

IMPLEMENTATION OF K-MEDOIDS METHOD FOR HEART DISEASE PREDICTION USING QUANTUM COMPUTING AND MANHATTAN DISTANCE

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Abstract— Heart disease is a severe health condition characterized by dysfunctions in the heart and blood vessels, which can be fatal if not properly managed. Early detection and prediction of heart disease are crucial for understanding the prevalence and determining patients' quality of life. In this study, quantum computing is applied to enhance the performance of the K-Medoids method. A comparative analysis of these methods is conducted, focusing on their performance. The investigation utilizes a dataset of heart disease patient medical records. This dataset includes various attributes used to predict heart disease patterns. The dataset is tested using both the classical and K-Medoids methods with a quantum computing approach, employing Manhattan distance calculations. This study's findings reveal that applying quantum computing to the K-Medoids method results in clustering accuracy stability of 85%, equivalent to the classical method. Although there is no increase in accuracy, the quantum computing approach demonstrates potential improvements in data processing efficiency. These results highlight that the K-Medoids method with a quantum computing approach can contribute significantly to faster and more efficient medical data analysis. However, further research is needed for optimization and testing on more extensive and more diverse datasets.

Keywords: data mining, clustering, K-Medoids, manhattan distance, quantum computing, qubit.

Intisari— Penyakit jantung adalah suatu kondisi kesehatan parah yang ditandai dengan disfungsi jantung dan pembuluh darah, yang dapat berakibat fatal jika tidak ditangani dengan baik. Deteksi dini dan prediksi penyakit jantung sangat penting untuk memahami prevalensi dan mengetahui kualitas hidup pasien. Dalam penelitian ini, komputasi kuantum diterapkan untuk meningkatkan kinerja metode K-Medoids. Analisis komparatif terhadap metode-metode ini dilakukan, dengan fokus pada kinerjanya. Penyelidikannya memanfaatkan dataset rekam medis pasien penyakit jantung. Kumpulan data ini mencakup berbagai atribut yang digunakan untuk memprediksi pola penyakit jantung. Dataset diuji menggunakan metode klasik dan K-Medoids dengan pendekatan komputasi kuantum, menggunakan perhitungan jarak Manhattan. Temuan penelitian ini mengungkapkan bahwa penerapan komputasi kuantum pada metode K-Medoids menghasilkan



stabilitas akurasi clustering sebesar 85%, setara dengan metode klasik. Meskipun tidak ada peningkatan akurasi, pendekatan komputasi kuantum menunjukkan potensi peningkatan efisiensi pemrosesan data. Hasil ini menyoroti bahwa metode K-Medoids dengan pendekatan komputasi kuantum dapat berkontribusi secara signifikan terhadap analisis data medis yang lebih cepat dan efisien. Namun, diperlukan penelitian lebih lanjut untuk optimasi dan pengujian pada dataset yang lebih luas dan beragam.

Kata Kunci: data mining, clustering, K-Medoids, jarak manhattan, komputasi kuantum, qubit.

INTRODUCTION

Heart disease is one of the leading causes of death worldwide [1][2][3]. According to the World Health Organization (WHO), cardiovascular diseases cause approximately 17,9 million deaths each year, accounting for about 31% of all global deaths [4][5][6]. Early identification and appropriate management are crucial to reducing mortality rates and improving the quality of life for patients. In recent decades, advancements in computing technology have significantly contributed to diagnosing and predicting heart disease through analyzing large and complex medical datasets. Clustering methods such as k-medoids have been widely used in medical data analysis to identify patterns and anomalies relevant to specific health conditions [7][8]. The k-medoids algorithm selects a number of medoids as cluster centers and groups data based on the nearest distance to these medoids. The main advantage of k-medoids over k-means is their robustness to outliers, often present in medical data.

Data mining is the process of discovering patterns and knowledge from large datasets [9][10][11]. In the medical context, data mining is used to extract valuable information from patient data, which includes diagnoses, treatments, and health outcomes [12][13]. Data mining techniques such as clustering, classification, and association are used to analyze medical data to improve clinical decisions and treatment outcomes. Clustering is one of the data mining techniques used to group data into homogeneous clusters [14]. Clustering algorithms work by identifying patterns in data and grouping data with similar characteristics. In heart disease analysis, clustering can identify groups of patients with similar risks, allowing for more precise and personalized interventions.

The k-medoid clustering method is a variant of k-means that is more robust to outliers [15][16]. The k-medoids algorithm selects several medoids or representative cluster centers and then clusters data based on the nearest distance to these medoids. Unlike k-means, which use the mean as cluster centers, k-medoids select actual data points as medoids, making them more robust against outliers and noise in the data. The k-medoids

algorithm begins with an initial random selection of medoids. It then iterates through two main steps: cluster assignment and medoid update. Each data point is assigned to its nearest medoid in the cluster assignment step. In the medoid update step, new medoids are selected for each cluster by minimizing the distance between data points within the cluster and the medoid. This process is repeated until convergence, where the medoids have no significant change.

Manhattan distance, also known as L1 norm or taxicab distance, is one method for measuring the distance between two points in Euclidean space [17]. Manhattan distance between two points is calculated by summing the absolute differences of their coordinates [18]. In the context of two dimensions, the Manhattan distance between two points (x_1, y_1) and (x_2, y_2) is calculated as:

$$d = |x_1 - x_2| + |y_1 - y_2| \quad (1)$$

This formula sums the absolute differences of their x-coordinates and y-coordinates.

Manhattan distance is often used in clustering due to its simplicity and its ability to handle high-dimensional data or features that are not comparable. In analyzing heart disease, using Manhattan distance can provide more interpretable and robust results in clustering patient data based on diverse clinical features.

Several related studies have explored using the K-Medoids algorithm in various medical applications. For instance, a study titled "Interpretation and Visualization of Clustering Results Using K-Medoids for Identifying the Spread of COVID-19 Virus" [19] demonstrates K-Medoids' effectiveness in clustering COVID-19 spread data in Indonesia. This research employs the K-Medoids method to identify virus spread patterns based on population density and geographical area attributes. The interpretation of clustering results revealed that areas with high population density and smaller geographical areas tend to have higher COVID-19 cases. Visualizing and interpreting clustering results helps gain a deeper understanding of virus spread and can support more effective prevention strategies. Another study, titled "Comparison of Distance Measure in K-

Medoids Clustering for Grouping ISPA Diseases"[20] utilized the K-Medoids algorithm to classify the spread of ISPA (Acute Respiratory Tract Infection) in the region. By comparing two distance measurement methods, Euclidean Distance and Chebyshev Distance, the study revealed that Euclidean Distance provided more optimal results with a Davies Bouldin Index (DBI) value of 0.088, compared to Chebyshev Distance, which had a DBI value of 0.116. The clustering results were divided into three groups: low, medium, and high, offering critical insights for local authorities to prioritize the handling of ISPA cases in Karawang District. Both studies affirm that the K-Medoids method is effective in clustering analysis for various diseases and health conditions. The implementation of visualization and interpretation of clustering results also play a crucial role in conveying information to stakeholders more understandably and beneficially. These studies provide a vital foundation for further research, including exploring the application of quantum computing in enhancing the efficiency and accuracy of the K-Medoids method for medical data analysis.

The main referenced study in this research is titled "Analysis of Cardiovascular Influence in Covid-19 Cases on Obesity Using the K-Medoids Method"[21]. The study aimed to analyze COVID-19 patients suffering from obesity, non-obesity, and patients experiencing both obesity and cardiovascular conditions. It utilized the K-Medoids method to classify and understand the comparisons and influences among attributes in the COVID-19 patient dataset. The research findings indicated that K-medoids effectively cluster data based on patient health conditions. Within the dataset, 62.62% of patients were not infected with COVID-19, while 37.38% were infected. Furthermore, 74.54% of the sample consisted of non-obese patients, whereas 25.46% were obese patients—only 0.57% of the sample suffered from both obesity and cardiovascular conditions simultaneously. The study revealed that attributes such as pneumonia and hypertension significantly influenced the obesity patient cluster, with respective impact levels of 150.15% and 172.04%. For non-obese patients, gender and hypertension attributes showed influence levels of 39.50% and 106.61%, respectively. Among obese patients also suffering from cardiovascular conditions, gender and pneumonia attributes had influences of 159.07% and 300%, respectively.

This research is beneficial as a reference because it shows how the K-Medoid method can identify and group patients based on various health conditions. However, this research has yet to apply

a quantum computing approach in its analysis. This study provides a solid basis for further development. Although the classical k-medoids algorithm is effective in many cases, its main challenge is computational efficiency, mainly when applied to large and complex datasets [22]. The iterative process in k-medoids requires significant computational time, which can be a hindrance in real-time applications such as medical diagnosis [23][24][25]. Additionally, the need to reduce data dimensions and handle outliers remains a challenge that needs to be addressed to improve prediction reliability.

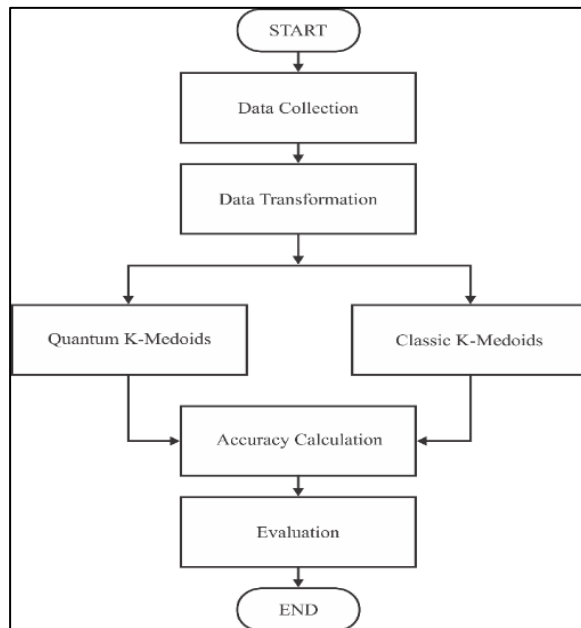
This study proposes using quantum K-medoids to overcome the limitations of the classical K-medoids method. By leveraging principles of quantum computing, quantum K-Medoids aim to reduce the computational time required for clustering processes. This algorithm utilizes qubits to represent data and applies quantum operations to optimize the selection of medoids and cluster assignments more efficiently. The main difference between this study and the primary reference is the practical application of quantum K-medoids in predicting heart disease. Few studies have applied this algorithm to real medical cases such as heart disease prediction. This research fills that gap by implementing and evaluating quantum K-Medoids using relevant heart disease datasets.

The uniqueness of this study lies in the practical application of quantum K-medoids for predicting heart disease and comparing its performance with classical K-medoids. This study represents one of the first evaluations of the effectiveness and efficiency of quantum K-medoids in a medical context, providing empirical evidence supporting the potential of quantum computing to enhance disease diagnosis and prediction. Additionally, the research introduces a new method for handling outliers and reducing data dimensions using quantum techniques.

MATERIALS AND METHODS

This study was conducted to analyze the comparative optimization techniques between classical k-medoids and quantum k-medoids in predicting heart disease based on medical data. The predictive results from this data help obtain comparative analysis information on the optimization techniques of classical k-medoids and quantum k-medoids models.

Research Stages



Source: (Research Results, 2024)

Figure 1. Research Stages

1. Method of Collecting Data

In researching to obtain data and information, the methods used in the data collection process are as follows: Using open source data taken from the kaggle.com site. You can explore these resources to create a research series with relevant data. Data from the Kaggle.com site.

2. Data Transformation

In this phase, the collected dataset is transformed into a binary representation (1 or 0) to facilitate further processing. This process involves normalizing or encoding categorical variables into binary variables to use the data in clustering methods.

3. Quantum Bit Transformation

Once the data is converted into a binary representation, the next step is to convert it into quantum bits (qubits). Qubits are the basic information units of quantum computing that allow information to be stored and manipulated quantumly. This transformation enables the K-Medoids algorithm to be used in quantum computing environments.

4. K-Medoids Method with Quantum Computing

The K-Medoids method using quantum computing refers to implementing the K-Medoids algorithm in a quantum computing environment. The

Manhattan distance is still used to calculate distances.

5. Results

At this stage, the data clustering results were analyzed using the conventional K-Medoids method and the quantum computing-based K-Medoids method. This analysis provides a deeper understanding of the data structure and patterns of the identified two clustering algorithms.

6. Evaluation

This evaluation stage includes assessing the performance of the classical K-Medoids method and quantum computing-based K-Medoids in predicting heart disease. Evaluations are carried out using metrics such as accuracy to measure the model's ability to predict cardiovascular health conditions from patient datasets.

Medical record data for heart disease patients is processed through a rule-based transformation process to achieve a standard representation: the data is transformed into qubits with values 0, 1, or both simultaneously. The notation used is Dirac notation, namely bra " $\langle$ " and ket " $\rangle$."

Dirac notation, also known as bra-ket notation, is an efficient and elegant way to write and manipulate vectors in Hilbert space, which is a vector space frequently used in quantum mechanics. Physicist Paul Dirac created this notation. In Dirac notation, the state vector is expressed as ket " $\rangle$ " or bra " $\langle$."

Ket is a vector in Hilbert space that is used to describe the system's quantum state.

Example: $|0\rangle$ and $|1\rangle$ is the ground state of a qubit.

The bra is the dual vector of ket. If $|\rangle$ is ket, then $\langle|$ is bra, which is the Hermitian conjugate (transpose conjugate) of $|\rangle$.

Example: If $|\rangle$ is ket, then $\langle|$ is the appropriate bra.

This quantum computing approach shows the potential to increase data processing efficiency. Heart disease prediction data transformation is carried out based on the rules in Table 1:

Table 1. Transformation Condition

No	Attribute	Rules
1.	BMI	Not normal = 1. If 18.5- 24.9 (normal) = 0.
2.	Smoke	Yes = 1. No = 0.
3.	Alcohol Drinking	Yes = 1. No = 0.
4.	Strokes	Yes = 1. No = 0.
5.	Physical Health	0-15 (Not good) = 1 . 16-30 (Good) = 0.
6.	Mental Health	0-15 (Not good) = 1. 16-30 (Good) = 0.
7.	Age	$\geq 55 = 1$.

No	Attribute	Rules
8.	Diabetic	<55 = 0. Yes = 1. No = 0.
9.	Physical Activity	Yes = 0. No = 1.
10.	Sleep Time	7-8 Hours (Normal) = 0. Otherwise 1.
11.	Asthma	Yes = 1. No = 0.
12.	Kidney Disease	Yes = 1. No = 0.
13.	Skin Cancer	Yes = 1. No = 0.
14.	Heart Disease	Yes = 1. No = 0.

Source: (Research Results, 2024)

These rules ensure that heart disease medical record data is standardized and can be used effectively for analysis and further processing in a uniform format. The coding results in the form of binary code can be seen in Table 2 below:

Table 2. Heart Disease Medical Record Dataset

No.	X1	X2	X3	X4	X5	X6	X7	...	T
1	1	1	0	0	1	0	1	...	0
2	0	0	0	1	1	1	1	...	0
3	1	1	0	0	0	0	1	...	0
4	0	0	0	0	1	1	1	...	0
5	0	0	0	0	0	1	0	...	0
6	1	1	0	0	1	1	1	...	1
7	0	0	0	0	1	1	1	...	0
8	1	1	0	0	1	1	1	...	0
9	1	0	0	0	1	1	1	...	0
10	1	0	0	0	1	1	1	...	0
11	1	1	0	0	0	1	1	...	1
12	1	1	0	0	1	1	1	...	0
13	1	1	0	0	1	1	1	...	0
14	1	0	0	0	1	1	1	...	0
15	1	1	0	0	1	0	1	...	0
16	1	0	0	0	1	1	0	...	0
17	1	0	0	0	1	1	1	...	0
18	0	1	0	0	1	0	1	...	0
19	1	1	0	0	1	1	1	...	0
...	...	...	...	...	...	...	...	...	...
500	1	1	0	0	1	1	1	...	0

Source: (Research Results, 2024)

For example, the sample is taken from dataset number 1, the binary code 1100101101010. Table 3 explains the first description of the data transformation.

Table 3. Description First Data Transformation

No.	Attribute	Rules
1.	BMI	Not Normal (<18.5 and >24.9).
2.	Smoke	Yes.
3.	Alcohol Drinking	No.
4.	Strokes	No = 0.
5.	Physical Health	Not Good (<=15).
6.	Mental Health	Good (>15).
7.	Age	>=55 years.
8.	Diabetic	Yes .

No.	Attribute	Rules
9.	Physical Activity	Yes (Good).
10.	Sleep Time	Not Normal (<7 hours and >8 hours).
11.	Asthma	Yes.
12.	Kidney Disease	No.
13.	Skin Cancer	Yes.
14.	Heart Disease	No. (Target)

Source: (Research Results, 2024)

The data in Table 1 above is converted into qubit form as in Table 4 below:

Table 4. Qubit Data for Heart Disease Medical Records

No.	X1	X2	X3	X4	X5	X6	X7	...	T
1	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	...	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$
2	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	...	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$
3	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	...	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$
4	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	...	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$
5	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	...	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$
6	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	...	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$
7	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	...	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$
8	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	...	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$
9	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	...	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$
10	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	...	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$
11	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	...	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$
12	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	...	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$
13	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	...	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$
14	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	...	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$
15	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	...	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$
16	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	...	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$
17	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	...	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$
18	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	...	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$
19	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	...	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$
...	...	...	...	...	...	...	...	...	...
500	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	$\begin{bmatrix} 0 \\ 1 \end{bmatrix}$	...	$\begin{bmatrix} 1 \\ 0 \end{bmatrix}$

Source: (Research Results, 2024)

Below is an example of developing K-Medoid with quantum computing using Manhattan distance calculations. The steps for the K-Medoids algorithm using Manhattan Distance are as follows:

1. Initialization Step

Randomly select k medoids from the data as initial cluster centers. These k medoids can be chosen randomly from the data or by a particular initialization strategy.

$$= \text{ABS}\left(\begin{bmatrix} 0 \\ 1 \end{bmatrix} - \begin{bmatrix} 1 \\ 0 \end{bmatrix}\right) + \text{ABS}\left(\begin{bmatrix} 0 \\ 1 \end{bmatrix} - \begin{bmatrix} 1 \\ 0 \end{bmatrix}\right) + \text{ABS}\left(\begin{bmatrix} 1 \\ 0 \end{bmatrix} - \begin{bmatrix} 1 \\ 0 \end{bmatrix}\right) + \text{ABS}\left(\begin{bmatrix} 1 \\ 0 \end{bmatrix} - \begin{bmatrix} 1 \\ 0 \end{bmatrix}\right) + \text{ABS}\left(\begin{bmatrix} 0 \\ 1 \end{bmatrix} - \begin{bmatrix} 0 \\ 1 \end{bmatrix}\right) + \text{ABS}\left(\begin{bmatrix} 0 \\ 1 \end{bmatrix} - \begin{bmatrix} 0 \\ 1 \end{bmatrix}\right) + \text{ABS}\left(\begin{bmatrix} 0 \\ 1 \end{bmatrix} - \begin{bmatrix} 1 \\ 0 \end{bmatrix}\right) + \text{ABS}\left(\begin{bmatrix} 1 \\ 0 \end{bmatrix} - \begin{bmatrix} 1 \\ 0 \end{bmatrix}\right) + \text{ABS}\left(\begin{bmatrix} 0 \\ 1 \end{bmatrix} - \begin{bmatrix} 1 \\ 0 \end{bmatrix}\right) + \text{ABS}\left(\begin{bmatrix} 0 \\ 1 \end{bmatrix} - \begin{bmatrix} 1 \\ 0 \end{bmatrix}\right) + \text{ABS}\left(\begin{bmatrix} 1 \\ 0 \end{bmatrix} - \begin{bmatrix} 1 \\ 0 \end{bmatrix}\right) + \text{ABS}\left(\begin{bmatrix} 1 \\ 0 \end{bmatrix} - \begin{bmatrix} 1 \\ 0 \end{bmatrix}\right)$$

ABS (absolute) Description:

$$\text{ABS}(1-1) = \text{ABS}(0) = 0$$

$$\text{ABS}(0-1) = \text{ABS}(-1) = 1$$

$$\text{ABS}(1-0) = \text{ABS}(1) = 1$$

$$\text{ABS}(0-0) = \text{ABS}(0) = 0$$

$$= \begin{bmatrix} 1 \\ 1 \end{bmatrix} + \begin{bmatrix} 1 \\ 1 \end{bmatrix} + \begin{bmatrix} 0 \\ 0 \end{bmatrix} + \begin{bmatrix} 0 \\ 0 \end{bmatrix} + \begin{bmatrix} 0 \\ 0 \end{bmatrix} + \begin{bmatrix} 1 \\ 1 \end{bmatrix} + \begin{bmatrix} 0 \\ 0 \end{bmatrix} + \begin{bmatrix} 1 \\ 1 \end{bmatrix} + \begin{bmatrix} 0 \\ 0 \end{bmatrix} + \begin{bmatrix} 1 \\ 1 \end{bmatrix} + \begin{bmatrix} 1 \\ 1 \end{bmatrix} + \begin{bmatrix} 0 \\ 0 \end{bmatrix} + \begin{bmatrix} 1 \\ 1 \end{bmatrix} = \begin{bmatrix} 7 \\ 7 \end{bmatrix}$$

2. Output $C_2 = d(a_x, b_y) = \sum_{z=1}^n ||a_{az} > - |b_{bz} > |$

$$\begin{aligned}
&= \text{ABS}\left(\begin{bmatrix} 0 \\ 1 \end{bmatrix} - \begin{bmatrix} 1 \\ 0 \end{bmatrix}\right) + \text{ABS}\left(\begin{bmatrix} 0 \\ 1 \end{bmatrix} - \begin{bmatrix} 0 \\ 1 \end{bmatrix}\right) + \text{ABS}\left(\begin{bmatrix} 1 \\ 0 \end{bmatrix} - \begin{bmatrix} 1 \\ 0 \end{bmatrix}\right) + \text{ABS}\left(\begin{bmatrix} 1 \\ 0 \end{bmatrix} - \begin{bmatrix} 0 \\ 1 \end{bmatrix}\right) \\
&+ \text{ABS}\left(\begin{bmatrix} 1 \\ 0 \end{bmatrix} - \begin{bmatrix} 0 \\ 1 \end{bmatrix}\right) + \text{ABS}\left(\begin{bmatrix} 0 \\ 1 \end{bmatrix} - \begin{bmatrix} 0 \\ 1 \end{bmatrix}\right) + \text{ABS}\left(\begin{bmatrix} 0 \\ 1 \end{bmatrix} - \begin{bmatrix} 1 \\ 0 \end{bmatrix}\right) + \text{ABS}\left(\begin{bmatrix} 1 \\ 0 \end{bmatrix} - \begin{bmatrix} 1 \\ 0 \end{bmatrix}\right) \\
&+ \text{ABS}\left(\begin{bmatrix} 0 \\ 1 \end{bmatrix} - \begin{bmatrix} 1 \\ 0 \end{bmatrix}\right) + \text{ABS}\left(\begin{bmatrix} 0 \\ 1 \end{bmatrix} - \begin{bmatrix} 0 \\ 1 \end{bmatrix}\right) + \text{ABS}\left(\begin{bmatrix} 1 \\ 0 \end{bmatrix} - \begin{bmatrix} 1 \\ 0 \end{bmatrix}\right) + \text{ABS}\left(\begin{bmatrix} 1 \\ 0 \end{bmatrix} - \begin{bmatrix} 0 \\ 1 \end{bmatrix}\right) \\
&+ \text{ABS}\left(\begin{bmatrix} 0 \\ 1 \end{bmatrix} - \begin{bmatrix} 1 \\ 0 \end{bmatrix}\right)
\end{aligned}$$

$$= \begin{bmatrix} 1 \\ 1 \end{bmatrix} + \begin{bmatrix} 0 \\ 1 \end{bmatrix} + \begin{bmatrix} 0 \\ 0 \end{bmatrix} + \begin{bmatrix} 0 \\ 0 \end{bmatrix} + \begin{bmatrix} 1 \\ 1 \end{bmatrix} + \begin{bmatrix} 0 \\ 0 \end{bmatrix} + \begin{bmatrix} 0 \\ 0 \end{bmatrix} + \begin{bmatrix} 1 \\ 1 \end{bmatrix} + \begin{bmatrix} 0 \\ 0 \end{bmatrix} + \begin{bmatrix} 1 \\ 1 \end{bmatrix} + \begin{bmatrix} 1 \\ 1 \end{bmatrix} + \begin{bmatrix} 0 \\ 0 \end{bmatrix} + \begin{bmatrix} 0 \\ 0 \end{bmatrix} = \begin{bmatrix} 5 \\ 5 \end{bmatrix}$$

Next is to calculate the Decimal C_1 and Decimal C_2 values:

1. Output Decimal $C_1 = \sqrt{C_1 \text{ top row}^2 + C_1 \text{ bottom row}^2}$.

$$= \sqrt{7^2 + 7^2} = \sqrt{49 + 49} = \sqrt{98} = \sqrt{9.899}$$

2. Output Decimal $C_2 = \sqrt{C_2 \text{ top row}^2 + C_2 \text{ bottom row}^2}$.

$$= \sqrt{5^2 + 5^2} = \sqrt{25 + 25} = \sqrt{50} = \sqrt{7.071}$$

Furthermore, it can be concluded that the closest distance between decimal C1 and decimal C2 is decimal C2 = 7.071. If the closest distance = Decimal C1, the result is 1; if the closest distance $\neq$ is Decimal C1, the result is 2.

To determine the Description results, the conditions are explained in Table 7:

Table 7. Conditions Description

Result	Target	Description
1	0	True
2	1	True
1	2	False
2	0	False
1	1	False

Source: (Research Results, 2024)

Table 8 is the test result of the K-Medoids algorithm with quantum computing from epoch-1 and Table 9 is the test result of the K-Medoids algorithm with quantum computing from epoch-2:

Table 8. K-Medoids with Quantum Computing
Epoch-1 Test Results

Epoch 1 Test Results							
C 1	C 2	C1 (Decimal)	C2 (Decimal)	Shortest Distance	Cluster	Data Real	Description
[5]	[6]	7.071	8.485	7.071	1	0	True
[3]	[4]	4.243	5.657	4.243	1	0	True
[4]	[7]	5.657	9.899	5.657	1	0	True
[5]	[4]	7.071	5.657	5.657	2	0	False
[4]	[7]	5.657	9.899	5.657	1	0	True
[4]	[3]	5.657	4.243	4.243	2	1	True
[5]	[6]	7.071	8.485	7.071	1	0	True
[4]	[5]	5.657	7.071	5.657	1	0	True
[4]	[5]	5.657	7.071	5.657	1	0	True
[2]	[5]	2.828	7.071	2.828	1	0	True
[5]	[6]	7.071	8.485	7.071	1	1	False
[3]	[4]	4.243	5.657	4.243	1	0	True
[1]	[4]	1.414	5.657	1.414	1	0	True
[2]	[3]	2.828	4.243	2.828	1	0	True
[5]	[4]	7.071	5.657	5.657	2	0	False
[3]	[6]	4.243	8.485	4.243	1	0	True
[3]	[4]	4.243	5.657	4.243	1	0	True
[4]	[5]	5.657	7.071	5.657	1	0	True
[4]	[5]	5.657	7.071	5.657	1	0	True
...	...	...	...	...	...	...	...
[4]	[3]	5.657	4.243	4.243	2	0	False
Total of Shortest Distance				1927.573	Accuracy		74 %

Source: (Research Results, 2024)

**Table 9. K-Medoids with Quantum Computing
Epoch-2 Test Results**

C 1	C 2	C1 (Deci mal)	C2 (Deci mal)	Short est Dista nce	Clus ter	Da ta Re al	Descrip tion
[7] [7]	[5] [5]	9.899	7.071	7.071	2	0	False
[1] [1]	[5] [5]	1.414	7.071	1.414	1	0	True
[6] [6]	[4] [4]	8.485	5.657	5.657	2	0	False
[3] [3]	[5] [5]	4.243	7.071	4.243	1	0	True
[2] [2]	[4] [4]	2.828	5.657	2.828	1	0	True
[4] [4]	[6] [6]	5.657	8.485	5.657	1	1	False
[3] [3]	[5] [5]	4.243	7.071	4.243	1	0	True
[6] [6]	[8] [8]	8.485	11.31 4	8.485	1	0	True
[4] [4]	[8] [8]	5.657	11.31 4	5.657	1	0	True
[2] [2]	[6] [6]	2.828	8.485	2.828	1	0	True
[7] [7]	[7] [7]	9.899	9.899	9.899	1	1	False
[3] [3]	[5] [5]	4.243	7.071	4.243	1	0	True
[3] [3]	[5] [5]	4.243	7.071	4.243	1	0	True
[2] [2]	[6] [6]	2.828	8.485	2.828	1	0	True
[5] [5]	[5] [5]	7.071	7.071	7.071	1	0	True
[3] [3]	[7] [7]	4.243	9.899	4.243	1	0	True
[3] [3]	[7] [7]	4.243	9.899	4.243	1	0	True
[2] [2]	[2] [2]	2.828	2.828	2.828	1	0	True
[6] [6]	[8] [8]	8.485	11.31 4	8.485	1	0	True
...	...	...	...	...	...	...	...
[4] [4]	[6] [6]	5.657	8.485	5.657	1	0	True
Total of Shortest Distance				2108. 592	Accuracy	85 %	

Source: (Research Results, 2024)

The findings of this research show significant progress in the K-Medoids method, namely the application of quantum computing using Manhattan distance calculations. Simulation results show that the K-Medoids method based on quantum computing reaches an accuracy level of 85% after two epochs. The test results show no change in the K-Medoids with the application of quantum computing compared to the classical K-Medoids method, which also achieved 85% accuracy.

CONCLUSION

This research explores the application of quantum computing in the K-Medoids clustering method using Manhattan distance calculations for heart disease prediction. The results indicate a stable accuracy of 85% for both quantum and classical implementations of the K-Medoids algorithm. While no significant improvement in accuracy was observed, the quantum approach presents potential advantages in data processing efficiency, particularly for larger and more complex datasets. However, this claim requires further validation through detailed comparisons of algorithm complexity and runtime performance between quantum and classical methods. The transformation of medical record data into qubits using Dirac notation successfully provided a standard and consistent data representation. Future work should focus on optimizing the quantum algorithm and testing it on a wider variety of medical datasets to assess the generalizability of the findings. Although the improvements in efficiency have not been fully demonstrated, the quantum computing-based K-Medoids method holds promise for enhancing the speed of medical data analysis, marking a step forward in the integration of quantum technologies within healthcare.

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