

1. Notations and Background

1.1. Set Partition

A partition of a set $S = \{1, \dots, n\}$ is a family of subsets $S_1, \dots, S_k \subset S$, satisfying the following.

1. $S_i \cap S_j = \emptyset$, if $i \neq j$
2. $S = \bigcup_{i=1}^k S_i$
3. $S_i \neq \emptyset$, for $i = 1, \dots, k$

1.2. Transductive Conformity Prediction (TCP)

The object space $\mathcal{X} \in \mathbb{R}^p$, where p is the number of features, and label space $\mathcal{Y} \in (0, 1)$, and example space $\mathcal{Z} := \mathcal{X} \times \mathcal{Y}$ are fixed throughout the article. We assume that each observation consists of an object and its label.

The typical classification problem is, given a training dataset $Z = \{z_1, \dots, z_n\}$ – where n is the number of observations in the training set, and each observation $z_i = (x_i, y_i)$ are labeled observations – we want to predict the label of a new observation x whose label is unknown.

First, we define a transductive non-conformity measure and transductive conformity score in the following.

Definition 1 (Transductive nonconformity measure). *A transductive non-conformity measure is a measurable function $\mathcal{A} : \mathcal{Z} \times \mathcal{Z} \rightarrow \mathbb{R}$ such that $\mathcal{A}(Z_1, Z_2)$ does not depend on the ordering of observations in the set Z_1 .*

Definition 2 (Transductive nonconformity score). *The transductive nonconformity score measures the lack of conformity of the “test observation” Z_2 to the “training set” Z_1 .*

Definition 3 (Transductive Conformity Prediction (TCP)). *Given a training dataset Z and a new observation x , the transductive conformal predictor (TCP), corresponding to a nonconformity measure \mathcal{A} , checks each of a set of hypothesis (for all possible labels) for the new observation x , and assigns it a p -value at a significance level $\epsilon \in (0, 1)$.*

Algorithm 1: TCP

Input: (training dataset: Z , test data: x , label set: Y , a nonconformity measure: \mathcal{A})

Output: p-values

for *each* $y \in \mathcal{Y}$ **do**

$z_{n+1} = (x, y)$;

$Z^* = (Z, z_{n+1})$;

 Compute the transductive nonconformity scores:

$\alpha_i = \mathcal{A}(Z^*, z_i)$ for each $z_i \in Z^*$;

 Compute p-value: $p(y) = \frac{|\{i=\{1,\dots,n+1\} | \alpha_i \geq \alpha_{n+1}\}|}{n}$;

end

p-values = $\{p(y) | y \in \mathcal{Y}\}$;

return p-values;
