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CHANGE POINT DETECTION FOR HIGH-DIMENSIONAL LINEAR MODELS: A GENERAL TAIL-ADAPTIVE APPROACH

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Abstract: We propose a novel approach for detecting change points in high-dimensional linear regression models. Unlike previous research that relies on strict Gaussian/sub-Gaussian error assumptions and has prior knowledge of change points, we propose a tail-adaptive method for change point detection and estimation. We use a weighted combination of composite quantile and least squared losses to build a new loss function, allowing us to leverage information from both conditional means and quantiles. For change point testing, we develop a family of individual testing statistics with different weights to account for unknown tail structures. These individual tests are further aggregated to construct a powerful tail-adaptive test for sparse regression coefficient changes. For change point estimation, we propose a family of argmax-based individual estimators. We provide theoretical justifications for the validity of these tests and change point estimators. Additionally, we introduce a new algorithm for detecting multiple change points in a tail-adaptive manner using the wild binary segmentation. Extensive numerical results show the effectiveness of our proposed method.

Key words and phrases: Binary segmentation, bootstrap, heterogeneity, multiple change points.

1. Introduction

With the advances of data collection and storage capacity, large scale/high-dimensional data are ubiquitous in many scientific fields ranging from genomics, finance, to social science. Due to the complex data generation mechanism, the heterogeneity, also known as the structural break, has become a common phenomenon for high-dimensional data, where the underlying model of data generation changes and the identically distributed assumption may not hold anymore. Change point analysis is a powerful tool for handling structural changes since the seminal work by Page (1955). It received considerable attentions in recent years and has a lot of real applications in various fields including genomics (Liu et al., 2020), social science (Roy, Atchadé and Michailidis, 2017), and even the recent COVID-19 pandemic studies (Jiang, Zhao and Shao, 2022). Motivated

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