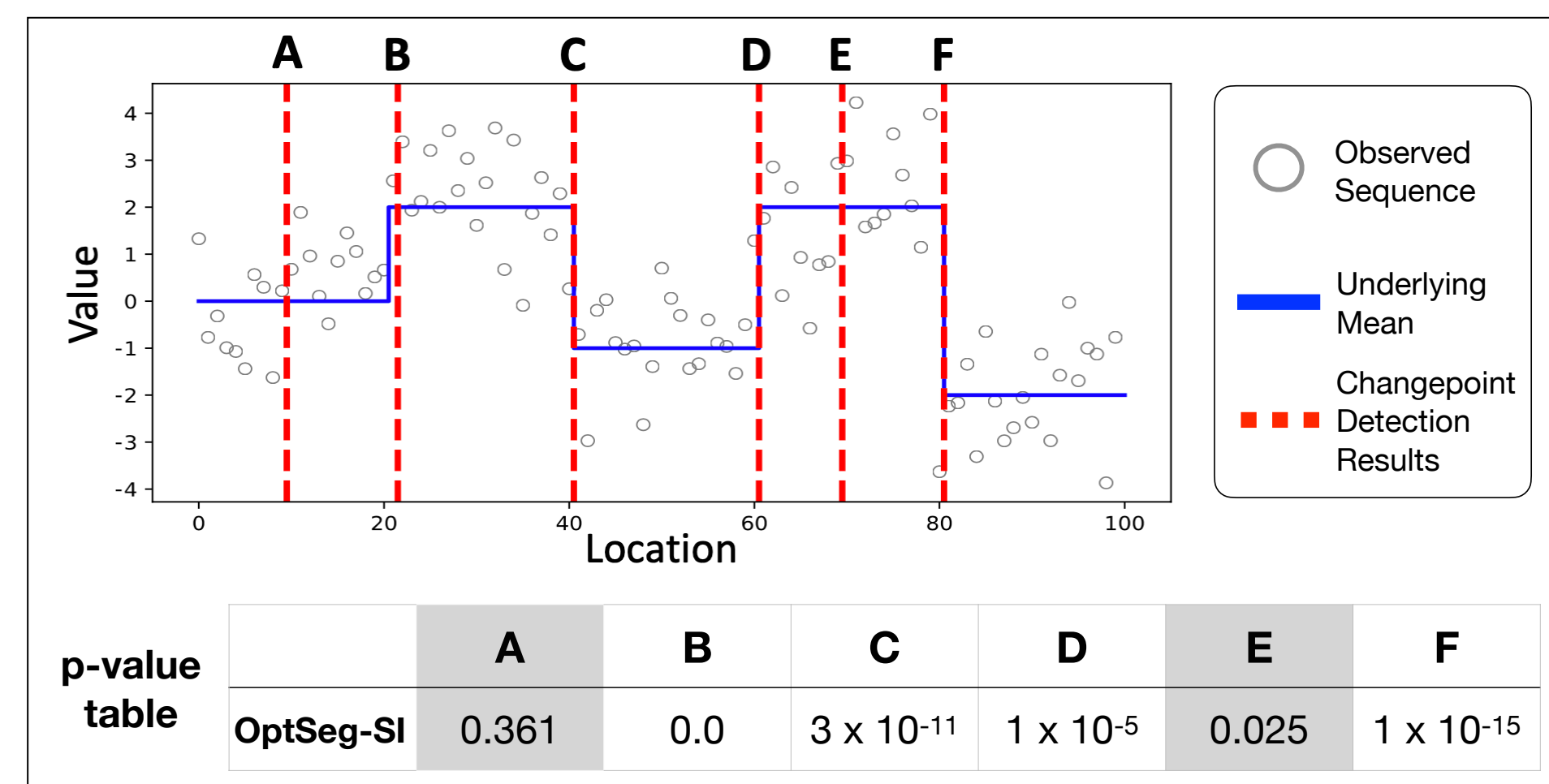


Computing Valid p -value for Optimal Changepoint by Selective Inference using Dynamic Programming

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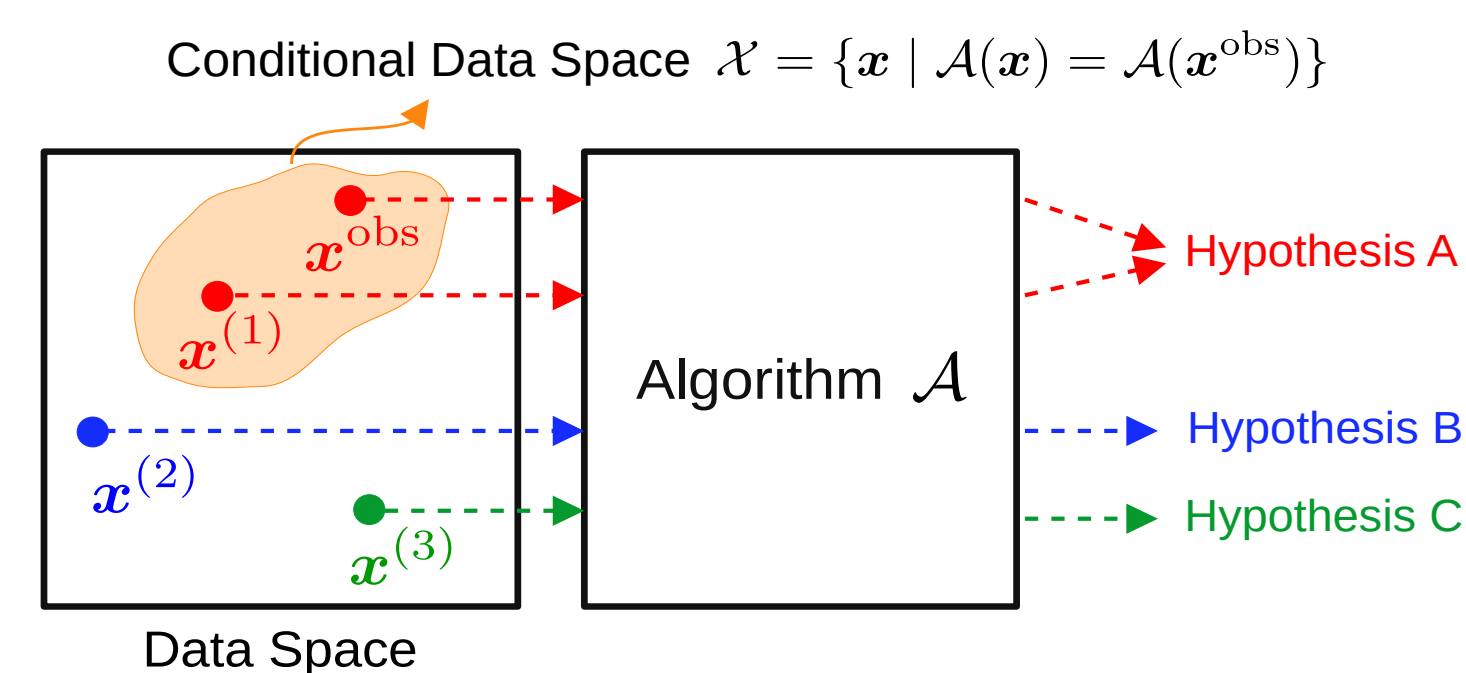
Introduction and Motivation

- ❖ **Changepoint (CP) detection**: find changes in the underlying mechanism of the observed sequential data.
- ❖ CP detection is usually formulated as the problem of minimizing the segmentation cost where **Dynamic Programming (DP)** is commonly used.
- ❖ There are several CP detection methods. However, **less attention** has been paid to **quantify the reliability** of the detected CPs.



- ❖ **A and E** are **falsely detected** CPs
 - ➔ Results from CP detection algorithms are **unreliable**
 - ➔ **Harmful** for high-stake decision making such as medical diagnosis
- ❖ We propose **OptSeg-SI** method to provide **valid p -value**, which is used as a criterion to **quantify the reliability** of the detected CPs, based on the concept of **Selective Inference (SI)**.
 - ➔ Large p -value indicates false detection (**A and E**) and small p -value indicates true detection (**B, C, D and F**)
 - ➔ OptSeg-SI can identify both false and true positive detections

Concept of Selective Inference (SI)

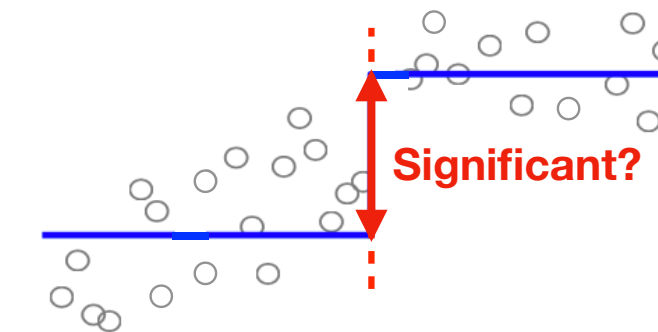


Conditional inference: $\Pr(T(x) \mid \mathcal{A}(x) = \mathcal{A}(x^{\text{obs}}))$, where $T(x)$ is the test statistic.

Problem Setting

- ❖ We consider the following statistical test

$$H_0 : \mu_{\text{left}} = \mu_{\text{right}} \quad \text{vs.} \quad H_1 : \mu_{\text{left}} \neq \mu_{\text{right}}$$



where μ is population mean.

- ❖ The conditional p -value (**selective p -value**) is defined as

$$p_{\text{selective}} = \mathbb{P}_{H_0}(|\Delta| \geq |\Delta^{\text{obs}}| \mid \mathcal{X})$$

- Δ^{obs} is the **difference in sample mean** between the left segment and right segment in the **observed** sequence
- Δ is the mean difference in **any random sequence**
- \mathcal{X} is the **conditional data space** defined as

$$\mathcal{X} = \{x : \{\text{left, right}\} \leftarrow \text{DP algorithm } \mathcal{A}(x)\}$$

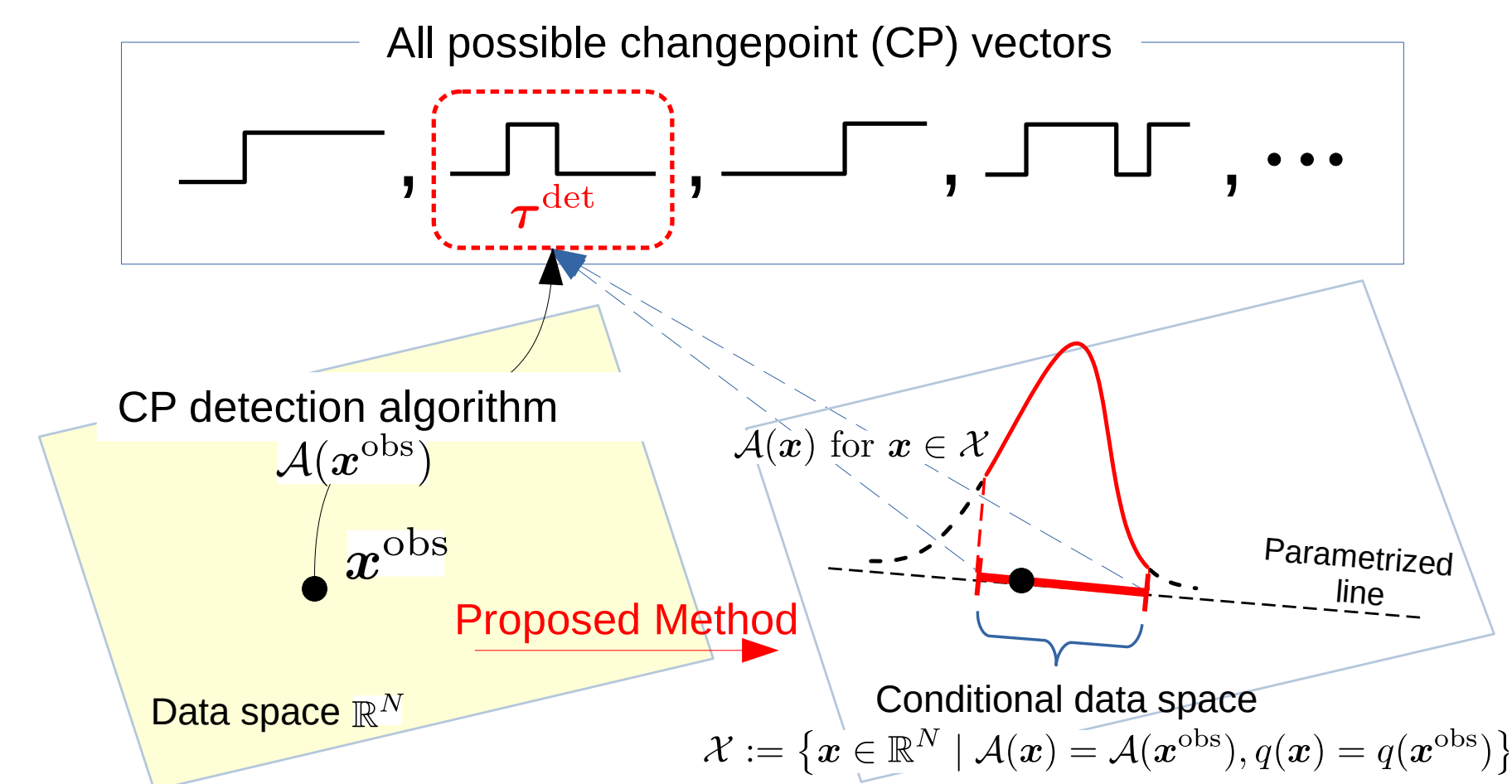
- ❖ In other words, \mathcal{X} is the data space whose data has the same detected CP as the observed sequence.

- ❖ The selective p -value is **valid** since

$$\mathbb{P}_{H_0}(p_{\text{selective}} < \alpha) = \alpha, \quad \forall \alpha \in [0, 1].$$

However, **characterization of the conditional data space \mathcal{X}** is challenging

Proposed Method - Schematic illustration



- ❖ **Step 1**: Obtain CP results from the observed data x^{obs}
- ❖ **Step 2**: By restricting data on the line, we perform DP on parametrized data and identify the sub-space whose data has the same CP results as x^{obs}

Proposed Method - Details

- ❖ We first restrict the data to the **line** by using a **scalar parameter** $z \in \mathbb{R}$

$$x(z) = a + bz,$$

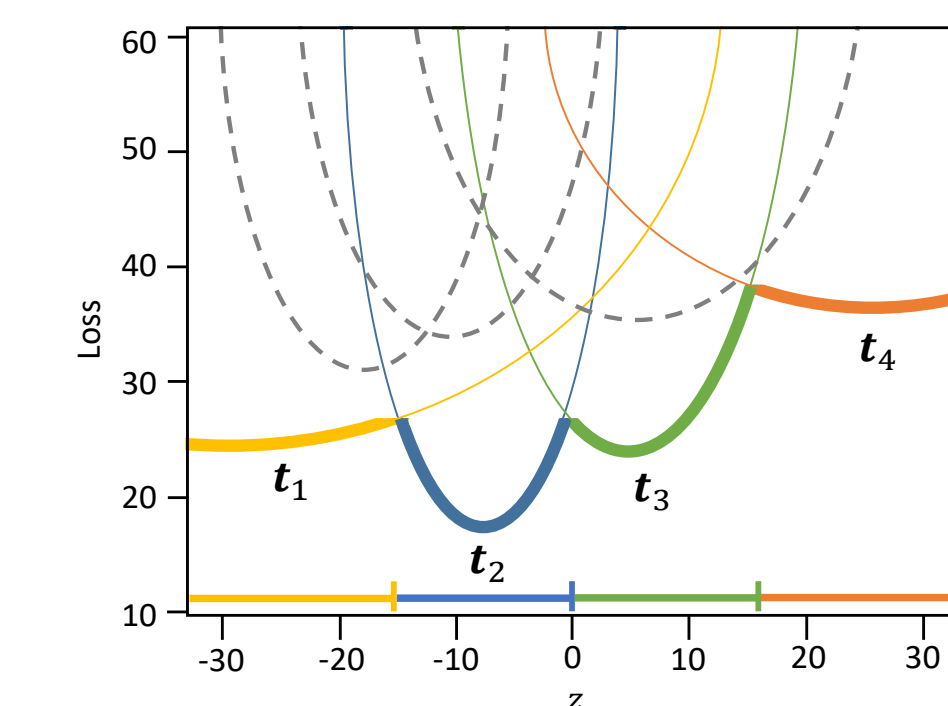
where a and b have specific forms.

- ❖ The conditional data space \mathcal{X} is then re-written as

$$\mathcal{X} = \{x(z) = a + bz \mid z \in \mathcal{Z}\},$$

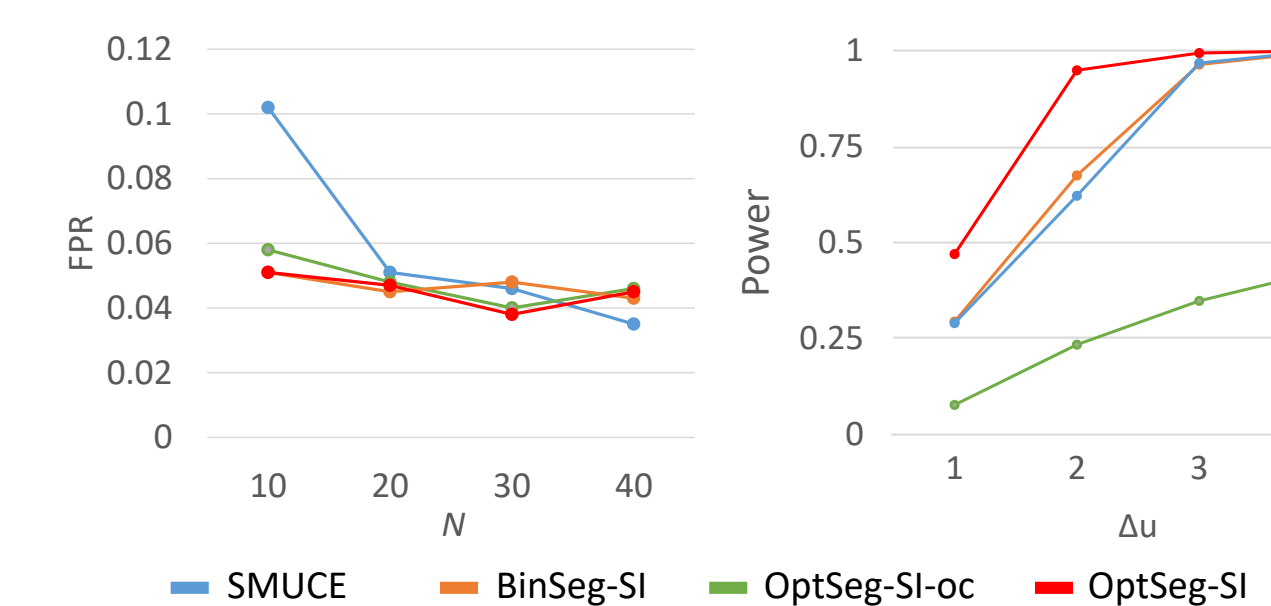
where $\mathcal{Z} = \{z \in \mathbb{R} : \{\text{left, right}\} \leftarrow \text{DP algorithm } \mathcal{A}(x(z))\}$.

⇒ **The remaining task is to identify truncation region \mathcal{Z}**

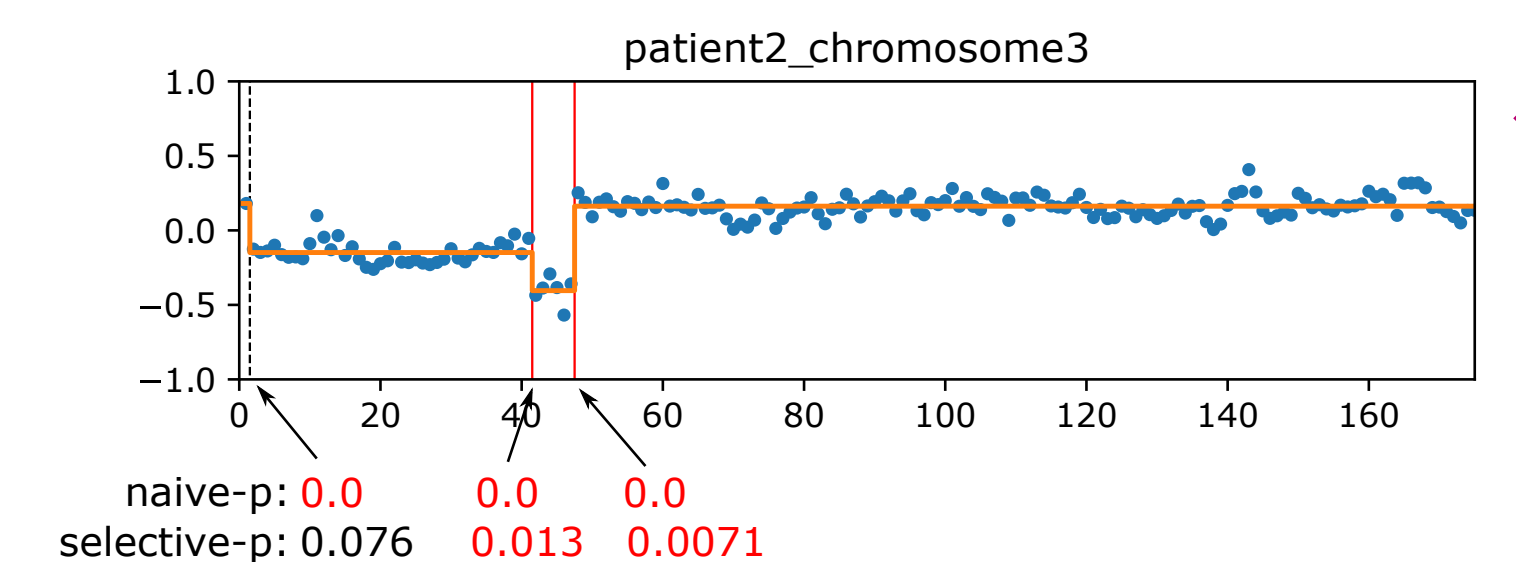


- ❖ We propose a **parametric DP** approach to compute CP results of $x(z)$ for all $z \in \mathbb{R}$
- ❖ The region \mathcal{Z} is then the union of **intervals of z** on which we obtain the same CP results as the observed data

Experimental Results



- ❖ The OptSeg-SI method (red) is powerful while successfully controlling the false positive rate (FPR)



- ❖ Application to real-world bioinformatics dataset

References

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