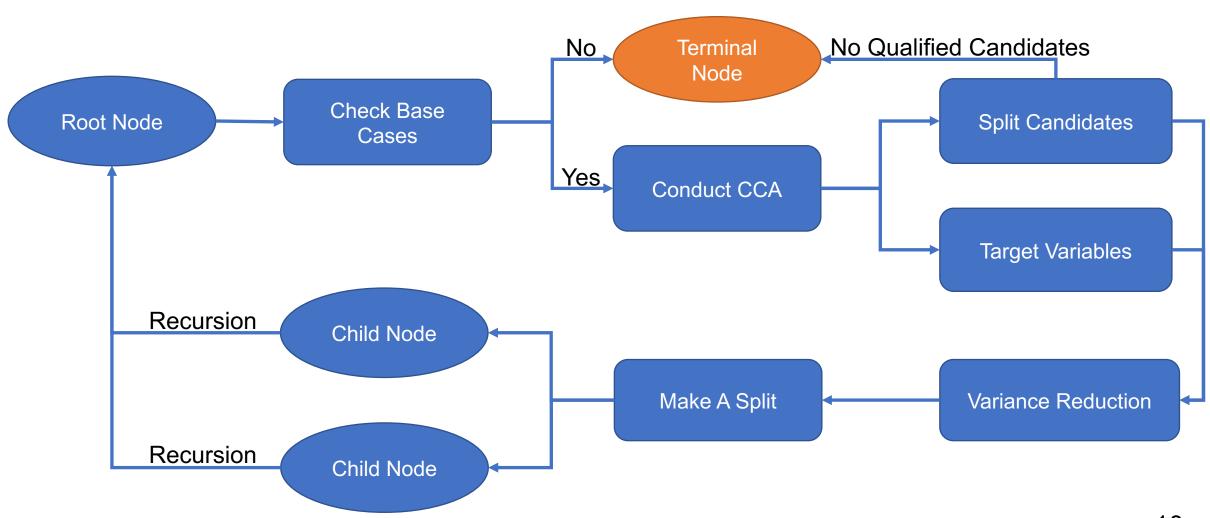
MedForests

- MedForests is an ensemble learning method that is based on random forests algorithm (Breiman, 2001)
- It consists n_{tree} distinct MedTrees, which is based on the regression tree algorithm (Breiman, 2017)
- Each MedTree recursively partitions a population, described by the pre-treatment covariates, into sub-populations where the treatment effects are similar
- When making predictions, MedForests collects the posttreatment responses that belong to the same sub-population from all MedTrees, and outputs the empirical means under each treatment arm.

Treatment Effect

- Measure of treatment effect
 - $\mathbb{E}(\Delta X|X^b,T) = \mathbb{E}(X^e X^b|X^b,T) = f'(X^b,T)$
 - $\mathbb{E}(\Delta Y|X^b,T) = \mathbb{E}(Y^e Y^b|X^b,T) \approx g(f'(X^b,T))$ under $g(\cdot)$ is linear
- Use canonical correlation analysis (CCA) to approximate $g(f'(\cdot,\cdot))$ while reducing dimensions
 - CCA (Hotelling, 1992) is a method for exploring the relationships between two multivariate sets of variables
 - $\underset{\rho,\beta_{T=1},\beta_{T=-1}}{arg\max} \left[corr(\rho X^b, \beta_{T=1} \Delta Y_{T=1}) + corr(\rho X^b, \beta_{T=-1} \Delta Y_{T=-1}) \right]$
 - ρX^b is the splitting variable, and $\beta_{T=1}\Delta Y_{T=1}$, $\beta_{T=-1}\Delta Y_{T=-1}$ are the target variables to reduce variance
 - Variance Reduction: $var(\beta_{T=1}\Delta Y_{T=1}) + var(\beta_{T=-1}\Delta Y_{T=-1})$

MedTree Algorithm



Simulation Study

- 64 Data Generating Mechanisms
 - Cover various settings of dimensionality, Sample Size, Correlation Structure
 - Treatment Effect Function $f(X,T) \in \{Linear, Circle, Box\}$
 - Link Function $g(X) \in \{\beta X, \beta X^2\}$ where $X^2 = x_{ij}^2$ for all pairs of i, j
 - 200 iterations
- Models Compared
 - £1-Penalized Least Square (Qian & Murphy, 2011)
 - GUIDE (Loh, He & Man, 2015)
- Performance Metric
 - Averaged recommendation error rate

Simulation Study Result (p=20, q=6)

		Uncorrelated				Correlated			
	Setting	MedTree	${f MedForest}$	$L_1\mathbf{PLS}$	GUIDE	MedTree	${f MedForest}$	$L_1\mathbf{PLS}$	GUIDE
N = 400	Linear	0.168	0.078	0.038	0.262	0.256	0.129	0.040	0.328
		(0.048)	(0.025)	(0.010)	(0.035)	(0.081)	(0.047)	(0.011)	(0.076)
	Circle	0.416	0.419	0.434	0.428	0.366	0.309	0.587	0.352
		(0.022)	(0.020)	(0.020)	(0.017)	(0.066)	(0.092)	(0.041)	(0.112)
	Box	0.222	0.188	0.189	0.202	0.267	0.204	0.258	0.321
		(0.034)	(0.012)	(0.012)	(0.046)	(0.048)	(0.021)	(0.014)	(0.081)
	Square	0.436	0.345	0.485	0.501	0.411	0.316	0.456	0.480
		(0.033)	(0.034)	(0.020)	(0.028)	(0.049)	(0.054)	(0.042)	(0.058)
N = 800	Linear	0.155	0.062	0.026	0.229	0.229	0.105	0.029	0.278
		(0.044)	(0.021)	(0.008)	(0.037)	(0.057)	(0.033)	(0.008)	(0.052)
	Circle	0.388	0.391	0.428	0.420	0.275	0.183	0.572	0.286
		(0.024)	(0.033)	(0.016)	(0.031)	(0.049)	(0.045)	(0.024)	(0.086)
	Box	0.215	0.188	0.189	0.199	0.237	0.177	0.259	0.269
		(0.023)	(0.013)	(0.013)	(0.029)	(0.030)	(0.016)	(0.015)	(0.064)
	Square	0.401	0.288	0.482	0.497	0.368	0.240	0.473	0.468
		(0.027)	(0.026)	(0.021)	(0.030)	(0.037)	(0.032)	(0.050)	(0.047)

Conclusion

MedForests & MedTree

- Learning models that require few assumptions
- Incorporate extra information to improve accuracy of estimation
- Utilize correlation structures to reduce dimensions.
- Outperform traditional models when treatment effect function is complicated

Future Directions

- Tuning Parameters
- Interpretability
 - variable importance measure

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Appendix: Treatment Effect

- $\mathbb{E}(\Delta Y|X^b,T) = \mathbb{E}(Y^e Y^b|X^b,T) = \mathbb{E}(g(X^e) g(X^b)|X^b,T)$
 - If $g(\cdot)$ is linear, $\mathbb{E}(\Delta Y|X^b,T) = \mathbb{E}(g(\Delta X)|X^b,T) = g(\mathbb{E}(\Delta X|X^b,T) = g(f'(X^b,T))$

Appendix: Simulation Setting

- 64 Data Generating Mechanisms
 - Dimensionality $(p,q) \in \{(10,3), (20,6)\}$
 - Training Sample Size N ∈ {400, 800}, Testing Sample Size N_{test} = 1000
 - Treatment Effect Function $f(X,T) \in \{Linear, Circle, Box\}$
 - Link Function $g(X) \in \{\beta X, \beta X^2\}$ where $X^2 = x_{ij}^2$ for all pairs of i, j
 - $X^b \sim MVN(0, \Sigma)$ where $\Sigma \in \{\sigma^2 \mathbb{I}, AR(0.8)\}$
 - $T \sim Bernolli(0.5)$
 - $Y = g(X) + MVN(0, \sigma_Y^2 \mathbb{I}), X^e = f(X^b, T) + MVN(0, \sigma_X^2 \mathbb{I})$
 - 200 iterations