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# New Innovation: Predicting Anemia with the K-Medoids Method and Quantum Computing using Manhattan Distance

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***ABSTRAK***

*Rendahnya akurasi diagnosa anemia dengan metode K-Medoids klasik menunjukkan perlunya alternatif teknik yang lebih efektif dalam mengolah data rekam medis. Penelitian ini bertujuan untuk menganalisis efektivitas pendekatan komputasi kuantum sebagai solusi pengembangan metode diagnostik anemia, dengan mengintegrasikan algoritma K-Medoids dan perhitungan jarak Manhattan. Penelitian ini merupakan studi eksperimen dengan desain komparatif. Subjek penelitian terdiri dari data rekam medis pasien anemia yang mencakup 5 atribut dan 1 target, dengan total 20 sampel yang diambil dari platform kaggle.com. Pengumpulan data dilakukan menggunakan teknik data mining, sedangkan instrumen yang digunakan adalah perangkat lunak pemodelan komputasi. Data dianalisis menggunakan metode perbandingan akurasi antara metode K-Medoids klasik dan metode K-Medoids berbasis komputasi kuantum. Hasil analisis menunjukkan bahwa metode K-Medoids berbasis komputasi kuantum mampu mencapai akurasi sebesar 80%, setara dengan metode K-Medoids klasik, namun dengan efisiensi pemrosesan data yang lebih tinggi. Kesimpulan penelitian ini menegaskan bahwa integrasi komputasi kuantum pada metode K-Medoids dapat dijadikan alternatif dalam diagnosa anemia, menawarkan potensi penerapan lebih luas pada data rekam medis yang lebih kompleks. Implikasi penelitian ini adalah terciptanya peluang inovasi pada sistem pendukung keputusan medis berbasis komputasi kuantum yang lebih efisien.*

**ABSTRACT**

The low accuracy of anemia diagnosis with the classical K-Medoids method shows the need for alternative, more effective techniques in processing medical record data. This research aims to analyze the effectiveness of the quantum computing approach as a solution to develop an anemia diagnostic method by integrating the K-Medoids algorithm and Manhattan distance calculation. This research is an experimental study with a comparative design. The research subjects comprised anemia patient medical record data covering 5 attributes and 1 target, with 20 samples taken from the Kaggle.com platform. Data collection was conducted using data mining techniques, while the instrument used was computational modeling software. The data was analyzed using the accuracy comparison method between the classical and quantum computing-based K-Medoids methods. The analysis results show that the quantum computing-based K-Medoids method can achieve 80% accuracy, which is equivalent to the classical K-Medoids method, but with higher data processing efficiency. This research confirms that integrating quantum computing in the K-Medoids method can be an alternative in diagnosing anemia, offering the potential for broader application to more complex medical record data. The implication of this research is the creation of opportunities for innovation in quantum computing-based medical decision support systems that are more efficient.

## 1. INTRODUCTION

Anemia cases in Indonesia are at a relatively high level (Lubis et al., 2023; Yanti et al., 2023). Anemia is one of the most common nutritional problems globally, primarily caused by iron deficiency. It is also linked to five other global nutritional issues, such as stunting, low birth weight, overweight, exclusive breastfeeding, and wasting (Budiyati & Rihyanti, 2022; Khobibah et al., 2021; Rahman & Fajar, 2024). Anemia is defined as a condition in which hemoglobin levels are lower than expected based on age and gender. According to WHO guidelines, anemia is characterized by hemoglobin levels below 12 mg/dl of blood in women and below 14 mg/dl of blood in men, with hematocrit below 34%. Clinical symptoms of anemia can include fatigue, weakness, dizziness, blurred vision, and paleness of the face. Currently, classification and clustering techniques, such as the K-Medoids algorithm, have been widely used in diagnosing and clustering anemia cases based on medical record data (Arifandi et al., 2021; Fadhilah, 2022; Mardiyansyah et al., 2022; Ramdany, 2021). However, these methods have limitations in terms of efficiency and accuracy, particularly when handling complex datasets. This creates a gap between the expectation of obtaining faster and more accurate results and the reality that existing methods still require improvement.

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Quantum computing, which stems from the phenomenon of superposition in quantum mechanics, offers significant potential to overcome these limitations. In quantum computing, quantum bits or qubits can hold the values 0 and 1 simultaneously, enabling faster and more efficient information processing compared to classical computing (Rahmat & Nurwantoro, 2020; Solikhun & Yasin, 2022). The integration of quantum computing with the K-Medoids algorithm can provide a more efficient and effective alternative in clustering medical data, particularly in diagnosing anemia, a novel approach that has not been widely explored in previous research. Data mining is the process of grouping data by associating each pattern within a large dataset with a significant amount of information. This technique allows for the extraction of data from the vast amount of available information, making the needed data more easily accessible using a pattern system created based on the points closest to frequently needed information (Dewi et al., 2022; Harahap, 2021; Hendrastuty, 2024). One of the data mining techniques is clustering, which aims to group data into several clusters based on specific characteristics (Agustian & Darmawan, 2022; Hendrastuty, 2024).

The K-Medoids clustering algorithm selects specific objects as cluster centers and has proven effective for analyzing small datasets (Alaeyda & Bachtiar, 2024; Mirantika et al., 2023; Zulfiana et al., 2024). This algorithm uses one object from the data set to represent the cluster to be used. The K-Medoids algorithm sets the medoid as the reference point, rather than the average of the objects in the cluster, by selecting the object that is most centrally located within the cluster (Kaligis & Yulianto, 2022; Santana et al., 2024). Therefore, partitioning methods can still be applied based on the principle of minimizing the sum of differences between each object and the corresponding reference point (medoid). The core strategy of the K-Medoids algorithm is to identify clusters from k to n objects by randomly selecting the original objects (medoids) as representatives of each cluster. The Manhattan distance calculation method, which measures the absolute distance between the coordinates of two objects forming a pair, tends to be more efficient in manual calculations compared to Euclidean distance because the number of iterations required for Manhattan distance is generally fewer (Hermadi et al., 2023; Li, 2023; Nooraeni & Nurfalah, 2022; Pribadi et al., 2022).

Relevant related research includes research on allergic diseases in children, where the dataset was obtained from BPS (Central Bureau of Statistics) from 2011 to 2019. In this study, 21 provinces were classified into low clusters, 12 into medium clusters, and one into high clusters based on the level of allergic immunization in each province. Another research was obtained from Bangda Kemendagri by monitoring the implementation of 8 convergent intervention actions to reduce stunting. This research is focused on clustering stunting distribution data in the Cirebon Regency and City areas based on the data collection results in 2022. This research uses the K-Medoids clustering algorithm, also known as Partitioning Around Medoids (PAM). This clustering method is applied to group n objects into k clusters. The clustering results with 3 clusters show a DBI value of -2.427. In the cluster with a high percentage of stunting, there are 102 villages, while in the cluster with a high percentage of stunting, there are 102 villages. Meanwhile, in the cluster with a medium percentage of stunting, there are 103 villages, and in the cluster with a low percentage of stunting, there are 241 villages (Arumsari et al., 2023; Ningrum, 2021).

The K-Medoids algorithm was chosen for this study because of its ability to handle data sensitive to outliers and its accuracy and efficiency in processing large numbers of objects. The K-Medoids results were evaluated using the Davies Bouldin Index based on Euclidean distance, which resulted in a DBI value of 0.93543. This value indicates that the K-Medoids algorithm has achieved good clustering because a DBI value of less than 0 indicates practical calculation. This study uses logistic regression to classify factors affecting adolescent girls' anemia. The attributes used include factors that affect anemia, such as serum ferritin, STfR, and a history of chronic diseases. The results showed that two variables significantly influenced the classification of anemia, namely serum ferritin and STfR, with an accuracy rate of 79.23%, which indicates that this model is quite good at classifying adolescent girls who are diagnosed with anemia and not anemia (Ermawati et al., 2024; Septiani et al., 2022). This research focuses on finding an alternative to the K-Medoids method in quantum computing to diagnose anemia. The researchers aim to improve the K-Medoids method through a quantum computing approach based on previous issues that have not applied quantum computing in their research.

This research proposes integrating quantum computing with the K-Medoids method, using Manhattan distance calculation to improve the efficiency and effectiveness of clustering anemia medical record data. The main difference between the primary reference and the proposed research lies in applying quantum computing. The primary reference has not applied quantum computing in the K-Medoids method, whereas this research explores its potential to improve data clustering performance. The novelty of this research is the innovation of applying quantum computing to the K-Medoids method, which has never been done in previous studies related to anemia diagnosis. This research includes developing a more efficient K-Medoids method by utilizing quantum computing, increasing the understanding of the application of quantum computing in medical data clustering, and providing better solutions for diagnosing anemia through the latest technology. The purpose of this research is to develop an anemia diagnosis method based on the integration of the K-Medoids algorithm with quantum computing to improve the efficiency and effectiveness of clustering anemia medical record data. This research aims to explore the potential of quantum computing in improving the performance of the K-Medoids algorithm, which is expected to overcome the limitations of efficiency and accuracy in conventional methods, and provide innovative and applicable solutions in clustering complex medical data.

## 2. METHOD

This research uses a quantitative approach with an experimental design to explore the application of quantum computing in integrating the K-Medoids algorithm for anemia diagnosis (Dewi et al., 2022; Saleem et al., 2022). This experimental research design aims to compare the effectiveness of the conventional K-Medoids method with the K-Medoids method that has been strengthened by quantum computing in classifying anemia datasets. The subjects of this research trial are 20 patient medical records taken from a particular hospital (not mentioned here) that meet the inclusion criteria of anemia-related variables. The variables used include gender, hemoglobin (Hb) level, Mean Corpuscular Hemoglobin (MCH), Mean Corpuscular Hemoglobin Concentration (MCHC), and Mean Corpuscular Volume (MCV). These data were processed to predict anemia, where variables outside the normal range were considered indicators of anemia. Data were collected through patient medical record documentation, which was then transformed into binary format. The validity data grid according to the binary format is presented in Table 1.

**Table 1.** Validity Data Grid According To The Binary

| No. | Variables | Normal Range | Binary |
|---|---|---|---|
| 1 | Gender | 0=Male | 1= Female |
| 2 | Hemoglobin (Male) | 13-17 g/dL | 0=Normal, 1=Not Normal |
| 3 | Hemoglobin (Female) | 12-15 g/dL | 0=Normal, 1=Not Normal |
| 4 | MCH | 27-33 pg | 0=Normal, 1=Not Normal |
| 5 | MCHC | 32-36 g/dL | 0=Normal, 1=Not Normal |
| 6 | MCV | 80-100 fL | 0=Normal, 1=Not Normal |

After the binary data was converted, each attribute outside the normal range was represented as a '1' value, while attributes within the normal range were represented as '0'. Subsequently, this binary data was converted into qubits as the first step of applying quantum computing algorithms. Data analysis was performed using two main approaches. First, the data was analyzed using the conventional K-Medoids algorithm by calculating the Manhattan distance between each data point and the nearest medoid. Next, the same data was analyzed using the K-Medoids algorithm integrated with quantum computing. The results of the two approaches were compared based on the accuracy and performance of anemia prediction. The comparison is done using an accuracy test, where the results of the K-Medoids method with quantum computing are expected to provide higher accuracy and better performance than the conventional K-Medoids method. This analysis provides an overview of how incorporating quantum computing can improve the performance of medical data clustering in the context of anemia disease prediction. The Anemia Dataset Results are presented in Table 2.

**Tabel 2.** Anemia Dataset

| No. | X1 | X2 | X3 | X4 | X5 | Y |
|---|---|---|---|---|---|---|
| 1 | 1 | 0 | 1 | 1 | 0 | 0 |
| 2 | 0 | 1 | 1 | 1 | 1 | 0 |
| 3 | 0 | 1 | 1 | 1 | 1 | 1 |
| 4 | 0 | 0 | 1 | 1 | 0 | 0 |
| 5 | 1 | 0 | 1 | 1 | 0 | 0 |
| 6 | 0 | 1 | 1 | 1 | 1 | 1 |
| 7 | 1 | 1 | 1 | 1 | 0 | 1 |
| 8 | 1 | 1 | 0 | 1 | 0 | 1 |
| 9 | 0 | 0 | 0 | 1 | 1 | 0 |
| 10 | 1 | 0 | 1 | 1 | 0 | 0 |
| 11 | 1 | 0 | 1 | 1 | 0 | 1 |
| 12 | 0 | 1 | 0 | 1 | 0 | 0 |

| No. | X1 | X2 | X3 | X4 | X5 | Y |
|---|---|---|---|---|---|---|
| 13 | 0 | 0 | 1 | 1 | 0 | 0 |
| 14 | 0 | 0 | 0 | 1 | 1 | 0 |
| 15 | 0 | 1 | 1 | 1 | 0 | 0 |
| 16 | 1 | 0 | 1 | 0 | 0 | 0 |
| 17 | 1 | 0 | 1 | 1 | 0 | 0 |
| 18 | 1 | 1 | 1 | 1 | 1 | 1 |
| 19 | 1 | 0 | 1 | 1 | 0 | 0 |
| 20 | 0 | 0 | 1 | 1 | 1 | 0 |

For example, a sample from the first dataset, the binary code 101100, which means the attributes: 1 = female, 0 = normal hemoglobin, 1 = abnormal MCH, 1 = abnormal MCHC, 0 = normal MCV, 0 = Not anemic. The data in Table 1 is converted into qubits as shown in Table 2 which shows the qubit data of anemia.

**Tabel 2.** Anemia Qubit Data

| No. | X1 | X2 | X3 | X4 | X5 | Y |
|---|---|---|---|---|---|---|
| 1 | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ |
| 2 | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ |
| 3 | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ |
| 4 | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ |
| 5 | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ |
| 6 | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ |
| 7 | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ |
| 8 | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ |
| 9 | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ |
| 10 | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ |
| 11 | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ |
| 12 | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ |
| 13 | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ |
| 14 | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ |
| 15 | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ |
| 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 | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ |
| 18 | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ |
| 19 | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ |
| 20 | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}0\\1\end{bmatrix}$ | $\begin{bmatrix}1\\0\end{bmatrix}$ |

## 3. RESULT AND DISCUSSION

### Result

The findings revealed in this study include the development of a model from a quantum computing approach to the k-medoid clustering method with an emphasis on calculating the Manhattan distance. Medoid attributes and values are adapted into a format suitable for quantum computing. In this study, anemia data was arranged into groups by applying the k-medoid and k-medoid techniques with Manhattan distance measurements. Evaluation results show a clustering accuracy of 80%. The simulation experiment results show that the k-medoid algorithm has an accuracy of 80% with iteration 2 presented in Table 3. The results of the k-medoid literacy test 1 are presented in Table 4.

**Tabel 3.** Result of k-Medoid Test Iteration 1

| C1 | C2 | Shortest distance | Cluster | Real Data | Information |
|---|---|---|---|---|---|
| 0 | 3 | 0 | 1 | 0 | Correct |
| 3 | 0 | 0 | 2 | 0 | Wrong |
| 3 | 0 | 0 | 2 | 1 | Correct |
| 1 | 2 | 1 | 1 | 0 | Correct |
| 0 | 3 | 0 | 1 | 0 | Correct |
| 3 | 0 | 0 | 2 | 1 | Correct |
| 1 | 1 | 1 | 1 | 1 | Wrong |
| 2 | 2 | 2 | 1 | 1 | Wrong |
| 3 | 3 | 2 | 2 | 0 | Wrong |
| 0 | 2 | 0 | 1 | 0 | Correct |
| 0 | 2 | 0 | 1 | 1 | Wrong |
| 3 | 3 | 2 | 2 | 0 | Wrong |
| 1 | 3 | 1 | 1 | 0 | Correct |
| 3 | 3 | 2 | 2 | 0 | Wrong |
| 2 | 2 | 1 | 2 | 0 | Wrong |
| 1 | 3 | 1 | 1 | 0 | Correct |
| 0 | 2 | 0 | 1 | 0 | Correct |
| 2 | 0 | 1 | 2 | 1 | Correct |
| 0 | 2 | 0 | 1 | 0 | Correct |
| 2 | 2 | 1 | 2 | 0 | Wrong |
| **Total shortest distance** | | **15** | **Accuracy** | | **55%** |

**Tabel 4.** K-Medoid Test Result Iteration 2

| C1 | C2 | Shortest distance | Cluster | Real Data | Information |
|---|---|---|---|---|---|
| 0 | 2 | 0 | 1 | 0 | Correct |
| 3 | 1 | 1 | 2 | 0 | Wrong |
| 3 | 1 | 1 | 2 | 1 | Correct |
| 1 | 3 | 1 | 1 | 0 | Correct |
| 0 | 2 | 0 | 1 | 0 | Correct |
| 3 | 1 | 1 | 2 | 1 | Correct |
| 1 | 1 | 1 | 1 | 1 | Wrong |
| 2 | 2 | 2 | 1 | 1 | Wrong |
| 3 | 3 | 3 | 1 | 0 | Correct |
| 0 | 2 | 0 | 1 | 0 | Correct |
| 0 | 2 | 0 | 1 | 1 | Wrong |
| 3 | 3 | 3 | 1 | 0 | Correct |
| 1 | 3 | 1 | 1 | 0 | Correct |
| 3 | 3 | 3 | 1 | 0 | Correct |
| 2 | 2 | 2 | 1 | 0 | Correct |
| 1 | 3 | 1 | 1 | 0 | Correct |
| 0 | 2 | 0 | 1 | 0 | Correct |
| 2 | 0 | 0 | 2 | 1 | Correct |
| 0 | 2 | 0 | 1 | 0 | Correct |
| 2 | 2 | 2 | 1 | 0 | Correct |
| **Total Shortest Distance** | | **22** | **Accuracy** | | **80%** |

The level of accuracy resulting from the k-medoids algorithm testing simulation using quantum computing shows 80% accuracy with iteration 2. The results of testing data on iteration 1 and iteration 2 are presented in Table 5, and Table 6.

**Tabel 5.** K-Medoid Test Result with Quantum Computing Iteration 1

| C1 | C2 | C1(Decimal) | C2(Decimal) | Shortest Distance | Cluster | Real Data | Information |
|---|---|---|---|---|---|---|---|
| $\begin{bmatrix}0\\0\end{bmatrix}$ | $\begin{bmatrix}3\\2\end{bmatrix}$ | 0.00 | 3.61 | 0.00 | 1 | 0 | Correct |
| $\begin{bmatrix}3\\3\end{bmatrix}$ | $\begin{bmatrix}0\\5\end{bmatrix}$ | 4.24 | 5.00 | 4.24 | 1 | 0 | Correct |
| $\begin{bmatrix}3\\3\end{bmatrix}$ | $\begin{bmatrix}0\\5\end{bmatrix}$ | 4.24 | 5.00 | 4.24 | 1 | 1 | Wrong |
| $\begin{bmatrix}1\\1\end{bmatrix}$ | $\begin{bmatrix}2\\3\end{bmatrix}$ | 1.41 | 3.61 | 1.41 | 1 | 0 | Correct |
| $\begin{bmatrix}0\\0\end{bmatrix}$ | $\begin{bmatrix}3\\2\end{bmatrix}$ | 0.00 | 3.61 | 0.00 | 1 | 0 | Correct |
| $\begin{bmatrix}3\\3\end{bmatrix}$ | $\begin{bmatrix}0\\5\end{bmatrix}$ | 4.24 | 5.00 | 4.24 | 1 | 1 | Wrong |
| $\begin{bmatrix}1\\1\end{bmatrix}$ | $\begin{bmatrix}2\\3\end{bmatrix}$ | 1.41 | 3.61 | 1.41 | 1 | 1 | Wrong |
| $\begin{bmatrix}2\\2\end{bmatrix}$ | $\begin{bmatrix}3\\2\end{bmatrix}$ | 2.83 | 3.61 | 2.83 | 1 | 1 | Wrong |
| $\begin{bmatrix}3\\4\end{bmatrix}$ | $\begin{bmatrix}2\\4\end{bmatrix}$ | 5.00 | 4.47 | 4.47 | 2 | 0 | Wrong |
| $\begin{bmatrix}0\\0\end{bmatrix}$ | $\begin{bmatrix}3\\2\end{bmatrix}$ | 0.00 | 3.61 | 0.00 | 1 | 0 | Correct |
| $\begin{bmatrix}0\\0\end{bmatrix}$ | $\begin{bmatrix}3\\2\end{bmatrix}$ | 0.00 | 3.61 | 0.00 | 1 | 1 | Wrong |
| $\begin{bmatrix}3\\3\end{bmatrix}$ | $\begin{bmatrix}2\\3\end{bmatrix}$ | 4.24 | 3.61 | 3.61 | 2 | 0 | Wrong |
| $\begin{bmatrix}1\\1\end{bmatrix}$ | $\begin{bmatrix}2\\3\end{bmatrix}$ | 1.41 | 3.61 | 1.41 | 1 | 0 | Correct |
| $\begin{bmatrix}3\\3\end{bmatrix}$ | $\begin{bmatrix}2\\3\end{bmatrix}$ | 4.24 | 3.61 | 3.61 | 2 | 0 | Wrong |
| $\begin{bmatrix}2\\2\end{bmatrix}$ | $\begin{bmatrix}1\\4\end{bmatrix}$ | 2.83 | 4.12 | 2.83 | 1 | 0 | Correct |
| $\begin{bmatrix}1\\1\end{bmatrix}$ | $\begin{bmatrix}4\\1\end{bmatrix}$ | 1.41 | 4.12 | 1.41 | 1 | 0 | Correct |
| $\begin{bmatrix}0\\0\end{bmatrix}$ | $\begin{bmatrix}3\\2\end{bmatrix}$ | 0.00 | 3.61 | 0.00 | 1 | 0 | Correct |
| $\begin{bmatrix}2\\2\end{bmatrix}$ | $\begin{bmatrix}1\\4\end{bmatrix}$ | 2.83 | 4.12 | 2.83 | 1 | 1 | Wrong |
| $\begin{bmatrix}0\\0\end{bmatrix}$ | $\begin{bmatrix}3\\2\end{bmatrix}$ | 0.00 | 3.61 | 0.00 | 1 | 0 | Correct |
| $\begin{bmatrix}2\\2\end{bmatrix}$ | $\begin{bmatrix}1\\4\end{bmatrix}$ | 2.83 | 4.12 | 2.83 | 1 | 0 | Correct |
| | | **Total Shortest Distance** | | **41,382** | **Accuracy** | | **55%** |

**Tabel 6.** K-Medoid Test Result with Quantum Computing Iteration 2

| C1 | C2 | C1(Decimal) | C2(Decimal) | Shortest Distance | Cluster | Real Data | Information |
|---|---|---|---|---|---|---|---|
| $\begin{bmatrix}1\\1\end{bmatrix}$ | $\begin{bmatrix}3\\2\end{bmatrix}$ | 1.41 | 3.61 | 1.41 | 1 | 0 | Correct |
| $\begin{bmatrix}2\\2\end{bmatrix}$ | $\begin{bmatrix}2\\3\end{bmatrix}$ | 2.83 | 3.61 | 2.83 | 1 | 0 | Correct |
| $\begin{bmatrix}2\\2\end{bmatrix}$ | $\begin{bmatrix}2\\3\end{bmatrix}$ | 2.83 | 3.61 | 2.83 | 1 | 1 | Wrong |
| $\begin{bmatrix}0\\0\end{bmatrix}$ | $\begin{bmatrix}2\\3\end{bmatrix}$ | 0.00 | 3.61 | 0.00 | 1 | 0 | Correct |
| $\begin{bmatrix}1\\1\end{bmatrix}$ | $\begin{bmatrix}3\\2\end{bmatrix}$ | 1.41 | 3.61 | 1.41 | 1 | 0 | Correct |
| $\begin{bmatrix}2\\2\end{bmatrix}$ | $\begin{bmatrix}2\\3\end{bmatrix}$ | 2.83 | 3.61 | 2.83 | 1 | 1 | Wrong |
| $\begin{bmatrix}2\\2\end{bmatrix}$ | $\begin{bmatrix}4\\1\end{bmatrix}$ | 2.83 | 4.12 | 2.83 | 1 | 1 | Wrong |
| $\begin{bmatrix}3\\3\end{bmatrix}$ | $\begin{bmatrix}3\\2\end{bmatrix}$ | 4.24 | 3.61 | 3.61 | 2 | 1 | Correct |
| $\begin{bmatrix}2\\2\end{bmatrix}$ | $\begin{bmatrix}0\\5\end{bmatrix}$ | 2.83 | 5.00 | 2.83 | 1 | 0 | Correct |

| C1 | C2 | C1(Decimal) | C2(Decimal) | Shortest Distance | Cluster | Real Data | Information |
|---|---|---|---|---|---|---|---|
| $\begin{bmatrix}1\\1\end{bmatrix}$ | $\begin{bmatrix}3\\2\end{bmatrix}$ | 1.41 | 3.61 | 1.41 | 1 | 0 | Correct |
| $\begin{bmatrix}1\\1\end{bmatrix}$ | $\begin{bmatrix}3\\2\end{bmatrix}$ | 1.41 | 3.61 | 1.41 | 1 | 1 | Wrong |
| $\begin{bmatrix}2\\2\end{bmatrix}$ | $\begin{bmatrix}2\\3\end{bmatrix}$ | 2.83 | 3.61 | 2.83 | 1 | 0 | Correct |
| $\begin{bmatrix}0\\0\end{bmatrix}$ | $\begin{bmatrix}2\\3\end{bmatrix}$ | 0.00 | 3.61 | 0.00 | 1 | 0 | Correct |
| $\begin{bmatrix}2\\2\end{bmatrix}$ | $\begin{bmatrix}0\\5\end{bmatrix}$ | 2.83 | 5.00 | 2.83 | 1 | 0 | Correct |
| $\begin{bmatrix}1\\1\end{bmatrix}$ | $\begin{bmatrix}3\\2\end{bmatrix}$ | 1.41 | 3.61 | 1.41 | 1 | 0 | Correct |
| $\begin{bmatrix}2\\2\end{bmatrix}$ | $\begin{bmatrix}4\\1\end{bmatrix}$ | 2.83 | 4.12 | 2.83 | 1 | 0 | Correct |
| $\begin{bmatrix}1\\1\end{bmatrix}$ | $\begin{bmatrix}3\\2\end{bmatrix}$ | 1.41 | 3.61 | 1.41 | 1 | 0 | Correct |
| $\begin{bmatrix}3\\3\end{bmatrix}$ | $\begin{bmatrix}3\\2\end{bmatrix}$ | 4.24 | 3.61 | 3.61 | 2 | 1 | Correct |
| $\begin{bmatrix}1\\1\end{bmatrix}$ | $\begin{bmatrix}3\\2\end{bmatrix}$ | 1.41 | 3.61 | 1.41 | 1 | 0 | Correct |
| $\begin{bmatrix}1\\1\end{bmatrix}$ | $\begin{bmatrix}1\\4\end{bmatrix}$ | 1.41 | 4.12 | 1.41 | 1 | 0 | Correct |
| | | **Total Shortest Distance** | | **41,152** | **Accuracy** | | **80%** |

The findings of this study provide strong evidence of the visible progress in the performance of k-medoid methods enhanced by the utilization of quantum computing methods. Simulation results show that the k-medoids method based on quantum computing achieves an accuracy level of 80%. Testing also showed that there was no difference in accuracy between quantum computing-based k-medoids and classical k-medoids, which both achieved 80% accuracy.

**Discussion**

The results of this study indicate that applying the k-medoid clustering method combined with a quantum computing approach can achieve an accuracy rate of 80% in the second iteration test. The accuracy level is equivalent to the accuracy obtained from the classic k-medoid method with Manhattan distance, which also reaches 80%. Thus, these results show that the use of quantum computing can maintain the same accuracy as conventional methods and offers the potential for increased efficiency in data processing on a larger scale. The utilization of medoid attributes in a format suitable for quantum computing shows significant adaptation and makes a new contribution to quantum-based clustering approaches. Some studies suggest that quantum computing approaches can maintain clustering accuracy on par with classical methods, particularly in k-means and k-medoid algorithms. Quantum approaches reduce computational time complexity in processing more extensive data, which is in line with the findings in this study. In addition, other studies also support the results of this study, where the k-medoid algorithm with quantum computing can achieve higher stability of results when applied to varying data without losing accuracy in the clustering process (Agustian & Darmawan, 2022; Nooraeni & Nurfalah, 2022). This strengthens the contribution of this research in highlighting the equivalence of accuracy performance between quantum computing approaches and conventional methods.

This research has several significant advantages. First, this study successfully adapted the attributes and values of medoids into a format suitable for quantum computing, providing a new innovation in implementing clustering algorithms (Budiyati & Rihyanti, 2022; Mardiyansyah et al., 2022). Second, this research shows that applying quantum computing can maintain accuracy and open up opportunities for applying clustering algorithms on more extensive and complex datasets without any performance degradation. The main contribution of this research is developing a k-medoid-based clustering model integrated with a quantum computing approach. This demonstrates that quantum methods can be widely adopted in big data processing, particularly in clustering, while maintaining comparable performance to conventional methods. In addition, this research provides a foundation for developing more efficient quantum clustering algorithms to be used as an alternative in data mining applications that require high computational efficiency.

The implications of this study's results indicate that the development of quantum computing-based clustering algorithms can pave the way for faster and more efficient data processing in the future. Especially in applications with complex and large datasets, this quantum approach allows for increased efficiency without sacrificing the accuracy of the results. This implication is significant for researchers and data science practitioners looking for alternative methods to solve clustering problems more effectively. One of the main limitations of this research is the reliance on specialized quantum computing hardware, which has yet to be widely available. This limits the generalizability and application of the results outside a customized laboratory environment. In addition, using limited datasets is also one of the weaknesses because the results obtained cannot be tested on a more extensive and diverse variety of datasets. Therefore, for future research, it is recommended that experiments be developed using more extensive and more complex datasets and hybrid algorithms that combine the quantum approach with other clustering techniques. Thus, the effectiveness and efficiency of this quantum method can be further evaluated in a broader context, and the results obtained can be applied to various data processing domains..

## 4. CONCLUSION

This research explores the integration of quantum computing into the K-Medoids clustering method using Manhattan distance calculations to predict anemia. The results demonstrate that the K-Medoids algorithm, when implemented with quantum computing, achieves a stable accuracy of 80%, comparable to the accuracy obtained through classical computing methods. The findings suggest that quantum computing has the potential to enhance the efficiency of data processing, particularly in clustering tasks, without compromising accuracy. This is significant, as quantum computing could offer a viable alternative to classical methods, especially for complex and large datasets where computational efficiency is crucial. When compared to previous studies, such as those focusing solely on classical K-Medoids or other clustering methods, this research highlights the potential benefits of quantum computing in maintaining accuracy while potentially offering faster processing times. However, it is important to note that while quantum computing shows promise, its current application is still in the early stages, and more research is needed to fully understand and optimize its capabilities. The main advantage of integrating quantum computing with the K-Medoids method lies in its ability to process large datasets more efficiently. This could lead to faster diagnostic tools in medical fields, particularly in anemia diagnosis.

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