

Investigating Heart Rate Variability Index Classification in *Macaca fascicularis* and Humans: Exploring Applications for Personal Identification and Anonymization Studies

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ABSTRACT

*In this paper, we determine the feasibility of differentiating between the heart rate patterns of *Macaca fascicularis* and human infants by comparing pertinent hyperparameters. This verification process was undertaken to ascertain the suitability of *Macaca fascicularis* heart rate data as a testbed for evaluating heart rate parameter privacy safeguarding methodologies. The biological characteristics of *Macaca fascicularis* bear significant resemblance to those of humans, which consequently renders them useful subjects in medical experiments alongside other laboratory animals. The process of capturing heartbeat data from *Macaca fascicularis* is notably akin to the methodologies used to record human cardiac activity. In other hand, the recent years have witnessed the construction of extensive heart rate databases, thus raising important considerations surrounding privacy in their usage. Heartbeat recordings, indeed, can provide a wealth of diverse information, necessitating careful handling to maintain data privacy. Specifically, a Holter monitor, a type of electrocardiogram device, can record cardiac electrical activity for over 24 hours. The statistical indices derived from these recordings prove useful for various types of analysis, and simultaneously hold information relating to individual behaviors and health conditions. The extent to which individuals can be identified within such expansive databases is a topic warranting exploration; however, few individuals have granted consent for their data to be used for such research purposes. Given this scenario, since the protection of personal data is not a requisite for *Macaca fascicularis*, the proposition of employing *Macaca fascicularis* data to investigate the potential for individual identification appears to be a plausible approach. The experiment verified the similarity of cynomolgus monkey heart rate data to human heart rate data. The results are similar, suggesting that it is appropriate to use cynomolgus monkey heart rate data for personality identification experiments.*

1. Introduction

Macaca fascicularis exhibit a significant similarity to humans in terms of biological characteristics, making them suitable subjects in medical experiments alongside other laboratory

animals [1] and [2]. Heartbeat data from *Macaca fascicularis* can also be recorded using methodologies similar to those employed for humans [3]. Concurrently, a large heart rate variability database has been developed in recent years [4], [5], [6] and [7]. Personal identity can be an issue when using large heart rate databases. Therefore, research is needed to verify individual identifiability, which is our overall goal.

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Heart rate recordings are rich sources of data. Notably, wearable Holter electrocardiogram devices have the capacity to record cardiac electrical activity over a span exceeding 24 hours. The statistical indices derived from these recordings serve multiple analytical purposes and can also aid in predicting individual behaviors and health conditions.

Analysis of these databases revealed that various personal attributes can be extracted from heart rate [8], [9] and [10]. It is therefore essential to consider the protection of personal data contained in heart rate variability. Therefore, it is important to ascertain the identifiability of heartbeats and explore methods to enhance their anonymization.

Information pertaining to such health conditions, particularly cardiac diseases, is of a private nature and ought to be safeguarded from public disclosure.

Hence, when disseminating such expansive databases for research purposes, it is imperative to apply processing techniques ensuring the heartbeat data contained therein cannot be attributed to a specific individual. Various methodologies have been proposed to hinder individual identification, including anonymization strategies.

There is no absolute method to confirm that personal identification has been entirely thwarted. The effectiveness of identification prevention measures is typically evaluated empirically. Public tests, wherein attempts are made to identify specific individuals using test data, will be carried out, with the resultant outcomes undergoing evaluation. This necessitates the availability of appropriate test data.

Nevertheless, employing human data for such public testing initiatives is untenable due to inherent privacy implications.

The crux of this matter lies in the fact that the data that needs to remain unidentified pertains to personal health characteristics—specifically diseases—that the individual would prefer to keep private. Should the test results lead to the identification of both the disease and the individual, this would pose serious ethical concerns. Contributing data to such tests would bring about substantial risks and minimal benefits to the subjects. Consequently, procuring consent for such use is virtually unfeasible.

Consequently, we propose the use of Macaca fascicularis data for identification trials. Given that there is no requirement for the protection of personal data pertaining to Macaca fascicularis, there exist no ethical issues associated with identifying individual entities or symptoms within this data set.

Nonetheless, if the heart rate data of Macaca fascicularis can be statistically distinguished from that of humans, it would be improper to incorporate the data of Macaca fascicularis into human data and investigate the feasibility of individual identification. This is due to the fact that if we can discern the data of Macaca fascicularis, it would inevitably lead to the recognition of data specific to an individual entity.

Hence, it is crucial to establish that distinguishing between Macaca fascicularis and humans is sufficiently challenging. The primary aim of this study is to undertake this verification.

In essence, within our research purpose, the data of Macaca fascicularis and humans do not have to be entirely indistinguishable. If we select human data that bears similarity to the data of Macaca fascicularis, our objective is to ensure that distinguishing between Macaca fascicularis and humans proves challenging. Should this validation be successful, we can draw the conclusion that the Macaca fascicularis data, which represents the ultimate objective of this study, can be effectively utilized.

2. Proposed method

2.1. Data preparation

Thirty seven neonatal human samples and Macaca fascicularis ECGs, a single case of ECG data obtained from a Macaca fascicularis were utilized for this study.

Thirty seven neonatal Human heartbeat samples were obtained from ALLSTAR (Allostatic State Mapping by Ambulatory ECG Repository) database, those are all available data in the database. ALLSTAR is database based in Japan (<https://allstar.jpn.org/>). The data contained within the ALLSTAR database was gathered utilizing a Holter electrocardiograph, a product of Suzuken Co., Ltd., Japan.

The Macaca fascicularis used in this study was male and it is the only data we could use. The heart rate data for these specimens were collected using a two-lead electrocardiograph provided by Tokyo University of Agriculture and Technology, Japan.

2.2. Analysis Method

A prevalent technique for the detection of R-waves in both the Macaca fascicularis and human neonatal data involves the extraction of baseline fluctuation components, followed by the isolation of feature points through waveform detection processing. For this study, we opted for a device that is capable of automatically calculating RRI.

Utilizing the heart rate variability index as a high-dimensional feature, we sought to determine whether it could be visualized using three representative methods of classification visualization.

Visualization using PCA, t-SNE, UMAP were executed.

PCA (Principal Component Analysis):

PCA stands for Principal Component Analysis and is a classical technique used for dimensionality reduction and information extraction of data. It transforms the data into a low-dimensional space, mainly by finding new axes (principal components) that maximize the variance of the data.

Since PCA extracts features in the range of linear transformations, it is specifically useful in this study to see the relationship between features and original variables in linear transformations.

t-SNE (t-Distributed Stochastic Neighbor Embedding) is a nonlinear dimensionality reduction technique. High-dimensional data can be mapped into a low-dimensional space while maintaining data similarity. This is particularly suitable for visualizing cluster structures. Neighborhoods in high-dimensional space are also mapped to neighborhoods in low-dimensional space.

This transformation not only provides visualization, but also gives insight into how each piece of data is categorized. In this study, it is useful to visualize nonlinear structures.

UMAP (Uniform Manifold Approximation and Projection) is a newer technique than t-SNE. It performs non-linear dimensionality reduction like t-SNE, but makes it possible to capture the overall structure while preserving the local structure of high-dimensional data. It is used for visualization and clustering of high-dimensional data.

It reflects the local and global structures of high-dimensional data in a well-balanced manner. In addition, it is resistant to noise and provides stable and good results.

In this experiment, we expected that PCA could confirm the relationship between the feature value and the original space in the linear transformation relationship, that visualization of the cluster structure by t-SNE and that UMAP would provide a well-balanced view of local and global structures.

Commonly utilized features of heart rate variability were computed and employed for multi-dimensional analysis. These features encompass HR, MNN, SDNN, SDNN, rMSSD, TPW, ULF, VLF, LF, HF, VHF, , and LFHF. These features are widely employed in various heart rate variability analyses[7][8].

3. 3D visualization

3.1. 3D visualization using PCA

Figure 1 presents a three-dimensional visualization created through the principal component analysis (PCA) method. In this visualization, the principal components are derived through PCA, with the three most significant components being transformed into a three-dimensional format. The data points corresponding to Macaca fascicularis are circled in red.

Since PCA is a technique used for converting high-dimensional data into lower dimensions, it amalgamates dimensions in a high-dimensional linear space and extracts the dimension contributing most significantly to the data's variability. Consequently, dimensions that do not illustrate data differences are minimized, allowing for a reduction in dimensions while preserving information vital for data identification to the maximum possible extent.

In the figure 1, Macaca fascicularis is situated peripherally within the overall distribution. Nonetheless, numerous human data points exist in proximity to those of Macaca fascicularis, including closely neighboring human samples, thereby rendering the differentiation between the two challenging.

3.2. 3D visualization using t-SNE

Figure 2 presents the data visualization in three dimensions via the t-SNE method.

Since t-SNE (t-Distributed Stochastic Neighbor Embedding) is a dimensionality reduction technique that is designed to maintain data differences while reducing the dimensionality of high-dimensional data to low dimensionality, a key feature of t-SNE is its inclusion of non-linear transformations, which enhances its performance in data clustering and the preservation of similarity.

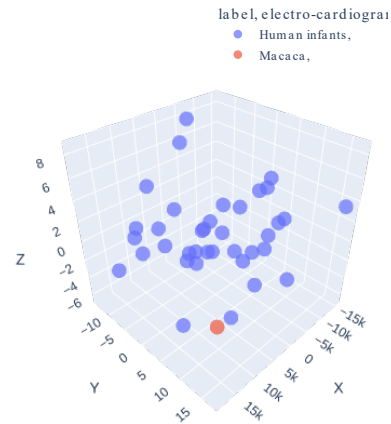


Figure 1: 3D visualization using PCA. 3-dimensional representation is obtained by selecting the top three eigenvectors associated with the largest eigenvalues of the covariance matrix. These eigenvectors capture the most significant variance in the original data, ensuring that the essential information is retained while reducing computational complexity and facilitating data interpretation. The selected 3-dimensional subspace preserves the main patterns and relationships present in the original data, enabling efficient data analysis and visualization. Macaca fascicularis is circled in red. It can be seen that there are human samples in the vicinity and it is difficult to distinguish them. Local structure in the cluster is not clear in case of PCA analysis.

In this analysis, t-SNE compresses from a high dimension to a 3-dimensional space.

This technique performs non-linear transformations to preserve the similarity of data. In other words, data points from the same class are located in close proximity to each other even in a three-dimensional space, while data points from different classes are more distantly spaced. Hence, some degree of clustering can be discerned in the figure, making it easier to understand the relationships between different groups of data in the original high-dimensional space.

Given that t-SNE reduces dimensions while preserving similarities between data points in the high-dimensional space, the figure tends to reflect some relative distances and similarities between the data in the original high-dimensional space.

Moreover, patterns and similarities within the data can be discerned more clearly with t-SNE than with PCA. This is attributed to t-SNE's ability to emphasize local data structures. Data points that were closely situated in high-dimensional space should also tend to be close together in 3D space, allowing local features to be more clearly discerned in the figure.

However, it should be noted that dimensionality reduction by t-SNE does not necessarily preserve the global structure. Therefore, it should be considered that the global arrangement in the 3D space may not necessarily reflect the global arrangement in the higher dimensions.

3.3. 3D visualization using UMAP

Figure 3 shows a three-dimensional visualization by UMAP.

UMAP embeds data in a three-dimensional space while preserving data similarity, resulting in a distribution that reflects the features and clusters of the original high-dimensional data.

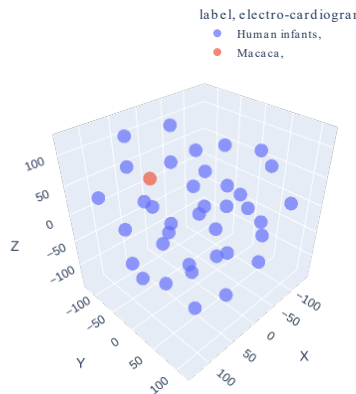


Figure 2: Visualization using t-SNE. Macaca fascicularis is circled in red. It can be seen that there are three or four clusters but local structure of the clusters are punctuated. It can be seen that there are human samples in all around it and it is difficult to distinguish from them.

Similar to t-SNA, data belonging to the same class are plotted close together in 3D space and data of different classes are plotted far apart. As a result, clusters of data are clearly visible in the figure, making it easier to understand the relationships between groups of data.

Also, like t-SNA, UMAP emphasizes local structures, so data that were close together are arranged close together in 3D space. Data that are plotted close together on the figure are likely to be nearby even in a high-dimensional space, making it easier to read the cluster structure.

Unlike t-SNA, UMAP also reflects global data placement to some extent. The structure between clusters can also be read in the figure, but in the case of UMAP, it is thought that this reflects the structure in a high-dimensional space.

This figure seems to be useful for understanding the characteristics of high-dimensional data by performing dimensionality reduction and visualization of data, but it is not true that there is no information loss due to dimensionality reduction.

4. 2D visualizations

Figures 4 to 6 provide two-dimensional (2D) visualizations, achieved through further dimensionality reduction from the previous three-dimensional (3D) representations. While 2D inherently contains fewer dimensions than 3D, this can actually be advantageous when visualizing data. When 3D visualizations are projected onto a 2D plane (such as a computer screen or printed page), some information can be lost due to the lack of depth perception. This could potentially obscure important features or relationships in the data. Therefore, if the 3D visualization isn't explored with a 3D viewer or software that allows for rotation and inspection from different angles, it can sometimes be more insightful to create a 2D visualization from the outset. This can ensure that the most significant data relationships are immediately visible, and are not hidden by the 3D to 2D transformation at the.

4.1. 2D visualization using PCA

Figure 4 presents a two-dimensional (2D) visualization using Principal Component Analysis (PCA). Here, the dimension that contributes the least to the variability of the data has been removed, effectively reducing the data from three dimensions down to two.

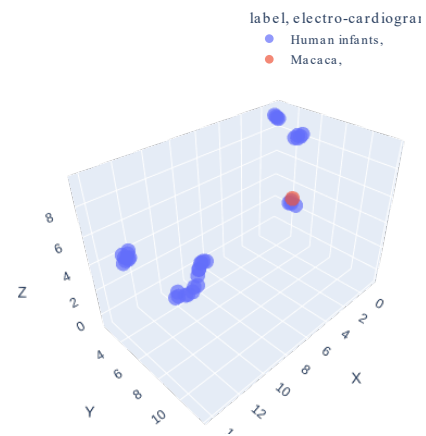


Figure 3: 3D visualization using UMAP. There are three or four clusters and the local structure of those are also visible. Macaca fascicularis is circled in red. It can be seen that it is in one of the clusters and there are human samples in the all-around it and it is difficult to distinguish from them.

The reduction process in PCA is designed to retain the features that account for the most variability in the data. Consequently, this 2D visualization is better suited to display the overall, or global, structure of the data. While PCA is very effective at illustrating these global trends and differences, it's worth noting that it may not accurately portray the more nuanced, local structures within the data set. These may become obscured or lost during the dimensionality reduction process. Thus, while PCA is an invaluable tool for examining broad trends in a data set, it may not fully capture the complexity of the data if there are intricate local patterns or clusters.

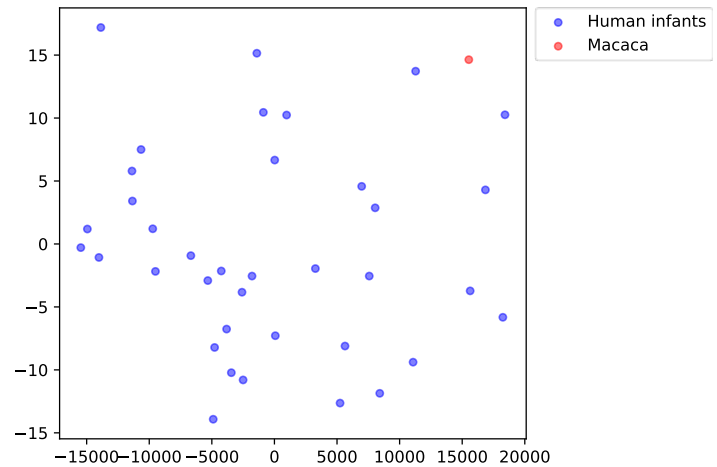


Figure 4: 2D visualization using PCA. Acquire the maximum 2D after PCA and convert it to 2D. Macaca fascicularis is circled in red. It can be seen that there are human samples in the vicinity and it is difficult to distinguish them. Local structure in the cluster is not clear.

4.2. 2D visualization using t-SNE

Figure 5 represents the data's compression into two dimensions using t-SNE (t-Distributed Stochastic Neighbor Embedding). Like in the case of Figure 4, this 2D visualization method emphasizes the preservation of local structures and similarities between data points. Therefore, it provides a more detailed view of the internal structure within each cluster, often producing a more intuitive representation than PCA.

This 2D visualization helps reveal four discernible clusters, with data from *Macaca fascicularis* appearing within one of these clusters. However, as previously mentioned, t-SNE may not necessarily preserve the global structure of the data. When comparing this t-SNE visualization with the PCA representation, this limitation becomes evident.

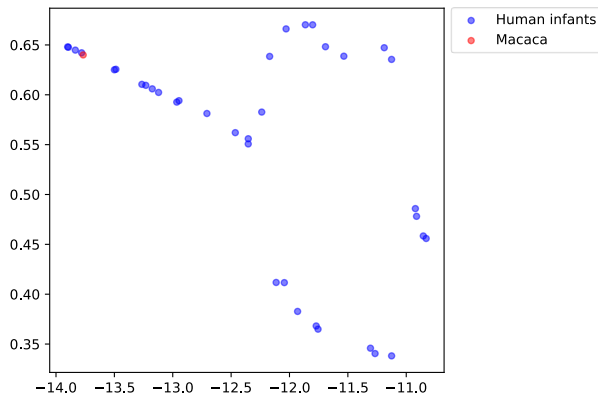


Figure 5: 2D visualization using t-SNE. It can be seen that there are three or four clusters but local structure of the clusters are punctuated. *Macaca fascicularis* is circled in red. It is difficult to distinguish *Macaca fascicularis*.

It's important to note that while t-SNE generally requires higher computational resources compared to PCA, in this case, due to the relatively small size of the dataset, this computational cost is not a significant concern.

4.3. 2D visualization using UMAP

Figure 6 illustrates a two-dimensional visualization using the UMAP (Uniform Manifold Approximation and Projection) method. UMAP is particularly adept at preserving both local and global structures in data, leading to robust and informative visualizations.

In this figure, UMAP outperforms t-SNE by capturing intricate local cluster structures in a more comprehensible manner. While t-SNE may cause some clusters to collapse, UMAP is able to differentiate within-cluster data points and maintain clearer demarcations.

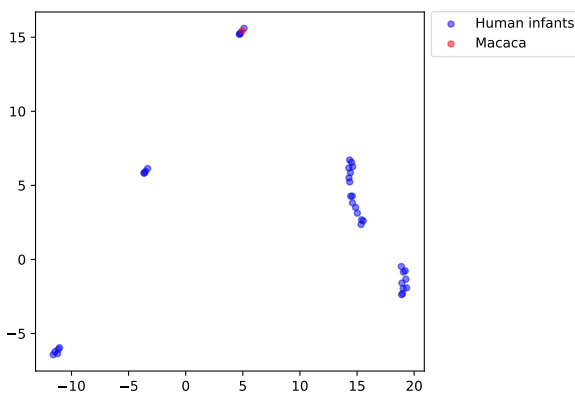


Figure 6: 2D visualization using UMAP. It can be seen that there are three or four clusters and the local structure of those are also visible. *Macaca fascicularis* is circled in red. It can be seen that it is in one of the clusters and there are human samples in the all-around it and it is difficult to distinguish from them.

Moreover, data points that were dispersed across separate clusters in the t-SNE visualization appear more integrated in this www.astesj.com

UMAP visualization. Consequently, it's easier to discern three or four distinct clusters. The data points for *Macaca fascicularis* are situated within one of these clusters, showcasing a fairly even distribution.

Since, UMAP is less sensitive to variations in parameters, allowing the global structure of the visualization to better represent the actual distribution of data in the high-dimensional space, global structure is best visualized in this figure.

5. PCA after UMAP

Figure 7 shows a 2D visualization of UMAP (Uniform Manifold Approximation and Projection) followed by PCA. UMAP is particularly good at preserving both local and global structure in your data, resulting in robust and informative visualizations. PCA can derive the principal factors by linear transformation of the obtained dimensions. By combining these, you can see the structure visualized by UMAP on the space where the factors of the overall structure are orthogonalized in this figure.

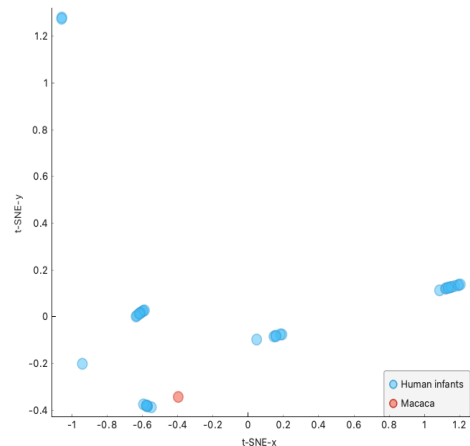


Figure 7: 2D visualization using UMAP (Uniform Manifold Approximation and Projection) followed by PCA. UMAP is preserving local and global structure in data, resulting in robust and informative visualizations. PCA can derive the principal factors by linear transformation of the obtained dimensions.

6. Discussion

Throughout the conducted analyses, our findings consistently validate that the *Macaca fascicularis* dataset exhibits a distribution pattern that closely aligns with that of the human data, posing difficulties in effectively distinguishing the *Macaca fascicularis* data. Furthermore, the cynomolgus dataset demonstrates integration within this structure, upon the cluster structure observed in the human data.

Therefore, the findings of this study indicate that straightforward visual features and dimensionality reduction techniques may not be sufficient to differentiate between the heart rate variability indices of *Macaca fascicularis* and humans when their heart rates are similar. This implies that when the mechanical pulsation mechanism (the mechanical model) of the heart is consistent, the heart rate variability index exhibits analogous characteristics, making it challenging to distinguish between *Macaca fascicularis* and humans using conventional methods.

These results provide an intriguing insight into the similar physiological patterns shared between certain primates and humans when observed through the specific lens of heart rate

variability indices. Furthermore, they also underscore the need for more nuanced or advanced methods for distinguishing between such closely aligned data sets.

This study might have significant implications for a range of applications where such differentiation could be crucial. For instance, in medical research involving primate models, or in the development of biometric identification systems that rely on heart rate variability as a distinguishing factor. Further research is needed to identify and develop more sophisticated techniques that can make this crucial differentiation more accurately and efficiently.

A clear limitation of this study is the scant amount of data for both *Macaca fascicularis* and humans. However, the ultimate aim of this research is to utilize *Macaca fascicularis* data to verify the individuality of human heartbeats. For this purpose, it is not strictly necessary to establish whether there is discrimination between humans and *Macaca fascicularis*; it is sufficient to demonstrate that the level of discrimination between humans and *Macaca fascicularis* is considerably low.

If *Macaca fascicularis* possess traits that humans do not, it's assumed that it would be particularly easy to identify individuals in human heartbeat data. Therefore, it could actually be beneficial for the experiments on individual identification and anonymization. This opens up opportunities for future research and experimentation with larger datasets, more sophisticated analytical techniques, and alternative data sources.

To bolster the reliability of these results, future research will need to gather a larger sample size and consider an approach that incorporates a variety of feature values. Techniques such as data co-mingling and masking are commonly employed to safeguard personally identifiable information, and it's imperative that datasets remain devoid of any personally identifiable information or personal identifiers.

Additionally, integrating different types of machine learning and statistical techniques may also improve the ability to differentiate between the two species. Involving more complex techniques, such as deep learning or support vector machines, could also be considered to help refine the model. Overall, this research provides an interesting starting point, but more extensive work is required to validate these results and to explore the potential implications further.

To bolster the reliability of these findings, our future work will encompass the collection of additional data samples and exploration of a methodology that integrates a variety of feature values. It is crucial to highlight that in the handling of such data, methods such as data commingling and masking are often employed to safeguard personally identifiable information. This ensures that the datasets remain void of personal identifiers and any information that can be traced back to individuals.

In summary, the objective of this experiment was that cynomolgus monkeys are highly similar to humans, and a highly reliable answer was obtained through a multifaceted investigation. In the future, as we acquire more data, we will be able to use these results to advance research toward the broader goal of identifying individual heartbeats.

7. Conclusion

This research substantiated the claim that the cardiac data of *Macaca fascicularis* are substantially analogous to human heart rhythms and thus can be aptly employed to validate various method intended to prevent personal identification of cardiac data. This research provided highly reliable answer, derived through a multifaceted investigation. The deployment of *Macaca fascicularis* cardiac rhythm data as a test set for such validation is expected to enable research on more secure processing of cardiac rhythm data. And once the privacy preservation technique for heart rhythm data is possible to be provided, large and efficient use of large-scale shared heart rhythm data repositories will be possible. Clear limitation of this study is the small number of *Macaca fascicularis* and we need to address this limitation in future research. Even current result is possible to support such result, still it is possible to improve precision and reliability of result by extending data size and analysis method.

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