

## 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.

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;

---