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Prediction Modeling: Basic Metabolic Panel

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Abstract

Blood test informatics is a field that combines data science, medical informatics, and research to improve management, treatment, and understanding of diseases. This field uses health data, wearable technology, artificial intelligence (AI), and electronic health records (EHRs) to optimize healthcare. EHR informatics focuses on the following: 1) Using AI and data analytics to tailor EHR data management for individuals, 2) Identifying early signs of complications or predicting blood sugar fluctuations, 3) Using continuous glucose monitors (CGMs) and insulin pumps to collect real-time data, 4) Assisting doctors and patients with real-time recommendations. In this paper, we will discuss the basic principles of EHR informatics focusing on assisting doctors and patients with accurate recommendations and data management. We will demonstrate a new prediction method that improves accuracy compared to other forecasting technologies.

Keywords

Artificial Intelligence, Electronic Health Records, Prediction Modeling, Metabolic Panel Prediction

1. Introduction

Predictive modeling in healthcare is the application of statistical, machine learning, or artificial intelligence methods to forecast outcomes based on historical or real-time health data. These models help in anticipating disease progression, readmission risk, treatment outcomes, and more, ultimately improving clinical decision-making and resource allocation.

Key applications include Disease risk prediction using Logistic Regression, Random Forest, Neural Networks, etc. Predictive modeling plays an important role in patient readmission. Hospitals use models to predict if a patient is likely to be readmitted within 30 days of discharge. It helps reduce readmission penalties and improve care plans.

Length of Stay (LOS) estimation focuses on predicting how long a patient will stay in the hospital. It is critical for hospital resource management and treatment response prediction.

Personalized medicine forecasts how a patient might respond to a drug or therapy. It represents an important element in early warning systems based on vital signs, lab results, and clinical notes.

Predictive modeling is often powered by real-time data and deep learning. It is widely used in public health forecasting such as modeling the spread of infectious diseases (e.g., COVID-19), syndromic surveillance and outbreak detection.

Predictive modeling uses the following types of data: Electronic Health Records (EHR), laboratory test results, imaging data (X-ray, CT scans), wearable device data, genomics and biomarkers, social determinants of health.

Over the past decade, the rapid increase in the availability of healthcare data and dramatic advances in machine learning stimulated predictive models, which estimate the probability of some event of interest occurring in a specified time frame in the future. These models have been developed for events such as heart failure, inpatient mortality, and patient deterioration. However, there have been relatively few success stories where these models led to impact on what matters to patients, providers, and healthcare decision makers.

Blood tests are widely utilized in primary care and serve critical roles in diagnosis, prognosis, and treatment [1]. Beyond their clinical functions, qualitative studies have shown that blood tests also play psychosocial roles during consultations. They can offer reassurance, foster empathetic interactions, and validate patients' symptoms [2].

Inflammatory markers, a specific category of blood test, are frequently used to diagnose and monitor infections, autoimmune disorders, and cancers. They are also employed as broad screening tools for patients presenting with nonspecific or unexplained symptoms [3]. While inflammatory markers seldom yield definitive diagnoses, they can provide diagnostic clues.

However, false-positive results may lead to unnecessary follow-up appointments, repeated testing, and referrals [4]. This highlights the importance of a shared understanding between clinicians and patients regarding both the rationale for ordering inflammatory marker tests and the limitations associated with their use.

Shared decision-making—a collaborative approach where clinicians and patients make health decisions together, integrating clinical evidence and patient values—is widely endorsed as a best practice [5]. Although its importance is well recognized, most existing research focuses on treatment decisions rather than diagnostic testing. When diagnostic decision-making is studied, attention is often limited to tests, such as prostate-specific antigen (PSA) for prostate cancer [6].

This study aimed to explore how communication and decision-making occur around the use of inflammatory marker blood tests in primary care. While the concept of shared decision-making provided a framework for our future investigation, we deliberately adopted a broader perspective to encompass the full communication process—from the initial consultation through to the delivery of test results.

Let us discuss major components of the blood test chemistry. Blood urea nitrogen (BUN) test: This test measures the volume of nitrogen in the blood. High levels can be caused by kidney damage or disease, while low levels may be a sign of malnutrition or severe liver damage.

Calcium test: This test measures the levels of calcium in the blood. If testing indicates low levels, this can indicate under-active parathyroid glands, insufficient calcium in the diet, or Vit D insufficiency, and other less common conditions. High levels can indicate conditions including over-active parathyroid glands, excessive Vit D supplementation, kidney problems as well as more concerning causes that usually require further investigation. Proper interpretation of calcium levels often requires testing of other parameters such as total serum protein and albumin.

Chloride test: This test measures the body's chloride levels. An increased level of chloride can indicate dehydration as well as kidney disorders and adrenal gland dysfunction.

Sodium test: Sodium is a mineral that aids nerve impulses and muscle contractions, as well as balancing water levels. Irregularities are a possible indication of dehydration, adrenal gland disorders, corticosteroids, and kidney or liver disorders.

Creatinine test: Creatinine is a chemical waste molecule that is important for creating muscle energy. Increased levels of creatinine can be a sign of kidney dysfunction.

Potassium test: Potassium aids communication between nerves and muscles, regulates the heart and maintains muscle function. Diuretics (a substance or medication used to increase urination) can cause potassium levels to fall.

Blood glucose: A blood glucose test measures the amount of sugar in the blood. It's a standard part of the electrolyte test panel. Blood sugar will vary depending on when you last ate. A normal range for a fasting blood sugar (meaning you haven't eaten for 8 hours) is 99 mg/dL or less. A normal range for a random blood sugar is less than 200 mg/dL.

Anion gap (or serum anion gap) is a measurement to check for how acidic blood is. Too much acid or too little acid in blood can be a sign of certain health conditions.

A carbon dioxide (CO_2) blood test helps healthcare providers determine if the body is balancing electrolytes properly. Results outside the normal range of 20 to 29 millimoles per liter (mmol/L) may point to a more serious issue with the kidneys or lungs. The following Table (**Table 1**) depicts normal values of BMP:

Table 1. Normal values for BMP panel.

BMP element	Normal numbers
Glucose:	74 to 99 mg/dL
Calcium:	8.5 to 10.2 mg/dL
BUN:	7 to 21 mg/dL
Creatinine:	0.58 to 0.96 mg/dL
Sodium:	136 to 144 mmol/L
Potassium:	3.7 to 5.1 mmol/L
Bicarbonate (CO_2):	22 to 30 mmol/L
Chloride:	98 to 107 mmol/L

2. Methods

2.1. Interpolation of Sparse Data

In this section, we will consider a traditional linear interpolation between the recorded data and show that the correlation between the features does not change much proving that unlike extrapolation, the interpolation is a stable process. In the next sections, we will demonstrate 2 methods PM GenAI and CAIHA that are able to make accurate predictions beyond the recorded data. a 73-year-old man complained about hypertension. The blood test was taken. The history of the bmp panel is given below (Table 2):

Table 2. BMP panel.

Glucose	Potassium	Sodium	Chloride	CO_2	Creatinine	AG	BUN	Month
98	4.0	142	106	24	0.84	12	30	1
93	4.3	142	108	25	0.97	9	21	9
99	4.0	141	107	22	1.03	12	17	10
112	3.8	138	105	23	0.95	10	22	19
100	4.3	139	109	21	0.95	9	27	24

Time is measured in months. Figure 1 shows the correlation between features (heatmap). For example, potassium highly correlates with chloride values while CO_2 correlates with sodium.

Figure 2 shows the interpolated data for Chloride (a) and CO_2 (b).

Figure 3 shows the heatmap (correlation between interpolated features). It demonstrates slightly different correlation values compared to original data correlation. This shows that correlation is a stable process.

2.2. Augmentation of Data

Augmented data can be calculated in the form of Gaussian posterior probabilities:

$$p(x) = \sum_{k=1}^{N} \pi_k \left(x_k, \mu, \Sigma_k \right) \tag{1}$$

which is the multivariate normal distribution of the data set x with mean μ and covariance matrix Σ_k. K is the number of Gaussian components and π_k is a coefficient for k-Gaussian distribution:

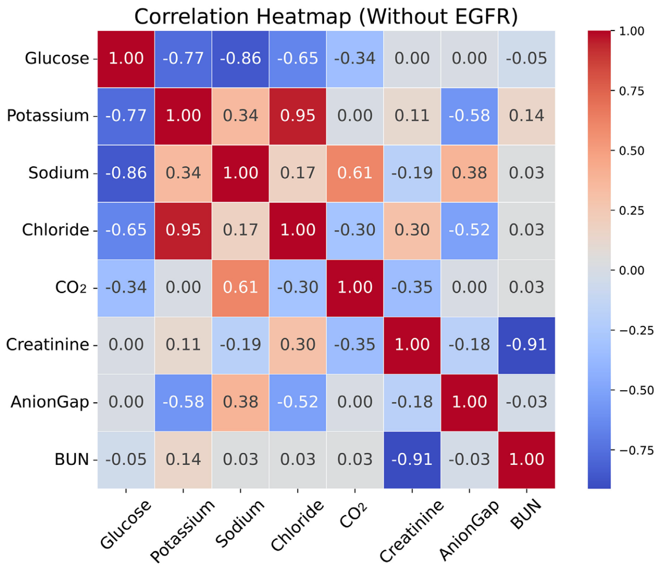
$$\sum_{k=1}^{N}\pi_k = 1$$

The covariance matrix is calculated from:

$$\Sigma_k = \frac{1}{N_k}\sum_{i=1}^{N}\gamma_{ik}\left(x_i - \mu_k\right)\left(x_i - \mu_k\right)^{\mathrm{T}} \tag{2}$$

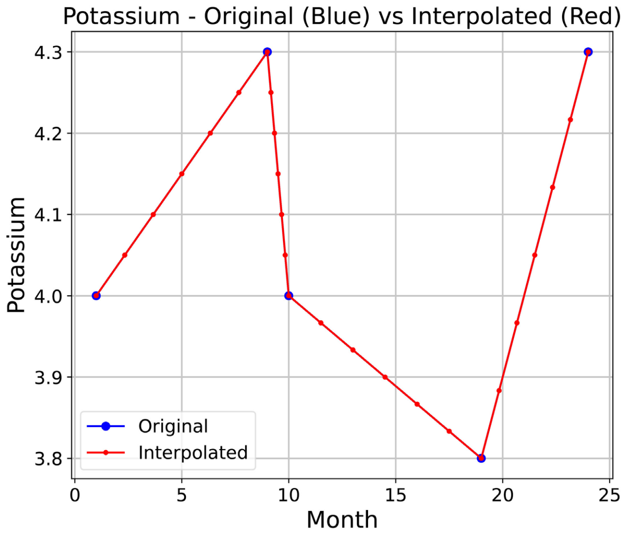
In this formula,

$$N_k = \sum_{i=1}^{N}\gamma_{ik}$$

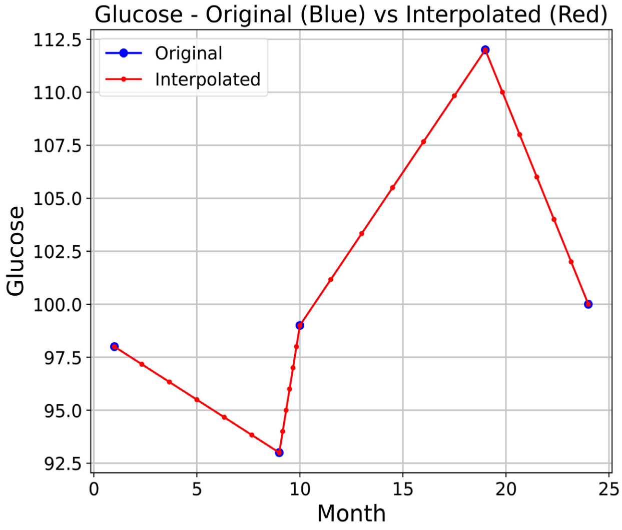

Correlation Heatmap (Without EGFR)

	Glucose	Potassium	Sodium	Chloride	CO2	Creatinine	AnionGap	BUN
Glucose	1.00	-0.77	-0.86	-0.65	-0.34	0.00	0.00	-0.05
Potassium	-0.77	1.00	0.34	0.95	0.00	0.11	-0.58	0.14
Sodium	-0.86	0.34	1.00	0.17	0.61	-0.19	0.38	0.03
Chloride	-0.65	0.95	0.17	1.00	-0.30	0.30	-0.52	0.03
CO2	-0.34	0.00	0.61	-0.30	1.00	-0.35	0.00	0.03
Creatinine	0.00	0.11	-0.19	0.30	-0.35	1.00	-0.18	-0.91
AnionGap	0.00	-0.58	0.38	-0.52	0.00	-0.18	1.00	-0.03
BUN	-0.05	0.14	0.03	0.03	0.03	-0.91	-0.03	1.00

Figure 1. Heatmap (correlation) of features.

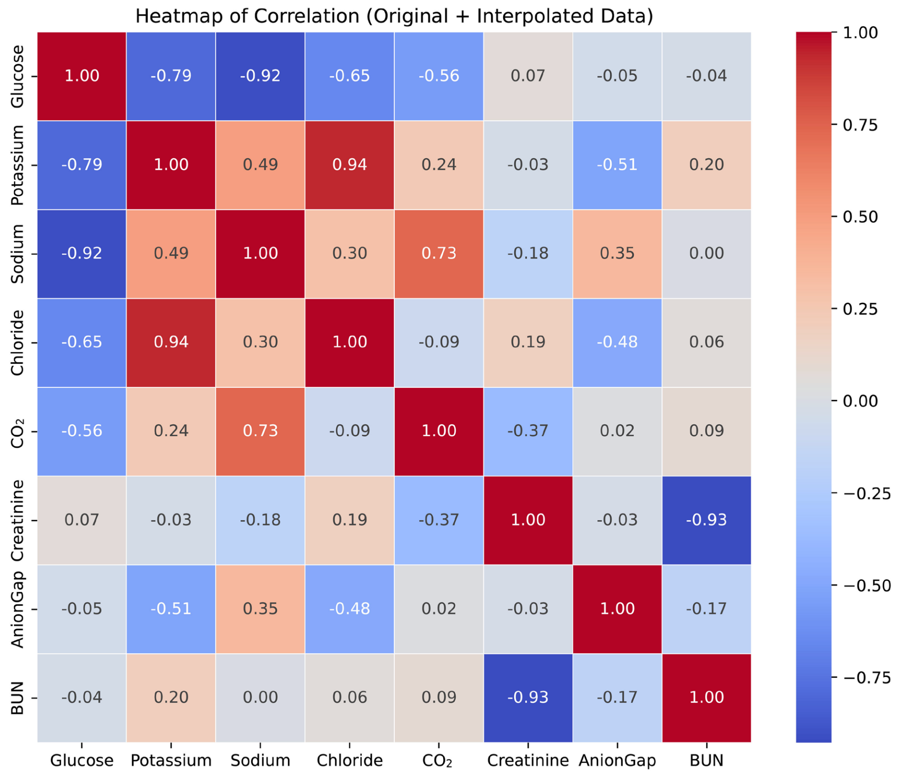

Potassium - Original (Blue) vs Interpolated (Red)

(a)



(b)

Figure 2. Original (blue dots) and interpolated data (red dots). (a) Potassium, (b) Glucose.



	Glucose	Potassium	Sodium	Chloride	CO₂	Creatinine	AnionGap	BUN
Glucose	1.00	-0.79	-0.92	-0.65	-0.56	0.07	-0.05	-0.04
Potassium	-0.79	1.00	0.49	0.94	0.24	-0.03	-0.51	0.20
Sodium	-0.92	0.49	1.00	0.30	0.73	-0.18	0.35	0.00
Chloride	-0.65	0.94	0.30	1.00	-0.09	0.19	-0.48	0.06
CO₂	-0.56	0.24	0.73	-0.09	1.00	-0.37	0.02	0.09
Creatinine	0.07	-0.03	-0.18	0.19	-0.37	1.00	-0.03	-0.93
AnionGap	-0.05	-0.51	0.35	-0.48	0.02	-0.03	1.00	-0.17
BUN	-0.04	0.20	0.00	0.06	0.09	-0.93	-0.17	1.00

Figure 3. Heatmap of the interpolated data.

Figure 4(a) and Figure 4(b) shows the scattered plots of augmented data. Figure 5(a) and Figure 5(b) depicts Gaussian and Gibbs data augmentation. Figure 6 depicts original + interpolated data and augmented data (red)

Let's build now the confidence ellipse. Given a 2D Gaussian distribution of variables $X =$ original chloride and $Y =$ augmented data. The ellipse is defined by:

$$\chi^2 = (x-\mu)^{\mathrm{T}} \Sigma^{-1} (x-\mu) \tag{3}$$

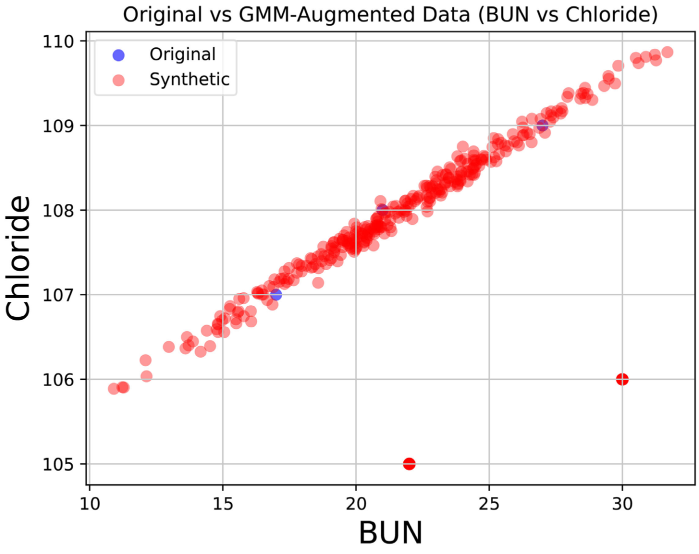
Here $\chi^2 = 5.99$ chi-squared critical value with 2 degrees of freedom.

Σ is the 2×2 covariance matrix between X and Y.

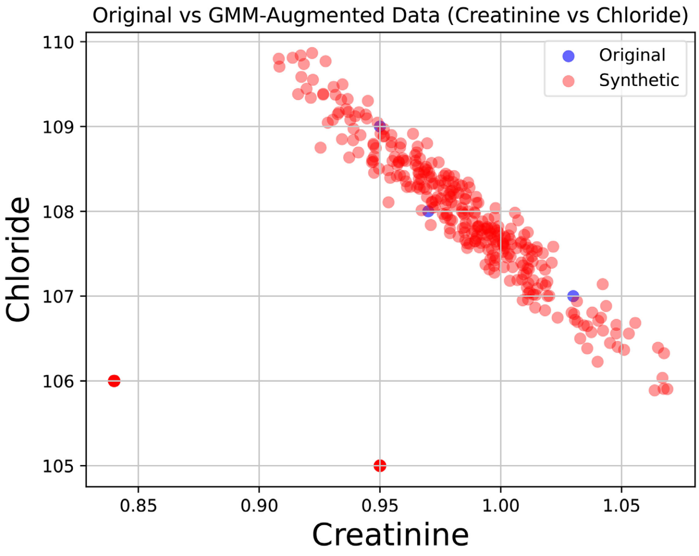
$\mu = (\mu_X, \mu_Y)$ is the mean vector of X and Y.

Figure 5(a) and **Figure 5(b)** illustrates Gaussian and Gibbs augmentation of the recorded data.

Figure 6(a) depicts the confidence ellipse of augmented and original + interpolated data (BUN vs. Chloride) and **Figure 6(b)** Chloride vs. creatinine. **Figure 7** shows the confidence ellipse of augmented and original + interpolated data (BUN vs. creatinine.

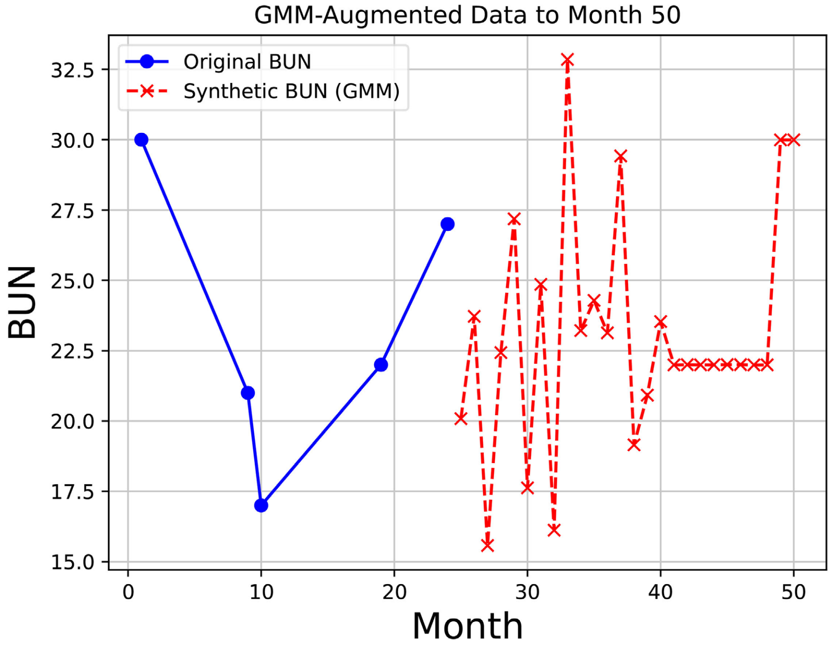


(a)

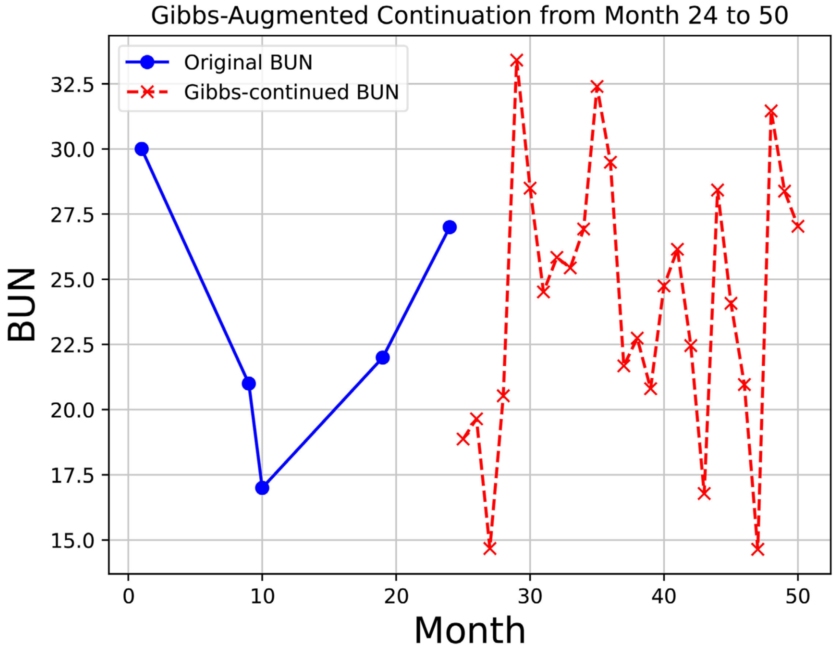


(b)

Figure 4. Gaussian (a) BUN vs. Chloride and (b) Creatinine vs. Chloride data augmentation.



(a)



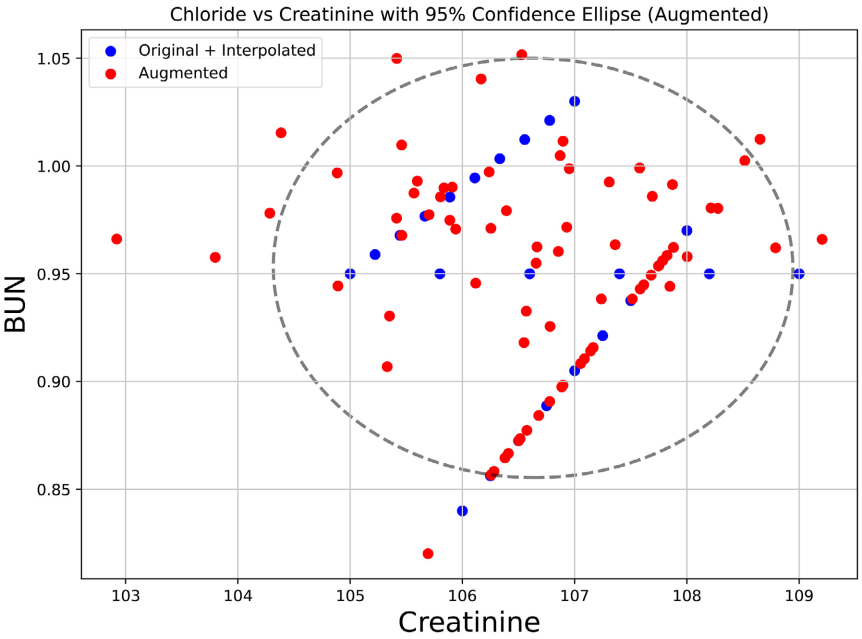
(b)

Figure 5. Gaussian (a) and Gibbs (b) data augmentation.

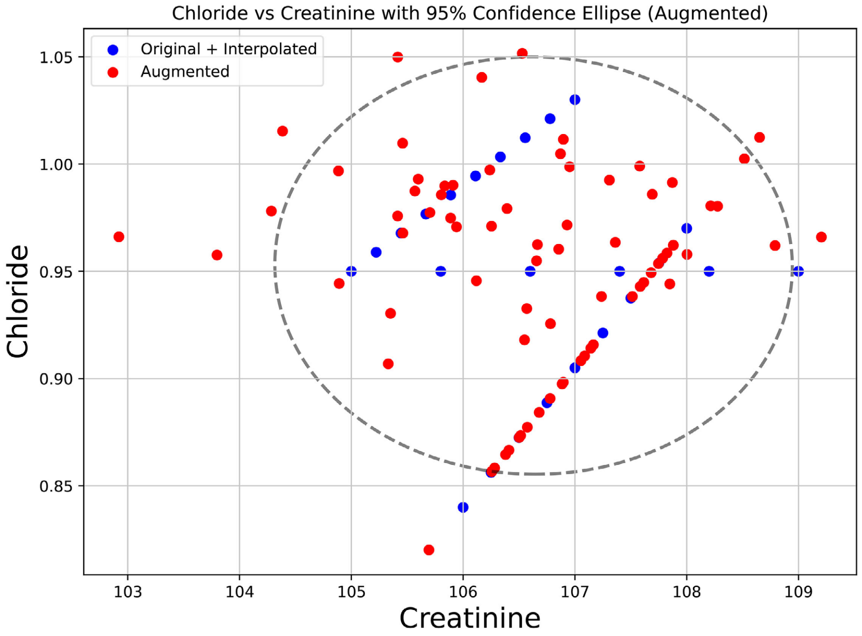
Let us build now the confidence ellipse.

A confidence ellipse is a graphical representation of the uncertainty (or confidence region) around an estimated mean vector in two dimensions. It is often used in statistics, regression analysis, and multivariate analysis to show where the "true" values are likely to fall with a certain probability (e.g., 95%).

Key Ideas:



(a)



(b)

Figure 6. 95% confidence ellipse between original + interpolated and augmented data. (a) Bun-Creatinine and (b) Chloride-Creatinine.

Shape: The ellipse is centered at the sample mean of two features. Axes: The major and minor axes of the ellipse correspond to the eigenvectors of the covariance matrix of the data, and their lengths depend on the eigenvalues (which reflect variance along each direction).

Confidence Level: A 95% confidence ellipse means that if you were to repeat the sampling many times, the true population mean would lie within the ellipse about 95% of the time. **Figure 7** shows the 95% confidence ellipse of creatinine and BUN.

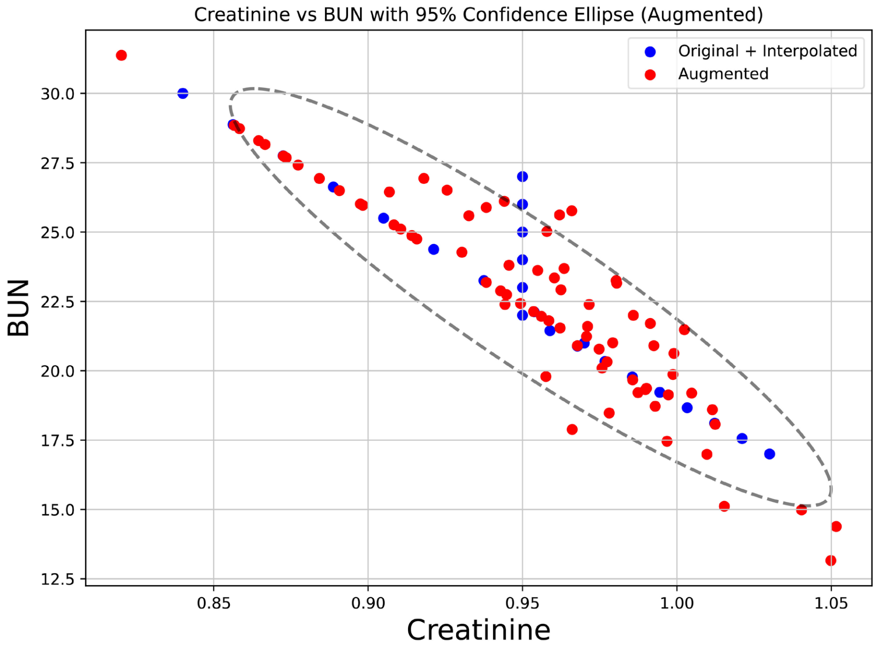


Figure 7. 95% confidence ellipse between original + interpolated and augmented data.

The characteristics of the confidence ellipse are given by:

Size of ellipse	Variance or spread in original/augmented data
Shape	Strength and direction of correlation
Tilted ellipse	Indicates linear correlation (positive/negative)
Circular ellipse	No correlation
Overlap with 45˚ line	High consistency between original and augmented values

2.3. Prediction Algorithms to Forecast the Blood Lab Tests

2.3.1. LSTM Prediction

LSTM (Long Short-Term Memory) is a refined version of Recurrent Neural Networks (RNNs), designed to better handle long-term dependencies by controlling information flow through special structures called gates. The core of LSTM consists of four interacting components:

1) Forget Gate

Controls what portion of the previous cell state c_{t-1} to retain (σ is a sigmoid function).

$$f_t = \sigma\left(W_f x_t + U_f h_{t-1} + b_f\right) \tag{4}$$

2) Input Gate

Controls what new information to write into the cell.

$$i_t = \sigma\left(W_i x_t + U_i h_{t-1} + b_i\right) \tag{5}$$

3) Cell Candidate (New Content)

Proposes new content to be added to the cell state.

$$\tilde{c}_t = \tanh\left(W_c x_t + U_c h_{t-1} + b_c\right) \tag{6}$$

4) Cell State Update combines old state and new candidate using the gates:

$$c_t = f_t \odot c_{t-1} + i_t \odot \tilde{c}_t \tag{7}$$

5) Output Gate decides how much of the cell state to expose:

$$o_t = \sigma\left(W_o x_t + U_o h_{t-1} + b_o\right) \tag{8}$$

LSTM prediction is highly inaccurate and unstable for small data sets. This is why the sparce data were interpolated (Time index 40 corresponds to month 24). Interpolation significantly stabilizes the LSTM algorithm (Figure 8 and Figure 9).

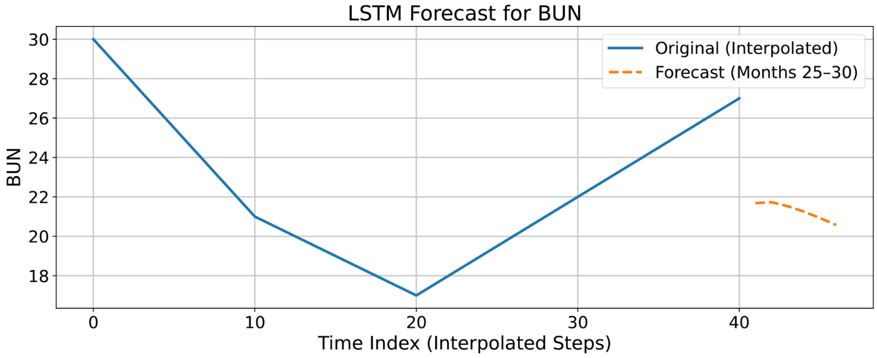


Figure 8. LSTM prediction of BUN (red solid line) for months 25 - 30.

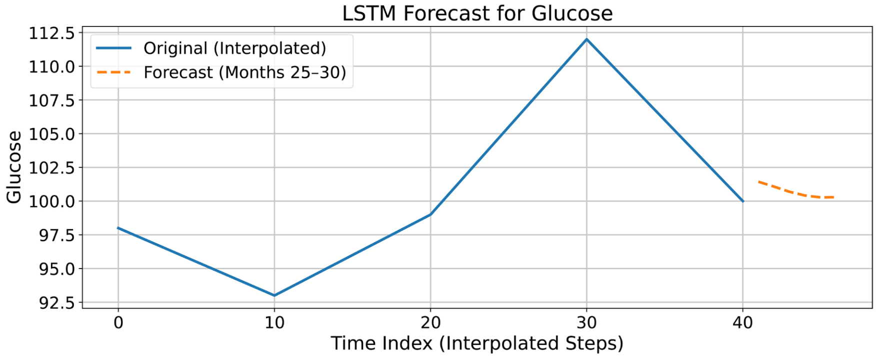


Figure 9. LSTM prediction of Glucose (red solid line) for months 25 - 30.

2.3.2. PM GenAI Prediction

PM GenAI (Principal Model Generative Algorithm) was introduced by Philip de Melo [7] [8].

The method consists of the following steps:

PM GenAI generates new data by sampling from the posterior distribution of the model weights. This allows it to create diverse outputs based on the learned distributions, rather than relying on a fixed, deterministic model.

By modeling uncertainty in the parameters, PM GenAI produces a distribution of outputs instead of a single prediction. This is particularly useful for tasks that benefit from multiple plausible outcomes, such as data generation or decision-making under uncertainty.

Design the neural network architecture and specify prior distributions for the model parameters. Use techniques such as variational inference or Markov Chain Monte Carlo (MCMC) to approximate the posterior distribution of the weights.

Once the posterior is approximated (typically via backpropagation), sample weights from the distribution and perform feedforward passes through the network to generate predictions or synthetic data points that reflect the learned uncertainty. PM GenAI generates data that resembles real data, which is especially valuable in scenarios with limited labeled examples. By incorporating uncertainty, PM GenAI enables models to be more robust to outliers and noise, ultimately improving generalization.

In summary, using Bayesian inference in deep learning for data generation enables the incorporation of uncertainty into models, generate realistic synthetic data, and make more reliable and accurate predictions as expressed in **Figures 10-12**.

To analyze the structure of the original data and predict (such as sharp variations), we use the CWT method (Continuous Wavelet Transform). The Continuous Wavelet Transform transforms a 1D signal into a 2D representation that shows how the frequency content of the data variations changes over time, using wavelets—localized oscillatory functions.

Larger scales capture low frequencies (slow trends) while smaller scales correspond to high frequencies (sharp changes). **Figure 13** and **Figure 14** show CWT of original and predicted values of BUN and Glucose.

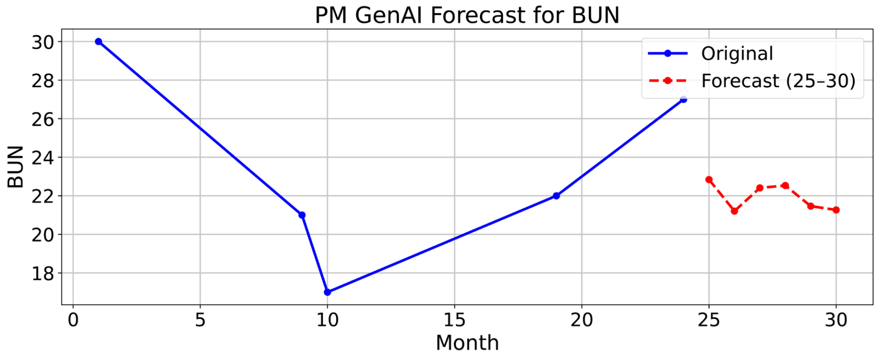


Figure 10. PM GenAI prediction of BUN (red solid line) for months 25 - 30.

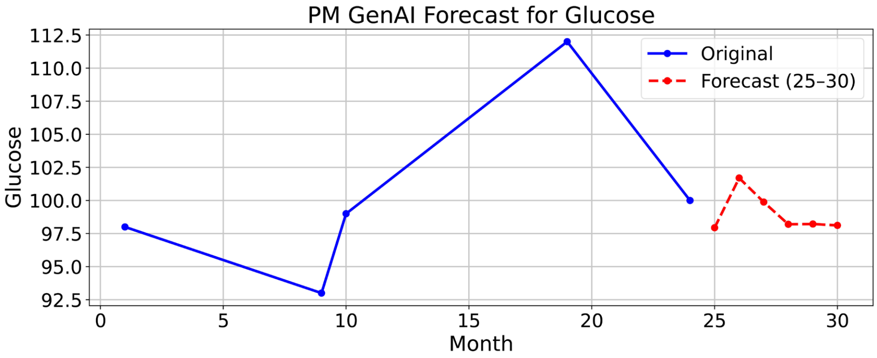


Figure 11. PM GenAI prediction of Glucose (red solid line) for months 25 - 30.

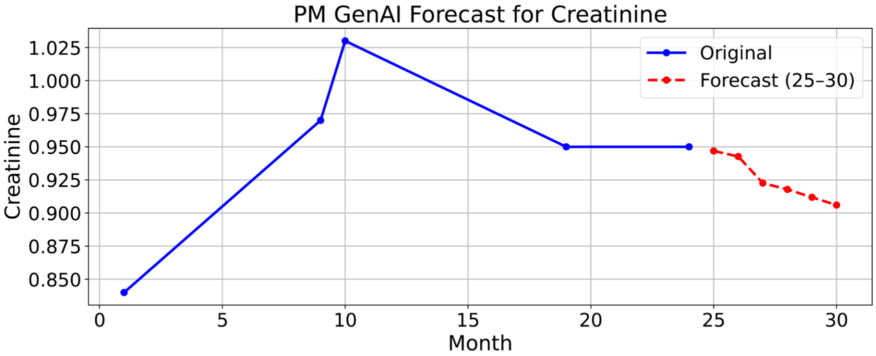


Figure 12. PM GenAI prediction of Creatinine (red solid line) for months 25 - 30.

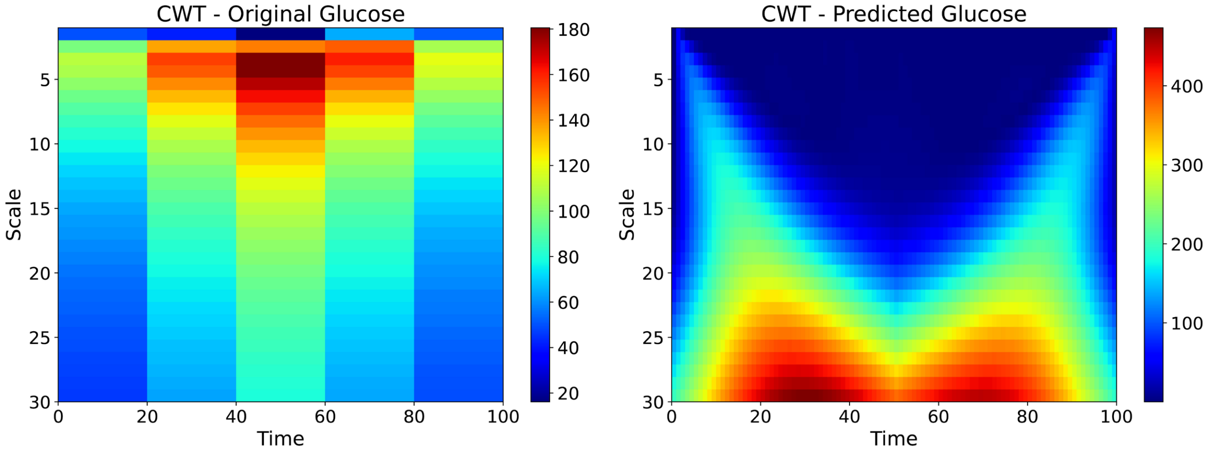


Figure 13. CWT analysis of original and predicted data (Glucose).

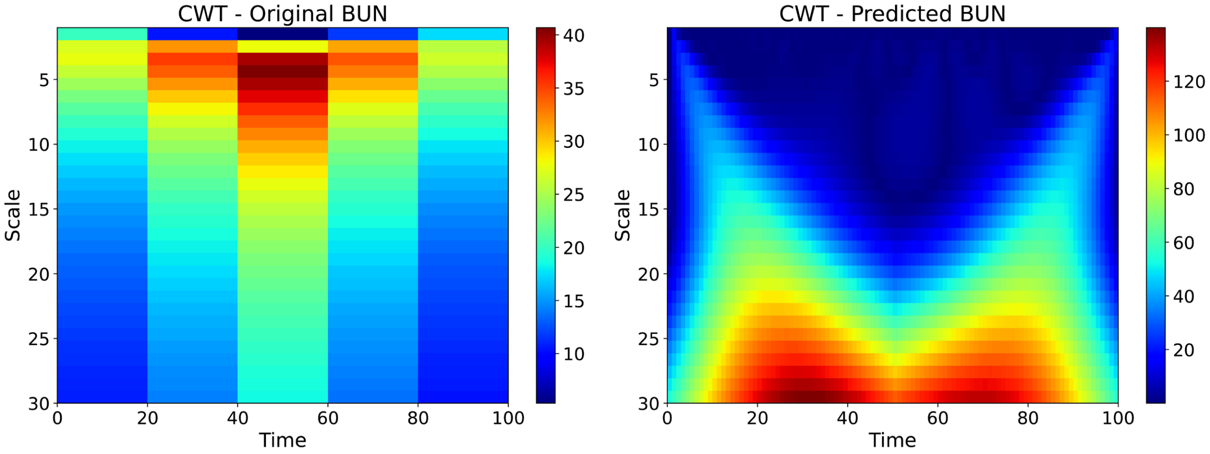


Figure 14. CWT analysis of original and predicted data (BUN).

2.3.3. SAIHA (Self-Adaptive Informed Healthcare Algorithm) Prediction

We will follow now [9] and consider a new algorithm that uses stochastic characteristics of the data to predict values such as vitals, etc. beyond the time of observations. We will consider real data (irregular, sparse, incomplete). [10] considered predicting disease progress with imprecise lab test results. [11] discussed time series prediction with Long Short-Term Memory (LSTM). [12] introduce fuzzy logics in biomedical prediction of time series. [13] demonstrated an advanced machine learning algorithm in diabetes dynamics. [14] used machine learning applied to blood glucose forecasting.

We generate augmented data in effort to identify the most likely predicted value for BUN from 20 to 30. We have chosen the center at 25 (**Figure 15**). Now we can explore other possibilities. **Table 3** shows statistical data of other possibilities with different centers. **Figure 16** shows KDE curves and BUN = 22 was chosen in accordance with **Table 3**.

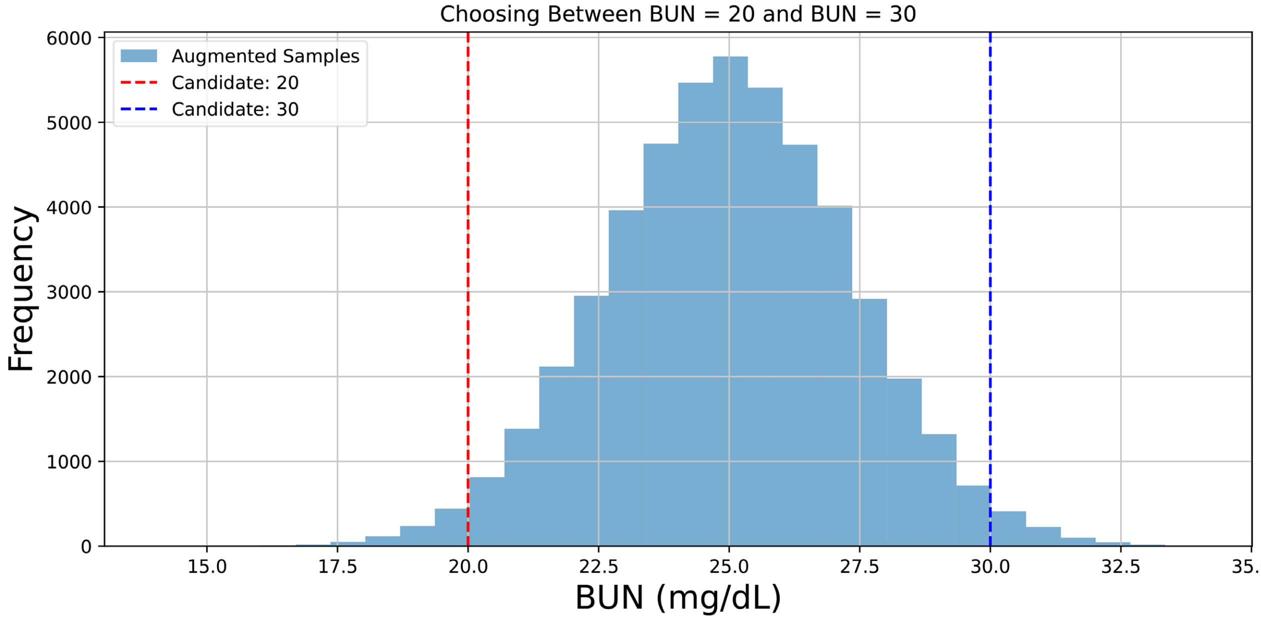


Figure 15. Histogram of augmented data center at BUN=25.

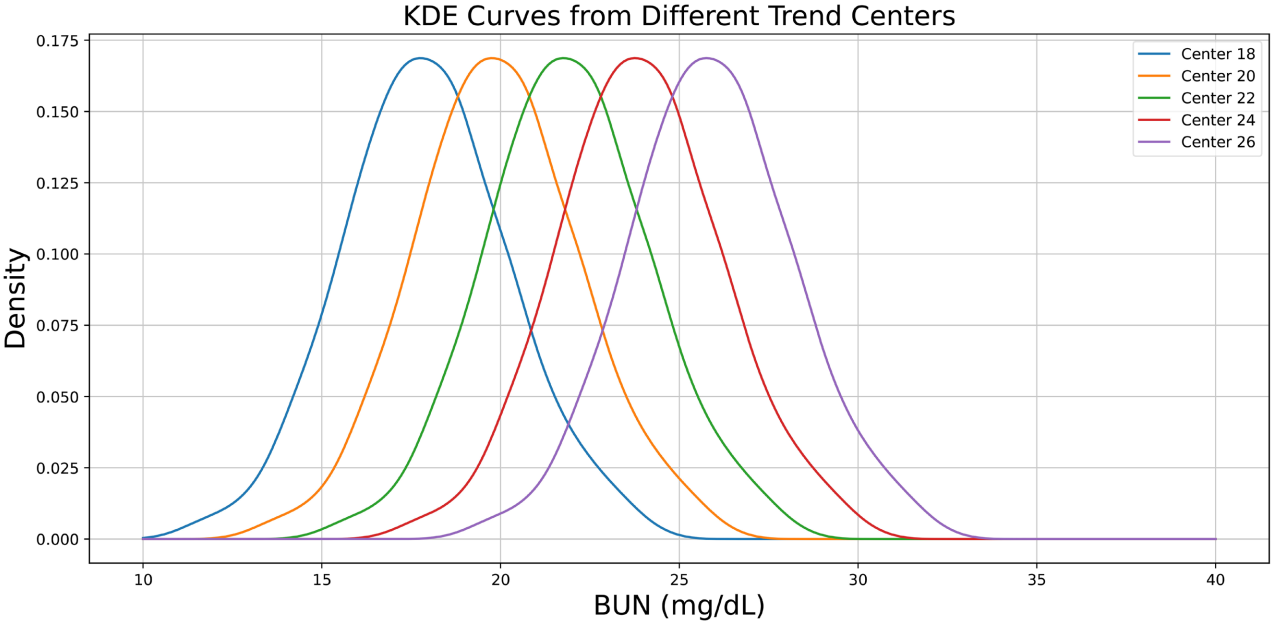


Figure 16. KDE values for different prediction values.

Table 3. Statistical characteristics of augmented data centered around various possibilities.

BUN	Center	Histogram	KDE	LogProb	Score
22	22	166	0.168	−0.99	0.997183
24	24	166	0.168	−1.02	0.996479
20	20	166	0.168	−1.70	0.972535
26	26	166	0.168	−1.76	0.970423
23	24	160	0.160	−0.92	0.967261
21	22	160	0.160	−1.26	0.955290
25	26	160	0.160	−1.30	0.953881
18	18	166	0.169	−3.13	0.922535
23	22	153	0.148	−0.92	0.921718
19	20	160	0.160	−2.32	0.917966

To decide which BUN value to choose, you want the value that best balances:

- Histogram count (frequency among GMM samples).
- KDE density (smooth estimate of likelihood).
- Log probability (true probability under GMM).
- WeightedScore (combined score—higher is better).

From this Table, it is seen that the next BUN value will be 22 which very well approximates the PM GenAI prediction (**Figure 10**).

BUN values 22, 24, 20, and 26 all have the same KDE value (0.168) and identical histogram count (166). However, BUN = 22 was still chosen because of its higher (less negative) log-probability, which leads to the highest weighted score. BUN = 22 served as the initial condition for AI time-series prediction.

The method is called "Self-Adaptive Informed Healthcare Algorithm" because it concurrently uses synthetic data and stochastic property of the recorded data. The method gives a number of solutions, but the choice is based on the maximum of log probability.

3. Results

Predicting laboratory test results is becoming increasingly vital in modern healthcare due to its potential to improve diagnostic accuracy, optimize resource allocation, and support proactive clinical decision-making. As healthcare systems shift toward precision medicine and data-driven strategies, predictive modeling of lab tests—using machine learning, artificial intelligence, and statistical methods—offers transformative advantages across several domains:

Predictive models can forecast abnormal lab values before they manifest clinically. For instance, trends in blood urea nitrogen (BUN), creatinine, or glucose levels can indicate impending kidney dysfunction or diabetes. Early warnings allow clinicians to intervene before the disease progresses, reducing morbidity and associated healthcare costs.

By anticipating which lab results are likely to be within normal limits, predictive algorithms can reduce redundant or low-yield testing. This not only minimizes patient discomfort and financial burden but also alleviates the strain on laboratory resources.

Prediction models can help tailor patient management plans based on expected future values. For example, forecasting a drop in hemoglobin or rise in inflammatory markers can prompt preemptive action such as medication adjustment or further diagnostics, improving patient outcomes.

Integrating lab prediction tools into electronic health record (EHR) systems empowers clinicians with real-time, data-driven insights. This enhances diagnostic accuracy, especially in complex cases where patterns in lab data may not be immediately obvious.

For patients with chronic illnesses (e.g., diabetes, renal failure, or cardiovascular disease), predictive modeling of lab trends supports longitudinal care. Forecasts of future lab values help monitor disease progression, treatment efficacy, and risk of complications.

In virtual care settings, where physical lab access may be limited, predicting lab results allows providers to make informed decisions even in the absence of immediate testing, ensuring continuity and quality of care.

On a broader scale, predictive lab analytics can be used to monitor public health trends, identify emerging disease patterns, and allocate resources effectively. This is especially relevant in epidemic preparedness and management.

Predictive models serve as educational tools for students and medical trainees, helping them understand the interplay between symptoms, disease progression, and laboratory findings.

The ability to predict laboratory test results represents a paradigm shift in clinical medicine—from reactive care to anticipatory care. As computational methods and access to large-scale health data improve, predictive lab testing will become a cornerstone of intelligent, efficient, and patient-centered healthcare delivery.

It is well known that many conventional prediction methods fail to give accurate results [15]. In most existing studies, the algorithm is designed under the implicit assumption that the target value for each sample is the only correct outcome, and the data quality is high (completeness, uncertainty-free, etc.). However, this assumption does not hold for laboratory test data known by irregularities and a lack regular time periods of timestamps between observations.

In this paper, we address the challenge of developing a robust predictive model that accounts for both measurement imprecision, lack of regular temporal information, and data sparsity. We introduce a novel accurate prediction algorithm SAIHA, which assigns probabilistic weight to each value within the defined range of augmented data, reflecting its likelihood of being the true value. The method is controlled by a stochastic controller that defines a range of possible values beyond the historical time of lab data defining the best choice within the imprecision range (**Figure 16**). The difference between SAIHA and PM GenAI is that SAIHA gives accurate results for each individual feature prediction, while PM GenAI is focused on the accuracy of the prediction of the combination of all features.

Experiments conducted on real-world datasets (chemical blood panel) demonstrate that the SAIHA can achieve higher accuracy across various tasks and learning algorithms. Additionally, our approach yields more stable and consistent predictions when test samples originate from within imprecision ranges or exhibit minimal temporal variation.

4. Discussion

4.1. Description

This paper tackles a critical challenge in healthcare analytics: the prediction of Basic Metabolic Panel (BMP) values from sparse and irregular clinical data, which is a common issue in real-world Electronic Health Records (EHRs).

Accurate forecasting of BMP components—such as blood urea nitrogen, creatinine, and electrolytes—is vital for monitoring metabolic function, especially in patients with chronic or acute conditions. However, the sparsity and irregular sampling of clinical lab data hinder the effectiveness of traditional time-series models.

To address this, the study introduces a multi-component methodology consisting of 1) data interpolation, 2) Gaussian Mixture Model (GMM)-based data augmentation, and 3) the development of two novel predictive algorithms: PM GenAI (Predictive Modeling with Generative AI) and SAIHA (Self-Adaptive Informed Healthcare Algorithm).

The interpolation step ensures a more continuous representation of patient data, while the GMM augmentation enriches the dataset with plausible synthetic samples that reflect the underlying statistical distribution of the observed values. This addresses the data sparsity problem and improves the robustness of downstream prediction models.

The core contribution lies in the design and application of PM GenAI and SAIHA. These algorithms are specifically tailored to leverage both real and synthetic data for enhanced predictive performance. PM GenAI integrates generative modeling with feature-aware prediction, while SAIHA introduces a self-adaptive mechanism that dynamically adjusts to the patient's evolving clinical state.

4.2. Limitations

While this study presents a novel and promising methodology for predicting Basic Metabolic Panel (BMP) values using sparse and irregular clinical data, several limitations must be acknowledged:

The methodology was evaluated on a single patient case study. While this allowed for a detailed analysis, it limits the generalizability of the findings. The variability across patient populations, disease profiles, and care pathways may significantly affect the model's performance in broader clinical settings.

The PM GenAI and SAIHA algorithms, while powerful, introduce an additional layer of model complexity that may hinder interpretability for clinicians. Clinical deployment requires transparency and explainability, which remains a challenge for generative and adaptive models.

The proposed methodology has not yet been validated on independent datasets or across multiple healthcare institutions. External validation is necessary to ensure robustness, reproducibility, and applicability in diverse clinical environments.

Conflicts of Interest

The author declares no conflicts of interest regarding the publication of this paper.

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