Conformal Prediction with missing values (2023 ICML)

Hwichang Jeong

February 26, 2025

◆□▶ ◆□▶ ◆ □▶ ◆ □▶ ─ □ ─ つへぐ

Table of Contents

Introduction

Method

Experiment

Introduction

Background

Conventional quantile regression-based conformal prediction methods tend to construct prediction intervals that undercover the response conditionally to some missing patterns.

Contribution

Suggest novel conformalized quantile regression framework, missing data augmentation, which yields prediction intervals that are valid conditionally to the patterns of missing values.

< □ > < 同 > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > <

Prove that the proposed algorithms satisfy desirable theoretical properties.

Table of Contents

Introduction

Method

Experiment

Notation

- ▶ $X = (X_1, \cdots, X_d) \in \mathbb{R}^d$: *d*-dimensional feature vector.
- ▶ $M = (M_1, \dots, M_d) \in \{0, 1\}^d$: A mask such that $M_j=0$ when X_j is observed and $M_j = 1$ otherwise.
- ▶ $Y \in \mathbb{R}$: Outcome.
- $\mathcal{M} = \{0, 1\}^d$: Set of masks.
- For a mask $m \in \mathcal{M}, X_{obs(m)}$ is the random vector of observed components, and $X_{mis(m)}$ is the random vector of unobserved one.

- ► For $(\overset{\circ}{m}, \breve{m}) \in \mathcal{M}^2$, $\overset{\circ}{m} \subset \breve{m}$ denotes $\overset{\circ}{m}_j = 1$ then $\breve{m}_j = 1$ for any $j \in \{1, \dots, d\}$, i.e. \breve{m} includes at least the same missing values than $\overset{\circ}{m}$.



 Create a proper training set, a calibration set, and keep your test set, by randomly splitting your data set.

イロト 不得 とくほ とくほとう

э

Proper training set : Tr / Calibration set : Cal / Test set : Te



On the proper training set:

▶ Learn \hat{q}_{low} and \hat{q}_{upp}

イロト 不得 とうほう イヨン





On the calibration set:

- ▶ Predict with *q̂*_{low} and *q̂*_{upp}
- ► Get the scores $s^{(k)} = \max \left\{ \hat{q}_{\text{low}} \left(x^{(k)} \right) - y^{(k)}, y^{(k)} - \hat{q}_{\text{upp}} \left(x^{(k)} \right) \right\}$
- Compute the (1 − α) × (1 + ¹/_{#Cal}) empirical quantile of the s^(k), noted Q
 _{1−α} (S)

▲□▶ ▲□▶ ▲□▶ ▲□▶ ▲□ ● のへで



On the test set:

- ▶ Predict with \hat{q}_{low} and \hat{q}_{upp}
- $\blacktriangleright \text{ Build } \hat{C}_{\hat{\alpha}}(x) \colon \left[\hat{q}_{\text{low}}(x) \hat{Q}_{1-\hat{\alpha}}\left(S\right), \hat{q}_{\text{upp}}(x) + \hat{Q}_{1-\hat{\alpha}}\left(S\right) \right]$

ヘロト 人間 とくほ とくほとう

æ

Theorem (1)

If $(X^{(k)}, Y^{(k)})$, k = 1, ..., n + 1 are exchangeable, then the prediction interval $\hat{C}(X^{(n+1)})$ constructed by the split CQR algorithm satisfies

$$\mathbb{P}\left\{Y^{(n+1)} \in \hat{C}\left(X^{(n+1)}\right)\right\} \ge 1 - \alpha$$

Moreover, if the conformity scores $s^{(k)}$ are almost surely distinct, then the prediction interval is nearly perfectly calibrated:

$$\mathbb{P}\left\{Y_{n+1}\in\hat{C}\left(X_{n+1}\right)\right\}\leq1-\alpha+1/\left(\#Cal+1\right)$$

< □ > < 同 > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > < □ > <

Validity with Missing values

$$1 - \alpha \leq \mathbb{P}\left\{Y_{n+1} \in \hat{C}\left(X^{(n+1)}, M^{(n+1)}\right)\right\} \leq 1 - \alpha + \frac{1}{(\#\text{Cal}+1)}$$

◆□▶ ◆□▶ ◆ □▶ ◆ □▶ ● □ ● ● ● ●

Impute then predict + conformalization

• Let $\phi^m : \mathbb{R}^{|obs(m)|} \to \mathbb{R}^{|mis(m)|}$ be a imputation function.

• Let $\Phi = (\Phi_1, \cdots, \Phi_d) : \mathbb{R}^d \times \{0, 1\}^d \to \mathbb{R}^d$ be a function such that

$$\Phi_j(X,M) = X_j \mathbb{I}_{M_j=0} + \phi_j^M(X_{obs(M)}) \mathbb{I}_{M_j=1}$$

Theorem (2)

Assume exchangeability holds and the imputation function Φ is the output of an algorithm \mathcal{I} treating its input data points symmetrically: $\mathcal{I}\left(\left(X^{(\sigma(k))}, M^{(\sigma(k))}\right)_{k=1}^{n+1}\right) \stackrel{(d)}{=} \mathcal{I}\left(\left(X^{(k)}, M^{(k)}\right)_{k=1}^{n+1}\right)$ conditionally on $\left(X^{(k)}, M^{(k)}\right)_{k=1}^{n+1}$ and for any permutation σ . Then, the prediction interval $\hat{C}\left(X^{(n+1)}, M^{(n+1)}\right)$ satisfies

$$1 - \alpha \leq \mathbb{P}\left\{Y_{n+1} \in \hat{C}\left(X^{(n+1)}, \boldsymbol{M}^{(n+1)}\right)\right\}$$

. Also if the conformity scores $s^{(k)}$ are almost surely distinct,

$$1 - \alpha \leq \mathbb{P}\left\{Y_{n+1} \in \hat{C}\left(X^{(n+1)}, M^{(n+1)}\right)\right\} \leq 1 - \alpha + \frac{1}{(\#Cal+1)}$$

▲□▶▲□▶▲□▶▲□▶ □ のQで

is holds.

Mask-Conditional-Validity(MCV)



ヘロト 人間 とくほ とくほとう

э.

- Gaussian linear regression with d = 3.
- Missingness mechanism : MCAR / Missing rate : 20%.
- Imputation : Iterative regression.

Mask-Conditional-Validity(MCV)

For any $m \in \mathcal{M}$,

$$1-\alpha \leq \mathbb{P}\left(Y^{(n+1)} \in \widehat{C}_{\alpha}\left(X^{(n+1)}, m\right) \mid \underline{M}^{(n+1)} = \underline{m}\right) \leq 1-\alpha + \frac{1}{\#\operatorname{Cal}^{\mathrm{m}} + 1},$$

◆□▶ ◆□▶ ◆ □▶ ◆ □▶ ─ □ ─ つへぐ

where ${\rm Cal}^m=\{k\in Cal \text{ such that } m^{(k)}\subset m \}.$

MCV

- CP-MDA-Exact : Select the data in the calibration set (Cal) that contains missing values included in the missing columns of the test data + Additional Masking
- CP-MDA-Nested : Masking the calibration set with max-mask + temporary test point (quantile of confidence interval induced by TTP).



Theorem - MCV

Assume missing mechanism is MCAR and $(Y \perp M)|X$

For all $m \in \mathcal{M}$, CP-MDA-Exact satisfies

$$1-\alpha \leq \mathbb{P}\left(Y^{(n+1)} \in \widehat{C}_{\alpha}\left(X^{(n+1)}, m\right) \mid M^{(n+1)} = m\right),$$

► If the conformity scores s^(k) are almost surely distinct, for all m ∈ M, CP-MDA-Exact satisfies,

$$1-\alpha \leq \mathbb{P}\left(Y^{(n+1)} \in \widehat{C}_{\alpha}\left(X^{(n+1)}, m\right) \mid \underline{M}^{(n+1)} = m\right) \leq 1-\alpha + \frac{1}{\#\operatorname{Cal}^{\mathsf{m}} + 1},$$

・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・
 ・

where $\operatorname{Cal}^m = \{k \in \text{Cal such that } m^{(k)} \subset m\}.$

Theorem - MCV

Assume missing mechanism is MCAR and $(Y \perp M)|X$

► Let
$$(\overset{\circ}{m}, \breve{m}) \in \mathcal{M}^2$$
. If $\overset{\circ}{m} \subset \breve{m}$ then for any $\delta \in [0, 0.5]$,
 $q_{1-\delta/2}^{Y|(X_{\text{obs}}(\breve{m}), M=\breve{m})} \leq q_{1-\delta/2}^{Y|(X_{\text{obs}}(\breve{m}), M=\breve{m})}, q_{\delta/2}^{Y|(X_{\text{obs}}(\breve{m}), M=\breve{m})} \geq q_{\delta/2}^{Y|(X_{\text{obs}}(\breve{m}), M=\breve{m})}$ are hold.
Then, CP-MDA-Nested satisfies

$$1-\alpha \leq \mathbb{P}\left(Y^{(n+1)} \in \widehat{C}_{\alpha}\left(X^{(n+1)}, m\right) \mid \underline{M}^{(n+1)} = \underline{m}\right),$$

(ロト・日本)・モン・モン・モー のへの

up to a technical minor modification of the output.

Table of Contents

Introduction

Method

Experiment

Experiment



▲□▶▲圖▶▲≣▶▲≣▶ ≣ のQ@