Physiological Reactions Profiling in Polygraph Testing: Insights from Fuzzy C-Means Clustering Analysis

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Abstract: The polygraph test, which is frequently employed for deception detection and truth verification, evaluates the accuracy of people's assertions by analyzing their physiological reactions. This study investigates the variety of physiological responses detected during polygraph tests using fuzzy C-means clustering analysis. 400 individuals undergoing polygraph testing provided a dataset containing physiological parameters, such as assessments of autonomic arousal, cardiovascular activity, respiration patterns, and electrodermal responses. Participants' varied patterns of physiological reaction were revealed using fuzzy clustering, which distinguished different physiological groupings among them. Cluster analysis revealed the physiological profiles linked to various levels of deception. Performance metrics, including cluster silhouette coefficient and within-cluster heterogeneity, were utilized to validate the clustering results. The findings provide valuable implications for improving the accuracy and reliability of polygraph testing, with potential applications in forensic investigations, law enforcement, and security screenings. This study contributes to the advancement of polygraph test interpretation techniques and underscores the importance of considering individual differences in physiological responses during deception detection.

Keywords: Polygraph testing; Fuzzy C-means clustering; physiological profiling; deception detection

1 Introduction

Polygraph testing, also known as lie detection testing, has been utilized for many years as a technique for detecting deception and evaluating honesty in forensic investigations, security screenings, and pre-employment screenings [1]. The polygraph measures physiological reactions to variations in heart rate, blood pressure, respiration, and skin conductivity. It is based on the concept that dishonest individuals react physically differently from truthful people [2]. The scientific community continues to scrutinize and discuss the accuracy and reliability of polygraph testing, despite its widespread usage [3]. The inherent variability in physiological responses across test subjects is an important aspect of polygraph testing that requires more research [4]. The interpretation of test results might be challenged by the fact that, whereas certain individuals may show prominent physiological reactions when engaging in deceptive activity, others may only show minor or inconclusive responses [5].

Improving the accuracy and reliability of polygraph testing requires an understanding of the physiological mechanisms behind these variations [6]. Advancements in machine learning, decision making with hard computing methods [7] and data analytics in recent times provide encouraging opportunities to investigate the complex relationships between dishonest conduct and physiological reactions during polygraph examinations [8]. Fuzzy C-means clustering, among other clustering methods, facilitates the identification of unique patterns or clusters in diverse datasets [9, 10, 11, 12, 13, 14], allowing for the categorization of individuals according to their physiological profiles [15]. Clustering approaches provide insights into the underlying physiological states linked with lying by grouping individuals into homogenous groups based on their physiological responses [16].

It is important to emphasize that this research is a novel addition to the field because it is the first to expressly use fuzzy C-means clustering to the setting of polygraph testing. The purpose of this research is to examine physiological data from subjects undergoing polygraph testing using fuzzy C-means clustering. We aim to clarify the variability of physiological responses during polygraph tests and provide insight into the physiological traits linked to deception detection by detecting unique physiological clusters among subjects. The results of this study have implications for strengthening polygraph testing's reliability and precision, which will increase its usefulness in forensic science, law enforcement, and other sectors that need truth verification.

2 Methodology

2.1 Objectives

This research aims to employ fuzzy C-means clustering analysis to discern distinct physiological clusters within individuals undergoing polygraph testing. It seeks to characterize the physiological profiles associated with these clusters, encompassing measures such as autonomic arousal, cardiovascular activity, respiratory patterns, and electrodermal responses. Additionally, the study intends to evaluate the effectiveness of the clustering algorithm in segregating individuals based on their physiological responses during polygraph examinations. It further aims to assess the validity and reliability of the identified clusters through various performance metrics. Finally, the research aims to discuss the implications of its findings for enhancing the accuracy and reliability of polygraph testing across different domains, including forensic science and law enforcement.

These objectives aim to advance our understanding of the physiological variability inherent in polygraph test scoring and contribute to the development of more effective techniques for interpreting polygraph test results.

2.2 Participants

The sample comprised 400 individuals selected randomly from a pool of 1072 offenders who had committed multiple crimes and underwent Polygraph testing administered by expert examiners from ten polygraph laboratories within the Romanian Police, under the supervision of Dr. Csaba Kiss. All 400 participants were repeat offenders involved in serious criminal activities, and they voluntarily confessed to their crimes, providing consent for their aggregated data to be utilized for scientific research purposes. Data utilized in this study were extracted from a minimum of three charts corresponding to each Polygraph examination conducted. Among the participants, 90% were male and 10% were female, with ages ranging from 18 to 65 years and an average age of 32 years. On average, participants had completed 8.6 years of formal education, indicating a relatively low level of educational attainment.

This study adhered to ethical guidelines for research involving human participants. Participants provided informed consent prior to participation and were assured of confidentiality and anonymity throughout the study.

2.3 Data Collection

Physiological data were collected using a standardized polygraph testing protocol. Participants underwent polygraph examinations administered by trained examiners in a controlled laboratory setting. The polygraph apparatus recorded physiological responses, including but not limited to electrodermal activity (EDA), heart rate, blood pressure, respiration, and skin conductivity, during the testing procedure [17].

A comprehensive set of physiological parameters derived from polygraph measurements was included in the analysis. These parameters encompassed measures of autonomic arousal, cardiovascular activity, respiratory patterns, and electrodermal responses. Specific physiological parameters included amplitude of electrodermal reaction (ARED), amplitude of blood pressure in brachial pulse (ATAB), change of baseline level in chest breathing (MNBRT), difference of altitude between breathing cycles (DIFA), duration of electrodermal reaction (TRED), abdominal breath line length (LLRA), arterial tension amplitude of the distal pulse (ATAD), heart rhythm (RC), voluntary repeated acts (REV), duration of brachial pulse arterial tension (TTAB), changing of the basic level of abdominal breathing (MNBRA), ratio of inspiration to expiration (I/E), average value of electrodermal reaction (EDA), thoracic breath line length (LLRT), reactive patterns (PATTR), duration of distal pulse arterial tension (TTAD), respiratory rhythm (RR), erratic breathing (RE), abdominal respiratory stop (TSTOPRA), average amplitude of abdominal breathing (ARA), length of electrodermal reaction (LRED), and thoracic respiratory stop (TSTOPR).

2.3 Data Analysis

Fuzzy C-means clustering was employed to analyze the physiological data and identify distinct clusters within the dataset. Fuzzy clustering allows for the classification of individuals into multiple clusters, with each individual assigned a membership value indicating their degree of association with each cluster. The algorithm iteratively assigns data points to clusters based on their proximity to cluster centroids, minimizing within-cluster variance while maximizing between-cluster variance [18].

Fuzzy C-Means (FCM) clustering is a soft clustering technique used for partitioning a dataset into a set of clusters where each data point belongs to every cluster with a certain degree of membership [19]. Unlike hard clustering methods, where each data point belongs exclusively to one cluster, FCM assigns a membership value to each data point for every cluster, indicating the degree of belongingness. This approach allows for the representation of uncertainty in cluster assignments.

Mathematically, FCM minimizes an objective function known as the fuzzy partition coefficient, which quantifies the degree of fuzziness in the clustering. The objective function is defined as follows:

$$J_m(U,V) = \sum_{i=1}^{N}\sum_{j=1}^{c} u_{ij}^{m} \cdot \|x_i - v_j\|^2$$

Where:

$J_m(U,V)$ is the objective function to be minimized.

N is the number of data points.

c is the number of clusters.

u_{ij} is the membership value of data point xi in cluster j.

v_j is the centroid of cluster j.

m is a fuzziness exponent (typically set to 2 in most applications).

$\|.\|$ denotes a distance measure (e.g., Euclidean distance).

The algorithm iteratively updates the membership values u_{ij} and cluster centroids v_j until convergence, based on the following update equations:

$$u_{ij} = \frac{1}{\sum_{k-1}^{c}\left(\frac{\|x_i - v_j\|}{\|x_i - v_k\|}\right)^{\frac{2}{m-1}}}$$

$$v_j = \frac{\sum_{i-1}^{N} u_{ij}^{m} \cdot x_i}{\sum_{i-1}^{N} u_{ij}^{m}}$$

Here, m is the fuzziness coefficient, controlling the degree of fuzziness in the clustering. As m approaches 1, the clustering becomes increasingly hard, whereas larger values of m lead to fuzzier clusters.

FCM is widely used in various fields, including pattern recognition [20], image processing [21], and data mining [19], due to its ability to handle complex data distributions and capture inherent uncertainty in data.

The clustering results were evaluated using performance metrics such as cluster silhouette coefficient, within-cluster heterogeneity, and explained variance [22]. These metrics provided quantitative measures of the clustering quality and the degree of separation between clusters.

Descriptive statistics were calculated for demographic variables and physiological parameters. Cluster means for each physiological parameter were computed to characterize the physiological profiles of each cluster. Statistical analyses were performed using JASP version 0.17.3.0.

3 Results

The fuzzy C-Means Clustering analysis (FCM) was conducted with a dataset comprising 400 observations, resulting in the formation of nine distinct clusters. The clustering performance metrics are summarized as follows: $R^2 = 0.371$, AIC = 8362.760, BIC = 9260.840, and Silhouette = 0.010 (Table 1).

Table 1
Fuzzy C-Means Clustering

Clusters	N	R^2	AIC	BIC	Silhouette
9	400	0.371	8362.760	9260.840	0.010

In the context of FCM, each observation is associated with membership degrees across all clusters, allowing for a cluster assignment.

The performance of the clustering analysis is evaluated using several metrics. The coefficient of determination (R2) measures the proportion of variance in the data explained by the clustering model, with a value of 0.371 indicating a moderate level of explanatory power. Additionally, the Akaike Information Criterion (AIC) and Bayesian Information Criterion (BIC) serve as measures of model complexity, with lower values indicating a better trade-off between model fit and complexity. The calculated AIC value of 8362.760 and BIC value of 9260.840 provide insights into the relative quality of the clustering model.

Furthermore, the Silhouette coefficient, a measure of cluster cohesion and separation, is reported as 0.010. The Silhouette coefficient ranges from -1 to 1, with higher values indicating better-defined clusters. Although the reported value is relatively low, it still suggests a reasonable degree of cluster separation.

Overall, these performance metrics provide a comprehensive assessment of the effectiveness of the FCM clustering algorithm in partitioning the dataset into meaningful clusters, with consideration given to both explanatory power and model complexity.

Cluster information (Table 2) is provided in terms of cluster size, explained proportion within-cluster heterogeneity, and within sum of squares. The clusters varied in size, ranging from 6 to 124 observations. The proportion of within-cluster heterogeneity explained ranged from 0.012 to 0.224, indicating varying degrees of compactness within clusters. The within sum of squares ranged from 91.494 to 1769.666, reflecting the dispersion of data points within each cluster.

The provided cluster information offers valuable insights into the characteristics of each cluster generated through the Fuzzy C-Means (FCM) Clustering analysis. This detailed breakdown facilitates a deeper understanding of the underlying patterns within the dataset and holds significant implications for various research domains.

Table 2
Cluster Information

Cluster	1	2	3	4	5	6	7	8	9
Size	6	27	66	25	38	19	124	18	77
Explained proportion within-cluster heterogeneity	0.01	0.11	0.20	0.07	0.07	0.08	0.22	0.03	0.18
Within sum of squares	91.49	887.44	1610.99	586.66	558.78	633.40	1769.66	284.01	1490.29

Firstly, the size of each cluster indicates the distribution of observations across the clusters. For instance, Cluster 7 appears to be the largest, containing 124 observations, while Cluster 1 is the smallest, comprising only 6 observations. This distribution provides researchers with an understanding of the prevalence and representation of different physiological profiles or patterns within the dataset.

Secondly, the explained proportion of within-cluster heterogeneity quantifies the degree to which the variability within each cluster is accounted for by the clustering model. Higher values, such as those observed in Clusters 3, 7, and 9, suggest that the physiological parameters within these clusters exhibit more consistent patterns or associations. Conversely, lower values, such as those in Clusters 1 and 2, indicate a greater degree of heterogeneity or variability within the cluster.

Furthermore, the within sum of squares offers insights into the dispersion of data points within each cluster. Clusters with higher within sum of squares, such as Clusters 3, 6, and 8, may indicate greater variability or spread of physiological parameters, potentially highlighting diverse subgroups or phenomena within the dataset.

Furthermore, the cluster means for each physiological parameter were computed. These parameters include amplitude of electrodermal reaction (ARED), amplitude of blood pressure in brachial pulse (ATAB), change of baseline level in chest breathing (MNBRT), difference of altitude between breathing cycles (DIFA), duration of the electrodermal reaction (TRED), abdominal breath line length (LLRA), arterial tension amplitude of the distal pulse (ATAD), heart rhythm (RC), voluntary repeated acts (REV), duration of brachial pulse arterial tension (TTAB), changing of the basic level of abdominal breathing (MNBRA), the ratio of inspiration to expiration (I/E), average value of the electrodermal reaction (EDA), thoracic breath line length (LLRT), reactive patterns (PATTR), duration of distal pulse arterial tension (TTAD), respiratory rhythm (RR), erratic breathing

(RE), abdominal respiratory stop (TSTOPRA), average amplitude of abdominal breathing (ARA), length of the electrodermal reaction (LRED), and thoracic respiratory stop (TSTOPR).

Each cluster exhibited distinct mean values for these parameters, providing insights into the physiological characteristics associated with each cluster (Table 3).

Table 3
Cluster Means

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9
ARED	2.40	-0.16	-0.29	0.87	0.18	-0.40	0.03	0.67	-0.36
ATAB	-0.10	-0.07	-0.34	0.43	-0.38	0.01	-0.32	0.59	0.75
ATAD	-0.25	0.08	0.35	-0.14	-0.32	0.14	-0.08	-0.10	0.01
ART	-0.45	-0.05	-0.15	0.66	0.39	-0.39	-0.36	0.26	0.38
ARA	-0.54	-0.15	-0.06	-0.33	0.93	0.74	-0.19	-0.22	-0.02
MNBRA	-0.52	0.77	0.57	-0.04	-0.44	-0.19	-0.31	-0.32	0.13
MNBRT	-0.25	0.69	0.43	0.07	-0.25	0.07	-0.30	-0.16	0.01
IR	-0.25	-1.19	0.33	0.15	1.00	0.07	-0.21	-0.23	-0.01
LLRT	0.32	-0.13	0.12	0.03	0.54	-0.17	-0.42	-0.35	0.43
LLRA	0.18	-0.45	0.43	-0.21	0.82	0.57	-0.41	0.45	-0.14
LRED	3.84	-0.12	-0.20	0.69	-0.01	-0.27	-0.04	0.79	-0.35
TRED	0.10	0.04	-0.04	0.21	-0.27	1.01	-0.13	-0.11	0.06
TTAB	0.08	0.09	-0.56	0.18	-0.46	1.25	-0.12	0.02	0.48
TTAD	0.03	0.50	0.19	0.02	-0.47	0.03	-0.09	-0.24	0.07
RR	0.14	-1.21	0.62	-0.10	0.19	-0.50	-0.11	0.17	0.08
RC	0.44	-0.07	0.52	-0.43	0.08	-0.73	-0.22	0.48	0.07
TSTOPR	-0.39	2.91	-0.15	-0.18	-0.36	-0.31	-0.23	-0.17	-0.13
TSTOPRA	-0.39	2.89	-0.15	-0.18	-0.36	-0.31	-0.24	-0.16	-0.13
RE	0.75	0.93	0.02	0.05	-0.54	-0.18	-0.44	-0.25	0.66
REV	2.48	0.79	-0.07	-0.06	-0.33	-0.33	-0.08	-0.14	0.02
PATTR	-0.66	0.87	0.30	0.80	-0.76	-0.22	-0.53	0.49	0.40
EDA	0.42	-0.07	-0.27	1.98	0.17	0.06	-0.03	-0.41	-0.38
MBT	0.54	0.35	-0.01	-0.20	-0.22	0.18	-0.18	1.38	-0.07
DIFA	-0.49	0.88	0.19	0.28	-0.36	0.75	-0.34	-0.09	0.04
TDIFA	-0.85	0.57	0.63	0.61	-0.52	0.92	-0.41	-0.30	-0.10

Analysing the cluster means for each physiological parameter provides researchers with a detailed characterization of the clusters. For example, Cluster 4 shows relatively high mean values for parameters such as ARED, ATAB, and ART, suggesting a distinct physiological profile associated with this cluster. Conversely, Cluster 5 exhibits lower mean values for several parameters, indicating a different physiological pattern.

In conclusion, the cluster information obtained from the FCM analysis serves as a valuable resource for researchers in elucidating complex physiological phenomena and identifying distinct subgroups within the dataset.

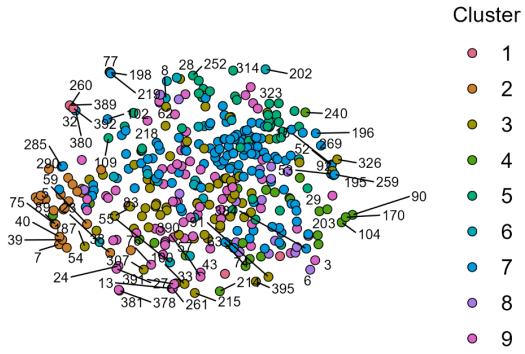

Figure 1
t-SNE Cluster Plot

The t-SNE (t-Distributed Stochastic Neighbor Embedding) cluster plot offers a visual representation of the high-dimensional data in a lower-dimensional space, allowing us to observe the spatial distribution of data points and the relationships between them (Figure 1). In the context of our analysis with nine clusters, a t-SNE cluster plot would condense the multidimensional physiological data into two dimensions while preserving local similarities between data points [23]. Each data point on the plot represents an individual observation, and its position is determined by its similarity to other data points.

In the t-SNE cluster plot, data points belonging to the same cluster are typically grouped together spatially, forming distinct clusters or clusters with cohesive neighborhoods. The plot enables us to visually identify the boundaries between clusters, their relative sizes, and any overlapping regions. By assigning different colors or labels to data points according to their cluster assignments, we can easily discern the membership of each point and visually inspect the distribution of clusters across the plot.

Interpreting the t-SNE cluster plot involves analyzing the spatial arrangement of clusters and identifying patterns such as tight clusters, scattered points, or clusters that overlap with one another. Clusters that are well-separated in the plot suggest distinct physiological profiles or patterns, while overlapping clusters indicate

similarities or relationships between different physiological states. The density of data points within each cluster on the t-SNE plot provides insights into the prevalence or concentration of certain physiological patterns within the dataset. Areas with higher data density represent clusters with more members or clusters exhibiting greater physiological homogeneity.

4 Discussion

The findings of this study contribute to our understanding of physiological variability as assessed through polygraph test scoring, shedding light on the distinct clusters identified through fuzzy C-means clustering. The analysis revealed nine distinct clusters, each characterized by unique physiological profiles represented by a combination of various parameters derived from polygraph measurements.

The identification of these clusters highlights the heterogeneity of physiological responses observed among the participants undergoing polygraph testing, reflecting diverse physiological states or patterns within the dataset. The clustering performance metrics, including R^2, AIC, BIC, and Silhouette, provide quantitative measures of the clustering quality and the effectiveness of the fuzzy C-means algorithm in partitioning the polygraph data into meaningful clusters.

Examining the cluster information, such as cluster size, explained proportion within-cluster heterogeneity, and within sum of squares, further elucidates the characteristics of each cluster and their relative homogeneity or heterogeneity in the context of polygraph test scoring. The cluster means analysis revealed distinct mean values for each physiological parameter derived from polygraph measurements across the clusters, indicating specific physiological characteristics associated with each cluster as assessed through the polygraph.

Interpreting the physiological significance of these clusters in the context of polygraph test scoring requires careful consideration of the underlying physiological processes represented by the parameters included in the analysis. For instance, clusters characterized by high values of parameters such as amplitude of electrodermal reaction (ARED) and amplitude of blood pressure in brachial pulse (ATAB) may indicate heightened physiological arousal or stress response among individuals undergoing polygraph testing. Conversely, clusters exhibiting lower values of these parameters may represent individuals with relatively subdued physiological responses during polygraph examinations.

The implications of these findings in the domain of polygraph testing extend beyond the scope of this study, offering insights into potential applications for improving the accuracy and reliability of polygraph examinations. Understanding the physiological variability among individuals undergoing polygraph testing can

inform the interpretation of test results and contribute to the development of more effective techniques for deception detection and truth verification.

In conclusion, the findings of this study underscore the importance of considering the heterogeneity of physiological responses in polygraph test scoring and highlight the potential utility of clustering techniques in identifying distinct physiological profiles associated with deception detection. Further research in this area holds promise for advancing our understanding of the physiological basis of polygraph testing and its implications for forensic science and investigative practices.

Conclusions

In conclusion, our study utilized fuzzy C-means clustering to identify distinct physiological clusters among individuals undergoing polygraph testing. The analysis revealed nine clusters characterized by unique physiological profiles, providing valuable insights into the heterogeneity of physiological responses during polygraph examinations. These findings contribute to a deeper understanding of the physiological variability inherent in polygraph test scoring and underscore the importance of considering individual differences in the interpretation of test results.

It is important to acknowledge the limitations of this study, including the reliance on a specific set of physiological parameters derived from polygraph measurements and the potential influence of confounding variables not accounted for in the analysis. Future research in the field of polygraph testing could explore alternative clustering algorithms, incorporate additional physiological parameters or contextual factors, and validate the identified clusters in larger and more diverse samples of individuals undergoing polygraph examinations.

Future research in the field of polygraph testing should aim to address these limitations and further advance our understanding of physiological clustering in this context. Investigating alternative clustering algorithms and incorporating additional physiological parameters or contextual factors may enhance the accuracy and reliability of cluster identification. Moreover, validation of the identified clusters in larger and more diverse samples of individuals undergoing polygraph examinations is essential to ensure the reproducibility and generalizability of the findings. Furthermore, longitudinal studies tracking changes in physiological clusters over time and in response to different stimuli could provide valuable insights into the dynamic nature of physiological responses during polygraph testing.

The implications of our findings for polygraph testing are significant. By identifying distinct physiological profiles associated with different degrees of deception, our study contributes to the development of more effective techniques for interpreting polygraph test results. Understanding the physiological variability among individuals undergoing polygraph examinations can inform the refinement

of existing polygraph protocols and the development of innovative approaches to enhance the accuracy and reliability of polygraph testing in forensic science and investigative practices. Ultimately, our study highlights the potential utility of physiological clustering in improving the effectiveness of polygraph examinations and advancing the field of deception detection.

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