

# Conformal Inference for Continuous Treatment Effect

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Our goal is to generate prediction intervals with certain coverage for heterogeneous treatment effect when treatment is continuous. Generally, we will use conformal prediction to get them. We first review the relating literature by topic, then we show some basic simulation results we already have.

## 1 Literature Review

**Conformal Inference** Conformal prediction (or inference) (Vovk et al. [2005], Lei et al. [2018]) is a method for uncertainty quantification. It's goal is to give an interval  $\hat{C}(X)$ , such that for a *i.i.d* test data pair  $(X_{n+1}, Y_{n+1})$ , we have

$$\mathbb{P}(Y_{n+1} \in \hat{C}(X_{n+1})) \geq 1 - \alpha$$

Original conformal prediction requires exchangeability, which is violated when there are distribution shifts. To solve this issue, Tibshirani et al. [2019] develop weighted conformal algorithm, and Romano et al. [2019] purpose conformal quantile regression to further simplify the process. Lei and Candès [2021] first introduce conformal prediction to causal inference framework. They show that covariate shift can be represented by propensity scores in causal settings with binary treatment. Zhang et al. [2023] use conformal inference on off-policy evaluation for multiple treatments. Fofano et al. [2023] base on their work to use conformal off-policy evaluation for markov decision process. As a result, the potential of this method is gradually being realized. The key procedure of this approach is the quantile adjustment after we get first step point estimation with either machine learning algorithm like Neural Networks or basic regressions.

**Continuous Treatment Effect** Continuous-treatment effect (CTE)/Dose Response Function has been explored in traditional Non-parametric/Semi-parametric framework Kennedy et al. [2017] and Galvao and Wang [2015]. The main area of practical problem concerning CTE is off-policy evaluation. Recently, some scholars have investigated how to integrate the framework of conformal inference with multiple treatment effects, as discussed in Zhang et al. [2023] and Taufiq et al. [2022]. Differently, off-policy evaluation has a known propensity score  $e(x, 1)$  but we need to estimate  $\hat{e}(x, 1)$  in causal inference framework. These papers propose a sampling method to approximate the evaluation policy (propensity score in the causal inference framework). Additionally, CTE has been explored in the balanced ML method presented in Kazemi and Ester [2022]. This paper

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proposes an encoder method to construct  $Z$  from  $X$  to address the confounding of treatment. Furthermore, it offers a possible alternative to the traditional propensity score.

**Generalized Propensity Score** The concept of propensity score was initially proposed by [Hirano and Imbens \[2004\]](#) and has since become a mature field with the development of numerous algorithms, such as the one proposed by [Wu et al. \[2022\]](#), which uses matching to use neighboring points to get an estimation. [Tu \[2019\]](#) compare several different machine learning algorithms for the precision of estimating GPS. In the continuous treatment setting, one problem we did not meet before is the sampling issue. Thus we might want to add  $t$  into the estimated functional form, as S-Learner did as in [Künzel et al. \[2019\]](#).

## 2 Preliminary Results

**Problem** Our current target is to do get a individual level prediction interval  $\hat{C}_i(t, X)$ , s.t.

$$P(\theta_i(t) - \theta_i(t_0) \in \hat{C}_i(t, X)) \geq 1 - \alpha$$

Some points to note for this problem:

- How to select samples? This time we focus on CTE, we can almost impossibly get samples s.t  $T = t$ .
- Above problems certainly heavily rely on exchangeability of data, it has been solved in 0-1 framework. Now we need to construct a new *Generalized Conformity Score* to weighted samples belong to  $[t - \delta, t + \delta]$

**Naive Algorithm** We only modified the [Lei and Candès \[2021\]](#) nested algorithm slightly for presentation. The differences only manifest in the **sampling method** and **GPS** used.

An initial algorithm was proposed to solve this problem; however, the coverage was not satisfactory, see example [Figure 1](#) and [Figure 2](#).

We use this data generating process:

$$Y_i = X_{1i} + 0.5 \times X_{2i} + T_i + \epsilon_i$$

where  $T_i \in [0, 6]$ . All RHS variables are generated randomly.

To estimate treatment effect  $Y_i(t) - Y_i(0)$ ,  $t > 0$

### Step I. data splitting

- 1: Split the data into two folds  $Z_1$  and  $Z_2$
- 2: Estimate general propensity score  $\hat{e}(x, t)$  on  $Z_1$

### Step II. counterfactual inference on $Z_2$

For  $i \in Z_2$  with  $T_i = t$ . Group samples  $\{Y_i, X_i, Y_t^{obs}\}_{i=1}^{n_t}$  and  $\{Y_i, X_i, Y_0^{obs}\}_{i=1}^{n_t}$

- 1: Compute  $[\hat{Y}_i^L(X_i, 0), \hat{Y}_i^R(X_i, 0)]$  by using CQR on  $Z_1$  with level  $\alpha$  and  $w(x, 0)$  (unbiased estimation with general propensity score  $E[Y(0)] = E[Y_0^{obs}w(x, 0)]$ )
- 2: Compute  $\hat{C}_i = [Y_i(X_i, t) - \hat{Y}_i^R(X_i, 0), Y_i(X_i, t) - \hat{Y}_i^L(X_i, 0)]$

Now reverse the order.

- 1: Compute  $[\hat{Y}_t^L(X_i, t), \hat{Y}_t^R(X_i, t)]$  by using CQR on  $z_1$  with level  $\alpha$  and  $w(x, t)$  (unbiased estimation with general propensity score  $E[Y(t)] = E[Y_t^{obs}w(x, t)]$ )
- 2: Compute  $\hat{C}_i = [\hat{Y}_t^L(X_i, t) - Y_i(0), \hat{Y}_t^R(X_i, t) - Y_i(0)]$  These two sets compose the set  $\Gamma = (X_i, C_i)$  and  $C_i = [C_i^L, C_i^R]$

### Step III Exact version of ITE on the testing point

Input: level  $\gamma$ , data  $\mathcal{Z} = (X_i, C_i)_{i \in \mathcal{I}}$  where  $C_i = [C_i^L, C_i^R]$ , testing point  $x$ , functions  $\hat{m}^L(x; \mathcal{D}), \hat{m}^R(x; \mathcal{D})$  to fit the conditional mean/median of  $C^L, C^R$

Procedure:

- 1: Split  $\mathcal{Z}$  into a training fold  $\mathcal{Z}_{tr} \triangleq (X_i, C_i)_{i \in \mathcal{I}_{tr}}$  and a calibration fold  $\mathcal{Z}_{ca} \triangleq (X_i, C_i)_{i \in \mathcal{I}_{ca}}$
  - 2: For each  $i \in \mathcal{I}_{ca}$ , compute score  $V_i = \max\{\hat{m}^L(X_i; \mathcal{Z}_{tr}) - C_i^L, C_i^R - \hat{m}^R(X_i; \mathcal{Z}_{tr})\}$
  - 3: Compute  $\eta$  as the  $(1 - \gamma)(1 + 1/|\mathcal{Z}_{ca}|)$  quantile of the empirical distribution of  $\{V_i : i \in \mathcal{I}_{ca}\}$
- Output:  $\hat{\mathcal{C}}(x) = [\hat{m}^L(x; \mathcal{Z}_{tr}) - \eta, \hat{m}^R(x; \mathcal{Z}_{tr}) + \eta]$

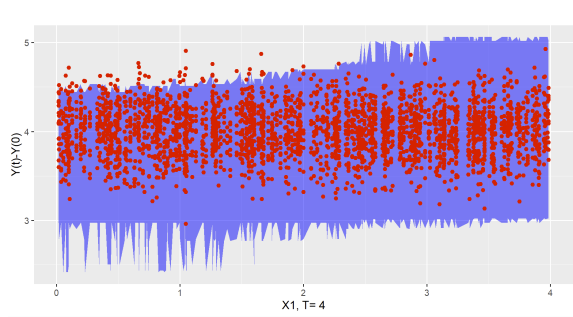


Figure 1:  $T = 4$

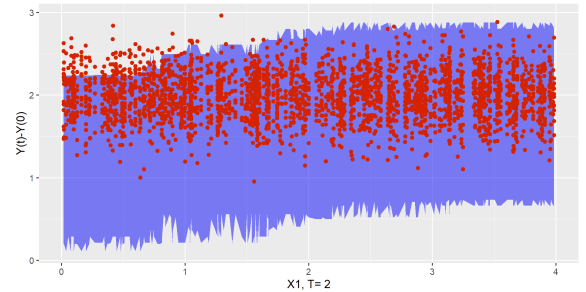


Figure 2:  $T = 2$

## 3 How to improve the naive approach?

**Generalized Conformity Score** The first problem need to solve is to modify the weighting strategy.  $\tilde{t} \neq t$ , therefore it doesn't follow exchangeability if we only use weight on test point  $t$ . We need to get a new Generalized Conformity Score  $g_i^w(x, \tilde{t}, t)$  like this:

$$S_i = \max\{q_{low}^w(X_i, \tilde{t}) - Y_i, Y_i - q_{high}^w(X_i, \tilde{t})\}$$

and the new empirical distribution

$$\sum_i g_i^w(x, \tilde{t}, t) \delta_{S_i}$$

we have not thought about the specific formula of  $g_i^w(x, \tilde{t}, t)$ , but it is possibly related to the distance between  $|\tilde{t} - t| \leq \bar{\delta}$ ,  $\bar{\delta}$  is the upper bound of band width for sampling.

**Encoding Method** Kazemi and Ester [2022] promotes a method that transfer  $X \rightarrow Z$  to make  $Y \perp T|Z$  to resolve confoundness. We can possibly recast the algorithm without using any "score".

### Step I. encoder

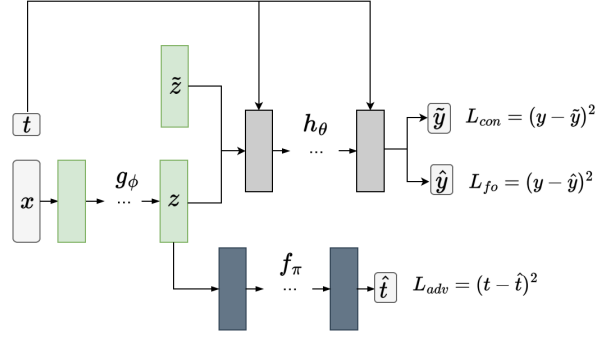


Figure 2: The architecture of ACFR network.

Figure 3: From [Kazemi and Ester \[2022\]](#)

$I$  is mutual information that can capture non-linear dependency between two variables. The latent representation  $Z$  extracted via a parametric encoder  $g_\phi(x)$  is assumed to be causally dependent to covariate  $X$ , and to be conditionally independent of treatment  $T$  and outcome  $Y$  given  $X$ .

$$\min_{\phi, \theta} I(Z, Y|T; \phi) - \gamma_1 I(Z, T; \phi)$$

this step generates  $g_\phi(x)$ , and  $h_\theta(z, t)$ . At treatment level  $t_e$  where there are no samples, we want to use this  $h_\theta$  to generate samples, and use conformality score quantiles to adjust the prediction interval to reach certain marginal coverage level.

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