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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. This study uses the K-Medoids method with a quantum computing approach to predict AIDS based on clinical and demographic data. K-Medoids is chosen to group large amounts of data using a clustering technique that determines the center point (medoid) of each cluster, minimizing the overall distance between data in a cluster. The Manhattan distance is used because it is easier to process data. The quantum computing approach is used to overcome the limitations of classical computing when processing large-scale medical data. This study shows that the application of quantum algorithms to the K-Medoids method allows for faster and more accurate predictions in the diagnosis of AIDS. The tests carried out showed that the prediction accuracy of classical and quantum methods was comparable, namely 85%. The results support the great potential of quantum computing to improve the efficiency of medical predictions. The research involves converting data into quantum format, processing it with the K-Medoids algorithm, and evaluating its performance based on metrics such as intercluster distance and computation time. The research will also identify patterns and risk factor for the spread of AIDS that can be used to develop more effective health interventions. The conclusion of the research is that integrating the K-Medoids techniques can only increase the speed of data processing but also provide competitive accuracy compared to traditional techniques. This research opens up new possibilities in medical data analysis, especially when managing large and complex data sets. The bottom line is that these findings can help make better medical decisions and strategically support AIDS prevention and treatment efforts.

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

Introduction

Data Mining is a collection of large data sets that undergo processing to identify relationships and extract valuable information [1], [2], [3]. 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. 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]. Its goal is to achieve the highest accuracy in grouping structured data, allowing users to obtain the best possible accuracy from the processed data. Some researchers have found that the K-Medoids clustering technique can assist in processing large-scale data and producing highly accurate predictions [7], [8].

Previous research has explored the use of clustering methods in medical data analysis. For instance, studies such as 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 [9].

The primary reference for this research is. This study employs a "network medicine" approach to investigate and validate population-level disease manifestations and drug repurposing for COVID-19 [10], [11], [12]. The findings of this research include identifying several disease manifestations associated with COVID-19 using network analysis,

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which allows for a deeper understanding of the complex pathways of the disease [13]. Additionally, the study identified several existing drugs that could be considered for repurposing in treating COVID-19 based on network analysis results [14]. These findings not only expand knowledge about the clinical manifestations of COVID-19 but also open new opportunities for therapy through drug repurposing [15], [16]. 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 [17]. 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 [17], [18], [19]. Additionally, another specific objective of this research is to identify key risk factors and patterns of AIDS disease spread [20], [21]. 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 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.

Quantum Computing is a mode of computation that processes large amounts of data compared to classical methods [22], [23], [24]. Quantum computing is a field in computer science that utilizes the principles of quantum mechanics to perform computations [25]. 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) are used, which can be in a superposition of both 0 and 1 simultaneously and can experience entanglement [26].

Method

A. Related Research

In In the study by Minyechil Alehegn [27], 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 [28], 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, derived from the disease-free equilibrium E0 using the fundamental Euler-Maruyama (EM) algorithm. Research involved clustering [29] 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 [30] 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).

By utilizing quantum solving procedures, it can produce more complex & realistic mathematical examples to predict the spread of HIV/AIDS. For example, the SIA (Susceptible, Infected, Abstained) or SIAT (Susceptible, Infected, Abstained, Treatment) examples can be optimized using quantum computing to analyze the equilibrium point & stability of the spread of the disease. In addition, quantum computing can help identify key factors that influence the spread of the disease & the effectiveness of hegemony such as education & ART (Antiretroviral Therapy) treatment. Thus, the application of quantum computing to the analysis of the spread of AIDS not only increases the accuracy of predictions, but also provides advantages in terms of processing speed & the ability to handle more complex data. This opens up new opportunities for research & development of more effective prevention & treatment tactics.

B. Dataset Collection

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

1. Trt (Treatment Indicator): This indicator provides crucial information regarding the effectiveness of antiretroviral therapy (ART), disease progression, and patient outcomes.
2. Homosexual Activity: This variable assists in analyzing epidemiological data to map patterns of HIV/AIDS transmission.
3. 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.
4. 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.
5. 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.
6. Hemo: Hemophilia is a disorder related to blood clotting processes.
7. Treat: This variable represents treatment strategies for the prevention of HIV/AIDS.
8. 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. Results

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:

1. Trt (Treatment Indicator): Receiving treatment = 1, not receiving treatment = 0.
2. Homo: No = 0, Yes = 1.
3. Drugs: If using drugs = 1, if not = 0.
4. Karnof: If health score ≤ 50 = 0, > 51 = 1.
5. Hemo (Hemophilia): If positive for hemophilia = 1, if not = 0.
6. Treat: If treatment is present = 0, if not = 1.
7. Symptom: If no symptoms = 0, if symptoms are present = 1.
8. 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	Treatment indicator	Homo	Drugs	Karnof	Hemophilia	Sympton	Treat	Infected
1	1	0	0	1	0	0	1	0
2	1	0	0	1	0	0	1	1
3	1	1	1	1	1	0	1	0
4	1	1	0	1	1	0	1	0
5	0	1	0	1	1	0	0	0
6	0	1	1	1	1	0	1	0
7	0	1	0	1	1	0	0	1
8	0	1	1	1	1	0	0	0
9	1	1	0	1	1	1	1	1
10	0	1	0	1	1	0	0	1
11	1	0	0	1	0	0	1	1
12	1	1	0	1	1	0	1	0
13	1	1	0	1	1	0	1	0
14	0	1	0	1	1	0	1	0
15	1	1	0	1	1	0	1	1
16	0	1	0	1	1	1	0	1
17	1	0	1	1	0	0	0	0
18	1	1	0	1	1	0	1	0
…	…	…	…	…	…	0	1	…
…	…	…	…	…	…	...	…	…
350	1	1	0	1	1	0	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	Treatment indicator	Homo	Drugs	Karnof	Hemophilia	Sympton	Treat	Infected
1	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$
2	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$
3	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$
4	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$
5	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$
6	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$
7	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$
8	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$
9	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$
10	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$
11	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$
12	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$
13	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$
14	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$
15	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$
16	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$
17	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$
18	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$
…	…	…	…	…	…	…	…	…
…	…	…	…	…	…	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	…
350	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}1\\0\end{bmatrix}$	$\begin{bmatrix}0\\1\end{bmatrix}$

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

1. Initialization Step: Determine the initial number of clusters to be established for data processing.
2. 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.

$$d(a_x, b_y) = \sum_{z=1}^{n} ||a_{az} > - |b_{bz} >| \tag{1}$$

3. 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.

In this study, clustering of AIDS medical record data was carried out using the K-medoids method with Manhattan distance calculations. The clustering process converts attribute values into a quantum computational form, allowing for parallel and efficient data processing. Known for its ability to handle data with noise and outliers, the K-Medoids algorithm has been tested with classical and quantum approaches. Based on the test results, the clustering accuracy of the quantum computing method and the classical computing method is the same, namely 85%.

Quantum computing has the potential to increase efficiency and processing speed, but there are several possible reasons why this study did not significantly increase accuracy. First, converting data to quantum form and back to classical form adds complexity that is not present in the classical process, potentially negating the benefits of quantum parallelism. Second, the K-Medoids algorithm itself may have reached the upper limit of accuracy that can be achieved with the data set and techniques used, so the improvement from quantum computing is unlikely to be significant. Finally, factors such as interference in qubits and the difficulty in physically implementing quantum algorithms can reduce the potential benefits obtained from other methods, given the potential and limitations of existing quantum computing.

Table 3. K-Medoids Epoch-1 Test Results

C1	C2	Shortest Distance	Cluster	Real Data	Description
2	2	2	1	0	True
2	2	2	1	1	False
3	1	1	2	0	False
2	0	0	2	0	False
2	2	2	1	0	True
2	2	2	1	0	True
2	2	2	1	1	False
3	3	3	1	0	True
3	1	1	2	1	True
2	2	2	1	1	False
2	2	2	1	1	False
2	0	0	2	0	False
2	0	0	2	0	False
1	1	1	1	0	False
2	0	0	2	1	False
3	3	3	1	1	False
3	5	3	1	0	True
2	0	0	2	0	False
…	…	…	…	…	…
2	0	0	2	0	False
Total of Shortest Distance		443	Accuracy		55 %

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

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

C1	C2	C1	C2	Shortest Distance	Cluster	Real Data	Description
$\begin{bmatrix}3\\4\end{bmatrix}$	$\begin{bmatrix}1\\6\end{bmatrix}$	5,00	6,08	5,00	1	0	True
$\begin{bmatrix}3\\4\end{bmatrix}$	$\begin{bmatrix}3\\4\end{bmatrix}$	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	2,83	1	1	False
…	…	…	…	…	…	…	…
…	…	…	…	…	…	…	…
$\begin{bmatrix}2\\5\end{bmatrix}$	$\begin{bmatrix}0\\7\end{bmatrix}$	5,38	7,00	5,38	1	0	True
Total of Shortest Distance				1899,558	Accuracy		75 %

Table 5. K-Medoids Epoch-2 Test Results

C1	C2	Shortest Distance	Cluster	Real Data	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	True
Total of Shortest Distance		923	Accuracy		85 %

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

C1	C2	C1	C2	Shortest Distance	Cluster	Real Data	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

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

This research is crucial to continue exploring the potential of quantum computing in improving the performance of clustering procedures such as K-Medoids. In addition to testing using a variety of larger and more complex datasets, further research can try to implement more sophisticated quantum optimization techniques or combine other methods such as quantum machine learning. Research can also focus on reducing noise in qubits and improving the stability of quantum systems, which can have a significant effect on the accuracy output. In addition, exploring the combination of quantum computing with classical computing in a hybrid system can also be a tactic to maximize the benefits of both approaches. With these steps, it is hoped that quantum computing can be further optimized to provide significant accuracy improvements in the analysis of medical data such as AIDS medical records.. 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.

Further research is recommended to focus on several aspects that can improve the accuracy and benefits of quantum computing. Improving the quality of qubits and reducing noise are important because more stable qubits allow for more accurate calculations. Applying more sophisticated quantum optimization algorithms such as the Quantum Approximate Optimization Algorithm (QAOA) and the Variational Quantum Eigensolver (VQE) can also help achieve better results. In addition, more effective quantum error correction techniques should be used to overcome possible errors. Combining quantum and classical computing (hybrid computing) can also be an effective strategy to maximize the benefits of both approaches. Testing larger, more complex, and different data sets will provide deeper insights into the benefits of quantum computing. Investment in the development of more advanced quantum computing infrastructure, including hardware and software, will also create a stronger foundation for research and application of this technology. Ultimately, interdisciplinary collaborations between computer science, physics, mathematics, and other disciplines will lead to more comprehensive and innovative solutions. These steps are expected to enable quantum computing to achieve higher precision and provide significant benefits in a variety of applications.

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