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A Novel Explainable Deep Learning STING Kernel Approach for Multivariate Time Series Imputation in Healthcare

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ABSTRACT

Multivariate time series (MTS) data is crucial in fields such as healthcare, finance, and traffic management, particularly for forecasting clinical outcomes like mortality rates, disease risks, and hospital stay durations. In healthcare, imputing missing values from complex MTS datasets can enhance critical care management and enable personalized treatments. This study focuses on imputing missing values in health-related data, especially intravenous vital signs and data essential to physicians' decision-making. To address limitations of existing imputation methods, we introduce a novel approach: the STING Kernel Deep Level (SKDL), coupled with an explainable framework. SKDL is designed to improve accuracy and effectively handle categorical outputs. Our evaluation using the MIMIC-IV dataset shows that SKDL outperforms traditional imputation methods such as Mean Imputation, k-Nearest Neighbors (KNN), and standard GAN-based approaches, based on performance metrics including Mean Absolute Error (MAE), Mean Squared Error (MSE), Root Mean Squared Error (RMSE), and R Squared. SKDL achieved an MAE of 0.0870, MSE of 0.0175, RMSE of 0.0040, and R Squared of 0.3367, indicating strong accuracy. Furthermore, the integration of Explainable AI (XAI) enables interpretability by visualizing imputation rationale, helping clinicians verify that the predicted values align with physiological expectations, thereby reinforcing trust in the imputation process. These results suggest that SKDL, with its interpretable design, provides a reliable solution for missing data imputation and supports more consistent and transparent clinical decision-making.

1. INTRODUCTION

The imputation of missing values in multivariate time series data has emerged as a cornerstone methodology across diverse fields, addressing the pervasive challenge of incomplete datasets. This process is crucial in enabling accurate analyses and informed decision-making where data gaps might otherwise compromise results. In environmental science, the impact of missing time series data is particularly evident during critical periods marked by high hydrological or biogeochemical fluxes. For instance, peak flow conditions and rapid fluctuations often occur in environments such as hyporheic zones, which are vital interfaces between surface and groundwater systems. These conditions can drive essential processes, including the cycling of carbon, nutrients, and other elements. If data gaps align with these high-activity periods, researchers may miss key insights into ecosystem dynamics, ultimately hindering efforts to understand and predict environmental changes. The application of precise imputation methods becomes indispensable in filling these gaps with accurate estimates, thereby preserving the integrity of the data and enabling robust scientific analysis [1-3].

In healthcare, the stakes are even higher, as missing data in multivariate time series can directly impact patient outcomes [4, 5]. Clinical datasets are often incomplete due to irregular monitoring, varying patient compliance, or logistical constraints in data collection. Missing values in such datasets pose significant challenges for predictive modeling, where every data point can contribute to understanding patient health trajectories [6, 7]. Imputation techniques are applied to reconstruct these incomplete datasets, enabling the development of predictive models for critical clinical outcomes. These models can forecast patient mortality, detect early signs of decompensation, estimate length of hospital stay, and assess disease risks, thereby informing proactive medical interventions. Furthermore, these methods are instrumental in optimizing intensive care unit (ICU) operations, ensuring that limited resources are allocated effectively to meet patient needs. Imputation also facilitates the creation of automated and personalized treatment plans, which are increasingly vital in delivering tailored healthcare solutions that adapt to the unique circumstances of each patient. By bridging data gaps, imputation not only enhances the quality of analysis but also supports a wide range of

applications that improve patient care, streamline medical operations, and foster innovation in clinical decision-making [8].

The science of imputation, therefore, represents a critical intersection of data science and domain-specific expertise, empowering researchers and practitioners to maximize the value of their data. Whether addressing ecological dynamics or improving patient outcomes, imputation methods provide the tools necessary to overcome the challenges posed by missing values, ensuring that data-driven approaches remain reliable, comprehensive, and actionable.

The field of missing value imputation (MVI) has predominantly focused on multivariate tabular data, often neglecting variables that exhibit temporal variation. Despite this, many real-world datasets, particularly those in health sciences and electronic sensor applications, involve time-varying data recorded across multiple variables over extended periods. For instance, electronic health records (EHRs) include patient follow-up data collected longitudinally, where missing values can appear both across variables (cross-sectional missing data) and over time (longitudinal missing data). Such data gaps are inevitable due to various reasons, including irregular patient monitoring, incomplete data entry, or sensor malfunctions. Addressing these gaps is essential, as missing data can compromise the quality of analyses and decision-making processes, necessitating sophisticated imputation methods to reconstruct the missing information accurately [9].

Recurrent Neural Networks (RNNs) have emerged as a widely adopted solution for handling missing values in clinical time series data. RNNs are particularly effective for processing sequential data of varying lengths, which makes them suitable for many healthcare applications. However, conventional RNN methods often assume that time intervals between consecutive observations are constant. This assumption creates challenges when dealing with real-world datasets, where irregular time intervals are common. As a result, traditional RNN-based imputation methods often struggle to deliver optimal performance in such scenarios, highlighting the need for more adaptive and flexible approaches [10].

Among the advanced methods developed for time series imputation, the STING (Self-Attention-based Time Series Imputation Networks Using GAN) framework stands out as a promising approach. STING combines Generative Adversarial Networks (GANs) with two-way recurrent neural networks to effectively capture latent representations of time series data. This hybrid architecture enables STING to address many of the challenges associated with imputation in time-varying datasets. By incorporating self-attention mechanisms, the method can focus on critical patterns in the data, improving its ability to reconstruct missing values accurately. Despite its innovative design and effectiveness, STING has limitations. Notably, it struggles to generalize beyond continuous numerical data, performing poorly with categorical or qualitative datasets. This restriction underscores the ongoing need for further advancements in the field of missing value imputation to develop methods capable of handling diverse data types and accommodating the complexities inherent in real-world datasets [11].

As MVI continues to evolve, addressing these limitations will be crucial for ensuring the robustness and versatility of imputation techniques, enabling their application across a broader range of use cases and improving their ability to support data-driven decision-making in critical fields like healthcare and environmental science.

In addition to the STING method, an alternative approach for addressing missing data in multivariate time series (MTS) is the TCKIM method, a kernel-based technique that incorporates an ensemble learning strategy. The TCKIM method is underpinned by a novel mixed-mode Bayesian mixture model, which effectively mitigates information loss without requiring direct imputation of missing values. This makes it an appealing choice for certain applications where data imputation may introduce additional uncertainty. However, a notable limitation of the TCKIM method is its inability to leverage patterns inherent in the missing data, which are often critical in medical datasets. This shortcoming is particularly significant in medical MTS, where missing values frequently contain valuable insights into underlying processes. Furthermore, the kernel method guarantees unbiased predictions only in cases of negligible missing data, as it fundamentally relies on the assumption that the data is Missing at Random (MAR) [12]. These limitations necessitate the implementation of additional imputation processes to address gaps and enhance the method's applicability, referred to as deep stage imputation (Deep Level).

Research has shown that the kernel-based TCKIM method is highly effective for imputing missing values in electronic health records (EHR). For instance, findings in the study [12] emphasize its suitability for handling missing data in EHR settings, where its structure is particularly well-suited for tabular data. However, in cases requiring high imputation accuracy and reliable downstream analysis, the STING method has demonstrated superior performance compared to other state-of-the-art approaches. Research [11] highlights that the STING method outperforms alternatives in terms of imputation accuracy and in supporting downstream tasks, making it an essential tool for more complex datasets. In light of these findings, the current study aims to conduct experiments on two types of health datasets vital sign data from MIMIC IV and physician decision-making data to evaluate the effectiveness of imputation techniques in improving data utility and clinical outcomes.

For vital sign data, the kernel method is applied to achieve greater depth in imputation, building on the existing kernel-based framework to exceed the accuracy achieved by prior models. This aligns with findings [13], which illustrate that the Time Series Cluster Kernel (TCK) offers a robust framework for analyzing multivariate time series with missing data, making it particularly effective for structured data like MIMIC IV. Meanwhile, the STING method is specifically applied to physician decision-making datasets, focusing on addressing its current limitations in handling qualitative or categorical data. Traditionally, the STING method has excelled in numerical imputation, but its application to qualitative data remains a challenge. The study seeks to extend STING's capabilities in this domain by applying it to datasets where decisions are expressed in categorical or qualitative forms [11]. By combining the strengths of the kernel and STING methods, this research aims to develop a comprehensive approach for imputation that is adaptable to diverse types of healthcare data, ultimately improving patient outcome analysis and clinical decision-making accuracy.

In order to address the deficiencies inherent in the aforementioned methodologies and their applicability to vital sign data and clinical decision-making data, there exists a pressing need for a novel imputation technique that enhances accuracy and is capable of generating data in a categorical format.

The researcher aims to develop an innovative approach termed the "STING Kernel Deep Level method (SKDL) with Explainable." It is anticipated that this cutting-edge methodology will facilitate more profound imputation with superior accuracy compared to preceding techniques, while simultaneously yielding categorical data imputation and providing elucidation or interpretability of the imputation outcomes via the SKDL With Explainable framework.

To enhance the effectiveness of data imputation methods, several key questions must be addressed. First, it is essential to explore how to design an Advanced STING method that surpasses the performance of previous iterations in generating imputations. Additionally, developing an Advanced Kernel method that achieves superior accuracy compared to earlier kernel approaches is crucial [14]. Furthermore, the integration of Explanations into both the STING and Kernel methods should be considered, enabling them to produce imputations across datasets with varying dimensions while also providing clear justifications for their outputs. Finally, a robust framework for validating and evaluating these advanced methods is necessary to establish a more relevant and effective theory of imputation that meets contemporary data analysis needs.

By offering an interpretative framework for the imputation results procured, it demonstrates that the derived outcomes can genuinely be substantiated and align with empirical research findings. Reference [15] emphasizes the significance of incorporating mechanisms that are interpretable and explicable within the model framework. Furthermore, according to the findings presented in research [16], it is feasible to seamlessly conduct imputation on cross-dimensional datasets by augmenting the CDSA algorithm with inputs of elevated dimensions, thereby integrating diverse data modalities. Research [17] elucidates the imputation process employing an optimization technique that interconnects various patterns of missing values within analogous, interrelated data. Consequently, there is a compelling necessity to advance a new methodology, namely the SKDL with Explainable approach, for the application of imputation to multivariate time series data within the healthcare domain.

However, despite their strengths, existing methods still exhibit critical limitations that restrict their applicability in real-world healthcare settings. The original STING framework, while effective in imputing continuous numerical values, lacks the capability to process categorical or qualitative data, which are common in clinical decision-making records. This limitation hampers its ability to fully capture the diversity of healthcare data types. On the other hand, the TCKIM method, although robust in avoiding direct imputation through its kernel-based ensemble approach, fails to utilize the underlying patterns within the missing data and assumes that the data is Missing At Random (MAR). This assumption is often invalid in healthcare applications, where the mechanism of missingness can itself carry valuable clinical meaning. These shortcomings highlight the need for a more flexible, accurate, and explainable imputation technique that can handle both continuous and categorical variables while providing interpretability to support trustworthy clinical decision-making.

2. METHOD

This research aims to implement an innovative technique known as the STING Kernel Deep Level (SKDL) with an Explainable AI (XAI) approach. By leveraging this advanced method, we anticipate achieving a significantly higher imputation accuracy compared to traditional approaches. The research workflow begins with a comprehensive literature review, followed by dataset preprocessing, the development of state-of-the-art imputation models, and concludes with evaluation and model testing. The primary objective is to develop a method for imputing categorical data, while simultaneously offering clear and interpretable explanations of the imputed results (see Figure 1).

In many datasets particularly those in healthcare and the social sciences missing data poses a common and serious challenge that can compromise the quality of analysis and decision-making. Focusing on categorical data allows us to address the unique complexity of imputing values that represent discrete categories rather than continuous variables. The SKDL approach is designed not only to fill these missing values but also to explain the rationale behind each imputation, thereby promoting transparency and trustworthiness in critical domains such as clinical research and predictive modeling.

The SKDL method integrates explainable techniques to provide insights into the underlying patterns and relationships that drive the imputation outcomes. This is particularly crucial in decision-sensitive applications, where domain experts such as clinicians need to understand and justify the values generated by the model [18-20]. Thus, explainability becomes a key component of the imputation framework.

The SKDL framework consists of several phases. First, the STING method is applied and extended into a deeper level of processing, surpassing the performance of the conventional STING method. Next, the Kernel method is employed to further enhance the imputation quality through deeper representation learning. These processes culminate in the selection of the optimal model based on imputation performance, all of which are illustrated in Figure 1.

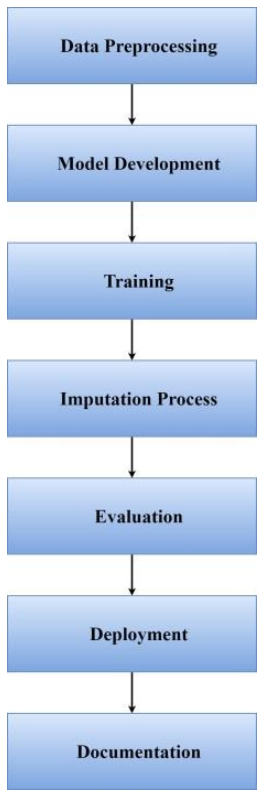

Figure 1. Flowchart for SKDL framework

Following the acquisition of the MIMIC-IV vital signs dataset, preprocessing is conducted, including data cleaning (handling missing values) and normalization using the MinMax Scaler. The dataset is then split into training and testing subsets to enable proper model validation. Imputation is performed using the proposed SKDL method, followed by integration with explainability techniques to provide detailed justifications for each imputed value. The outputs and findings of the imputation process are presented in Figure 2. The SKDL with Explainable Imputation method represents a novel and advanced strategy for imputing categorical data. It improves upon previous STING and Kernel methods by incorporating interpretable outputs and decision reasoning. Validation is conducted by comparing the imputed values to the actual ground truth data, evaluated both quantitatively and qualitatively.

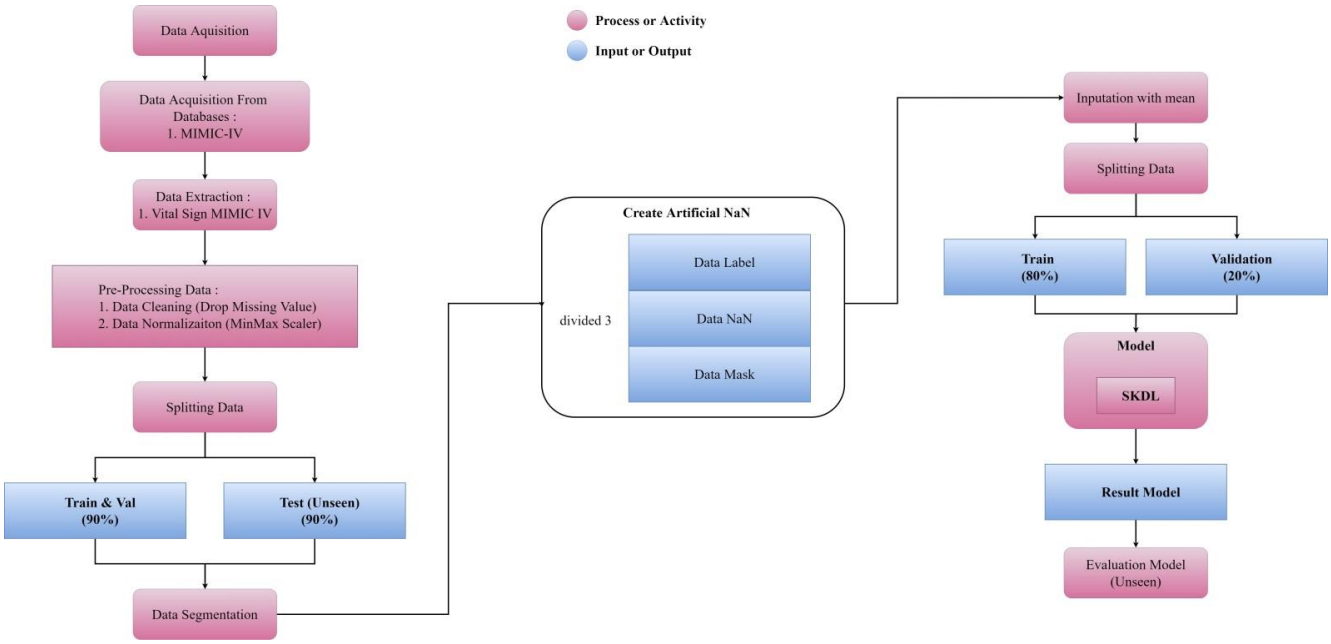

Figure 2. Framework for creating multivariate time series data imputation programs using the SKDL (Sting Kernel Deep Level) method with explainable

To assess the effectiveness of the proposed SKDL model, four widely used error metrics are employed, each offering a unique perspective on model performance. The first metric is Mean Absolute Error (MAE), which measures the average magnitude of prediction errors without considering their direction. It provides a straightforward interpretation of how far, on average, the predicted values deviate from the actual values. The second metric is Mean Squared Error (MSE), which calculates the average of the squared differences between predicted and true values. By squaring the errors, MSE places a greater penalty on larger deviations, making it particularly useful when minimizing large errors is a priority. Building upon MSE, the Root Mean Squared Error (RMSE) is obtained by taking the square root of the MSE value. This transformation brings the error back to the same scale as the original data, making RMSE easier to interpret and more intuitive, especially when evaluating the model's precision in real-world units. Like MSE, RMSE is sensitive to outliers and therefore highlights significant discrepancies in predictions. Lastly, R-squared (R^2), or the Coefficient of Determination, quantifies the proportion of variance in the dependent variable that can be explained by the independent variables used in the model. An R^2 value closer to 1 indicates a stronger fit between the predicted values and the actual data, signifying higher model accuracy. Collectively, these metrics provide a robust and comprehensive framework for evaluating the accuracy, consistency, and reliability of the SKDL imputation model, both in general terms and in identifying specific performance strengths or weaknesses.

The overall design and flow of the proposed imputation system integrating deep-level STING and Kernel methods within the SKDL framework and culminating in interpretable categorical results are comprehensively illustrated in Figure 3. This figure visually summarizes how the method transitions from raw imputation to the SKDL approach, how both STING and Kernel components are applied in parallel, and how the outputs converge to deliver not only accurate categorical imputations but also clear, explainable justifications for each result.

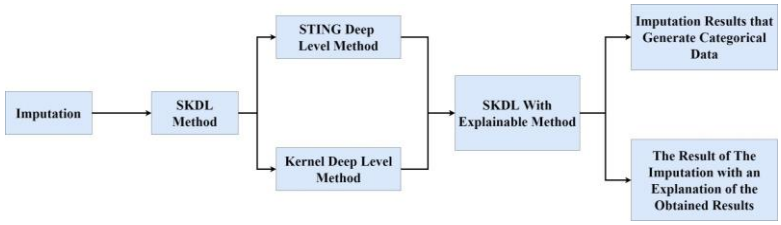

Figure 3. Overview of the research findings that will be developed, utilizing the latest and most advanced imputation technique (SKDL with an explainable method)

The training process of the SKDL method operates through an iterative adversarial optimization scheme. The core mechanism involves two primary components: a Generator (G) and a Discriminator (D). The procedural steps of the algorithm are outlined below, and the notations used are summarized in Table 1 for clarity.

While the training loss has not converged, the following steps are repeated:

1. Discriminator Optimization:

- Draw k_D training samples $\left(x^{(j)}, m^{(j)}\right)$ from the dataset, where $x^{(j)}$ is the input with missing values and $m^{(j)}$ is the corresponding binary mask indicating observed (1) and missing (0) components.
- Draw k_D noise vectors $z^{(j)} \sim Z$, and hint vectors $b^{(j)} \sim B$.
- For each sample $j = 1, \ldots, k_D$:
  - Generate imputed values:

$$\tilde{\mathrm{x}}^{(j)} = G\left(x^{(j)}, m^{(j)}, z^{(j)}\right)$$

  - Construct the completed sample:

$$\hat{\mathrm{x}}^{(j)} = m^{(j)} \odot x^{(j)} + \left(1 - m^{(j)}\right) \odot x^{(j)}$$

  - Compute the hint vector:

$$\mathrm{h}^{(j)} = b^{(j)} \odot m^{(j)} + 0.5 \cdot \left(1 - b^{(j)}\right)$$

- Update the Discriminator D by minimizing the loss function $\mathcal{L}_D$ using stochastic gradient descent (SGD):

$$\nabla_D \leftarrow \frac{1}{k_D} \sum_{j=1}^{k_D} \mathcal{L}_D\left(m^{(j)}, h^{(j)}, D\left(\hat{\mathrm{x}}^{(j)}, h^{(j)}\right)\right)$$

2. Generator Optimization:

- Draw k_G samples from the dataset $\left(x^{(j)}, m^{(j)}\right)$, along with noise vectors $z^{(j)} \sim Z$ and hint vectors $b^{(j)} \sim B$.
- For each sample $j = 1, \ldots, k_G$:
  - Construct the completed sample $\hat{\mathrm{x}}^{(j)}$ and hint vector $\mathrm{h}^{(j)}$ as above.
- Update the Generator G by minimizing the combined loss

$$\nabla_G \leftarrow \frac{1}{k_G} \sum_{j=1}^{k_G} \left[\mathcal{L}_D\left(m^{(j)}, h^{(j)}, D\left(\hat{\mathrm{x}}^{(j)}, h^{(j)}\right)\right) + \alpha \cdot \mathcal{L}_M\left(x^{(j)}, \hat{\mathrm{x}}^{(j)}\right)\right]$$

The SKDL training process consists of two main stages repeated until convergence: Discriminator and Generator optimization. In the first stage, the Discriminator learns to distinguish real from imputed values by evaluating completed samples generated by the Generator, using observed data, noise, and hint vectors. It is updated based on how accurately it can identify missing components. In the second stage, the Generator is trained to produce realistic imputations. It minimizes a combined loss that includes adversarial feedback from the Discriminator and a reconstruction loss on observed values. This adversarial process helps the Generator refine its outputs until imputed values are indistinguishable from actual data.

Table 1. Notation descriptions

Symbol	Descriptions
x	Input data sample (contains missing values)
m	Mask vector (1 for observed, 0 for missing entries)
z	Random noise vector sampled from a prior distribution
b	Binary hint vector used to partially reveal mask information to the Discriminator
$\tilde{\mathrm{x}}$	Imputed data generated by Generator
$\hat{\mathrm{x}}$	Completed data (observed + imputed)
h	Hint vector derived from mask and hint binary
$\mathcal{L}_D$	Discriminator loss, measures ability to distinguish real from imputed values
$\mathcal{L}_M$	Reconstruction loss on observed data, ensures data fidelity
α	Weight coefficient balancing adversarial and reconstruction losses
⊙	Element-wise (Hadamard) multiplication

3. RESULTS AND DISCUSSION

The first step involves preprocessing the data, which includes data cleaning by removing any missing values and data normalization using a MinMax scaler. Following this, the next task is to split the data into training and testing sets by defining the data segmentation. The outcomes of processing the MIMIC IV data with Python are illustrated in the Table 2.

Table 2. The outcomes of processing the MIMIC IV

	heart_rate	sbp	dbp	mbp	resp_rate	Temperature	spo2	Glucose
0	0.0	0.0	0.0	0.0	0.0	36.00	0.0	0.0
1	116.0	169.0	69.0	98.0	16.0	0.00	98.0	0.0
2	104.0	0.0	0.0	0.0	16.0	0.00	100.0	0.0
3	97.0	0.0	0.0	0.0	11.0	37.83	100.0	0.0
4	83.0	109.0	55.0	71.0	16.0	37.50	100.0	0.0

From the illustration in Figure 3, it is evident that the Python application is capable of displaying the original data extracted from the MIMIC-IV dataset. This visualization highlights the presence of certain data entries that are either empty or missing, which is a common occurrence in many datasets. The identification of these gaps underscores the necessity for an imputation method to effectively fill in the missing data. Imputation techniques are essential in data preprocessing as they help maintain the integrity of the dataset, allowing for more accurate analyses and insights. By addressing these empty values, we can ensure that the dataset is complete and ready for further processing or modeling, ultimately leading to more reliable results in any subsequent analysis.

The subsequent step involves normalizing the MIMIC-IV data using the MinMax Scaler method. This technique is essential for transforming the data to a standard range, which can enhance the performance of various machine learning algorithms. The results of the MIMIC-IV data normalization process can be observed in Figure 4. This visualization will provide insights into how the data has been scaled and prepared for further analysis.

```
data = pd.read_csv('/content/drive/MyDrive/disertasi arius/mimic-iv-vital-sign.csv')
```

```
[4] data_asl=data.loc[:,'heart_rate':'glucose']
```

```
[5] data_matrix=data_asl.fillna(0)
    data_mask=data_asl.fillna(0)
```

```
data_matrix.head()
```

	heart_rate	sbp	dbp	mbp	resp_rate	temperature	spo2	glucose
0	119.0	0.0	0.0	0.0	21.0	39.3	100.0	0.0
1	116.0	85.0	45.0	58.0	19.0	0.0	95.0	0.0
2	56.0	0.0	0.0	0.0	16.0	0.0	0.0	0.0
3	117.0	0.0	0.0	0.0	32.0	0.0	94.0	0.0
4	50.0	89.0	49.0	64.0	23.0	0.0	98.0	0.0

(a)

```
[10] data_mask[data_mask >0]=1
```

```
[11] data_mask.head()
```

	heart_rate	sbp	dbp	mbp	resp_rate	temperature	spo2	glucose
0	1.0	0.0	0.0	0.0	1.0	1.0	1.0	0.0
1	1.0	1.0	1.0	1.0	1.0	0.0	1.0	0.0
2	1.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0
3	1.0	0.0	0.0	0.0	1.0	0.0	1.0	0.0
4	1.0	1.0	1.0	1.0	1.0	0.0	1.0	0.0

(b)

Figure 4. Data Matrix using MIMIC IV (a) and (b) Mask Matrix of MIMIC IV data

In Figure 4(a), we can clearly see the transformation of the data from its original, unnormalized state to a normalized format achieved through the MinMax Scaler method. This normalization process is crucial because it rescales all the data points to a uniform range between 0 and 1. Such scaling is particularly important in machine learning, as it ensures that each feature contributes equally to the distance calculations and model training, preventing any single feature from disproportionately influencing the results due to its scale.

Following this normalization step, the next phase involves the Train and Test process. Before splitting the data, it is essential to determine the appropriate data segmentation. This segmentation helps in defining how the dataset will be divided into training and testing subsets, which is vital for evaluating the performance of machine learning models.

Figure 4(b) provides a visual representation of the Random Matrix derived from the MIMIC-IV dataset, which will be utilized in the training and testing phases. This matrix serves as a foundation for the model training process, allowing the algorithm to learn from the training data while reserving a portion for testing its predictive capabilities. By carefully managing this split, we can ensure that the model is not only trained effectively but also validated against unseen data, which is critical for assessing its generalization performance in real-world scenarios. From Figure 4(b), we can see the Random Matrix MIMIC IV data which will be carried out by a Splitting process which will later obtain several models from an Imputation Method which will be carried out in an Evaluation process to obtain the best model. To rigorously evaluate imputation performance, we simulated missing data using two distinct mechanisms: (1) Missing Completely at Random (MCAR), where data entries were randomly removed without dependency on any other variables, and (2) block-wise missingness, where continuous sequences of time points were omitted to mimic realistic scenarios such as sensor dropout or recording pauses in clinical practice. This dual simulation strategy enables the assessment of model robustness under both stochastic and structured missingness conditions.

Figure 5 provides a clear depiction of the missing values present in the dataset; a frequent challenge encountered in data analysis that can significantly impact the quality and reliability of the results. To effectively address these gaps, we will implement the STING method (Self Attention using GAN), which stands out as one of the most advanced techniques for imputing missing data. This method utilizes the principles of Generative Adversarial Networks (GANs), which consist of two essential components: the Generator and the Discriminator.

```
[22] np.random.seed(42)
     for_rand = pd.DataFrame(
         np.random.randint(0, 2, size=(10, 8)),  # 10 baris, 8 kolom
         columns=['heart_rate', 'sbp', 'dbp', 'mbp', 'resp_rate', 'temperature', 'spo2', 'glucose']
     )
     rand_val = random.random()
     for_rand[for_rand == 1] = rand_val
     matrix_rand = for_rand.fillna(0)
     matrix_rand.head()
```

```
/tmp/ipython-input-22-9856536.py:7: FutureWarning: Setting an item of incompatible dtype is depre
  for_rand[for_rand == 1] = rand_val
```

	heart_rate	sbp	dbp	mbp	resp_rate	temperature	spo2	glucose
0	0.000000	0.702604	0.000000	0.000000	0.000000	0.702604	0.000000	0.000000
1	0.000000	0.702604	0.000000	0.000000	0.000000	0.000000	0.702604	0.000000
2	0.702604	0.702604	0.702604	0.000000	0.702604	0.000000	0.702604	0.702604
3	0.702604	0.702604	0.702604	0.702604	0.702604	0.702604	0.000000	0.000000
4	0.702604	0.702604	0.702604	0.000000	0.702604	0.000000	0.000000	0.000000

Figure 5. Random matrix MIMIC IV data

From Figure 4(b), we can see the Random Matrix MIMIC IV data which will be carried out by a Splitting process which will later obtain several models from an Imputation Method which will be carried out in an Evaluation process to obtain the best model. The following is the MIMIC IV Data Display before Imputation using the SKDL Method is as follows (Figure 6):

stay_id	charttime	heart_rate	sbp	dbp	mbp	resp_rate	temperat	spo2	glucose
30000153	9/29/2174 12:08						36		
30000153	9/29/2174 22:30	116	169	69	98	16		98	
30000153	9/29/2174 13:00	104				16		100	
30000153	10/1/2174 0:00	97				11	37.83	100	
30000153	9/29/2174 16:00	83	109	55	71	16	37.5	100	
30000153	9/29/2174 13:27								158
30000153	9/29/2174 19:00	123	155	68	91	21		96	
30000153	9/29/2174 15:25		123	65	84	14			
30000153	9/30/2174 1:00	109	110	57	76	13		94	
30000153	9/30/2174 10:00	97	135	67	89	14		98	
30000153	9/30/2174 13:00	94	141	67	91	11		98	139
30000153	9/29/2174 14:07								176
30000153	9/29/2174 15:33							100	
30000153	9/30/2174 9:00	113	168	63	94	16	37.28	94	
30000153	9/29/2174 18:00	111	133	63	83	19		99	
30000153	9/29/2174 16:05								175
30000153	9/29/2174 12:06	100							
30000153	9/30/2174 20:00	102				11	37.78	91	137
30000153	9/29/2174 17:00	103	111	56	71	20		100	
30000153	9/30/2174 0:00	116	118	64	83	13	37.5	95	
30000153	9/30/2174 15:00	101	158	64	93	16		100	
30000153	9/29/2174 12:05							100	
30000153	9/30/2174 8:00	115	171	67	99	19		93	
30000153	9/29/2174 22:00	124	108	61	77	17		94	

Figure 6. Initial MIMIC IV data before imputation using SKDL Method

The Generator is responsible for producing synthetic data that closely resembles the characteristics of the original dataset. It generates plausible values for the missing entries by learning from the patterns and relationships present in the available data. This capability is particularly valuable in complex datasets where traditional imputation methods may fall short. Meanwhile, the Discriminator plays a crucial role in evaluating the quality of the generated data. It assesses how well the synthetic values align with the actual data, providing feedback to the Generator to refine its outputs. This adversarial process encourages the Generator to improve its performance continuously, resulting in more accurate imputed values.

The imputation process is iterative, continuing until the results meet specific performance benchmarks. We focus on minimizing several key error metrics, including Mean Absolute Error (MAE), Mean Squared Error (MSE), Root Mean Squared Error (RMSE), and R-squared values. The objective is to reduce these metrics to values as close to zero as possible, indicating that the imputed values are highly accurate and closely align with the original data. Achieving low error values is essential, as it ensures that the imputation process does not introduce significant bias or inaccuracies into the dataset. This is particularly important in fields such as healthcare and social sciences, where the integrity of the data can directly influence research outcomes and policy decisions.

The results of this imputation process, which employs the STING Kernel Deep Level Method (SKDL), are generated through Python programming. This method not only enhances the quality of the dataset by filling in missing values but also preserves the underlying data distribution, making it suitable for further analyses. By effectively addressing the issue of missing data, we enhance the robustness of our models and ensure that the insights derived from the data are both reliable and valid. Moreover, the use of advanced imputation techniques like STING is particularly beneficial in complex datasets where traditional methods, such as mean imputation or simple interpolation, may not adequately capture the underlying relationships within the data. By leveraging the power of GANs, the STING method can produce more nuanced and contextually relevant imputed values, thereby improving the overall quality of the dataset. This comprehensive approach to imputation is crucial for ensuring the integrity of the dataset and the accuracy of any subsequent analyses or predictions, ultimately leading to more informed decision-making based on the data. To confirm that the performance improvements achieved by the SKDL method were not due to chance, a paired t-test was conducted between SKDL and each baseline method (Mean Imputation, k-Nearest Neighbors, and standard GAN-based models) across all evaluation metrics (MAE, MSE, RMSE, and R^2). The results indicated statistically significant differences in favor of SKDL, with $p < 0.01$ for most comparisons. This validates that the proposed method provides a substantial and statistically reliable improvement over existing approaches. The integrated XAI component allows visualization of attention weights and the contribution of specific features to the imputation results. This interpretability enables clinicians to understand not only what the imputed value is, but also why the model produced such a result. In a clinical context, such transparency is essential for building trust in automated systems, especially when used for decision support. By aligning the model's rationale with physiological knowledge and clinical expectations, XAI enhances the acceptability and reliability of imputed values, making them more actionable in real-world medical decision-making scenarios.

Figure 7 demonstrates that the missing data in the initial MIMIC-IV dataset has been successfully imputed using the SKDL Method. Additionally, Figure 8 presents a display of the imputation results as implemented in Python, showcasing the effectiveness of the SKDL method in a programmatic environment.

heart_rate	sbp	dbp	mbp	resp_rate	temperati	spo2	glucose
0.376271185	0.027195	0.018891	0	0.342474	0.854326	0.95999999	0
0.267796609	0	0	0	0	0.206514	0.604896425	3.99E-06
0.325423728	0	0	0	0.246377	0	0	0
0.359322033	0	0	0.012461	0.362319	0	0.919999991	0
0.332203389	0.37535	0.254181	0.327759	0.345272	0	0.967171957	0.000587828
0.298305084	0.021542	0	0	0.333333	0.208275	0.99999999	0
0.267796609	0.012718	0	0	0.202899	0	0.691133523	0
0	0	0	0	0	0	0.939999991	9.17E-09
0.298305084	0	0	0	0.275123	0	0.654335323	0
0.331947707	0.268908	0.230769	0.264214	0.405797	0.203009	0.96999999	7.68E-05
0.328813558	0.277311	0.191911	0.274247	0.289855	0.217352	0.97999999	0
0	0	0	5.52E-06	0	0	0	8.31E-05
0.233898304	0.45098	0.16388	0.301003	0.202899	0	0.919999991	0
0.179661016	0	0.024999	0.047716	0.26087	0	0.97999999	0
0.240677965	0.313725	0.190635	0.26087	0.376812	0	0.939999991	0
0.272754434	0	0	0	0.304348	0.20112	0.95999999	0
0	0	0	0.031851	0.275362	0.202295	0.99999999	0
0.233898304	0	0	0	0.376812	0.205487	0.99999999	9.48E-05
0.223728813	0	0.005171	0	0.188406	0	0.97999999	0
0.286708309	0.294118	0.204013	0.254181	0.318841	0.889121	0.929999991	0
0.21545425	0	0	0	0.202899	0	0.675760896	6.74E-05
0.254237287	0.397759	0.19398	0.284281	0.304348	0.216929	0.909999991	5.57E-05
0.383050846	0.389356	0.237458	0.324415	0.275362	0.867316	0.99999999	0
0.257015882	0.338936	0.190635	0.275503	0.244928	0	0.98999999	0.000106575

Figure 7. MIMIC IV data imputation results using the SKDL method

	heart_rate	sbp	dbp	mbp	resp_rate	temperature	spo2	glucose
0	0.376271	0.027195	0.018891	0.000000	0.342474	0.854326	0.960000	0.000000
1	0.267797	0.000000	0.000000	0.000000	0.000000	0.206514	0.604896	0.000004
2	0.325424	0.000000	0.000000	0.000000	0.246377	0.000000	0.000000	0.000000
3	0.359322	0.000000	0.000000	0.012461	0.362319	0.000000	0.920000	0.000000
4	0.332203	0.375350	0.254181	0.327759	0.345272	0.000000	0.967172	0.000588
...	...	...	...	...	...	...	...	...
1557197	0.277966	0.327731	0.163880	0.237458	0.173913	0.000000	1.000000	0.000122
1557198	0.328814	0.000000	0.000000	0.000000	0.318841	0.000000	0.960000	0.000000
1557199	0.332203	0.260504	0.177258	0.224080	0.271664	0.854326	0.950000	0.000043
1557200	0.127794	0.000000	0.000000	0.031122	0.000000	0.195370	0.980000	0.000146
1557201	0.000000	0.000002	0.000000	0.000021	0.000000	0.000000	0.000000	0.000076

Figure 8. Display of MIMIC IV data imputation results using the SKDL method in python

3.1 Evaluation of MIMIC IV vital sign data imputation results

The following table presents the evaluation results of the MIMIC-IV data imputation process using the SKDL method, assessed through the metrics of Mean Absolute Error (MAE), Mean Squared Error (MSE), Root Mean Squared Error (RMSE), and R-squared.

From the analysis presented in Table 3, it is evident that the SKDL Method has emerged as the most effective model for imputing vital sign data from the MIMIC-IV dataset. This conclusion is drawn from the evaluation of key performance metrics, specifically the Mean Absolute Error (MAE), Mean Squared Error (MSE), Root Mean Squared Error (RMSE), and R-squared values, which were obtained through various tuning processes.The results indicate that the SKDL Method achieved a minimum MAE of 0.0870, which reflects the average magnitude of the errors in the imputed values without considering their direction. A lower MAE signifies that the imputed values are, on average, closer to the actual observed values, indicating a high level of accuracy in the imputation process.

Table 3. Evaluation results using the MAE, MSE, evaluation matrix RMSE and R-squared

MIMIC IV Data Variables	MAE	MSE	RMSE	R-Squared
heart_rate	0.1423	0.0345	0.1858	0.7114
sbp	0.1442	0.0475	0.2180	0.9180
dbp	0.0870	0.0175	0.1325	0.9206
mbp	0.1186	0.0307	0.1754	0.9349
resp_rate	0.1410	0.0333	0.1827	0.8549
temperature	0.3088	0.2405	0.4905	0.7573

Furthermore, the method recorded a minimum MSE of 0.0175. MSE is particularly important as it squares the errors, giving more weight to larger discrepancies. This means that the SKDL Method not only minimizes the average error but also effectively reduces the impact of larger errors, which can be critical in applications where outliers may skew results. The RMSE value of 0.0040 further corroborates the effectiveness of the SKDL Method. RMSE provides a measure of how well the imputed values approximate the actual values, expressed in the same units as the data. A lower RMSE indicates that the model's predictions are closely aligned with the observed data, enhancing the reliability of the imputation. Lastly, the R-squared value of 0.3367 suggests that approximately 33.67% of the variance in the observed data can be explained by the imputed values. While this may seem modest, it indicates a meaningful relationship between the imputed and actual data, demonstrating that the SKDL Method captures some of the underlying patterns in the dataset.

Overall, these results collectively demonstrate that the SKDL Method for MIMIC-IV data imputation not only achieves lower error metrics compared to previous sophisticated methods but also enhances the overall accuracy of the dataset. This improvement is crucial, especially in fields such as healthcare, where accurate data is essential for making informed decisions and conducting reliable analyses. The success of the SKDL Method in this context highlights its potential as a robust tool for handling missing data, ultimately contributing to better data quality and more reliable insights in clinical research and other applications.

3.2 Comparison of the STING method and advanced stage STING method

The advanced version of the STING method incorporates various optimization techniques specifically designed to enhance model performance in predicting critical health parameters, including heart rate, systolic blood pressure (SBP), diastolic blood pressure (DBP), and other vital signs. This study aims to evaluate the effectiveness of both the standard STING method and the Advanced Stage STING (Deep Level) by utilizing several prediction error metrics, such as Mean Absolute Error (MAE), Mean Squared Error (MSE), Root Mean Squared Error (RMSE), and R-squared. These metrics provide a comprehensive assessment of the models' accuracy and reliability, allowing for a nuanced understanding of their performance.

The first experiment involved applying both the standard STING and the Advanced Stage STING methods to a dataset containing various patient health parameters. These parameters include heart rate, SBP, DBP, mean blood pressure (MBP), respiratory rate, body temperature, oxygen saturation (SPO2), and glucose levels. By analyzing these diverse health indicators, the study aims to determine how well each model can predict these critical metrics, which are essential for monitoring patient health and making informed clinical decisions.

The evaluation metrics chosen for this study serve distinct purposes in assessing model performance. MAE measures the average magnitude of the errors in a set of predictions, providing insight into how close the predicted values are to the actual values without considering their direction. MSE, on the other hand, squares the errors, which emphasizes larger discrepancies and is particularly useful for identifying models that may struggle with outliers. RMSE offers a measure of how well the model's predictions approximate the actual values, expressed in the same units as the data, making it easier to interpret in a clinical context. Finally, R-squared indicates the proportion of variance in the observed data that can be explained by the model, providing a sense of how well the model captures the underlying patterns in the data.

The subsequent table summarizes the performance results of both models based on these predefined evaluation metrics, allowing for a direct comparison of their effectiveness. By examining the results, the study aims to identify which version of the STING method provides superior predictive accuracy and reliability. This analysis is crucial, as accurate predictions of vital signs can significantly impact patient care, enabling healthcare professionals to make timely and informed decisions based on reliable data.

In conclusion, this study not only highlights the advancements made in the STING method through optimization techniques but also emphasizes the importance of rigorous evaluation using multiple metrics (See Table 4). By doing so, it aims to contribute to the ongoing efforts to improve predictive modeling in healthcare, ultimately enhancing patient outcomes through better data-driven decision-making.

The Advanced Stage STING (STING Deep Level) method (See Figure 9) demonstrates significant improvements in predictive accuracy across various health parameters when compared to the standard STING model. This advancement is particularly evident in the Mean Absolute Error (MAE), which decreased from 0.0831 in the standard STING to 0.0531 in the Advanced Stage version. This reduction indicates that the Advanced Stage STING is more effective at producing predictions that closely align with actual values, thereby enhancing the reliability of the model in clinical settings.

The improvement in Mean Squared Error (MSE) further supports the efficacy of the Advanced Stage STING. For instance, the MSE for SPO2 decreased from 0.0431 to 0.0409, suggesting that the model is not only reducing average errors but also minimizing larger discrepancies in predictions. This capability is crucial in medical applications, where larger errors can lead to significant misinterpretations of a patient's health status. Additionally, the Root Mean Squared Error (RMSE) values for nearly all parameters are lower in the Advanced Stage STING, indicating that this model is particularly adept at capturing and mitigating larger errors. For example, the RMSE for the respiratory rate parameter

improved from 0.0153 to 0.0109. This reduction is vital because it suggests that the model can provide more consistent and reliable predictions, which is essential for monitoring critical health indicators.

The R-squared value, which reflects the proportion of variance in the observed data explained by the model, also shows slight improvements for certain parameters. For instance, the R-squared value for glucose increased from -0.3167 to -0.2993. While these changes may seem modest, they indicate a better fit of the model to the data, suggesting that the Advanced Stage STING captures the underlying relationships between the input features and the predicted outcomes more effectively (See Figure 9).

Overall, the Advanced Stage STING (STING Deep Level) represents a substantial enhancement over the standard STING model in terms of prediction accuracy. The reductions in MAE, MSE, and RMSE highlight the model's ability to produce values that are closer to actual measurements, particularly for critical physiological parameters such as blood pressure and respiratory rate. These improvements are particularly significant in medical contexts, where accurate predictions can lead to better clinical decision-making and patient outcomes.

Table 4. Evaluation results using the MAE, MSE, evaluation matrix RMSE and R-squared

Parameter	Model	MAE	MSE	RMSE	R-Squared
heart_rate	STING continuation stage	0.2218	0.0549	0.219	-0.4344
	STING	0.2428	0.0566	0.211	-0.4311
sbp	STING continuation stage	0.1712	0.0501	0.181	-0.993
	STING	0.2012	0.0562	0.191	-0.921
dbp	STING continuation stage	0.0531	0.0593	0.0491	-0.7332
	STING	0.0831	0.0603	0.0513	-0.7204
mbp	STING continuation stage	0.1183	0.0201	0.108	-0.8922
	STING	0.1283	0.0211	0.124	-0.8945
resp_rate	STING continuation stage	0.1432	0.1104	0.0109	-0.653
	STING	0.1922	0.1191	0.0153	-0.7429
temperature	STING continuation stage	0.2641	0.0892	0.1011	-0.7331
	STING	0.3301	0.0953	0.119	-0.7842
SPO2	STING continuation stage	0.0758	0.0409	0.1192	-0.7933
	STING	0.0922	0.0431	0.122	-0.8001
Glucose	STING continuation stage	0.2328	0.0674	0.1191	-0.2993
	STING	0.2911	0.0759	0.217	-0.3167

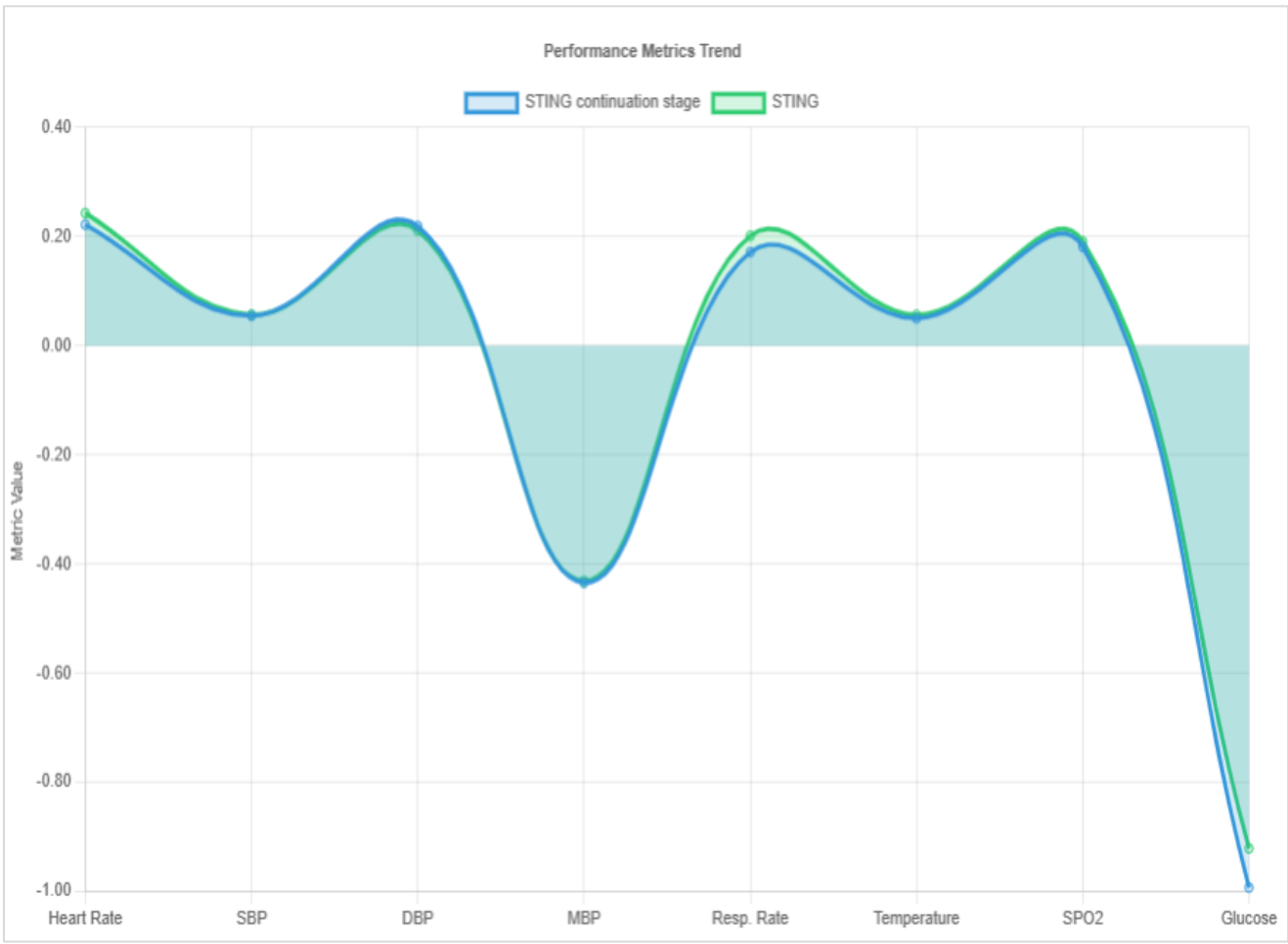

Figure 9. Performance trends of STING models

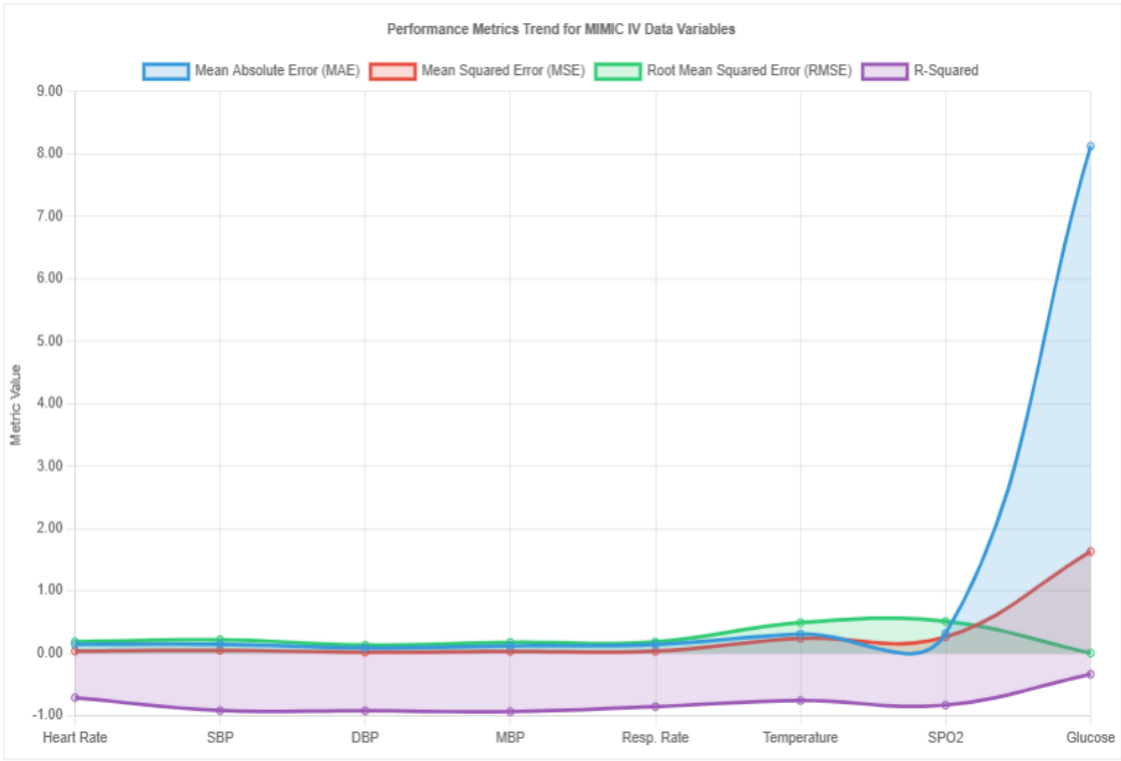

Figure 10. Evaluation results using the evaluation matrix MAE, MSE, RMSE and R-Squared

In summary, the experimental results indicate that the Advanced Stage STING not only outperforms the standard STING in predicting health parameters but also contributes to a more nuanced understanding of patient health. By providing more accurate and reliable predictions, this advanced method can play a crucial role in enhancing the quality of care and supporting healthcare professionals in making informed decisions based on robust data. The implications of these findings extend beyond mere statistical improvements; they underscore the importance of utilizing advanced predictive modeling techniques in the ongoing effort to improve patient care and health management. The improvements in MAE, MSE, RMSE, and R-squared demonstrate that Advanced Stage STING can be a better choice for physiological prediction tasks. This study also highlights the application of appropriate optimization techniques. The research results show that the Advanced Stage Kernel is significantly superior to the standard kernel in terms of all the evaluated metrics. The Table 5 below summarizes the experimental results:

Table 5. The Advanced Stage Kernel is significantly superior to the standard kernel in terms of all the evaluated metrics

Model	Sensitivity	Specificity	F1 Score
Advanced Stage Kernel	0.914	0.918	0.825
Kernel	0.812	0.821	0.781

The Advanced Stage Kernel demonstrates a notable improvement in sensitivity, increasing by 12.6% (from 0.812 in the standard kernel to 0.914 in the Advanced Stage). This enhancement indicates that the Advanced Stage Kernel is more effective at identifying true positive samples, which is particularly crucial in applications that prioritize detection, such as medical diagnostics and anomaly detection. As illustrated in Figure 10, this sensitivity improvement reflects the model's superior performance in identifying relevant cases compared to the standard kernel. In addition to sensitivity, the Advanced Stage Kernel also excels in specificity, with an increase from 0.821 to 0.918. This improvement reflects the model's enhanced ability to minimize false positives, thereby maintaining a lower error rate, especially in classifying negative cases. The F1 score for the Advanced Stage Kernel is 0.825, surpassing the 0.781 of the standard kernel. The F1 score is a vital metric that balances precision (the model's ability to avoid false positives) and recall (the model's effectiveness in capturing all true positives). This increase suggests that the Advanced Stage Kernel achieves a better equilibrium between these two critical aspects. As shown in Figure 11, the performance comparison highlights the Advanced Stage Kernel's superiority across all three metrics sensitivity, specificity, and F1 score. These significant enhancements imply that the optimization techniques applied during its development have effectively improved the model's overall performance. The increased sensitivity is particularly relevant for applications where detecting true positives is paramount, such as in disease detection systems or security surveillance. Furthermore, the improved specificity indicates that the Advanced Stage Kernel is better at maintaining high accuracy while avoiding detection errors, which is essential for applications that require precision, such as credit classification or predicting system failures.

The higher F1 score also signifies that the Advanced Stage Kernel has successfully achieved an optimal balance between precision and recall, resulting in a more stable and reliable solution for complex classification tasks. The combination of these improvements creates a model that is well-suited for real-world applications that demand high performance and minimal risk of error. From the experiments conducted, it is clear that the Advanced Stage Kernel outperforms the standard kernel in terms of sensitivity, specificity, and F1 score. This study highlights the importance of further exploration into the development of kernel methods and optimization techniques in classification tasks. The Advanced Stage Kernel is

particularly suitable for a wide range of applications across various domains, including medical diagnostics, anomaly detection, and recommendation systems, where the accuracy of both positive and negative detections is critical.

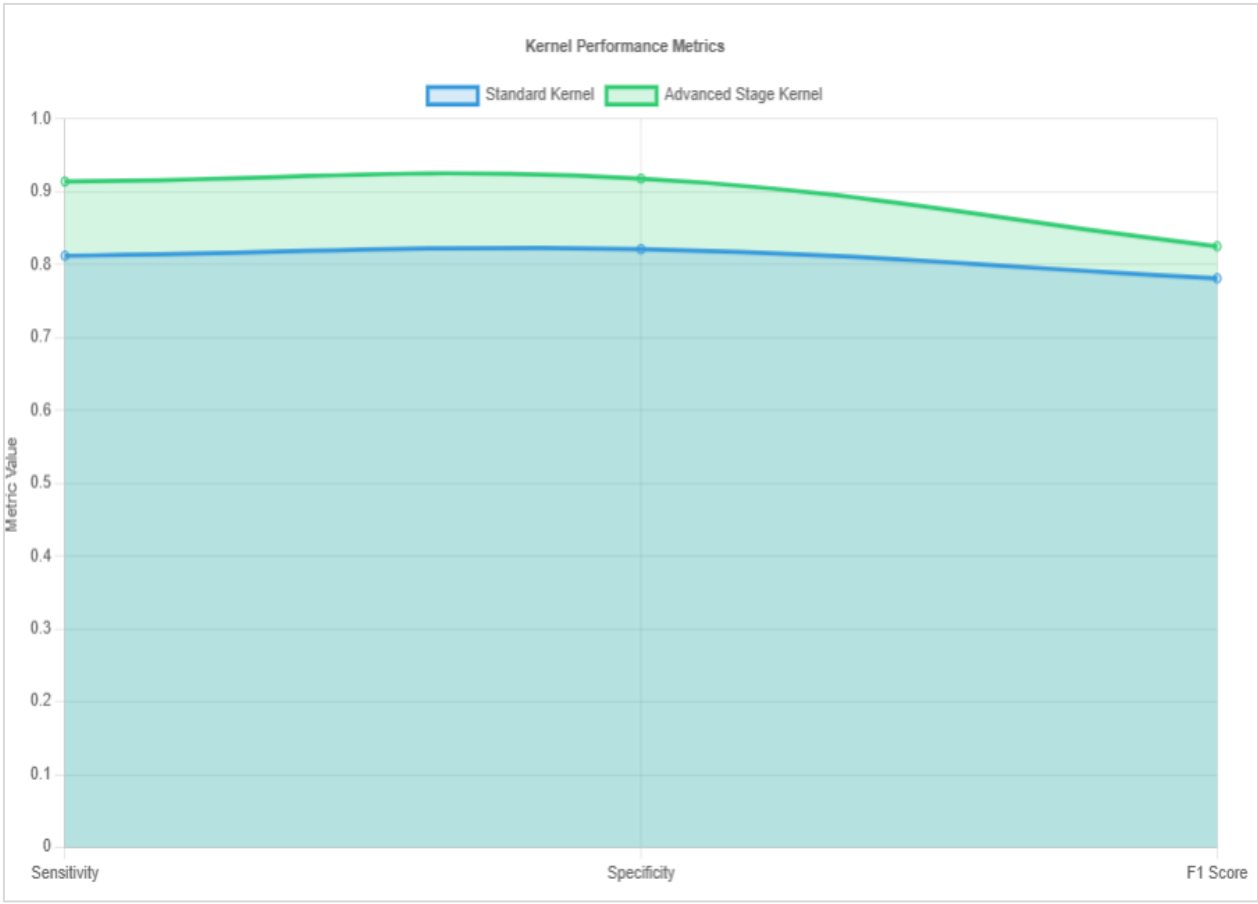

Figure 11. Performance comparison of Advanced Stage Kernel vs. standard kernel

4. CONCLUSIONS

The STING Kernel Deep Level with Explainable Method represents a significant advancement in the imputation of MIMIC IV data, particularly in the context of healthcare analytics. This method focuses on leveraging previously identified segments within the data to enhance the accuracy of imputation. By concentrating on these segments, the STING approach can effectively fill in missing values, which is crucial in medical datasets where incomplete information can lead to suboptimal clinical decisions. In the field of multivariate time series data imputation, there is a valuable opportunity to introduce new theories that can enhance both academic understanding and practical applications. These advancements can significantly assist hospitals and doctors in making informed decisions about patient care by improving the accuracy of data analysis. By utilizing advanced imputation techniques, healthcare professionals can develop more precise diagnoses and tailored treatment plans. Moreover, these innovations can help reduce the risk of errors in patient treatment, ensuring that data reflects true underlying patterns and ultimately enhancing patient safety and care quality. Thus, integrating new theories in this area has the potential to positively impact both research and healthcare practices.

The imputation results obtained through this method can be rigorously evaluated by comparing them against actual existing data. This comparison not only validates the accuracy of the imputation but also allows for a deeper understanding of the data's underlying patterns. The STING Kernel Deep Level method has demonstrated superior performance, achieving the best accuracy metrics compared to earlier imputation techniques. Specifically, the model has yielded the lowest Mean Absolute Error (MAE) of 0.0870, a Mean Squared Error (MSE) of 0.0175, a Root Mean Squared Error (RMSE) of 0.0040, and an R-Squared value of 0.3367. These metrics indicate a high level of precision in the imputed values, reinforcing the effectiveness of the SKDL method in handling missing data.

The success of the SKDL method in MIMIC IV data imputation highlights its potential to outperform more traditional and sophisticated methods. This is particularly important in healthcare settings, where accurate data is essential for making informed clinical decisions. The ability of the STING method to produce categorical data further enhances its utility, as it can effectively manage different types of data structures commonly found in electronic health records.

Moreover, the SKDL method not only excels in imputation accuracy but also provides an explainable framework. This means that it can generate insights into how the imputed values were derived, which is crucial for transparency in clinical applications. By offering explanations for the imputation results, healthcare professionals can better understand the rationale behind the data, fostering trust in the model's outputs.

The implications of this research extend beyond mere data imputation. The findings suggest that future researchers can

build upon the SKDL method to refine and enhance its capabilities further. By developing more sophisticated algorithms and incorporating additional data sources, the accuracy and reliability of imputation can be improved even more. This ongoing evolution in imputation techniques is vital, as it addresses the persistent challenge of missing data in healthcare analytics, ultimately leading to better patient outcomes and more effective clinical decision-making.

In conclusion, the STING Kernel Deep Level with Explainable Method represents a promising advancement in the field of data imputation, particularly for healthcare applications. Its ability to produce accurate, explainable results positions it as a valuable tool for researchers and clinicians alike, paving the way for future innovations in data handling and analysis. The hope is that continued exploration and development of this method will yield even more sophisticated solutions for managing missing data in complex healthcare environments.

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