EN.625.725 Formal Methods

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Abstract

For years, medical literature has supported a link between genetics, age, and heart disease and stroke risk. There is also evidence that suggests a gender-based difference. Whether these differences are causative is a natural question. The goal here will be to predict heart-based anomalies based on biological sex. We will also observe the performance of a Bayesian Regression Tree (BART) model on heterogeneous treatment effects, as detailed in [1]. This strategy employs techniques from causal data analysis, regression testing, and Bayesian inference, so their exploration will be our primary focus. Also included in the collection of methods are the tools employed in the initial data-testing phase, including sample estimator calculation, covariate hypothesis testing and data plotting.

1 Preliminary Analysis Methods

1.1 Participants & Data

Our sample consists of $n = 1025$ individuals under 14 categories. Of the 1025 participants, 713 (roughly 70 percent) are men and 312 (around 30 percent) are women. This data, collected in 1988, originates from four databases: Cleveland, Hungary, Switzerland, and Long Beach V. In particular, we are interested in evaluating the role of biological sex as a predictor of heart disease.

1.2 Initial Analysis, Covariates & Outcomes

To justify our suspicions, we first do some plotting. This will help us develop hypotheses for the relationships between variables in our dataset. In particular, we have chosen to segregate the visualizations by gender.

Below are a few of the ways we might test for heart disease: [5]

Sample Means by Gender (m=713, f=312)		
	Male	Female
Pain Level	0.92	1.0
Blood Pressure	130.7	133.7
Number Visible Arteries	2.4	2.1
Cholesterol Levels (mg/l)	239.3	261.5
Heart Disease True (% of Participants)	42.1	72.4

Table 1: Sample means between men and women in the heart disease dataset.

1. Exercise Tests
2. Fluoroscopy Tests
3. Cholesterol Level Exams
4. Electrocardiogram (EKG) Tests

Given these tests, the diagnostic criteria for heart disease includes (but is not limited to) lack of presence of arteries in fluoroscpy, high blood pressure, high cholesterol, and poor electrical response.

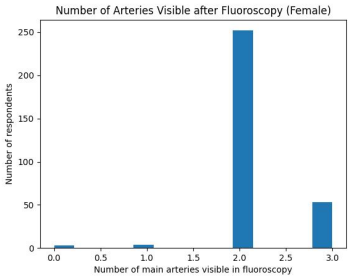
1.2.1 Observations of Sample Mean, Variance, and Standard Error & Categories For Testing

As our sample size is large (> 30), faith in the sample mean, variance, and standard deviation is reasonable, by the Law of Large Numbers. Still, segregation by biological sex gently reduces the quality of our estimation.

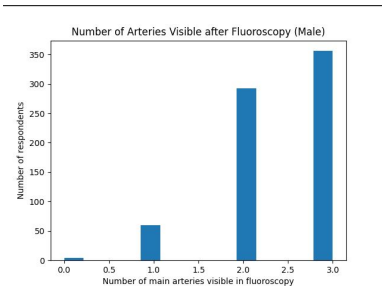
For simplicity, we will include those categories listed in Table 1 (including more if necessary.) By observation, it seems that a larger number of women than men in the dataset have outcomes which indicate heart disease, but, due to the sizeable difference in sample size between men and women, we cannot know for certain the nature of this difference. which makes this dataset a good candidate for a study of causal inference.

We will also calculate the sample variance $\hat{\sigma^2}$ and standard error $\hat{se}$ of the male versus female data for each category.

This is easy to do in python. We can initially make a surface-level comparison of the significance between each estimated parameter. This can be done



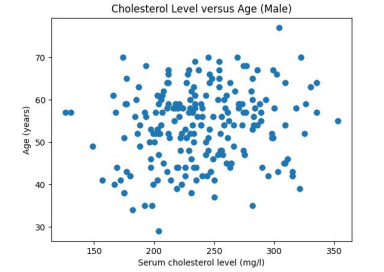
(a) Female Results



(b) Male Results

Figure 1: Visibility of Main Arteries Between Male and Female Patients

(a) Female Results



(b) Male Results

Figure 2: Age Versus Cholesterol Levels (mg/l) Between Male and Female Patients

using BART techniques; see Section 2.3.2 for more details on how this will be incorporated into our analysis.

The examples in Figure 1 and Figure 2 illustrate a level of ambiguity when comparing each of the heterogeneous risk factors between men and women. We will perform multiple bayesian regression tree techniques over a subset of the 14 columns of data (`age`, `sex`, `cp`, `trestbps`, `chol`, `fbs`, `restecg`, `thalach`, `exang`, `oldpeak`, `slope`, `ca`, `thal`, `target`).

2 Bayesian Causal Forests

An **inference** over a data point x is defined to be

$$Y = f(x) + \epsilon, \epsilon \sim \mathcal{N}(0, \sigma^2). \qquad [9]$$

A Bayesian Additive Regression Tree (BART) model wishes to approximate $f(x)$ by obtaining $\mathbb{E}(Y|f(x))$, where $f(x)$ is expressed as the sum of bayesian regression trees g_i over x. In other words, $f(x) \approx \sum_{i=1}^{N} g_i(x)$. This expression for f is also the prior distribution for the BART model. [9] Though the classic BART model is historically good for inference [1][7], this inference does not necessarily imply causality.

Causal inference is the study of bidirectionality in causality; if X, Y are random variables, and X impacts Y, causal inference tools wish to know whether Y also impacts X. [3]

This project is devoted to applying a proposed improvement on the BART-based model, known as Bayesian Causal Forests (BCF), for the sake of flexible causal inference. In particular, we want to examine whether biological sex is not only a prediction, but a *cause* of aggregated heart-related issues.

The main difference between BART and BCF is that the latter is more concerned with reparameterizing its priors to accomodate additional conditional causal effect statistics. This impacts where its decision trees must split, and provides greater flexibility (and resistance to regression phenomena such as RIC) when examining heterogeneous effects.

In the first part of this section, we will develop the basic tools necessary for producing a discussion of causality. We will then demonstrate how they will be used in our experimentation. Finally, we will examine the formation of priors for the BART and BCF models, and enumerate the regression techniques that will be used in conjunction with our application of the causal forest model.

2.1 Modeling Overview

We wish to develop and compare 2 models for this project. We will use the `bartMachine` package in R to perform a default BART analysis of the data (estimating `target`), in addition to propensity score calculation. Finally, the bulk of the BCF simulation will be done using the `grf` and `BCF` packages. We will compare the strength of inference in both models. For simplicity, we will

employ each with default settings (the explicit prior parameterizations for `grf` are mentioned in later sections.) We will estimate `target` under the constraint of biological sex, in addition to the various risk factors (heterogeneous effects) associated with heart disease, which belong to the categories listed in Table 1.

2.2 Causal Inference Analysis Tools

To examine random variables for causality, we refer to **treatment** as an effect. Typically (but not always), this takes on a binary meaning; for example, drinking 12 cups of coffee per day is a treatment. If a treatment variable X is associated with drinking 12 cups of coffee per day, we can denote $X = 1$ as "treated" and $X = 0$ as "not treated."

Define C_0 to be the outcome if a subject is not treated, and define C_1 to be the outcome if the subject is treated.

Then the **average causal effect** is said to be the consistent estimator

$$\theta = \mathbb{E}(C_1) - \mathbb{E}(C_0)$$

.

For our purposes, we will consider as treatments whether the subject is a man or a women. The outcomes of the treatment are simply the data points that occur for men and women, respectively. Let $X = 0$ be representative of women and $X = 1$ representative of men. Then according to [3], the conditional causal effect for relative to men is described as

$$\theta_1 = \mathbb{E}(C_1|X = 1) - \mathbb{E}(C_0|X = 1)$$

and likewise, θ_0 is defined similarly for women. Thus, C_0 is the outcome if the subject is a woman, and similarly, C_1 is the outcome if the subject is a man. However, conditional causal effect is not to be confused with **association**, which is defined by

$$\alpha = \mathbb{E}(Y|X = 1) - \mathbb{E}(Y|X = 0),$$

where Y is the **consistency relationship**

$$Y = \begin{cases} C_0 & X = 0 \\ C_1 & X = 1 \end{cases}$$

The following sections are dedicated to each of the causative tools we will use

to build and analyze our model.

2.2.1 Random Variable Definition & Consistency Relationship

For this project, let $C* = (X, Y, C_0, C_1)$ be a vector whose representations are described above. That is, X is a binary treatment variable representative of biological sex; Y is its consistency relationship. C_0 and C_1 are the outcomes for female and male subjects, respectively, in a particular heart disease category belonging to those listed in Table 1.

2.2.2 Conditional Causal Effect Estimator Calculation

Consider a subset of the heart disease data relative to the outcome of heart disease in men and women.
Recall the sample means for both $X = 0$ and $X = 1$, as described in Table 1, which are $\mathbb{E}(C_0|X = 0) = 42.1$ and $\mathbb{E}(C_1|X = 1) = 72.4$. Then $\theta_1 = 42.1$ and $\theta_0 = 72.4$, since both C_1 and C_0 are counterfactuals - that is, if $X = 1$, we don't observe C_0, and vice versa. [3]

For our purposes, we'll use expected values for Age, Pain Level, Blood Pressure, Artery Visibility, and Cholesterol Level for both men and women to describe the conditional causal parameters θ_1 and θ_0.

The model will then validate these parameters against the true outcomes (heart disease or no heart disease.)

2.3 Development of the BCF prior

In the BART methodology, a prior $f(x)$ is chosen by approximating a sum of binary regression trees. The trees themselves contain internal decision nodes The splitting rules for a binary regression tree are determined by this distribution. We can express a prior as the additive regression forest $f(x) = \sum_{i=1}^{N} g_i(x)$, where $g_i(x)$ maps to some scalar. In ordinary Bayesian analysis, choice of prior is designed to be an uninformed event, meaning that we will select a prior distribution $f(\theta)$ and statistical model $f(x|\theta)$ over some parameter θ with little insight into the true distribution. After viewing our results, we then update our parameters.

Per the initial introduction of BART into statistical literature, probability that a node at depth h splits is precisely $\eta(1 + h)^{-\beta}$, where $\eta \in (0, 1)$ and $\beta \in [0, \infty)$. [5]

For BART, quality of prior does matter. It is also assumed that the structure of each decision tree T_i and its leaves M_i are independent. Hence, prior specification can be segregated into parts if desired. For our purposes, we will be going with the naive approach, avoiding this option.

Per [5], large, deep trees take $\eta = 0.95$ and $\beta = 2$. Nth leaves are distributed according to $\mathcal{N}(0, \sigma^2)$, with $\sigma = \frac{\sigma_0}{\sqrt{N}}$.

2.3.1 Implications for Causal Inference

For causal analysis, however, the BART prior selection criteria do not necessarily account for causal priors; e.g., the inference of $\theta(x) = f(x|1) - f(x|0)$, or the mean conditional causal effect described in previous sections.

We will be following the prior selection criteria given by [1]. This will ultimately be a more naive approach. Set $\eta = 0.25$ and $\beta = 3$. In addition, we will reparamaterize the model to fit into a $\mathcal{N}(\mu + \theta, \sigma^2)$ distribution, as opposed to $\mathcal{N}(\mu, \sigma^2)$.

2.3.2 Additional Hypothesis Testing

Let H_0 be the statement that heart-disease risk is not significantly motivated by biological sex. Let H_1 be the alternate hypothesis, that biological sex has causes inflated heart disease risk.

"Heart disease risk" here means:

1. significantly higher blood pressure measurements
2. fewer visible arteries in fluoroscopy
3. higher cholesterol levels
4. greater chest pain measurements

We should test whether biological sex strongly impacts each of these factors.

The `bartMachine` R package has a `cov_importance_test` function, which is designed to test H_0 (that the covariates $X = 1$ and $X = 0$ do not affect the response under the BART) and H_1, that they do. While this association does **not** imply causality, it does inform some level of significance. We will use the sample means of the 4 categories listed above as our parameters for comparison.

We will use this function to communicate results and refine testing.

2.4 Regression Testing Tools

Unsurprisingly, the *regression* aspect of the BART and BCF methods is what drives the inference and learning of $f(x)$. It is not typical for us to have access to extensive knowledge of our parameters. Therefore, BART and BCF are **nonparametric** learning models, which makes them particularly flexible.

In the BART model, regression is expressed as the output of multiple decision trees over data point estimation given some prior distribution. In a BCF, this idea is still supported.

2.4.1 Fitting

[discuss how fitting is used in the paper]

Though advanced fitting options are explored in a variety of causal forest models, we will use the `grf`, `BCF`, and `bartMachine` default settings for simplicity. Time permitting, suggestions like those detailed above will be explored, though that is not necessarily the focus of this project.

2.4.2 Targeted Selection

[talk about how [1] and others implement this shi- and how it's used in coursework]

As noted in [1],[5], and [6], estimation risks bias. The regression model proposed in [1] attempts to alleviate bias by honing in on confounding. Recall the casual effect calculations above. An additional regression-assistance tool is known as **targeted selection**, or estimation of what a value *would* be in the absence of a treatment effect. [1]

[talk briefly about how it will be implemented here]

2.4.3 Propensity Scoring

We will use `bartMachine` to calculate propensity scores for the classic BART model and `BCF` to calculate propensity scores for the BCF variant.

2.4.4 Computation of Bias

3 Working Bibliography

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   : :text=Bayesian%20Additive%20Regression%

   20Trees%20(BART)%20is%20a%20sum%2Dof,particular%20kind%20ca

   lled%20decision%20trees.

3.1 (Updated) Dataset(s) & Links

Heart Disease Dataset Link:

https://www.kaggle.com/datasets/johnsmith88/heart-disease-dataset

BartPy Repository: https://github.com/JakeColtman/bartpy

bartMachine Docs: https://cran.r-project.org/web/packages/bartMachine/bartMachine.pdf

BCF Docs: https://cran.r-project.org/web/packages/bcf/bcf.pdf

grf Docs: https://cran.r-project.org/web/packages/grf/grf.pdf

GitHub Repository: https://github.com/le-kimpel/heart-disease-and-gender