Framework for unveiling change points in multivariate signals with non-Gaussian patterns

1st Justyna Witulska
Faculty of Pure and Applied Mathematics
Wrocław University of Science and Technology
Wrocław, Poland
justyna.witulska@pwr.edu.pl

2nd Marta Hendler
Faculty of Fundamental Problems of Technology
Wrocław University of Science and Technology
Wrocław, Poland
marta.hendler@pwr.edu.pl

3rd Magdalena Kasprowicz
Faculty of Fundamental Problems of Technology
Wrocław University of Science and Technology
Wrocław, Poland
magdalena.kasprowicz@pwr.edu.pl

4th Marek Czosnyka
Department of Clinical Neurosciences
Addenbrooke's Hospital
University of Cambridge
Cambridge, UK
mc141@medschl.cam.ac.uk

5th Agnieszka Wyłomańska
Faculty of Pure and Applied Mathematics
Wrocław University of Science and Technology
Wrocław, Poland
agnieszka.wylomanska@pwr.edu.pl

6th Ireneusz Jabłoński
Fraunhofer IPMS
Dresden, Germany
Faculty MINT
Brandenburg University of Technology
Cottbus, Germany
ireneusz.jablonski@ipms.fraunhofer.de

***Abstract*—This study focuses on the challenge of monitoring and managing complex systems by distinguishing sequential states while observing multiple variables. We introduce a methodology for change point detection in multivariate data with non-Gaussian distribution based on fusion techniques, underpinned by multivariate statistical test based on the Cramer-von-Mises approach. To evaluate the performance of our method, we conducted a comparative analysis with established baseline techniques, namely e-Divisive and Kernel Change Point Analysis methods, using a multivariate sub-Gaussian distribution. Finally, we demonstrate the practical applicability of our approach by showing its ability to reduce invasiveness in detecting intracranial hypertension events during neurointensive monitoring of traumatic brain injury patient by identifying the temporal distribution structure in multivariate data.**

***Index Terms*—multivariate data change point detection, two-sample test, non-Gaussian distributions, multisensor fusion, intracranial hypertension detection**

I. Introduction

From finance and healthcare to industrial purposes and beyond, efficient time series modeling underpins a wide range of applications. While measurement data exploration strategies originated in the artificial intelligence/machine learning have achieved success, their requirement to access relatively big-size training data and reliance on global context limits scalability for lengthy sequences due to an increase in computational cost with sequence length. Recent research on statistical techniques suggests that they can achieve comparable performance with lower complexity [1]. However, the heterogeneity and non-stationary characteristics of time series data continue to challenge the ability of single models to capture complex temporal dynamics, especially in the long-term monitoring of complex systems and processes, relevant, for example, for the conception of autonomous systems. The challenge is even greater regarding the need for joint inference of multisensor data streams, required to understand and manage this complexity, which can exhibit non-Gaussian patterns.

Detecting change points that indicate transitions between different statistical regimes is a fundamental requirement in various scientific and engineering fields, such as seismic, climatic, bioinformatics, quality control, monitoring complex systems, and financial data analysis, see e.g. [2], [3]. Change point estimation techniques are designed to identify shifts in univariate or multivariate data. For univariate data, the variety of segmentation methods is considerably wider, encompassing both parametric and nonparametric approaches. Notably, there are specific segmentation methods tailored for non-Gaussian univariate data, see e.g. [4], [5]. There are significantly fewer methods that effectively detect changes in multivariate data, and most of these approaches assume a Gaussian distribution [6]. Despite the focus on multivariate data analysis, researchers often concentrate on a single attribute of the multivariate sample, leading to methods that are typically designed for specific, well-defined tasks rather than general-purpose applications, see e.g. [7]. Although more general methods do exist, their effectiveness can vary depending on the characteristics of the sample being analyzed. A general segmentation methods for univariate or multivariate data include e-Divisive [7] and Kernel Change Point Analysis (KCPA) [8], which rely on energy statistics and kernel-based measures, respectively. Other examples of methods for segmenting multivariate data include MultiRank, which is based on rank statistics [9], and DeCon, a procedure [10] for detecting emotional concordance, particularly when identifying changes in mean and covariance.

In this article a general framework for change point identification in a multivariate data is proposed. The method aims

to identify the locations of change points by examining the distributional characteristics of multivariate data with a non-Gaussian distribution, which is particularly important in practical applications. We utilize here the methodology based on the Cramer-von-Mises (CvM) test [11] dedicated to the analysis of multivariate random samples. Although we propose using the CvM test, however, any other test for equal distributions could be applied in this general framework; see, e.g. [12]. Our approach does not assume any specific distribution of the data and can be efficient regardless of which parameter(s) of the multivariate distribution changes over time.

The efficiency of the algorithm proposed in this article is verified for the general class of multivariate non-Gaussian distributions, namely $\alpha-$stable class [13] with special emphasis on the sub-Gaussian distribution. The results received are compared with the general benchmark techniques dedicated to multivariate data segmentation, namely e-Divisive and KCPA. Finally, the illustrative example presents a possible application of presented methodology to the multimodal brain monitoring performed in the intensive care setting. There are two advantages demonstrated by this use case: a) fundamental - the work contributes to the so-called hybrid modeling, which combines data-driven and model-based approaches and b) applications - it is possible to indirectly monitor changes in a signal that is typically accessible only through invasive means, by tracking and segmenting related quantities measured non-invasively.

II. Mathematical formulation of the problem and description of the segmentation technique

The problem discussed in this article, i.e. partitioning a multivariate random sample into segments exhibiting identical probabilistic properties, can be expressed in mathematical terms. Let $\mathbf{X}_1, \mathbf{X}_2, ..., \mathbf{X}_N$ $(N \in \mathbb{N})$ be a $d-$dimensional random sample that follows the following model

$$\mathbf{X}_i \stackrel{d}{=} \begin{cases} \mathbf{X}^{(1)} \sim F_1, & \text{for } 1 \leq i < n_1, \\ \mathbf{X}^{(2)} \sim F_2, & \text{for } n_1 \leq i < n_2, \\ ... & \\ \mathbf{X}^{(R)} \sim F_R, & \text{for } n_{R-1} \leq i < N. \end{cases} \tag{1}$$

In this context, $n_1, n_2, ..., n_{R-1}$ denote the change points, while $F_1, F_2, ..., F_R$ correspond to the cumulative distribution functions (CDFs) of the $d-$dimensional random vectors associated with the respective regimes.

Generally, dividing $\mathbf{X}_1, \mathbf{X}_2, ..., \mathbf{X}_N$ into homogeneous segments based on change points is called *segmentation* [14]. By homogeneous segments, we mean that the $d-$dimensional random variables within each segment share the same CDF. The goal of our research is to estimate the change points using the $d-$dimensional data, without requiring prior knowledge of the CDFs $F_1, F_2, ..., F_R$.

The proposed change point detection algorithm is as follows. First, a given realization $\mathbf{x}_1, \mathbf{x}_2, ..., \mathbf{x}_N$ of the $d-$dimensional random sample $\mathbf{X}_1, \mathbf{X}_2, ..., \mathbf{X}_N$ from the model (1) is divided into subsamples of length ω. Specifically, the subsamples consist of consecutive $d-$dimensional vectors of length ω derived from $\mathbf{x}_1, \mathbf{x}_2, ..., \mathbf{x}_N$ with a specified overlap of o. The subsamples are defined as follows

$$\begin{cases} \vec{\mathbf{y}}_1 = (\mathbf{x}_1, \mathbf{x}_2, ..., \mathbf{x}_\omega), \ \vec{\mathbf{v}}_1 = (\mathbf{x}_{\omega+1}, \mathbf{x}_{\omega+2}, ..., \mathbf{x}_{2\omega}) \\ \vec{\mathbf{y}}_2 = (\mathbf{x}_{1+o}, ..., \mathbf{x}_{\omega+o}), \ \vec{\mathbf{v}}_2 = (\mathbf{x}_{\omega+1+o}, ..., \mathbf{x}_{2\omega+o}) \\ \dots \\ \vec{\mathbf{y}}_K = (\mathbf{x}_{N-2\omega+1}, ..., \mathbf{x}_{N-\omega}), \ \vec{\mathbf{v}}_K = (\mathbf{x}_{N-\omega+1}, ..., \mathbf{x}_N). \end{cases}$$

Then, for K pairs of subsamples $\vec{\mathbf{y}}_1$ and $\vec{\mathbf{v}}_1$, $\vec{\mathbf{y}}_2$ and $\vec{\mathbf{v}}_2$, ..., $\vec{\mathbf{y}}_K$ and $\vec{\mathbf{v}}_K$ we perform the statistical test with the null hypothesis that two $d-$dimensional samples have the same distributions assuming significance level c. Thus, as a consequence, we receive K $p-$values of the test. We denote them as $p_1, p_2, ..., p_K$. In our study, we propose using the CvM test tailored to $d-$dimensional samples proposed in [11]. The details of the test statistic and the corresponding testing methodology are presented in the next part of this section.

As the next step, we select such values from $p_1, p_2, ..., p_K$ which are higher than the assumed significance level c. They will be used to identify potential regime change points. Change points are detected based on maximizing the probability of a change in the distribution (statistical test result). However, in order to avoid such situations where the selected change points are "close to each other" and actually correspond to the same regime, in the algorithm we select such $p-$values that are at a distance from each other not less than the neighborhood e. Otherwise, they are assigned to the same group. For each of these groups, the index with the smallest $p-$value is determined and added to the set $\mathcal{C}$. If the number of change points is known (in the model (1) we assume $R-1$ change points) then we select the highest maximum $R-1$ values from the set $\mathcal{C}$. We assign the change points as the indexes of the highest selected $p-$values.

As mentioned, the proposed algorithm is based on the CvM test adapted to $d-$dimensional random samples. In the following part, we recall the general idea of the test. Let $\vec{\mathbf{z}} = (\mathbf{z}_1, \mathbf{z}_1, ..., \mathbf{z}_N)$ and $\vec{\mathbf{w}} = (\mathbf{w}_1, \mathbf{w}_2, ..., \mathbf{w}_N)$ be two $d-$dimensional random vectors of length N. To verify if the corresponding distributions are the same at the given significance level c, the following test statistic is used

$$T = \frac{1}{2N} \sum_{i,j=1}^{N} 2\phi(||\vec{\mathbf{z}}_i - \vec{\mathbf{w}}_j||^2) - \phi(||\vec{\mathbf{z}}_i - \vec{\mathbf{z}}_j||^2) - \phi(||\vec{\mathbf{w}}_i - \vec{\mathbf{w}}_j||^2).$$

The function ϕ used above is a kernel function that plays a fundamental role in defining the distance measure used in the test, influencing both statistical power and consistency. A kernel function ϕ must satisfy several mathematical properties to ensure that the test is well-defined and performs optimally. It should be continuous and negative definite. For more details, see [11]. In this study, following kernel function is used: $\phi(z) = 1 - (1+z)^{-1}$. The selection is based on the simulation study described in [11]. The statistical test was implemented using the *cramer* package in R [15]. In our study, the critical value of the test (and thus $p-$value) was computed via the Monte Carlo bootstrap method with 1000 replications. A default significance level of 5% was used. In Algorithm 1 we present the pseudocode of the proposed procedure. We note that the parameters used in the proposed methodology (see first line of Algorithm 1) can affect the results. Due to space

limitations, we do not discuss this issue in this article and leave it for future studies.

Algorithm 1 CvM test-based segmentation algoritm

Require: $\omega > 2,\ o > 0,\ e > 0,\ 0 < c < 1$
Ensure: data: $x_1, x_2, ..., x_N$
prepare segments: $\vec{\mathbf{y}}_1, \vec{\mathbf{y}}_2, ..., \vec{\mathbf{y}}_K,\ \ \vec{\mathbf{v}}_1, \vec{\mathbf{v}}_2, ..., \vec{\mathbf{v}}_K$ for given $\omega,\ o$.
for all $k \in \{1, 2, ..., K\}$ **do**
calculate p-value obtained in CvM test for $\vec{\mathbf{y}}_k$ and $\vec{\mathbf{v}}_k : p_k$
end for
define $\mathcal{P} := \{k \in \{1, 2, ..., K\} : p_k < c\}$
for all $i, j \in \mathcal{P} : i < j$ **do**
if $|i - j| < e$ **then** ▷ The neighborhood determining
assign indices i and j to the same group
end if
end for
for all groups $g \in \{1, 2, ..., G\}$ **do**
select index k with the smallest p_k value
if for given group there are many indexes with the same minimum **then**
calculate median of these indices and assign to $\mathcal{C}(g)$
else
$\mathcal{C}(g) \leftarrow k$
end if
end for
if R is given **then**
return $R - 1$ indices (from $\{\mathcal{C}(1), \mathcal{C}(2), ..., \mathcal{C}(G)\}$) with the smallest p-values.
else
return $\mathcal{C}(1), \mathcal{C}(2), ..., \mathcal{C}(G)$ as change points
end if

III. Simulation study

The efficiency of the proposed algorithm is demonstrated for a general class of $d-$dimensional distributions, specifically the $d-$dimensional α-stable family [13]. As per the Generalized Central Limit Theory [16], the α-stable distribution is the only limiting distribution for the sum of random variables with diverging variance, similar to how the Gaussian distribution is the limiting distribution for the sum of random variables with finite variance, as described by the Central Limit Theorem. For specific parameter values, the α-stable distribution reduces to the Gaussian case. Hence, the α-stable family is regarded as a natural generalization of the Gaussian distribution. In addition, the α-stable distribution can be considered in both univariate and multivariate scenarios.

For simplicity, we focus on the subclass of $d-$dimensional α-stable distributions, namely the sub-Gaussian distribution, where the dependence between components is controlled by a single parameter. In contrast, for the general class of α-stable distributions, such dependence is characterized by the so-called spectral measure [17] defined on unit sphere in $\mathbb{R}^d$, which may involve multiple parameters.

Let $\mathbf{G} = (G_1, ..., G_d)$ be as a zero-mean Gaussian vector in $\mathbb{R}^d$ with the covariance matrix $\mathbf{\Sigma} := \{\rho_{ij}\}_{i,j=1}^d$, where $\rho_{ij} = E[G_i G_j]$. Furthermore, we assume that A is the one-dimensional totally skewed $\alpha-$stable random variable (independent on $\mathbf{G}$) with the following characteristic function

$$\mathbb{E}\left(e^{itA}\right) = exp\left\{-\gamma^{\alpha/2}|t|^{\alpha/2}\left(1 - isgn(t)tan\left(\frac{\pi\alpha}{4}\right)\right)\right\},$$

where $\gamma = \left(cos\left(\frac{\pi\alpha}{4}\right)\right)^{2/\alpha}$ and $\alpha \in (0, 2)$. When $\alpha = 2$, then random variable A is just a constant. The vector defined as

$$\mathbf{X} = (X_1, X_2, ..., X_d) = (A^{1/2}G_1, ..., A^{1/2}G_d)$$

is called sub-Gaussian random vector in $\mathbb{R}^d$ and has the following characteristic function

$$E\left[exp\left\{i\sum_{k=1}^{d} t_k X_k\right\}\right] = exp\left\{-\left|\frac{1}{2}\sum_{i=1}^{d}\sum_{j=1}^{d} t_i t_j \rho_{ij}\right|^{\alpha/2}\right\}.$$

For each $\alpha \in (0, 2)$, the one-dimensional random variables $X_1, X_2, ...X_d$ (being the components of sub-Gaussian vector) have infinite-variance and thus the corresponding distribution belong to the heavy-tailed class of distributions. In contrast, when $\alpha = 2$, then $\mathbf{X}$ reduces to a $d-$dimensional Gaussian.

In our simulation study, we consider the simplified model (1), namely the model with one change point (i.e. $R = 2$). In addition, we assume $d = 2$ and $\rho_{11} = \rho_{22} = 1$. Taking the notation $\rho = \rho_{12} = \rho_{21}$, we consider the model with two parameters, namely α and ρ. The α parameter is responsible here for the heavy-tailed behavior of the random variables X_1 and X_2 while ρ controls their dependence. In the further analysis, we take the notation $\mathbf{X} \sim SG_{\alpha,\rho}$ to refer to a two-dimensional sub-Gaussian random vector with parameters α and ρ. Thus the model under consideration can be formulated as follows

$$\mathbf{X}_i \overset{d}{=} \begin{cases} \mathbf{X}^{(1)} \sim SG_{\alpha_1,\rho_1}, & \text{for } i < n^*, \\ \mathbf{X}^{(2)} \sim SG_{\alpha_2,\rho_2} & \text{for } i \geq n^*, \end{cases} \tag{2}$$

where $i = 1, 2, ..., N$. In our analysis presented in this section in the first scenario we assume $\rho_1 = \rho_2$ and the regime change corresponds to the shift in the α parameter. In the second scenario, we assume $\alpha_1 = \alpha_2$ and the regime change corresponds to the change in the ρ value.

For both scenarios, $N = 1000$ was used. The algorithm was performed with the following parameters: $\omega = 200,\ o = 10,\ c = 0.05,\ e = 10$ and $R = 2$. First, we consider the case where the change point is located at the midpoint of the data ($n^* = 500$). In the first scenario, the parameters set is as follows: $\alpha_1 = 1.5, \rho_1 = \rho_2 = 0.5$, and $\alpha_2 \in \{1.51, 1.55, 1.6, 1.7, 1.8, 1.9, 1.95, 1.98\}$. Fig. 1 presents the detected change points, where the dashed line represents the true change point. The boxplots are received based on 500 Monte Carlo simulations of the two-dimensional data from the model (2). In our analysis we compare the results with the baseline methods, namely e-Divisive [7] and KCPA [8], considered in the literature as efficient techniques for the detection of change points in multivariate data. The medians of the estimated change points obtained using the proposed approach are closest to the true value compared to e-Divisive and KCPA. Furthermore, the precision of the proposed method improves as the difference between α_1 and α_2 increases, which is attributed to a significant reduction in the detected change points range. For each parameter set (different α_2), the Mean Absolute Error (MAE) was computed. On average, the

proposed approach achieves 2.06 times smaller MAE than e-Divisive (exceeding 4 times smaller in extreme cases) and 9.78 times smaller MAE than KCPA (exceeding 15 times smaller in extreme cases).

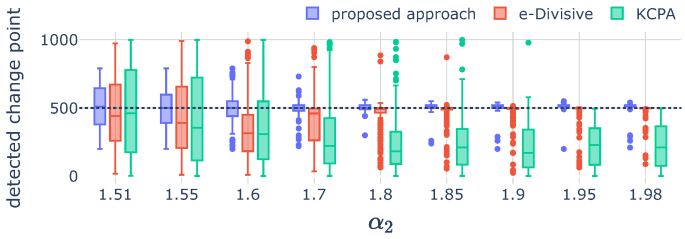

Fig. 1. Change points detected by various methods for samples described by Eq. (2) with the following parameters: $\alpha_1 = 1.5, \rho_1 = \rho_2 = 0.5, N = 1000$. The number of Monte Carlo trials for each considered α_2 is equal to 500.

For the second scenario, the following parameters were used: $\alpha_1 = \alpha_2 = 1.5, \rho_1 = 0.5$, and $\rho_2 \in \{-0.9, -0.8, \ldots, 0.9\}$ excluding $\rho_2 = 0.5$. As before, a total of 500 Monte Carlo trials were conducted for each parameter combination. Fig. 2 presents boxplots of estimated change points obtained using various methods. Similarly to the first scenario, the proposed approach outperforms e-Divisive and KCPA in the estimation of change points, particularly for negative ρ_2 values. The median of the estimated change points using the proposed method remains close to the true change point across all values ρ_2. Additionally, the variability in estimated change points is smallest for the proposed method compared to e-Divisive and KCPA. The MAE was also computed for each parameter set (different ρ_2), where the proposed approach achieved, on average, 3.62 times smaller MAE than e-Divisive (exceeding 11 times smaller in extreme cases) and 4.58 times smaller MAE than KCPA (exceeding 15 times smaller in extreme cases).

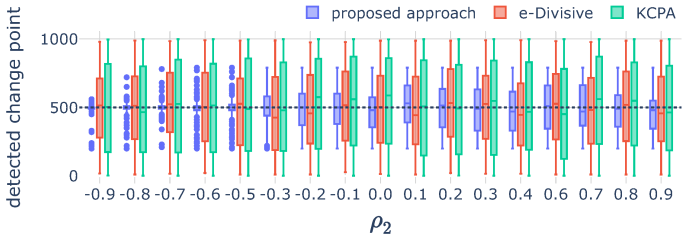

Fig. 2. Change points detected by various methods for samples described by Eq. (2) with the following parameters: $\alpha_1 = \alpha_2 = 1.5, \rho_1 = 0.5, N = 1000$. The number of Monte Carlo trials for each considered ρ_2 is equal to 500.

The subsequent stage of the analysis aimed to evaluate the impact of the change point's position within the sample on segmentation accuracy. For a selected set of parameters ($\alpha_1 = \alpha_2 = 1.5, \rho_1 = 0.5, \rho_2 = 1.9$), a total of 500 trajectories of length 1000 were simulated, with the change point n^* varying within $\{\lfloor 0.1N \rfloor, \lfloor 0.2N \rfloor, \ldots, \lfloor 0.9N \rfloor\}$. The accuracy of the estimated change points detected by various methods was assessed using MAE along with the corresponding standard error (SE). The results presented in Fig. 3 show that the performance of all methods are worse as the change point approaches the sample edges (i.e., $n^*/N \in \{0.1, 0.9\}$). However, for all analyzed values of n^*/N, the proposed approach consistently demonstrated the highest accuracy, producing the lowest MAE. Additionally, the time complexity of the proposed segmentation method was evaluated via simulation for sample lengths $N = \{1000, \ldots, 7000\}$ and dimensions $d = \{2, 3, 5, 10\}$, using data generated from model (2) with parameters $\rho_1 = 0.5$, $\rho_2 = 1.9$, and $\alpha_1 = \alpha_2 = 1.5$. A fixed window length of 200 was used, with the change point positioned in the middle of the data. Results indicate linear time complexity.

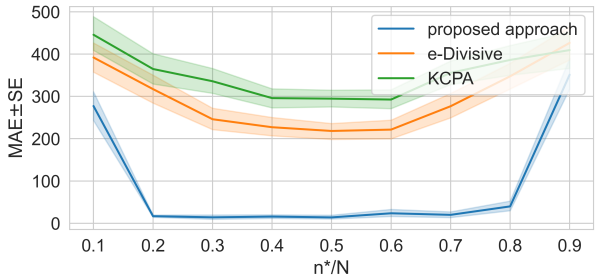

Fig. 3. Results of the comparative analyses for samples described by Eq. (2): MAE $\pm$ SE obtained for $\alpha_1 = \alpha_2 = 1.5, \rho_1 = 0.5, \rho_2 = -0.9, N = 1000$. For each value of n^*, 500 Monte Carlo trials were conducted.

IV. Real Data Analysis

In this section the potential of the proposed algorithm is shown by applying it to real data related to the detection of the episode of elevated intracranial pressure (ICP) in a patient requiring neurointensive care. ICP monitoring is an invasive procedure, often associated with serious complications such as infections. However, its monitoring enables detection of intracranial hypertension (IH), a highly dangerous condition that can lead to decreased cerebral perfusion pressure or secondary brain injury, and greatly affects the patient's outcome [18]. In clinical practice, it is not always advised to monitor ICP [19], therefore, a method to detect or predict changes in ICP based on less-invasive methods is sought-after [20].

The data presented were collected from a patient after traumatic brain injury admitted to the neurointensive care unit at Addenbrooke's Hospital (Cambridge, UK). Arterial blood pressure (ABP) in the radial artery, non-invasive transcranial Doppler cerebral blood flow velocity (FVX) in middle cerebral artery, and ICP were recorded simultaneously as described in [21] with a sampling rate of 30 Hz. The recording was cut to capture the most significant change in ICP. Data were processed anonymously to ensure the protection of sensitive information. The study protocol was approved by the Neurocritical Care User Committee of Addenbrooke's Hospital with additional approval to use retrospective data stored in the Brain Physics Lab research database (REC 23/YH/0085).

Like most biomedical signals, the presented data do not exhibit Gaussian distribution (see the artifactory spike around 200th sample). As a pre-processing step, ABP and FVX are averaged over one second. The proposed algorithm is used to detect change points in ICP using averaged ABP and FVX signals treated as two-dimensional input.

The segmentation outcomes are illustrated in Fig. 4. The algorithm was performed with the following parameters: $\omega = 100$, $o = 10$, $c = 0.05$, $e = 10$ and $R = None$, indicating

that there is no limitation on the total number of change points that should be provided as output of the algorithm.

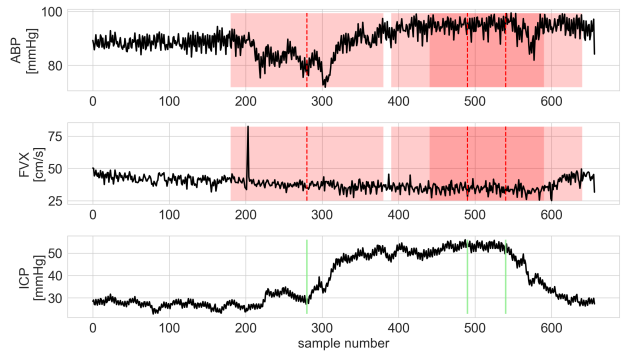

Fig. 4. Averaged ICP, ABP, and FVX signals. Red lines indicate change points detected by proposed approach using ABP and FVX as inputs. Light red shaded areas represent the sliding windows used for detection, with the corresponding change points located at their centers. Green lines illustrate the alignment between change points detected from ABP and FVX and the ICP signal.

The first change point is identified directly before the prominent rise in ICP, which demonstrates that the proposed approach can be used for ICP elevation detection. The third change point is a notable result, as the proposed algorithm is able to accurately spot the moment in time just before the decrease of ICP towards the initial value range. Finally, the middle change point is associated with approximately stable values of ICP (around 50 mmHg), and captures the underlying changes in the ABP and FVX distribution (Spearman correlation coefficient), which cannot be inspected visually. It should be highlighted that the proposed algorithm is capable of accurate segmentation despite the occurrence of FVX artifact (spike around 200th observation), which adds to the strengths of the proposed approach.

V. Conclusions

The paper provides fundamental and applied contributions. Firts, we introduce a methodology dedicated to the segmentation of random multivariate data exhibiting non-Gaussian patterns. The proposed mechanism involves the use of the CvM test to identify the location of change points by examining the temporal and multivariate distribution characteristics of measurement data. Comparative computer simulation studies reveal that the designed procedure outperforms benchmark techniques while preserving robustness to a parasitic measurement artifacts at the same time, which typically require an additional step in the data processing pipeline (increasing its complexity). Secondly, we proved that proposed methodology allows for robust detection of the changes in cerebral pressure-volume state without reliance on the ICP measurement, relying on readily available and less-invasive measurement methods, which might be beneficial in clinical scenarios where ICP monitoring is not indicated.

Acknowledgements

The work of JW was supported by the project Minigrants for doctoral students of the Wroclaw University of Science and Technology. The work of AW was supported by NCN OPUS project No. 2024/53/B/HS4/00433.

References

[1] J. Witulska, A. Zaleska, N. Kremzer-Osiadacz, A. Wyłomańska, and I. Jabłoński, "Robust variance estimators in application to segmentation of measurement data distorted by impulsive and non-Gaussian noise," *Measurement*, vol. 239, p. 115472, 2025.

[2] J.-L. Chapman, I. Eckley, and R. Killick, "A nonparametric approach to detecting changes in variance in locally stationary time series," *Environmetrics*, vol. 31, no. 1, p. e2576, 2020.

[3] G. J. Ross, "Modelling financial volatility in the presence of abrupt changes," *Physica A: Statistical Mechanics and its Applications*, vol. 392, no. 2, pp. 350–360, 2013.

[4] M. Li and Y. Yu, "Adversarially robust change point detection," *Advances in Neural Information Processing Systems*, vol. 34, pp. 22 955–22 967, 2021.

[5] Z. Chen, Z. Tian, and C. Zhao, "Monitoring persistence change in infinite variance observations," *Journal of the Korean Statistical Society*, vol. 41, no. 1, pp. 61–73, 2012.

[6] Z. Li and F. Tsung, "A control scheme for monitoring process covariance matrices with more variables than observations," *Quality and Reliability Engineering International*, vol. 35, no. 1, pp. 351–367, 2019.

[7] D. S. Matteson and N. A. James, "A nonparametric approach for multiple change point analysis of multivariate data," *Journal of the American Statistical Association*, vol. 109, no. 505, pp. 334–345, 2014.

[8] S. Arlot, A. Celisse, and Z. Harchaoui, "A kernel multiple change-point algorithm via model selection," *Journal of Machine Learning Research*, vol. 20, no. 162, pp. 1–56, 2019.

[9] A. Lung-Yut-Fong, C. Lévy-Leduc, and O. Cappé, "Homogeneity and change-point detection tests for multivariate data using rank statistics," *Journal de la Société Française de Statistique*, vol. 156, no. 4, pp. 133–162, 2015.

[10] K. Bulteel, E. Ceulemans, R. J. Thompson, C. E. Waugh, I. H. Gotlib, F. Tuerlinckx, and P. Kuppens, "DeCon: A tool to detect emotional concordance in multivariate time series data of emotional responding," *Biological Psychology*, vol. 98, pp. 29–42, 2014.

[11] L. Baringhaus and C. Franz, "Rigid motion invariant two-sample tests," *Statistica Sinica*, pp. 1333–1361, 2010.

[12] G. Fasano and A. Franceschini, "A multidimensional version of the Kolmogorov–Smirnov test," *Monthly Notices of the Royal Astronomical Society*, vol. 225, no. 1, pp. 155–170, 1987.

[13] J. P. Nolan, *Univariate Stable Distributions: Models for Heavy Tailed Data*. Springer, 2021.

[14] C. Raphael, "Automatic segmentation of acoustic musical signals using Hidden Markov Models," *IEEE Transactions on Pattern Analysis and Machine Intelligence*, vol. 21, no. 4, pp. 360–370, 1999.

[15] C. Franz and M. C. Franz, "Package 'cramer'," *cran.r-project.org*, 2019.

[16] H. Fischer, *A history of the central limit theorem: from classical to modern probability theory*. Springer, 2011, vol. 4.

[17] G. Samoradnitsky and M. S. Taqqu, *Stable Non-Gaussian Random Processes: Stochastic Models with Infinite Variance*. Routledge, 1994.

[18] C. A. Åkerlund, J. Donnelly, F. A. Zeiler, R. Helbok, A. Holst, M. Cabeleira, F. Güiza, G. Meyfroidt, M. Czosnyka, P. Smielewski, N. Stocchetti, A. Ercole, D. W. Nelson, the CENTER-TBI High Resolution ICU Sub-Study Participants, and Investigators, "Impact of duration and magnitude of raised intracranial pressure on outcome after severe traumatic brain injury: A center-tbi high-resolution group study," *PLOS ONE*, vol. 15, no. 12, pp. 1–20, 2020.

[19] J.-P. A. Jantzen, "Prevention and treatment of intracranial hypertension," *Best Practice & Research Clinical Anaesthesiology*, vol. 21, no. 4, pp. 517–538, 2007.

[20] H. Kristiansson, E. Nissborg, J. Bartek Jr, M. Andresen, P. Reinstrup, and B. Romner, "Measuring elevated intracranial pressure through non-invasive methods: a review of the literature," *Journal of Neurosurgical Anesthesiology*, vol. 25, no. 4, pp. 372–385, 2013.

[21] M. Czosnyka, P. Smielewski, S. Piechnik, E. A. Schmidt, P. G. Al-Rawi, P. J. Kirkpatrick, and J. D. Pickard, "Hemodynamic characterization of intracranial pressure plateau waves in head-injured patients," *Journal of Neurosurgery*, vol. 91, no. 1, pp. 11–19, 1999.