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Quantum Computing Approach in K-Medoids Method for AIDS Disease Prediction Using Manhattan Distance

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Abstract

Acquired Immunodeficiency Syndrome (AIDS) caused by the Human Immunodeficiency Virus (HIV) is one of the deadliest infectious diseases in the world. Understanding its spread and epidemiological characteristics is crucial for developing and preventing more effective treatments. The K-Medoids method was chosen to address this issue using several clinical and demographic variables. K-Medoids were selected for their ability to process large amounts of data with a clustering technique that selects central points within each cluster and minimizes the total distance. The choice of Manhattan distance is based on its ability to handle data simply. Applying quantum computing approaches overcomes the limitations of classical computing in processing large medical datasets. This study demonstrates that implementing a quantum algorithm on K-Medoids results in faster and more accurate predictions in diagnosing AIDS. The research findings show that the predictive accuracy between quantum and classical computing is equivalent, at 85%. These findings indicate the significant potential of quantum computing in improving medical prediction efficiency. This can provide patterns of AIDS spread and risk factors that can assist in the development of more effective health interventions for the community.

Keywords: Data Mining; K-Medoids; Manhattan Distance; Quantum Computing; Clustering.

Introduction

Data Mining is a collection of large data sets that undergo processing to identify relationships and extract valuable information [1]. Data Mining is widely used for data processing in business, science, healthcare, and financial calculations because it can effectively process large amounts of data to yield optimal decision-making results [2][3]. Some key areas encompassed by Data Mining include various clustering techniques, classification, physics and mathematics techniques, regression, Artificial Intelligence, association, and others [4].

K-Medoids is a clustering method in Data Mining that can provide accurate decision-making results [5][6][7]. Its goal is to achieve the highest accuracy in grouping structured data, allowing users to obtain the best possible accuracy from the processed data.

Quantum Computing is a mode of computation that processes large amounts of data compared to classical methods [8]. Quantum computing is a field in computer science [9][10] that utilizes the principles of quantum mechanics to perform computations. It differs from classical computing, which uses classical bits as the basic unit of information, where a bit can be in one of two states: 0 or 1. However, in quantum computing, qubits (quantum bits) [11][12] are used, which can be in superposition of both 0 and 1 simultaneously and can experience entanglement. This allows quantum computers to perform multiple operations in parallel and process information differently from classical computers.

Quantum computing can potentially solve some computational problems [13] much more efficiently than classical computers [14]. Examples include quantum cryptography, optimization, molecular simulation, and solving problems involving the factorization of large numbers.

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Although still in the developmental stage and facing significant technical challenges [15], quantum computing's potential to revolutionize the computational landscape has generated considerable interest within the scientific and industrial communities.

Some researchers have found that the K-Medoids clustering technique [16] can assist in processing large-scale data and producing highly accurate predictions [17]. AIDS (Acquired Immunodeficiency Syndrome) is a disease caused by HIV (Human Immunodeficiency Virus) that disrupts the human immune system. Research on the detection and treatment of AIDS patients is crucial for understanding the dynamics of the disease and developing more effective prevention strategies. Data collection methods, particularly K-Medoids, have been widely used to gather medical data to identify abnormal patterns that assist in developing medical reports. This study employs a quantum K-Medoids algorithm to detect AIDS.

Previous research has explored the use of clustering methods in medical data analysis. For instance, studies such as [18] demonstrate that the K-Medoids method effectively clusters patient data based on symptoms and laboratory test results, which aids in identifying disease spread patterns. Additionally, quantum computing approaches have begun to be applied in various fields to enhance the efficiency and accuracy of data processing.

The primary reference for this research is [19]. This study employs a "network medicine" approach to investigate and validate population-level disease manifestations and drug repurposing for COVID-19. The findings of this research include identifying several disease manifestations associated with COVID-19 using network analysis, which allows for a deeper understanding of the complex pathways of the disease. Additionally, the study identified several existing drugs that could be considered for repurposing in treating COVID-19 based on network analysis results. These findings not only expand knowledge about the clinical manifestations of COVID-19 but also open new opportunities for therapy through drug repurposing. The research demonstrates the significant potential of quantum computing to process large data sets with greater speed and accuracy compared to classical methods. However, the application of quantum computing in medical data clustering, particularly using the K-Medoids method, remains underexplored, especially for diseases such as AIDS. This creates a gap in the literature that needs to be addressed to maximize the potential of medical data analysis with higher accuracy and efficiency.

This research aims to develop a K-Medoids algorithm using a quantum computing approach to enhance the performance and efficiency of clustering large-scale data relevant to AIDS disease prediction. This study compares the accuracy and data processing speed of quantum computing-based K-Medoids with traditional K-Medoids. Additionally, another specific objective of this research is to identify key risk factors and patterns of AIDS disease spread.

The difference between this research and the primary reference is the application of quantum computing to the K-Medoids method for clustering medical records of AIDS disease.

The novelty of this research lies in integrating the K-Medoids clustering method with a quantum computing approach using the Manhattan Distance [20] for analyzing AIDS medical records. This approach efficiently and accurately transforms data attributes. This study significantly contributes to medical data analysis by offering a new method. The findings of this research can aid in better medical decision-making through accurate clustering of medical records and open new opportunities for the application of quantum computing in medical data analysis.

Method

A. Related Research

In the study by Minyechil Alehegn [21], an evaluation of deep learning models revealed superior accuracy, precision, and F-Score compared to machine learning models. However, machine learning models performed better for sensitivity metrics than deep learning models. Specifically, the machine learning algorithms SVM, RF, and NB achieved accuracies of 89.00%, 87.00%, and 86.94%, respectively, with precisions of 75.89%, 74.97%, and 75.87%, and sensitivities of 87.96%, 84.00%, and 84.12%. In contrast, LSTM and GRU models yielded 97.65% and 96.00% accuracies, with 77.35% and 84.00% precisions and sensitivities of 87.93% and 82.98%. The F-Scores for LSTM and GRU were 82.03% and 83.20%. Thus, it can be concluded that the sensitivity of the SVM machine learning model is better at 87.96%. The LSTM model achieves the highest accuracy of 97.65%, precision of 77.35%, sensitivity of 87.93%, and an F-Score of 82.03%.

In research [22], a mathematical model of the Human Immunodeficiency Virus (HIV) was used to investigate behaviors influenced by stochastic disturbances. This study addresses the global exponential stability of nonlinear stochastic HIV systems [23], derived from the disease-free equilibrium E0 using the fundamental Euler-Maruyama (EM) algorithm.

Research [24] involved clustering AIDS cases by province using the K-Means clustering method, creating two clusters: provinces with the highest and lowest AIDS cases. The centroid data calculations within these clusters targeted AIDS mitigation efforts in the provinces with the highest incidence.

Research [25] applied the K-Means clustering method to group data based on the distance from data centroids to collect similar characteristics within regions with comparable HIV spread. This method assists in implementing appropriate prevention and treatment measures. The study identified three clusters among 27 cities in West Java: 13 cities in the high-level cluster (C1), 13 cities in the moderate-level cluster (C2), and 1 city in the low-level cluster (C3).

B. Data Collection

Data collection involves gathering medical record data necessary for predicting AIDS through the following variables:

a. **Trt (Treatment Indicator)**: This indicator provides crucial information regarding the effectiveness of antiretroviral therapy (ART), disease progression, and patient outcomes.

b. **Homosexual Activity**: This variable assists in analyzing epidemiological data to map patterns of HIV/AIDS transmission.

c. **Drugs**: The use of injectable medications is one of the most effective methods of HIV transmission. Drug injection can cause damage to blood vessels and lead to other infections, increasing the risk of HIV transmission.

d. **Karnof**: This variable is important in clinical trials for classifying patients based on their health status, with a health score ranging from 1 to 100.

e. **Symptoms**: This variable provides insight into the patient’s general health and quality of life. Chronic symptoms can indicate the need for more intensive care, enabling more accurate identification of disease stages.

f. **Hemo**: Hemophilia is a disorder related to blood clotting processes.

g. **Treat**: This variable represents treatment strategies for the prevention of HIV/AIDS.

h. **Infected**: This variable denotes whether an individual has been diagnosed with AIDS. unavoidable.

C. Data Transformation

In this process, data transformation is carried out by changing the binary representation to 0 and 1 format to facilitate clustering and data processing and obtain optimal results.

D. Quantum Bit Transformation

In this process, data is transformed into quantum bits (qubits) to enable quantum data processing using quantum K-Medoids, making the data processing more complex than classical methods. The information is linked to prior research undertaken by the author. The Introduction must have at least five references, while a minimum of 20 citations should be included in all other sections. The sources must consist of publications written in foreign languages and are required to be sourced from reputable journals and proceedings that are relevant to your topic. The information should be current, with a maximum age of five years from the date of publishing. Scopus, Clarivate Analytics Web of Science (SCIE & SSCI), PubMed, DOAJ, IEEE, ACM, Proquest, CABI, Gale, and EBSCO database entries are the primary indexes for journals and proceedings. Ensure that every citation mentioned in the texts is included in the reference table, and vice versa. Non-scholarly sources such as Wikipedia, blogs, or periodicals are prohibited.

E. K-Medoids Method with Quantum Computing

Quantum computing in the K-Medoids method offers several advantages, such as increased computational speed, the ability to handle large datasets, improved stability, and error correction in qubits with distance calculations using Manhattan Distance.

The author has conducted prior research that is relevant to the content. The Introduction must have at least five references, while a minimum of 20 citations should be included in all other sections. The sources must consist of publications written in international languages and must be sourced from reputable journals and conference proceedings relevant to your topic. The information should be current, not exceeding a five-year period from the date of publishing. Scopus, Clarivate Analytics Web of Science (SCIE & SSCI), PubMed, DOAJ, IEEE, ACM, Proquest, CABI, Gale, and EBSCO database entries are the primary indexes for journals and proceedings. Ensure that every citation mentioned in the text is included in the reference table, and vice versa. Non-scholarly sources, including Wikipedia, blogs, and magazines, are prohibited.

F. Result

At this stage, the data processing results are clustered using the classical K-Medoids method and the quantum K-Medoids method. The clustered data results can provide information and insights into the patterns that have been discovered.

G. Evaluation

At this stage, the clustered data is evaluated using both classical and quantum computing methods to predict AIDS. The evaluation involves metrics such as accuracy and prediction, which determine how well the models perform in predicting AIDS.

In the medical records of AIDS patients transforming the standard representation, the data is converted into qubits, represented as 0 and 1, with bra ">" and ket “<” notation. The use of quantum computing aims to achieve more accurate results in predicting AIDS based on the following rules:

a. Trt (Treatment Indicator): Receiving treatment = 1, not receiving treatment = 0.
b. Homo: No = 0, Yes = 1.
c. Drugs: If using drugs = 1, if not = 0.
d. Karnof: If health score $\leq 50 = 0$, $> 51 = 1$.
e. Hemo (Hemophilia): If positive for hemophilia = 1, if not = 0.
f. Treat: If treatment is present = 0, if not = 1.
g. Symptom: If no symptoms = 0, if symptoms are present = 1.
h. Infected: No = 0, Yes = 1.

These rules are established to ensure that AIDS medical record data is standardized accurately and can be further processed. Table 1 shows the results of the binary encoding.

Table 1. AIDS Medical Record Dataset

No	X1	X2	X3	X4	X5	…	Y
1	1	0	0	1	0	…	0
2	1	0	0	1	0	…	1
3	1	1	1	1	1	…	0
4	1	1	0	1	1	…	0
5	0	1	0	1	1	…	0
6	0	1	1	1	1	…	0
7	0	1	0	1	1	…	1
8	0	1	1	1	1	…	0
9	1	1	0	1	1	…	1
10	0	1	0	1	1	…	1
11	1	0	0	1	0	…	1
12	1	1	0	1	1	…	0
13	1	1	0	1	1	…	0
14	0	1	0	1	1	…	0
15	1	1	0	1	1	…	1
16	0	1	0	1	1	…	1
17	1	0	1	1	0	…	0
18	1	1	0	1	1	…	0
…	…	…	…	…	…	…	…
…	…	…	…	…	…	...	…
350	1	1	0	1	1	…	1

For example, in dataset entry number 1, with the binary code 10010010, this code is derived from the attributes described above as follows: Trt: Receiving treatment (1), Homo: No (0), Drugs: No (0), Karnof: Health score ≥ 51

(1), Hemo: No hemophilia (0), Treat: Treatment present (0), Symptom: No symptoms (0), and Target (HIV/AIDS): No (0). The data in Table 1 is converted into qubits as shown in Table 2 below:

Table 2. Qubit Data

No	X1	X2	X3	X4	X5	…	Y
1	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	…	$\begin{bmatrix}0\\1\end{bmatrix}$
2	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	…	$\begin{bmatrix}1\\0\end{bmatrix}$
3	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	…	$\begin{bmatrix}0\\1\end{bmatrix}$
4	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	…	$\begin{bmatrix}0\\1\end{bmatrix}$
5	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	…	$\begin{bmatrix}0\\1\end{bmatrix}$
6	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	…	$\begin{bmatrix}0\\1\end{bmatrix}$
7	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	…	$\begin{bmatrix}0\\1\end{bmatrix}$
8	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	…	$\begin{bmatrix}0\\1\end{bmatrix}$
9	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	…	$\begin{bmatrix}1\\0\end{bmatrix}$
10	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	…	$\begin{bmatrix}1\\0\end{bmatrix}$
11	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	…	$\begin{bmatrix}1\\0\end{bmatrix}$
12	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	…	$\begin{bmatrix}0\\1\end{bmatrix}$
13	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	…	$\begin{bmatrix}0\\1\end{bmatrix}$
14	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	…	$\begin{bmatrix}0\\1\end{bmatrix}$
15	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	…	$\begin{bmatrix}1\\0\end{bmatrix}$
16	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	…	$\begin{bmatrix}1\\0\end{bmatrix}$
17	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	…	$\begin{bmatrix}0\\1\end{bmatrix}$
18	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	…	$\begin{bmatrix}0\\1\end{bmatrix}$
…	…	…	…	….	….	…	…
…	…	…	…	…	…	…	…
350	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	…	$\begin{bmatrix}0\\1\end{bmatrix}$

In the development of K-Medoids using quantum computing with Manhattan Distance calculations, the following formula steps are involved in the data processing:

a. **Initialization Step**: Determine the initial number of clusters to be established for data processing.
b. **Assignment Step**: Once the number of clusters is determined, calculate the Manhattan distance between each data point and all existing medoids. Assign each data point to the cluster with the nearest medoid based on the Manhattan Distance.

$$d(a_x,b_y)=\sum_{z=1}^{n} \left| |a_{az}\rangle - |b_{bz}\rangle \right| \quad (1)$$

c. **Update Step**: Select non-medoid data points within each cluster in this stage. Calculate the total Manhattan distance from all points in the cluster to each candidate medoid. Choose the medoid with the lowest distance as the new medoid for the cluster. Repeat this step until the desired results are achieved.

Results and Discussion

The findings from this research involve the development of the K-Medoids clustering method with a quantum computing approach using Manhattan Distance calculations. The values of each attribute are transformed into quantum computing form to be processed using quantum computing techniques. The K-Medoids algorithm was tested with an accuracy of 85% over two epochs. Below are the results of testing for epochs 1 and 2.

Table 3. K-Medoids Epoch-1 Test Results

C1	C2	Shortest Distance	Cluster	Data Real	Description
2	2	2	1	0	Benar

2	2	2	1	1	Salah
3	1	1	2	0	Salah
2	0	0	2	0	Salah
2	2	2	1	0	Benar
2	2	2	1	0	Benar
2	2	2	1	1	Salah
3	3	3	1	0	Benar
3	1	1	2	1	Benar
2	2	2	1	1	Salah
2	2	2	1	1	Salah
2	0	0	2	0	Salah
2	0	0	2	0	Salah
1	1	1	1	0	Benar
2	0	0	2	1	Benar
3	3	3	1	1	Salah
3	5	3	1	0	Benar
2	0	0	2	0	Salah
…	…	…	…	…	…
2	0	0	2	0	Salah
Total of Shortest Distance		443	Accuracy		55 %

Table 4. K-Medoids with Quantum Computing Epoch-1 Test Results

C1	C2	C1 (Decimal)	C2 (Decimal)	Shortest Distance	Cluster	Data Real	Description
$\begin{bmatrix}2\\5\end{bmatrix}$	$\begin{bmatrix}2\\5\end{bmatrix}$	5,38	5,38	5,38	1	0	True
$\begin{bmatrix}2\\5\end{bmatrix}$	$\begin{bmatrix}2\\5\end{bmatrix}$	5,38	5,38	5,38	1	1	False
$\begin{bmatrix}3\\4\end{bmatrix}$	$\begin{bmatrix}1\\6\end{bmatrix}$	5,00	6,08	5,00	1	0	True
$\begin{bmatrix}2\\5\end{bmatrix}$	$\begin{bmatrix}0\\7\end{bmatrix}$	5,38	7,00	5,38	1	0	True
$\begin{bmatrix}2\\5\end{bmatrix}$	$\begin{bmatrix}2\\5\end{bmatrix}$	5,38	5,38	5,38	1	0	True
$\begin{bmatrix}2\\5\end{bmatrix}$	$\begin{bmatrix}2\\5\end{bmatrix}$	5,38	5,38	5,38	1	0	True
$\begin{bmatrix}2\\5\end{bmatrix}$	$\begin{bmatrix}2\\5\end{bmatrix}$	5,38	5,38	5,38	1	1	False
$\begin{bmatrix}3\\4\end{bmatrix}$	$\begin{bmatrix}3\\4\end{bmatrix}$	5,00	5,00	5,00	1	0	True
$\begin{bmatrix}3\\4\end{bmatrix}$	$\begin{bmatrix}1\\6\end{bmatrix}$	5,00	6,08	5,00	1	1	False

[illegible]	[illegible]	5,38	5,38	5,38	1	1	False
[illegible]	[illegible]	5,38	5,38	5,38	1	1	False
[illegible]	[illegible]	5,38	7,00	5,38	1	0	True
[illegible]	[illegible]	5,38	7,00	5,38	1	1	False
[illegible]	[illegible]	6,08	6,08	6,08	1	0	True
[illegible]	[illegible]	5,38	7,00	5,38	1	0	True
[illegible]	[illegible]	5,00	6,08	5,00	1	0	True
[illegible]	[illegible]	5,00	5,00	5,00	1	0	True
[illegible]	[illegible]	5,38	5,38	2,83	1	1	False
…	…	…	…	…	…	…	…
…	…	…	…	…	…	…	…
[illegible]	[illegible]	5,38	7,00	5,38	1	0	Benar
Total of Shortest Distance				1899,558	Accuracy		75 %

Table 5. K-Medoids Epoch-2 Test Results

C1	C2	Shortest Distance	Cluster	Data Real	Description
0	0	0	1	0	True
0	0	0	1	1	False
3	3	3	1	0	True
2	2	2	1	0	True
4	4	4	1	0	True
4	4	4	1	0	True
4	4	4	1	1	False
5	5	5	1	0	True
3	3	3	1	1	False
4	4	4	1	1	False
0	0	0	1	1	False
2	2	2	1	0	True
2	2	2	1	0	True
3	3	3	1	0	True
2	2	2	1	1	False

5	5	5	1	1	False
3	3	3	1	0	True
2	2	2	1	0	True
…	…	…	…	…	…
…	…	…	…	…	…
2	2	2	1	0	Benar
Total of Shortest Distance		923	Accuracy		85 %

Table 6. K-Medoids with Quantum Computing Epoch-2 Test Results

C1	C2	C1 (Decimal)	C2 (Decimal)	Shortest Distance	Cluster	Data Real	Description
$\begin{bmatrix}0\\7\end{bmatrix}$	$\begin{bmatrix}0\\7\end{bmatrix}$	7,00	7,00	7,00	1	0	True
$\begin{bmatrix}0\\7\end{bmatrix}$	$\begin{bmatrix}0\\7\end{bmatrix}$	7,00	7,00	7,00	1	1	False
$\begin{bmatrix}3\\4\end{bmatrix}$	$\begin{bmatrix}3\\4\end{bmatrix}$	5,00	5,00	5,00	1	0	True
$\begin{bmatrix}2\\5\end{bmatrix}$	$\begin{bmatrix}2\\5\end{bmatrix}$	5,38	5,38	5,38	1	0	True
$\begin{bmatrix}4\\3\end{bmatrix}$	$\begin{bmatrix}4\\3\end{bmatrix}$	5,00	5,00	5,00	1	0	True
$\begin{bmatrix}4\\3\end{bmatrix}$	$\begin{bmatrix}4\\3\end{bmatrix}$	5,00	5,00	5,00	1	0	True
$\begin{bmatrix}4\\3\end{bmatrix}$	$\begin{bmatrix}4\\3\end{bmatrix}$	5,00	5,00	5,00	1	1	False
$\begin{bmatrix}5\\2\end{bmatrix}$	$\begin{bmatrix}5\\2\end{bmatrix}$	5,38	5,38	5,38	1	0	True
$\begin{bmatrix}3\\4\end{bmatrix}$	$\begin{bmatrix}3\\4\end{bmatrix}$	5,00	5,00	5,00	1	1	False
$\begin{bmatrix}4\\3\end{bmatrix}$	$\begin{bmatrix}4\\3\end{bmatrix}$	5,00	5,00	5,00	1	1	False
$\begin{bmatrix}0\\7\end{bmatrix}$	$\begin{bmatrix}0\\7\end{bmatrix}$	7,00	7,00	7,00	1	1	False
$\begin{bmatrix}4\\3\end{bmatrix}$	$\begin{bmatrix}4\\3\end{bmatrix}$	5,00	5,00	5,00	1	1	True
$\begin{bmatrix}2\\5\end{bmatrix}$	$\begin{bmatrix}2\\5\end{bmatrix}$	5,38	5,38	5,38	1	0	True
$\begin{bmatrix}2\\5\end{bmatrix}$	$\begin{bmatrix}2\\5\end{bmatrix}$	5,38	5,38	5,38	1	0	True
$\begin{bmatrix}3\\4\end{bmatrix}$	$\begin{bmatrix}3\\4\end{bmatrix}$	5,00	5,00	5,00	1	0	Benar
$\begin{bmatrix}2\\5\end{bmatrix}$	$\begin{bmatrix}2\\5\end{bmatrix}$	5,38	5,38	5,38	1	1	Salah
$\begin{bmatrix}5\\2\end{bmatrix}$	$\begin{bmatrix}5\\2\end{bmatrix}$	5,38	5,38	5,38	1	1	Salah
$\begin{bmatrix}3\\4\end{bmatrix}$	$\begin{bmatrix}3\\4\end{bmatrix}$	5,00	5,00	5,00	1	0	True
…	…	…	…	…	…	…	…
…	…	…	…	…	…	…	…
$\begin{bmatrix}2\\5\end{bmatrix}$	$\begin{bmatrix}2\\5\end{bmatrix}$	5,38	5,38	5,38	1	0	Benar
Total of Shortest Distance				1890,71	Accuracy		85 %

=

In this study, data clustering from AIDS medical records was performed using the K-Medoids method with Manhattan Distance calculations. The testing results showed that the clustering accuracy for both quantum and classical computing methods was the same, at 85%.

Conclusion

This study thoroughly evaluates the use of quantum computing with Manhattan Distance calculations to predict AIDS. The results indicate that the prediction accuracy for classical and quantum computing is the same, suggesting that the K-Medoids algorithm with quantum computing can serve as an alternative method for clustering AIDS data. These findings can be applied to clustering processes in the medical field, especially when handling large datasets.

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