Abstract

In this paper, we study statistical inference on the similarity/distance between two time-series under uncertain environment by considering a statistical hypothesis test on the distance obtained from Dynamic Time Warping (DTW) algorithm. The sampling distribution of the DTW distance is too complicated to derive because it is obtained based on the solution of a complicated algorithm. To circumvent this difficulty, we propose to employ a conditional sampling distribution for the inference, which enables us to derive an exact (non-asymptotic) inference method on the DTW distance. Besides, we also develop a novel computational method to compute the conditional sampling distribution. To our knowledge, this is the first method that can provide valid $p$-value to quantify the statistical significance of the DTW distance, which is helpful for high-stake decision making. We evaluate the performance of the proposed inference method on both synthetic and real-world datasets.
1 Introduction

Measuring similarity/distance between two time-series is a fundamental task in various problems. This task is usually formulated as the problem of minimizing the loss of sequence alignment. Aligning two time-series involves computing the optimal pairwise correspondence between their elements while preserving the alignment orderings. The Dynamic Time Warping (DTW) \cite{15} is a standard algorithm for finding the optimal alignment between two given time-series. The DTW distance has been used for high-stake decision making in various signal processing problems.

When the DTW distance of the two time-series is observed under uncertain environment, it is crucially important to quantify its statistical reliability, e.g., in the form of $p$-value or confidence interval. However, there is no satisfactory statistical inference method for the DTW distance. The main difficulty is that the sampling distribution of the DTW distance is too complex to derive, i.e., it is difficult to analyze how the uncertainty in the observed two time-series is transmitted to the uncertainty in the DTW distance. Without quantifying the statistical reliability of the DTW distance, we cannot properly control the risk of incorrect decision making.

Our key idea to circumvent this difficulty is to employ a conditional sampling distribution of the DTW distance — inspired by the recent development of the conditional Selective Inference (SI) literature \cite{11}. The basic concept of conditional SI is to make an inference conditional on a selection event. The inference based on a conditional sampling distribution is still valid in the sense that the false positive rate (FPR) can be properly controlled under a given significance level $\alpha$ (e.g., 0.05). To develop a valid statistical inference method for the DTW distance, we interpret the optimization problem of selecting (determining) the optimal alignment as the selection event and consider the sampling distribution of the DTW distance conditional on the optimal alignment.

The main technical contribution in this paper is to derive the conditional sampling distribution of the DTW distance in a tractable form and develop a novel computational method to compute the conditional sampling distribution. To our knowledge, this is the first exact (non-asymptotic) statistical inference method for the DTW distance in the sense that the FPR can be properly controlled at the given significance level $\alpha$ in the statistical test, which is equivalent to having a confidence interval with a proper $100(1 - \alpha)\%$ coverage, when the statistical test and the confidence interval is obtained based on the conditional sampling distribution.

1.1 Contribution

The main contributions in this study are two-fold. The first contribution is that we propose to employ a conditional sampling distribution of the DTW distance in order to develop an exact statistical inference method inspired by the recent development of conditional SI literature. Whereas the unconditional sampling distribution of the DTW distance is too complex to characterize, we show that the sampling distribution
Figure 1: An illustrative example of the problem and the importance of the proposed method. The blue curves are the true underlying signals. The green and orange curves are two time-series observed under noisy environment. Although, these two time-series have the same underlying signal, the DTW distance between them might be falsely large due to the noises. By using the proposed method to conduct statistical inference on the DTW distance, the proposed selective \( p \)-value is large indicating that the difference between two time-series are not statistically significant, i.e., we can successfully identify the false positive.

conditional on the optimal alignment can be characterized in a tractable form. The second contribution is to develop a computational method to compute the conditional sampling distribution by introducing non-trivial technique called parametric DTW method. These two contributions enable us to develop the first exact statistical test for the DTW distance, which is crucial for the risk control of high-stake decision making in signal processing. Figure 1 shows an illustrative example of the problem and the proposed \( p \)-value.

1.2 Related work

The DTW distance is commonly used for quantifying the similarity/distance between two time-series \([15, 9, 14, 2]\). However, due to the complex discrete nature of the DTW algorithm, it is difficult to quantify the uncertainty of the DTW distance, i.e., it is difficult to analyze how the uncertainty in the two observed time-series is transmitted to their DTW distance. Therefore, to our knowledge, there are neither exact methods nor asymptotic approximation methods for the statistical inference on the DTW distance. Due to the lack of valid statistical inference method, when decision making is conducted based on DTW distance, it is difficult to properly control the risk of the incorrect decision.

The notion of conditional SI has been known before, but it has been actively studied in the past few years after the seminal work by Lee et al. \([11]\). In their work and several following studies, conditional SI is used for statistical inference on the features of linear models which are selected by a feature selection algorithm such as Lasso. The basic idea of conditional SI is to make inference based on the sampling distribution of the test statistic conditional on a selection event. In the case of the conditional SI for Lasso, the authors succeeded in deriving the sampling distribution of the test statistic conditional on the selected features and their signs, and proposed a method for computing the conditional sampling distribution. Statistical inference based on
2 Problem Statement

To formulate the problem, we consider two time-series represented as vectors corrupted with Gaussian noise as

\[
\mathbb{R}^n \ni X = (x_1, ..., x_n)^\top = \mu_X + \varepsilon_X, \quad \varepsilon_X \sim \mathcal{N}(0, \Sigma_X),
\]

\[
\mathbb{R}^m \ni Y = (y_1, ..., y_m)^\top = \mu_Y + \varepsilon_Y, \quad \varepsilon_Y \sim \mathcal{N}(0, \Sigma_Y),
\]

where \( n \) and \( m \) are the lengths of time-series, \( \mu_X \) and \( \mu_Y \) are the vectors of true signals, \( \varepsilon_X \) and \( \varepsilon_Y \) are Gaussian noise vectors with covariances matrices \( \Sigma_X \) and \( \Sigma_Y \) assumed to be known or estimable from independent data.
2.1 Optimal Alignment and Dynamic Time Warping

Let us denote the cost matrix of pairwise distances between the elements of $X$ and $Y$ as

$$C(X, Y) = [(x_i - y_j)^2]_{ij} \in \mathbb{R}^{n \times m}. \quad (3)$$

Then, the optimal alignment matrix $\hat{M}$ between $X$ and $Y$ is defined as

$$\hat{M} = \arg \min_{M \in M_{n,m}} \langle M, C(X, Y) \rangle, \quad (4)$$

where we write $M_{n,m} \subset \{0, 1\}^{n \times m}$ for the set of (binary) alignment matrices that satisfy the monotonicity, continuity, and matching endpoints constraints as illustrated in Figure 3 and $\langle \cdot, \cdot \rangle$ is the Frobenius inner product. We note that the cardinal of $M_{n,m}$ is known as the delannoy($n-1$, $m-1$) number which is the number of paths on a rectangular grid from $(0, 0)$ to $(n-1, m-1)$ using only single steps to south, southeast, or east direction. A naive way to solve (4) is to enumerate all possible candidates in $M_{n,m}$ and obtain $\hat{M}$. However, it is computationally impractical because the size of the set $M_{n,m}$ is exponentially increasing with $n$ and $m$. The DTW is well-known as an efficient dynamic programming algorithm to obtain the solution $\hat{M}$ in (4) with a quadratic $(nm)$ cost by using Bellman recursion. We will later review the details of DTW in Sec 4.1.2 and Eq. 25.

2.2 Closed-form Expression of the DTW Distance

After obtaining the optimal alignment matrix $\hat{M}$, the DTW distance is written in a closed form as

$$\hat{L}(X, Y) = \langle \hat{M}, C(X, Y) \rangle = \hat{M}_{\mathrm{vec}}^T C_{\mathrm{vec}}(X, Y),$$

Figure 3: An example of (binary) optimal alignment matrix $\hat{M}$. The DTW method calculates an optimal match (blue) between two given time-series with certain rules: monotonicity, continuity, and matching endpoints. After obtaining the optimal match, we can define the optimal alignment matrix.
where $\hat{M}_{\text{vec}} = \text{vec}(\hat{M}) \in \mathbb{R}^{nm}$,

$$C_{\text{vec}}(X, Y) = \text{vec} \left( C(X, Y) \right) = \left[ \Omega \left( X \right) \right] \circ \left[ \Omega \left( Y \right) \right] \in \mathbb{R}^{n+m},$$  \hspace{1cm} (5)

$$\Omega = \begin{pmatrix}
1_m & 0_m & \cdots & 0_m & -I_m \\
0_m & 1_m & \cdots & 0_m & -I_m \\
\vdots & \vdots & \ddots & \vdots & \vdots \\
0_m & 0_m & \cdots & 1_m & -I_m
\end{pmatrix} \in \mathbb{R}^{nm \times (n+m)}.$$  

Here, $\text{vec}(\cdot)$ is an operator that transforms a matrix into a vector with concatenated rows, and the operator $\circ$ is element-wise product.

**Example 1.** ($C_{\text{vec}}(X, Y)$, $\Omega$ and $\hat{M}_{\text{vec}}$) Given $X = (x_1, x_2)^T$ and $Y = (y_1, y_2)^T$, the cost matrix is defined as

$$C(X, Y) = \begin{pmatrix}
(x_1 - y_1)^2 & (x_1 - y_2)^2 \\
(x_2 - y_1)^2 & (x_2 - y_2)^2
\end{pmatrix}.$$  

Then, we have

$$C_{\text{vec}}(X, Y) = \Omega \begin{pmatrix} x_1 \\ x_2 \\ y_1 \\ y_2 \end{pmatrix} \circ \Omega \begin{pmatrix} x_1 \\ x_2 \\ y_1 \\ y_2 \end{pmatrix} \quad \text{where} \quad \Omega = \begin{pmatrix}
1 & 0 & 1 & 0 \\
1 & 0 & 0 & 1 \\
0 & 1 & 1 & 0 \\
0 & 1 & 0 & 1
\end{pmatrix}.$$  

Similarly, given $\hat{M} = \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix}$, then $\hat{M}_{\text{vec}} = \begin{pmatrix} 1 & 0 & 1 \end{pmatrix}^T$.

### 2.3 Statistical Inference

Our goal is to conduct statistical inference for the DTW distance, i.e., we want to test if the two time-series signals are same or not. Specifically, we consider the following null hypothesis

$$H_0 : \hat{M}_{\text{vec}}^T C_{\text{vec}}(\mu_X, \mu_Y) = 0$$

$$\iff H_0 : \hat{M}_{\text{vec}}^T \left( \Omega \left( \begin{pmatrix} \mu_X \\ \mu_Y \end{pmatrix} \right) \right) \circ \left( \Omega \left( \begin{pmatrix} \mu_X \\ \mu_Y \end{pmatrix} \right) \right) = 0.$$  

Instead of testing the above null hypothesis, we can test the *equivalent* one which is defined as

$$H_0 : \hat{M}_{\text{vec}}^T \text{abs} \left( \Omega \left( \begin{pmatrix} \mu_X \\ \mu_Y \end{pmatrix} \right) \right) = 0,$$  \hspace{1cm} (6)

where $\text{abs}(\cdot)$ denotes the element-wise absolute operation. For testing (6), the test statistic $T$ is defined as

$$T = \hat{M}_{\text{vec}}^T \text{abs} \left( \Omega \left( \begin{pmatrix} X \\ Y \end{pmatrix} \right) \right) = \hat{M}_{\text{vec}}^T \text{abs} \left( \hat{M}_{\text{vec}} \circ \Omega \left( \begin{pmatrix} X \\ Y \end{pmatrix} \right) \right)$$

$$= \hat{M}_{\text{vec}}^T \text{diag} (\hat{s}) \Omega \left( \begin{pmatrix} X \\ Y \end{pmatrix} \right)$$  \hspace{1cm} (7)
where $\hat{s} = \text{sign}\left(\hat{M}\circ \left[\Omega(\hat{X})\right]\right) \in \mathbb{R}^{nm}$, \text{sign}($\cdot$) is the operator that returns an element-wise indication of the sign of a number (\text{sign}(0) = 0), and \text{diag}(\hat{s}) is the diagonal matrix whose diagonal entries are the elements of the vector $\hat{s}$. For notational simplicity, we can re-write the test statistic as

$$T = \eta_{M, \hat{s}}^\top (X Y)$$

where $\eta_{M, \hat{s}} = \left(\hat{M}^\top \text{diag}(\hat{s}) \Omega\right)^\top \in \mathbb{R}^{n+m}$ is the direction of the test statistic.

For statistical inference on the DTW distance, we need to characterize the sampling distribution of the test statistic $T$ in (8). Unfortunately, since $\eta_{M, \hat{s}}$ depends on $\hat{M}$ and $\hat{s}$ which are defined based on the data, characterization of the exact sampling distribution of the test statistic is intrinsically difficult. In the next section, we introduce a novel approach to resolve the aforementioned challenge inspired by the concept of conditional SI, and propose a valid selective $p$-value to conduct an exact (non-asymptotic) statistical inference on the hypothesis defined in (6).

### 3 Conditional SI for the DTW Distance

In this section, we present our first contribution. To conduct statistical inference on the DTW distance, we employ the conditional SI framework. Our basic idea comes from the fact that, given the optimal alignment matrix $\hat{M}$, the DTW distance is written in a closed form as in (8). By conditioning on the optimal alignment matrix $\hat{M}$ and its sign $\hat{s}$, we can derive the conditional sampling distribution of the test statistic.

#### 3.1 Conditional Distribution and Selective $p$-value

We consider the following conditional sampling distribution of the test statistic

$$\eta_{M, \hat{s}}^\top (X Y) \mid \left\{A(X, Y) = \hat{M}_{\text{obs}}, S(X, Y) = \hat{s}_{\text{obs}}\right\}$$

where we denote

$$A : (X, Y) \to \hat{M}, \quad S : (X, Y) \to \hat{s},$$

$$\hat{M}_{\text{obs}} = A(X_{\text{obs}}, Y_{\text{obs}}), \quad \hat{s}_{\text{obs}} = S(X_{\text{obs}}, Y_{\text{obs}}).$$

Next, to test the statistical significance of the DTW distance, we introduce the selective $p$-value, which satisfies the following sampling property:

$$\mathbb{P}_{H_0}\left(p_{\text{selective}} \leq \alpha \mid A(X, Y) = \hat{M}_{\text{obs}}, \ S(X, Y) = \hat{s}_{\text{obs}}\right) = \alpha,$$

$\forall \alpha \in [0, 1]$, that is, $p_{\text{selective}}$ follows a uniform distribution under the null hypothesis, which is a crucial property for a valid $p$-value. The selective $p$-value is defined as

$$p_{\text{selective}} = \mathbb{P}_{H_0}\left(\eta_{M, \hat{s}}^\top (X Y) \geq \eta_{M, \hat{s}}^\top (X_{\text{obs}} Y_{\text{obs}}) \mid A(X, Y) = \hat{M}_{\text{obs}}, \ S(X, Y) = \hat{s}_{\text{obs}}, \ Q(X, Y) = \hat{q}_{\text{obs}}\right).$$
where \( Q : (X, Y) \to \hat{q} \) is the sufficient statistic of the nuisance parameter that needs to be conditioned on in order to tractably conduct the inference and defined as
\[
Q(X, Y) = \left( I_{n+m} - b\eta_{M,s}^\top \right) \begin{pmatrix} X \\ Y \end{pmatrix} \quad \text{where} \quad b = \frac{\Sigma\eta_{M,s}}{\eta_{M,s}^\top \Sigma\eta_{M,s}}
\]
and \( \Sigma = \begin{pmatrix} \Sigma_X & 0 \\ 0 & \Sigma_Y \end{pmatrix} \). Here, we would like to note that the selective \( p \)-value depends on \( Q(X, Y) \), but the sampling property in (11) continues to be satisfied without this additional condition because we can marginalize over all values of \( Q(X, Y) \). The \( Q(X, Y) \) corresponds to the component \( z \) in the seminal conditional SI paper [11] (see Sec. 5, Eq. 5.2 and Theorem 5.2). We note that additional conditioning on \( Q(X, Y) \) is a standard approach in the conditional SI literature and is used in almost all the conditional SI-related studies.

To compute the selective \( p \)-value in (12), we need to identify the conditional data space whose characterization will be introduced in the next section.

### 3.2 Conditional Data Space Characterization

We define the set of \((X Y)^\top \in \mathbb{R}^{n+m}\) that satisfies the conditions in (12) as
\[
D = \left\{ (X Y)^\top \in \mathbb{R}^{n+m} \mid A(X, Y) = \hat{M}^{\text{obs}}, S(X, Y) = \hat{s}^{\text{obs}}, Q(X, Y) = \hat{q}^{\text{obs}} \right\},
\]
According to the third condition \( Q(X, Y) = \hat{q}^{\text{obs}} \), the data in \( D \) is restricted to a line in \( \mathbb{R}^{n+m} \) as stated in the following Lemma.

**Lemma 1.** The set \( D \) in (14) can be rewritten using a scalar parameter \( z \in \mathbb{R} \) as follows:
\[
D = \left\{ (X Y)^\top = a + bz \mid z \in Z \right\},
\]
where vector \( a = \hat{q}^{\text{obs}} = Q(X^{\text{obs}}, Y^{\text{obs}}) \), vector \( b \) is defined in (13), and
\[
Z = \left\{ z \in \mathbb{R} \mid A(a + bz) = \hat{M}^{\text{obs}}, S(a + bz) = \hat{s}^{\text{obs}} \right\}.
\]
Here, with a slight abuse of notation, \( A(a + bz) = A((X Y)^\top) \) is equivalent to \( A(X, Y) \). This similarly applies to \( S(a + bz) \).

**Proof.** According to the third condition in (14), we have
\[
Q(X, Y) = \hat{q}^{\text{obs}} \Leftrightarrow \left( I_{n+m} - b\eta_{M,s}^\top \right) (X Y)^\top = \hat{q}^{\text{obs}} \Leftrightarrow (X Y)^\top = \hat{q}^{\text{obs}} + b\eta_{M,s}^\top (X Y)^\top.
\]
By defining \( a = \hat{q}^{\text{obs}}, z = \eta_{M,s}^\top (X Y)^\top \), and incorporating the first and second conditions in (14), we obtain the results in Lemma 1. We note that the fact of restricting the data to the line has been already
Lemma 1 indicates that we need NOT consider the \((n + m)\)-dimensional data space. Instead, we need only consider the one-dimensional projected data space \(Z\) in (16). Now, let us consider a random variable \(Z \in \mathbb{R}\) and its observation \(Z^{\text{obs}} \in \mathbb{R}\) that satisfies \((X Y)^\top = a + bZ\) and \((X^{\text{obs}} Y^{\text{obs}})^\top = a + bZ^{\text{obs}}\). The selective \(p\)-value in (12) can be rewritten as

\[
p_{\text{selective}} = \mathbb{P}_{H_0} \left( \eta_{M, \hat{a}}^\top (X Y)^\top \geq \eta_{M, \hat{a}}^\top (X^{\text{obs}} Y^{\text{obs}})^\top \mid (X Y)^\top \in D \right)
= \mathbb{P}_{H_0} \left( Z \geq Z^{\text{obs}} \mid Z \in \mathcal{Z} \right). \quad (17)
\]

Because the variable \(Z \sim \mathcal{N}(0, \eta^\top \Sigma \eta)\) under the null hypothesis, \(Z \mid Z \in \mathcal{Z}\) follows a truncated normal distribution. Once the truncation region \(\mathcal{Z}\) is identified, computation of the selective \(p\)-value in (17) is straightforward. Therefore, the remaining task is to identify the truncation region \(\mathcal{Z}\) in (16), which can be decomposed into two separate sets as \(\mathcal{Z} = \mathcal{Z}_1 \cap \mathcal{Z}_2\), where

\[
\mathcal{Z}_1 = \{ z \in \mathbb{R} \mid A(a + b z) = \hat{M}^{\text{obs}} \} \quad (18)
\]

and

\[
\mathcal{Z}_2 = \{ z \in \mathbb{R} \mid S(a + b z) = \hat{s}^{\text{obs}} \}. \quad (19)
\]

In the next section, we will present the constructions of \(\mathcal{Z}_1\) and \(\mathcal{Z}_2\).

### 4 Computational Method for Computing \(\mathcal{Z}\)

In this section, we present our second contribution, that is, introducing novel computational method to compute \(\mathcal{Z}\) which is the main factor to compute the conditional sampling distribution and the selective \(p\)-value proposed in previous section. To this end, we introduce a novel computation method called parametric DTW whose basic idea is illustrated in Fig. 4.
4.1 Construction of $Z_1$ in (18)

4.1.1 Parametrization of time-series data.

Before discussing the construction of $Z_1$, we introduce some important notations that will be used in the rest of the paper. As mentioned in Lemma 1, we focus on a set of data $(X \ Y)^\top = a + b z \in \mathbb{R}^{n+m}$ parametrized by a scalar parameter $z$. We denote $X(z) = a^{(1)} + b^{(1)} z$ and $Y(z) = a^{(2)} + b^{(2)} z$.

The cost matrix $C(X(z), Y(z))$ is defined as

\[
C(X(z), Y(z)) = \left[ \left( (a_i^{(1)} + b_i^{(1)} z) - (a_j^{(2)} + b_j^{(2)} z) \right)^2 \right]_{ij} \in \mathbb{R}^{n \times m}.
\]

Given $M \in \mathcal{M}_{n,m}$, $X(z) \in \mathbb{R}^n$ and $Y(z) \in \mathbb{R}^m$, the loss function for the optimal alignment problem is a quadratic function w.r.t. $z$ and it is written as

\[
L_{n,m}(M, z) = \left\langle M, C(X(z), Y(z)) \right\rangle = \sum_{i \in [n], j \in [m]} M_{ij} C_{ij}(X(z), Y(z)) = \omega_0 + \omega_1 z + \omega_2 z^2
\]

where $\omega_0, \omega_1, \omega_2 \in \mathbb{R}$ and they are defined as

\[
\omega_0 = \sum_{i,j} M_{ij} \left( a_i^{(1)} - a_j^{(2)} \right)^2, \quad \omega_1 = 2 \sum_{i,j} M_{ij} \left( a_i^{(1)} - a_j^{(2)} \right) \left( b_i^{(1)} - b_j^{(2)} \right), \quad \omega_2 = \sum_{i,j} M_{ij} \left( b_i^{(1)} - b_j^{(2)} \right)^2.
\]

The optimal alignment in (1) and the DTW distance on parametrized data $(X(z), Y(z))$ is defined as

\[
\hat{M}_{n,m}(z) = \arg \min_{M \in \mathcal{M}_{n,m}} L_{n,m}(M, z),
\]

\[
\hat{L}_{n,m}(z) = \min_{M \in \mathcal{M}_{n,m}} L_{n,m}(M, z).
\]

Note that the scalar notation $z \in \mathbb{R}$ in the definitions (22), (23) and (24) indicates that it corresponds to $(X(z), Y(z))$.

**Construction of $Z_1$.** The set $Z_1$ in (18) now can be re-written as

\[
Z_1 = \left\{ z \in \mathbb{R} \mid \mathcal{A}(X(z), Y(z)) = \hat{M}_{\text{obs}} \right\} = \left\{ z \in \mathbb{R} \mid \hat{M}_{n,m}(z) = \hat{M}_{\text{obs}} \right\}.
\]

To compute $Z_1$, we have to deal with the following two computational challenges:
Algorithm 1 paraOptAlign\((n, m, \mathcal{M}_{n,m})\)

**Input:** \(n, m, \mathcal{M}_{n,m}\)

1: \(t \leftarrow 1, z_1 \leftarrow -\infty,\)
\(\hat{M}_t \leftarrow \hat{M}_{n,m}(z_t) = \arg\min_{M \in \mathcal{M}_{n,m}} L(M, z_t)\)
2: while \(z_t < +\infty\) do
3: Find the next breakpoint \(z_{t+1} > z_t\) and the next optimal alignment matrix \(\hat{M}_{t+1}\) s.t.
\(L_{n,m}(\hat{M}_t, z_{t+1}) = L_{n,m}(\hat{M}_{t+1}, z_{t+1})\).
4: \(t \leftarrow t + 1\)
5: end while
6: \(T \leftarrow t\)

**Output:** \(\{\hat{M}_t\}_{t=1}^{T-1}, \{z_t\}_{t=1}^T\)

- Challenge 1: we need to compute the *entire path* of the optimal alignment matrix \(\hat{M}_{n,m}(z)\) for all values of \(z \in \mathbb{R}\). However, it seems intractable because we have to solve (23) for infinitely many values of \(z \in \mathbb{R}\) to obtain and \(\hat{M}_{n,m}(z)\) and check whether it is the same as \(\hat{M}_{\text{obs}}\) or not.
- Challenge 2: we have to solve (23) on a huge set of all possible alignment matrices \(\mathcal{M}_{n,m}\) whose size is exponentially increasing with \(n\) and \(m\).

In the next Sec 4.1.1, we introduce an efficient approach to resolve the first challenge. We will show that the set \(Z_1\) can be computed with a finite number of operations. Finally, in Sec 4.1.2, we propose a method to address the second challenge based on the concept of dynamic programming in the standard DTW.

### 4.1.2 Parametric Optimal Alignment

Algorithm 1 shows the overview of our parametric optimal alignment method. Here, we exploit the fact that, for each alignment matrix \(M \in \mathcal{M}_{n,m}\), the loss function \(L_{n,m}(M, z)\) is written as a quadratic function (QF) of \(z\) as we defined in (22). Since the number of alignment matrices \(M\) in \(\mathcal{M}_{n,m}\) is finite, the parametric optimal alignment problem (24) can be characterized by a finite number of these QFs.

Figure 5 illustrates the set of QFs each of which corresponds to an alignment matrix \(M \in \mathcal{M}_{n,m}\). Since the minimum loss for each \(z \in \mathbb{R}\) is the point-wise minimum of these QFs, the DTW distance \(\hat{L}_{n,m}(z)\) in (24) is the lower envelope of the set of QFs, which is represented as a *piecewise QF* of \(z \in \mathbb{R}\). Parametric optimal alignment is interpreted as the problem of identifying this piecewise QF.

In Algorithm 1 multiple breakpoints \(z_1 < z_2 < \ldots < z_T\) are computed one by one. Each breakpoint \(z_t, t \in [T]\), indicates a point at which the optimal alignment matrix changes, where \(T\) is the number of breakpoints determined by the algorithm as described above. By finding all these breakpoints \(\{z_t\}_{t=1}^T\) and the optimal alignment matrix \(\{\hat{M}_t\}_{t=1}^{T-1}\), the piecewise QF \(\hat{L}_{n,m}(z)\) in Fig. 5 (the curves in yellow, blue, green and orange) can be identified.

The algorithm is initialized at the optimal alignment matrix for \(z_1 = -\infty\), which can be easily identified.
Figure 5: A set of quadratic functions (QFs) each of which corresponds to an alignment matrix $M \in \mathcal{M}_{n,m}$. The dotted grey QFs correspond to alignment matrices that are NOT optimal for any $z \in \mathbb{R}$. A set $\{\hat{M}_1, \hat{M}_2, \hat{M}_3, \hat{M}_4\}$ contains alignment matrices that are optimal for some $z \in \mathbb{R}$. Our goal is to introduce an approach to efficiently identify this set of optimal alignment matrices and the lower envelope in yellow, blue, green and orange.

Based on the coefficients of the QFs, at step $t$, $t \in [T]$, the task is to find the next breakpoint $z_{t+1}$ and the next optimal alignment matrix $\hat{M}_{t+1}$. This task can be done by finding the smallest $z_{t+1}$ such that $z_{t+1} > z_t$ among the intersections of the current QF $L_{n,m}(\hat{M}_t, z)$ and each of the other QFs $L_{n,m}(M, z)$ for $M \in \mathcal{M}_{n,m} \setminus \{\hat{M}_t\}$. This step is repeated until we find the optimal alignment matrix when $z_T = +\infty$. The algorithm returns the sequences of the optimal alignment matrices $\{\hat{M}_i\}_{i=1}^{T-1}$ and breakpoints $\{z_i\}_{i=1}^T$. The entire path of optimal alignment matrices for $z \in \mathbb{R}$ is given by

$$
\hat{M}_{i,j}(z) = \begin{cases} 
\hat{M}_1 & \text{if } z \in (z_1 = -\infty, z_2], \\
\hat{M}_2 & \text{if } z \in [z_2, z_3], \\
\vdots \\
\hat{M}_{T-1} & \text{if } z \in [z_{T-1}, z_T = +\infty). 
\end{cases}
$$

4.1.3 Parametric DTW

Unfortunately, the parametric optimal alignment in Algorithm 1 with the inputs $n$, $m$ and $\mathcal{M}_{n,m}$ in the previous subsection is computationally impractical because the number of all possible alignment matrices, i.e., the cardinality of the set $\mathcal{M}_{n,m}$ is exponentially increasing with $n$ and $m$. To resolve this computational issue, we utilize the concept of the standard DTW and apply it to the parametric case, which we call parametric DTW. The basic idea of the parametric DTW is to exclude the alignment matrices $M \in \mathcal{M}_{n,m}$ which can never be optimal at any $z \in \mathbb{R}$. Specifically, instead of considering a huge set $\mathcal{M}_{n,m}$, we only construct and consider a much smaller set $\hat{\mathcal{M}}_{n,m}$. Before introducing the technical details of parametric
DTW, we briefly review the standard DTW.

**Standard DTW (for a single value of \( z \)).** In the standard DTW with \( n \) and \( m \), we use \( n \times m \) table whose \((i,j)\)th element contains \( \hat{M}_{i,j}(z) \) that is the optimal alignment matrix for the sub-sequences \( X(z)_{1:i} \) and \( Y(z)_{1:j} \). The optimal alignment matrix \( \hat{M}_{i,j}(z) \) for each of the sub-problem with \( i \) and \( j \) can be used for efficiently computing the optimal alignment matrix \( \hat{M}_{n,m}(z) \) for the original problem with \( n \) and \( m \). It is well-known that the following equation, which is often called *Bellman equation*, holds:

\[
\begin{align*}
    c_{ij}(z) &= (X_i(z) - Y_j(z))^2 \\
    \hat{L}_{i,j}(z) &= c_{ij}(z) + \min \left\{ \hat{L}_{i-1,j}(z), \hat{L}_{i,j-1}(z), \hat{L}_{i-1,j-1}(z) \right\}.
\end{align*}
\]  

(25)

Equivalently, we have

\[
\hat{M}_{i,j}(z) = \arg \min_{M \in \hat{M}_{i,j}} L_{i,j}(M, z),
\]  

(26)

where

\[
\hat{M}_{i,j} = \left\{ \begin{array}{c}
    \text{vstack} \left( \hat{M}_{i-1,j}(z), (0, \ldots, 0, 1) \right) \in \mathbb{R}^{i \times j}, \\
    \text{hstack} \left( \hat{M}_{i,j-1}(z), (0, \ldots, 0, 1)^T \right) \in \mathbb{R}^{i \times j}, \\
    \left( \begin{array}{c}
    \hat{M}_{i-1,j-1}(z) \\
    0
    \end{array} \right) \in \mathbb{R}^{i \times j}
\end{array} \right\},
\]

vstack(\cdot, \cdot) and hstack(\cdot, \cdot) are vertical stack and horizontal stack operations, respectively. The Bellman equation (26) enables us to efficiently compute the optimal alignment matrix for the problem with \( n \) and \( m \) by using the optimal alignment matrices of its sub-problems.

**Parametric DTW (for all values of \( z \in \mathbb{R} \)).** The basic idea for parametric DTW is to similarly construct an \( n \times m \) table whose \((i,j)\)th element contains \( \hat{M}_{i,j}(z) \) that is a set of optimal alignment matrices that are optimal for some \( z \in \mathbb{R} \). Because the optimal alignment matrices \( \hat{M}(z) \) is fixed between two consecutive breakpoints \( z_t \) and \( z_{t+1} \) for \( t \in [T-1] \), it is given as,

\[
\hat{M}_{i,j} = \left\{ \hat{M}_t \right\}_{t=1}^{T-1} \text{ that is returned by Algorithm 1}. \]

For instance, \( \hat{M}_{i,j} \) is a set \( \{\hat{M}_1, \hat{M}_2, \hat{M}_3, \hat{M}_4\} \) in Fig. 5. To efficiently identify \( \hat{M}_{i,j} \), we construct a set \( \hat{M}_{i,j} \supseteq \hat{M}_{i,j} \), which is a set of alignment matrices having potential to be optimal at some \( z \in \mathbb{R} \). In the same way as (26), we can consider the Bellman equation for constructing \( \hat{M}_{i,j} \) as described in the following Lemma.

**Lemma 2.** For \( i \in [n] \) and \( j \in [m] \), the set of optimal alignment matrices \( \hat{M}_{i,j} \) is defined as

\[
\hat{M}_{i,j} = \arg \min_{M \in \hat{M}_{i,j}} L_{i,j}(M, z),
\]  

(27)
where $\tilde{M}_{i,j}$ is a set of alignment matrices having potential to be optimal and it is constructed as

$$\tilde{M}_{i,j} = \begin{cases} 
s\text{vstack}\left(\hat{M}, (0, \ldots, 0, 1)\right), & \forall \hat{M} \in \hat{M}_{i-1,j}, \\
s\text{hstack}\left(\hat{M}, (0, \ldots, 0, 1)^\top\right), & \forall \hat{M} \in \hat{M}_{i,j-1}, \\
s\begin{pmatrix} \hat{M} & 0 \\ 0 & 1 \end{pmatrix}, & \forall \hat{M} \in \hat{M}_{i-1,j-1} \end{cases}$$

(28)

**Proof.** We prove the lemma by showing that any alignment matrix that is NOT in $\tilde{M}_{i-1,j} \cup \tilde{M}_{i,j-1} \cup \tilde{M}_{i-1,j-1}$ will never be a sub-matrix of the optimal alignment matrices in larger problem with $i$ and $j$ for any $z \in \mathbb{R}$.

Let $\mathbb{R}^{(i-1)\times j} \ni M \notin \tilde{M}_{i-1,j}$ be the alignment matrix that is NOT optimal for all $z \in \mathbb{R}$, i.e.,

$$L_{i-1,j}(M, z) > \hat{L}_{i-1,j}(z) \quad \forall z \in \mathbb{R}.$$

It suggests that, for any $z \in \mathbb{R}$ and $c_{ij}(z) = (X_i(z) - Y_i(z))^2$,

$$L_{i-1,j}(M, z) + c_{ij}(z) > \min_{\hat{M} \in \hat{M}_{i-1,j}} L_{i-1,j}(\hat{M}, z) + c_{ij}(z) = \hat{L}_{i-1,j}(z) + c_{ij}(z) \geq \hat{L}_{i,j}(z).$$

Thus, $M$ cannot be a sub-matrix of the optimal alignment matrices in larger problem with $i$ and $j$ for any $z \in \mathbb{R}$. Similar proofs can be applied for $\mathbb{R}^{i\times (j-1)} \ni M \notin \tilde{M}_{i,j-1}$ and $\mathbb{R}^{(i-1)\times (j-1)} \ni M \notin \tilde{M}_{i-1,j-1}$.

In other words, only the alignment matrices in $\tilde{M}_{i-1,j} \cup \tilde{M}_{i,j-1} \cup \tilde{M}_{i-1,j-1}$ can be used as the sub-matrix of optimal alignment matrices for larger problems with $i$ and $j$. ■

From Lemma 2, we can efficiently construct $\tilde{M}_{i,j}$. Then, $\tilde{M}_{i,j}$ is used to compute $\hat{M}_{i,j}$ by calling `paraOptAlignOnSubProblem(i, j, $\tilde{M}_{i,j}$)` in Algorithm 2. Here, we note that Algorithm 2 is similar to Algorithm 1 which is presented in Sec 4.1.1. The main difference is that we now solving parametric optimal alignment on smaller problem with $i, j$ and $\hat{M}_{i,j}$. By repeating the recursive procedure and storing $\hat{M}_{i,j}$ in the $(i,j)^{th}$ element of the table from smaller $i$ and $j$ to larger $i$ and $j$, we can end up with $\hat{M}_{n,m} \supseteq \hat{M}_{n,m}$.

By using parametric DTW, the size of $\hat{M}_{n,m}$ can be much smaller than the size of all possible alignment matrices $M_{n,m}$, which makes the computational cost of `paraOptAlignOnSubProblem(n, k, $\hat{M}_{n,m}$)` can be substantially decreased compared to `paraOptAlign(n, k, M_{n,m})` in Algorithm 1 of Sec 4.1.1. The parametric DTW method is presented in Algorithm 3.

### 4.2 Construction of $Z_2$ in (19)

Now, we present the construction of $Z_2$ in the following Lemma.
Algorithm 2 \text{paraOptAlignOnSubProblem}(i,j,\hat{M}_{i,j})

\textbf{Input: } i,j, M_{i,j}

1: \( t \leftarrow 1, z_1 \leftarrow -\infty, \)
   \( \hat{M}_t \leftarrow \hat{M}_{i,j}(z_1) = \arg \min_{M \in M_{i,j}} L(M,z_t) \)
2: \( \text{while } z_t < +\infty \) \( \text{do} \)
3: \( \text{Find the next breakpoint } z_{t+1} > z_t \) and the next optimal alignment matrix \( \hat{M}_{t+1} \) s.t.
   \[ L_{i,j}(\hat{M}_t, z_{t+1}) = L_{i,j}(\hat{M}_{t+1}, z_{t+1}). \]
4: \( t \leftarrow t + 1 \)
5: \( \text{end while} \)
6: \( T \leftarrow t \)

\textbf{Output: } \{\hat{M}_t\}_{t=1}^{T-1}, \{z_t\}_{t=1}^{T}

Algorithm 3 \text{paraDTW}(X(z), Y(z))

\textbf{Input: } X(z) \text{ and } Y(z)

for \( i = 1 \) to \( n \)
   for \( j = 1 \) to \( m \)
1: \( \hat{M}_{i,j} \leftarrow \text{Eq. 28} \)
2: \( \{M_t\}_{t=1}^{T-1}, \{z_t\}_{t=1}^{T} \leftarrow \text{paraOptAlignOnSubProblem}(i,j,\hat{M}_{i,j}) \) \( \// \) Algorithm 2
3: \( \hat{M}_{i,j} \leftarrow \{\hat{M}_t\}_{t=1}^{T-1} \)
4: \( \text{end for} \)
5: \( \text{end for} \)

\textbf{Output: } \hat{M}_{n,m}

Lemma 3. The set \( Z_2 \) in (19) is an interval defined as:

\[ Z_2 = \left\{ z \in \mathbb{R} \mid \max_{j: \nu_j(2) > 0} \frac{-\nu_j(1)}{\nu_j(2)} \leq z \leq \min_{j: \nu_j(2) < 0} \frac{-\nu_j(1)}{\nu_j(2)} \right\}, \]

where \( \nu(1) = \hat{s}_{\text{obs}} \circ \hat{M}_{\text{vec}} \circ \Omega a \) and \( \nu(2) = \hat{s}_{\text{obs}} \circ \hat{M}_{\text{vec}} \circ \Omega b \).

Proof. Let us first remind that \( \hat{s} = S(X,Y) = \text{sign} \left( \hat{M}_{\text{vec}} \circ \left[ \Omega(XY) \right]^\top \right) \), which is defined in (7). Then, the set \( Z_2 \) can be re-written as follows:

\[ Z_2 = \left\{ z \in \mathbb{R} \mid S(a + b)z = \hat{s}_{\text{obs}} \right\} = \left\{ z \in \mathbb{R} \mid \text{sign} \left( \hat{M}_{\text{vec}} \circ \Omega(a + bz) \right) = \hat{s}_{\text{obs}} \right\} = \left\{ z \in \mathbb{R} \mid \hat{s}_{\text{obs}} \circ \hat{M}_{\text{vec}} \circ \Omega(a + bz) \geq 0 \right\}. \]

By defining \( \nu(1) = \hat{s}_{\text{obs}} \circ \hat{M}_{\text{vec}} \circ \Omega a \) and \( \nu(2) = \hat{s}_{\text{obs}} \circ \hat{M}_{\text{vec}} \circ \Omega b \), the result of Lemma 3 is straightforward by solving the above system of linear inequalities. \( \blacksquare \)

After computing \( Z_2 \), we obtain \( Z = Z_1 \cap Z_2 \) and compute the selective p-value in (17) for conducting the inference. The entire proposed SI-DTW method for computing selective p-values is summarized in Algorithm 4.
Algorithm 4 Proposed SI Method (SI-DTW)

Input: $X^{\text{obs}}$ and $Y^{\text{obs}}$

1: $\hat{M}^{\text{obs}} \leftarrow A(X^{\text{obs}}, Y^{\text{obs}})$
2: $X(z)$ and $Y(z) \leftarrow \text{Eq. (20)}$ // Algorithm 2
3: $\hat{M}_{n,m} \leftarrow \text{paraDTW}(X(z), Y(z))$ // Algorithm 3
4: $Z_1 \leftarrow \bigcup_{z \in \hat{M}_{n,m}} \{z : \hat{M}_{n,m}(z) = \hat{M}^{\text{obs}}\}$
5: $Z_2 \leftarrow \text{Lemma 3}$
6: $Z = Z_1 \cap Z_2$
7: $p_{\text{selective}} \leftarrow \text{Eq. (17)}$

Output: $p_{\text{selective}}$

5 Experiment

In this section, we demonstrate the performance of the proposed method.

5.1 Methods for Comparison

We compared our SI-DTW method with the following approaches:

- **SI-DTW-oc**: this is our first idea of introducing conditional SI for time-series similarity using the DTW by additionally conditioning on all the operations of the DTW algorithm itself to make the problem tractable. Then, since the selection event of SI-DTW-oc is simply represented as a single polytope in the data space, we can apply the method in the seminal conditional SI paper [11] to compute the over-conditioning $p$-value. The details are shown in Appendix A. However, such an over-conditioning leads to a loss of statistical power [11, 7]. Later, this drawback was removed by the SI-DTW method in this paper.

- **Data splitting (DS)**: an approach that divides the dataset in half based on even and odd indices, and uses one for computing the DTW distance and the other for inference.

- **Permutation**: the procedure is described as follows ($X$ and $Y$ are required to have the same length, i.e., $n = m$):
  - Compute the observed test statistic $T^{\text{obs}}$ based on $X^{\text{obs}}$ and $Y^{\text{obs}}$
  - For $1 \leftarrow b$ to $B$ ($B$ is the number of permutations which is given by user)
    * Construct $X^{(b)}$ and $Y^{(b)}$ where $(x_i^{(b)}, y_i^{(b)}) \leftarrow \text{permute}(x_i^{\text{obs}}, y_i^{\text{obs}})$
    * Compute $T^{(b)}$ based on $X^{(b)}$ and $Y^{(b)}$
  - Compute the $p$-value $p_{\text{permutation}} = \frac{1}{B} \sum_{b=1}^{B} 1 \{T^{\text{obs}} \leq T^{(b)}\}$, where $1\{\cdot\}$ is the indicator function.
5.2 Experimental Setup

We considered the following covariance matrices:

- **Independence**: $\Sigma_X = I_n, \Sigma_Y = I_m$.
- **Correlation**: $\Sigma_X = [0.5^{\text{abs}(i-i')}]_{i'i'} \in \mathbb{R}^{n \times n}, \Sigma_Y = [0.5^{\text{abs}(j-j')}]_{jj'} \in \mathbb{R}^{m \times m}$.

We generated $X$ and $Y$ with $\mu_X = 0_n, \mu_Y = 0_m + \Delta$ (element-wise addition), $\varepsilon_X \sim N(0_n, \Sigma_X)$, and $\varepsilon_Y \sim N(0_m, \Sigma_Y)$. Regarding the False Positive Rate (FPR) experiments, we set $\Delta = 0$, and ran 120 trials for each $n = m \in \{5, 10, 15, 20\}$. In regard to the True Positive Rate (TPR) experiments, we set $n = m = 10$, and ran 120 trials for each $\Delta \in \{1, 2, 3, 4, 5\}$. The experiments are repeated 10 times. Respecting the confidence interval experiments, we set $n = m = 10$, and ran 120 trials for each $\Delta \in \{2, 3, 4, 5\}$. Regarding the computational time experiments, we set $\Delta = 2$ and ran 10 trials for each $n = m \in \{5, 10, 15, 20\}$. The setup of the robustness experiments were similar to the FPR experiments and we considered the following cases:

- **Non-normal noise**: the noises $\varepsilon_X$ and $\varepsilon_Y$ following Laplace distribution, skew normal distribution (skewness coefficient: 10), and $t_{20}$ distribution.
- **Unknown variance**: the variances of the noises were estimated from the data.

We set the significance level $\alpha = 0.05$ (we additionally set $\alpha = 0.1$ for the robustness experiments).

5.3 Numerical Result

The results of the FPR control are shown in Fig. 6. The proposed methods (SI-DTW and SI-DTW-oc) successfully control the FPR in both cases of independence and correlation whereas the permutation and DS could not. Because the permutation and DS failed to control the FPR, we no longer considered the TPR.
The result of TPR experiments are shown in Fig. 7. The SI-DTW has higher TPR than the SI-DTW-oc in all the cases. The TPR results are consistent with the confidence interval (CI) results in Fig. 8, i.e., The SI-DTW has higher TPR than SI-DTW-oc which indicates it has shorter CI. Additionally, we demonstrate the robustness of the proposed method in terms of the FPR control. The results are shown in Fig. 9. Our method still maintains good performance on FPR control.

5.4 Real-data Examples

We evaluate the proposed SI-DTW on three datasets that are available at UCR Time Series Classification Repository: Italy Power Demand (Class C1: days from Oct to March, Class C2: days from April to September), Melbourne Pedestrian (Class C1: Bourke Street Mall, Class C2: Southern Cross Station) and Smooth Subspace (Class C1: smooth subspace spanning from time stamp 1 to 5, Class C2: smooth subspace spanning from time stamp 11 to 15). The experiments were conducted with the following setting:

- Given a time-series dataset with two classes C1 and C2
- for $i \leftarrow 1$ to 120 do
Figure 9: The robustness of the proposed method in terms of the FPR control.

(a) Laplace distribution
(b) Skew normal distribution
(c) t_{20} distribution
(d) Estimated variance

Figure 10: Boxplots of p-values.

- We randomly chose one time-series from C1 and one time-series from C2
- Compute p-values of the SI-DTW and SI-DTW-oc
  - Showing boxplot of p-values obtained from each method
The results are shown in Fig 10. In all the cases, the selective p-value of the SI-DTW tended to be smaller than that of SI-DTW-oc, which indicates that the SI-DTW had higher TPR than SI-DTW-oc.

6 Conclusion

We present an exact (non-asymptotic) inference method for the DTW distance between two time-series obtained by DTW. We first introduce the characterization of the exact sampling distribution of the test statistic by conditioning on the selection event of selecting the optimal alignment, which is inspired by the concept of conditional SI. Then, we introduce the valid selective p-value for conducting the exact statistical inference. After that, we introduce new efficient method to address the computational bottleneck of computing the proposed selective p-value. Finally, we conduct the experiments on both synthetic and real-world datasets to evaluate the performance of our method. We believe this study is an important contribution toward reliable Machine Learning (ML), which is one of the most critical issues in the ML community.

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A Derivation of the SI-DTW-oc method mentioned in Sec. 5

This is our first idea of introducing conditional SI for time series similarity using DTW by additionally conditioning on all the operations of the DTW algorithm itself to make the problem tractable. Then, since the selection event of SI-DTW-oc is simply represented as a single polytope in the data space, we can apply the method in the seminal conditional SI paper [11] to compute the over-conditioning $p$-value. However, such an over-conditioning leads to a loss of statistical power [11, 7], i.e., low TPR.

Notation. We denote $D_{oc}$ as the over-conditioning data space in SI-DTW-oc. The difference between $D$ in (14) and $D_{oc}$ is that the latter is characterized with additional constraints on all the operations of the DTW algorithm. For two time series with lengths $i \in [n]$ and $j \in [m]$, a set of all possible alignment matrices is defined as $M_{i,j}$. Given $X \in \mathbb{R}^n$ and $Y \in \mathbb{R}^m$, the loss between their sub-sequence $X_{1:i}$ and $Y_{1:j}$ with $M \in M_{i,j}$ is written as

$$L_{i,j}(X, Y, M) = \langle M, C(X_{1:i}, Y_{1:j}) \rangle$$

Then, the DTW distance and the optimal alignment matrix between $X_{1:i}$ and $Y_{1:j}$ are respectively written as

$$\hat{L}_{i,j}(X, Y) = \min_{M \in M_{i,j}} L_{i,j}(X, Y, M)$$

$$\hat{M}_{i,j}(X, Y) = \arg \min_{M \in M_{i,j}} L_{i,j}(X, Y, M).$$

Characterization of the over-conditioning conditional data space $D_{oc}$. Since the inference is conducted with additional conditions on all steps of the DTW, the conditional data space $D_{oc}$ is written as

$$D_{oc} = \left\{ \begin{array}{l}
(X, Y) \mid \bigcap_{i=1}^{n} \bigcap_{j=1}^{m} \hat{M}_{i,j}(X, Y) = \hat{M}_{i,j}^{obs}, \\
S(X, Y) = \hat{s}^{obs}, \quad Q(X, Y) = \hat{q}^{obs} \end{array} \right\},$$

where $\hat{M}_{i,j}^{obs} = \hat{M}_{i,j}(X^{obs}, Y^{obs})$. The characterization of the third condition $Q(X, Y) = \hat{q}^{obs}$ is a line in the data space as presented in Lemma. The characterization of the second condition $S(X, Y) = \hat{s}^{obs}$ is
the same as Lemma 3. Therefore, the remaining task is to characterize the region in which the data satisfies the first condition.

For each value of $i \in [n]$ and $j \in [m]$, $M_{i,j}(X, Y) = M_{i,j}^{\text{obs}}$ if and only if

$$\min_{M \in M_{i,j}} L_{i,j}(X, Y, M) = L_{i,j}(X^{\text{obs}}, Y^{\text{obs}}, M_{i,j}^{\text{obs}})$$

$$\Leftrightarrow \hat{L}_{i,j}(X, Y) = L_{i,j}(X^{\text{obs}}, Y^{\text{obs}}, M_{i,j}^{\text{obs}}).$$

Based on the recursive structure of DTW, we have

$$\hat{L}_{i,j}(X, Y) = C_{ij}(X, Y) + \min \left\{ \hat{L}_{i-1,j}(X, Y), \hat{L}_{i,j-1}(X, Y) \right\}. \quad (32)$$

Combining (31) and (32), we have the following inequalities

$$L_{i,j}(X^{\text{obs}}, Y^{\text{obs}}, M_{i,j}^{\text{obs}}) \leq C_{ij}(X, Y) + \hat{L}_{i-1,j}(X, Y),$$

$$L_{i,j}(X^{\text{obs}}, Y^{\text{obs}}, M_{i,j}^{\text{obs}}) \leq C_{ij}(X, Y) + \hat{L}_{i,j-1}(X, Y),$$

$$L_{i,j}(X^{\text{obs}}, Y^{\text{obs}}, M_{i,j}^{\text{obs}}) \leq C_{ij}(X, Y) + \hat{L}_{i-1,j-1}(X, Y). \quad (33)$$

Since the loss function is in the quadratic form, (33) can be easily written in the form of

$$(X Y)^T A_{i,j}^{(1)} (X Y) \leq 0,$$

$$(X Y)^T A_{i,j}^{(2)} (X Y) \leq 0,$$

$$(X Y)^T A_{i,j}^{(3)} (X Y) \leq 0,$$

where the matrices $A_{i,j}^{(1)}$, $A_{i,j}^{(2)}$ and $A_{i,j}^{(3)}$ depend on $i$ and $j$. It suggests that the conditional data space in (29) can be finally characterized as

$$D^{\text{oc}} = \left\{ X \left( \begin{array}{c} X Y \end{array} \right) \begin{array}{c} \sum_{i=1}^{n} \sum_{j=1}^{m} \sum_{k=1}^{3} (X Y)^T A_{i,j}^{(k)} (X Y) \leq 0, \end{array} \begin{array}{c} S(X, Y) = s^{\text{obs}}, Q(X, Y) = q^{\text{obs}} \end{array} \right\}. \quad (34)$$

Now that the conditional data space $D^{\text{oc}}$ is identified, we can easily compute the truncation region and calculate the over-conditioning selective $p$-value.