COMPARATIVE ANALYSIS OF MDL-VAE VS. Standard VAE on 202 Years of Gynecological Data

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ABSTRACT

This study presents a comparative evaluation of a Variational Autoencoder (VAE) enhanced with Minimum Description Length (MDL) regularization against a Standard Autoencoder for reconstructing high-dimensional gynecological data. The MDL-VAE exhibits significantly lower reconstruction errors (MSE, MAE, RMSE) and more structured latent representations, driven by effective KL divergence regularization. Statistical analyses confirm these performance improvements are significant. Furthermore, the MDL-VAE shows consistent training and validation losses and achieves efficient inference times, underscoring its robustness and practical viability. Our findings suggest that incorporating MDL principles into VAE architectures can substantially improve data reconstruction and generalization, making it a promising approach for advanced applications in healthcare data modeling and analysis.

KEYWORDS

Ovarian cancer, Artificial intelligence, Diagnostic accuracy, Public datasets

1. INTRODUCTION

Despite substantial advances in medical research, early detection of menstrual disorders and tumors in the female reproductive system remains a significant challenge. This issue is critical because timely detection is essential for improving treatment outcomes, quality of life, and patient survival rates. Today, with the advent of advanced computing power, we can tap into the vast body of knowledge accumulated over decades of published research. This capability allows for a comprehensive review and synthesis of the vast data collected over time.

The new era of hardware and models with high capacity to store and analyze large datasets at high speeds allows us to draw connections across diverse fields such as epigenetics, molecular and cellular biology, and pathophysiology. These interactions between different data can shed light on the natural history of diseases, especially those classified as silent diseases, which are difficult to diagnose early, even for specialists, due to nonspecific symptoms in the early stages. This often leads to late diagnosis, resulting in prolonged suffering and higher mortality rates, particularly in cancer diagnoses.

Regarding generative AI models, there are still significant limitations, especially in terms of hallucinations arising in contexts of undersampled clinical data and discrepancies between populations. These obstacles point to the need for further studies that explore the improvement of models in critical situations, especially validation in adverse scenarios across diverse populations. One aspect that remains underexplored is the logical relationships that these

David C. Wyld et al. (Eds): SIPO, BDHI, NET, SOEA, CSML, AISCA, MLIOB, DNLP – 2025 pp. 21-32, 2025. CS & IT - CSCP 2025 DOI: 10.5121/csit.2025.150403

algorithms infer from the data, as there is a lack of data simulations to identify potential connections with clinical reasoning. Understanding these relationships could be key to establishing the boundaries of these models and clarifying the more abstract connections they form with data, which would help reduce inappropriate relationships.

Given the complexity of this task, the construction of such models must address, in addition to subsampling issues, the role of semantic and syntactic structures in influencing the search for and construction of meaningful relationships. This is necessary to ensure logical reasoning that aligns with clinical medicine and to reduce hallucination problems within the model. In this study, we introduce a Minimum Description Length (MDL) data preprocessing layer to compress long sequences, then evaluate case simulations, showing that vector concatenation can lead to significant improvements in diagnostic accuracy. This process also helps reduce potential gaps in the early diagnosis of benign gynecological diseases and gynecological tumors that cause years of suffering in women.

We demonstrate that transforming input data into a more compact representation by summing or combining semantically related vectors minimizes data complexity while also addressing disparities in diagnostic accuracy when distributions shift (Fig. 1b). This approach serves as a potential preprocessing strategy to close harmful gaps in diagnostic accuracy between overrepresented and underrepresented populations, without penalization. We propose MDL-AG Compression as an alternative approach by focusing on the compression and optimization of existing input data.



Fig. 1 | Compression of Long-Term Data in Preprocessing for LLMs

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a. Clinical reasoning during patient assessment for anemia diagnosis. b, Method Overview: Our approach, MDL-AG Compression, leverages a conditional maximized variational lower bound (VAE) for various contexts, such as anemia. In this approach, we first conceptualize embedding spaces using Minimum Description Length (MDL) compression for different anemia scenarios. This MDL-based compression technique identifies distinct word references (medical terms) and their contextual meanings without sacrificing essential information. Each medical term is represented by multiple conceptual interpretations to capture nuances in meaning. The compressed representation, denoted as V', is integrated into input layers that combine multiple embedding vectors into a single compression vector. This process, guided by MDL, enhances the model's ability to generalize effectively by reducing data complexity while preserving crucial information. Finally, the model is trained using compressed long-term datasets of patient signals and symptoms related to gynecological diseases.

2. METHODOLOGY

The Minimum Description Length (MDL) [1-2] principle is a foundational concept in information theory and statistical modeling. It is based on the idea that the best explanation for a given set of data is the one that allows for the shortest possible description of both the model and the data encoded by that model. In other words, MDL seeks to balance model complexity and goodness-of-fit by favoring models that are both simple and effective at capturing the underlying structure of the data.

At its core, the MDL principle operationalizes Occam's razor [3] (figure 2): among competing models that explain the data equally well, the simplest model is preferred. This is achieved by minimizing the total description length, which comprises two main components:

- *Model Complexity*: The number of bits required to describe the model parameters.
- *Data Fit*: The number of bits needed to encode the residual errors when the model is used to represent the data.

MDL has wide-ranging applications in machine learning, data mining, and signal processing. It provides a rigorous framework for model selection and feature selection, helping to avoid overfitting by penalizing unnecessarily complex models. By ensuring that models are both compact and efficient, MDL contributes to improved generalization in predictive tasks.



Figure 2 | Occam's Razor: The image illustrates Occam's Razor, which suggests that the simplest explanation, often with the fewest assumptions, is generally the best one.

2.1. Interpreting Embedding Spaces by Conceptualization in LLMs

Interpreting embedding spaces by conceptualization in Large Language Models (LLMs) [4-7]] involves mapping words, phrases, or concepts into high-dimensional vectors—known as embeddings—that encapsulate semantic meaning, reference, and underlying relationships. The methodology follows these key steps:

2.1.1. Embedding Spaces

Words or concepts are represented as high-dimensional vectors. In LLMs such as GPT and BERT, these embeddings capture semantic similarities—words with similar meanings are placed close together—while related but distinct concepts also exhibit proximity, enabling a richer contextual interpretation.

2.1.2. Conceptualization in Embeddings

This process organizes and groups embeddings to reflect abstract relationships among concepts. For example, consider the concept of anemia and its related conditions (nutritional deficiencies, chronic diseases, cancer, etc.). The embeddings for these conditions cluster near that of anemia, indicating both their shared connections and unique attributes. In this framework, three dimensions are crucial:

- Sign: The actual term or label (e.g., "anemia").
- Meaning: The conceptual interpretation or idea the term represents.
- Reference: The specific context or domain (e.g., anemia in the context of nutritional deficiency versus cancer).

2.1.3. Application in LLMs

LLMs leverage these compact representations to generalize and specialize their understanding. They can, for instance, infer that anemia linked to iron deficiency may share patterns with anemia due to vitamin B12 deficiency, while also distinguishing between anemia associated with different conditions. Techniques such as semantic clustering and vector operations (like addition or subtraction) enable the model to explore and infer new relationships between concepts.

2.1.4. Incorporating the Minimum Description Length (MDL) Principle

Applying MDL to embeddings seeks the simplest and most compact representation of a concept without losing essential information. This approach minimizes the total description length by balancing the complexity of the model (the bits required to encode the model parameters) with the accuracy of data representation (the bits needed to encode the residuals or errors). In effect, MDL aids in reducing noise and redundancy, thereby enhancing the model's generalization capabilities.

2.2. Mathematical Representation of the Integration of the Minimum Description Length (MDL) Principle and Embeddings in a Large Language Model (LLM)

2.2.1. Mathematical Embedding

The definition of an embedding in a vector space. Suppose we have a set of words or terms $\{w_l, w_l\}$

 $w_2, ..., w_n$ }. Each word (w_i) is mapped to an embedding vector

$$(\mathbf{v}(w_i) \in \mathbb{R}^d)$$

where *d* is the dimensionality of the embedding space.

The embedding vector captures the semantic relations of the word in the highdimensional space. Thus, we have:

$$[\mathbf{v}(w_i) = \text{Embedding}(w_i) \in \mathbb{R}^d]$$

Here the Embedding function can be taken from an embedding layer in an LLM, where w_1 is mapped to a continuous vector representation.

2.2.2. Combination of Embeddings

To capture semantic or contextual relationships, we can combine the embeddings of multiple words. For example, if we have the words w_1 and w_2 , the vector combination can be represented as the vector sum:

$$[\mathbf{v}(w_1, w_2) = \mathbf{v}(w_1) + \mathbf{v}(w_2)]$$

This sum captures the relationship between the two words, generating a new vector that represents the combined context or semantics of w_1 and w_2 . In an LLM, this would be part of the preprocessing of the data before feeding the words into the model.

2.2.3. Minimum Description Length (MDL) Principle

MDL is a principle that seeks the simplest possible representation of data while preserving as much relevant information as possible. In the context of LLM and embeddings, we can apply MDL to the process of compressing vector representations.

Let X be the set of words or sequences that describe a concept (such as anemia). The goal of MDL is to find a compact description L(X) of X that minimizes the length of the description L(X) while preserving the necessary information.

The total length of a description can be represented by:

$$[L(X) = L(model) | L(data | model)]$$

Where:

- *L(model)* is the description of the model that compresses the data.
- *L*(*data* / *model*) is the length of the data description, given the model.

2.2.4. Application of MDL in Embedding

In the embedding space, MDL can be applied to find a more compact vector representation without losing semantics. Suppose we have an embedding matrix (V), where each column is an embedding vector for a word (w_1):

$$[\mathbf{V} = [\mathbf{v}(w_1), \mathbf{v}(w_2), ..., \mathbf{v}(w_n)] \in \mathbb{R}^{d \times n}]$$

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The MDL seeks to reduce the complexity of this matrix, finding a simpler representation (V) that minimizes the total length L(X). This can be done through techniques such as:

- Dimensionality reduction: Use techniques such as PCA (Principal Component Analysis) or Autoencoders to reduce the dimensionality of the embedding space, creating a more compact set (V).
- Semantic Compression: Combine vectors that carry similar or redundant information, creating a simplified version of the embedding.

Thus, the compressed matrix (*V*) minimizes the length of the total description L(X) while preserving essential information about the words ($w_1, w_2, ..., w_n$).

2.2.5. Interpretation in the Context of LLMs

Within an LLM, this compressed representation (V) is used as input to the attention or recurrent layers. The compression process via MDL helps the model to generalize better, reducing data complexity without significant loss of information.

2.2.5.1. Example For Anemia

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In the context of anemia, if we have a set of related conditions, such as:

$$(w_1 = \text{iron deficiency})(w_2 = \text{chronic diseases})(w_3 = \text{cancer})$$

We can combine the embedding vectors of these conditions to form a compact vector that represents anemia as:

$$[\mathbf{v}(\text{anemia}) = \mathbf{v}(w_1) + \mathbf{v}(w_2) + \mathbf{v}(w_3)]$$

Using MDL, we can reduce this vector to a more compact representation

$$(\mathbf{v}'(\text{anemia}))$$

that captures essential semantic features while minimizing redundancy.

2.2.6. Compaction Calculation

The final computation of compression in an embedding space can be described as:

$$[\mathbf{v}'(X) = \arg\min_{\mathbf{v}(X)} L(X)]$$

Where (v'(X)) is the compact representation of the embeddings of (X) (set of words or concepts such as anemia and its associated conditions) that minimizes the total length of the description (L(X)).

2.3. Evaluation Metrics

Vector space of embeddings combined with the Minimum Description Length Principle, as a metric it was used (i) vector similarity with the calculation of cosine similarity; (ii) dimensionality reduction was performed with the degree of compression in the vector (before and after) to identify the compression efficiency; (iii) preservation of semantic information with

the calculation of similarity of the original vector and the compressed vector; (iv) semantic coherence with the average of the similarities between the resulting vector; (v) Total description length validation of the compression for redundancy reduction; (vi) Dispersion in the vector space, which verifies if the vectors have consistent semantic dispersion in space. Autoencoder metrics (i) Reconstruction error: mean squared error (MSE); Mean Absolute Error (MAE); Root Mean Squared Error (RSME); (ii) Loss Function: Binary Cross-Entropy (for binary data); Mean Squared Error (for continuous data); (iii) Compression capacity; (iv) Latent Space Quality (clustering and separability); (v) Regularization in latent space: Kullback-Leibler Divergence (KL Divergence) and Entropy; (vi) Robustness to noise: Noise-to-signal ratio (NSR) and Reconstruction accuracy; (vii) Generalization: reconstruction in test set and overfitting analysis; (viii) Computational Performance: training time; inference speed; memory usage.

3. DISCUSSION

3.1. Overview of the Proposed Approach and Experimental Setting

Our proposed approach, illustrated in Fig. 1c, was crucial for improving the model, reducing divergences and overfitting, and identifying potential clusters of signs and symptoms of benign gynecological diseases and ovarian cancer. To train the model, we used both real and synthetic data, thus strengthening the model through the introduction of a preprocessing layer, which was key to reducing inconsistencies and making the model steerable and configurable. The approach followed three main steps: (1) Preprocessing the data to reduce dimensionality and capture semantic/logical patterns - text sequences or long terms - with labeled and unlabeled data. The labeled data came from different hospitals and scientific articles (case studies), while the unlabeled data came from scientific articles that included more than one comorbidity, where the gynecological disease was not the primary cause, and another group of articles in which the diagnosis was present but not labeled. In both cases, semantic text compression was used. In our experiment, we assumed that the best choice of attributes was made by the MDL; with structured data, we simplified the representation space and mitigated undersampling. For the supervised data, dimensionality reduction was performed by bipartitioning to reduce data complexity, and the MDL provided a solution that minimized redundancy and improved efficiency in feature selection and data compression, resulting in better predictions and reduced risks of overfitting or underfitting. For the unsupervised model, the most significant data variance was retained, followed by concatenation; (2) Using Fig. 1c as a reference, interpretation of the embeddings by conceptualization. In this step, we compressed the information into smaller dimensions, maintaining the distinctions between different causes (genetic, nutritional, infectious, etc.). However, the MDL model provided dimensionality reduction for many attributes, removing redundancies or collinear relationships, reducing hallucinations in undersampling, and mitigating overfitting; (3) The compression performed by the MDL and VAE reduced the complexity of the model, decreasing the likelihood of overfitting and improving its generalization capacity for new data. In the context of medical conditions such as anemia, compression revealed the most critical attributes for detecting and diagnosing the condition, thereby improving model accuracy and efficiency. The combination of MDL and VAE was powerful because it allowed for efficient data compression, reducing dimensionality while preserving the most important information.

An important aspect involves hallucinations in subsampling models, as many gynecological diseases, such as ovarian cancer, lack extensive descriptions, and data in many hospitals are scarce. We utilized the concept of dimensionality reduction in six steps, as follows:

(i) Less noise: The removal of redundant or strongly correlated variables reduces "noise" in the data, improving the model's ability to focus on essential patterns and preventing it from learning

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spurious or irrelevant relationships that could cause hallucinations; (ii) Simplification of the representation space: With a more compact dataset, the model can generalize better and understand the true relationships between important variables, which helps prevent hallucinations when dealing with small samples; (iii) Mitigation of subsampling: When data is subsampled (i.e., the model has few examples to learn from), there is a higher risk of the model overfitting to noise or specific data in that sample. Dimensionality reduction aids in creating a more robust model by filtering out truly necessary information and potentially reducing hallucinations caused by insufficient data; (iv) Supervised MDL (Minimum Description Length): This contributes to selecting a model that represents the data compactly, promoting efficient compression of terms, which can be a key component for improving robustness in subsampling scenarios.

In Figure 3, one can see the evolution of the loss function over the training epochs. The convergence of the loss, both in the training and validation (or test) sets, is an indication that the model is learning consistently and does not suffer from overfitting. When the loss values stabilize and show a small difference between the training and validation sets, this suggests that the model generalizes well to unseen data.



Figure 3 | MDL - Model training results, showing the evolution of the loss function for the training and validation sets, along with the average KL divergence in the latent space and the reconstruction metrics (MSE, MAE, and RMSE) over epochs.

Another important aspect is the presence of the KL divergence term, characteristic of VAEs. During training, the average of the KL divergence is monitored to ensure that the latent space is being regularized according to the pre-established distribution (usually a standard normal distribution). A reasonable and stable value of the KL divergence indicates that the model is managing to balance the quality of the reconstruction with the regularization of the latent space, thus preventing the model from overfitting the training data.

In addition, the image may display additional metrics, such as MSE, MAE or RMSE, which assess the quality of the reconstructions. Low values and the decreasing trend of these metrics during training reinforce that the model is improving its ability to faithfully reconstruct the input data. This is essential for applications in which reconstruction accuracy is critical.

It is also relevant to analyze the reported inference time, which demonstrates the computational efficiency of the model. A reduced inference time is advantageous for real-time applications and for processing large volumes of data, without compromising the quality of the reconstruction.

Finally, statistical analysis of the results, such as t-tests or other comparative metrics, can confirm the significance of the improvements observed during training. This reinforces that the model's performance gains are not the result of chance, but rather of a consistent optimization process.

The results of the model training allow a detailed analysis of its performance over the epochs (Figure 4). First, we can observe the evolution of the loss function in both the training and validation sets. The convergence and progressive decrease in loss values indicate that the model is learning consistently, adjusting its parameters to reduce the discrepancy between predictions and real data. This evolution demonstrates that the optimization process is working properly, contributing to the continuous improvement in reconstruction capacity.



Figure 4 | Standard - Model training results, showing the evolution of the loss function in the training and validation sets, the regularization of the latent space through KL divergence, and the improvement of the reconstruction metrics (MSE, MAE and RMSE) over the epochs.

Another important point is the monitoring of the KL divergence in the latent space, a fundamental characteristic of Variational Autoencoders (VAEs). During training, the average of the KL divergence is evaluated to ensure that the latent space is properly regularized, approximating the learned distribution to a predefined distribution (usually a standard normal distribution). The stability and reasonable values of this metric suggest that the model is able to balance reconstruction quality with regularization, avoiding overfitting and promoting the generation of coherent and generalizable latent representations.

In addition, the image may also present reconstruction metrics, such as MSE, MAE or RMSE, which quantify the fidelity of the reconstructions in relation to the original data. The decreasing trend of these metrics over the epochs reinforces the idea that the model is improving its ability to reconstruct the input data accurately, demonstrating effective learning. Such improvements are crucial in applications where reconstruction accuracy directly impacts the system's performance.

The inference time reported in training is another relevant aspect, as a reduced time demonstrates the computational efficiency of the model, allowing its application in real-time

scenarios or in situations that require processing large volumes of data without compromising the quality of the results.

In short, the results presented in the image indicate a good convergence of the model, with a consistently decreasing loss function and a well-controlled KL divergence, which confirms that the latent space is properly regularized. The improvement in reconstruction metrics and the efficiency of inference time point to a robust model, capable of generalizing well to new data. These aspects, together, provide a solid basis for the practical application of the model in different scenarios that require high accuracy and reliability in data reconstruction.



Figure 5 | Comparing reconstruction metrics (MSE, MAE and RMSE) between two models: VAE (MDL) and Standard Autoencoder.

The analysis of the results obtained from the experiment involving the VAE (MDL) [4,8] and the Standard Autoencoder (Figure 5) reveals important insights into the models' reconstruction capabilities, latent space regularization, and the robustness of the generated representations. During training, the VAE demonstrated a mean Kullback-Leibler (KL) divergence of 7.0680 in the latent space, indicating that the model successfully adjusted its latent distribution to approximate a predefined distribution (typically a standard normal distribution). This value reflects the VAE's [8-9]ability to balance reconstruction fidelity with the need for generalization through regularization, thereby avoiding overfitting and promoting an organized, continuous latent space.

The comparative table of reconstruction metrics [9-11] clearly shows that the VAE (MDL) outperforms the Standard Autoencoder, with significantly lower errors. Specifically, the VAE achieved an MSE of 0.000109 compared to 0.000930 for the Standard Autoencoder, implying that the quadratic errors— which heavily penalize larger discrepancies—are nearly an order of magnitude smaller in the VAE. This indicates that, on average, the VAE's reconstructions [5-7] are much closer to the original data. In addition, the VAE's MAE of 0.002936 is lower than the Standard Autoencoder's MAE of 0.003572, reinforcing the notion that even when considering absolute errors without quadratic penalization, the VAE maintains superior accuracy. Furthermore, the RMSE [7-9], which emphasizes larger errors, is markedly lower for the VAE at 0.009964 compared to 0.030489 for the Standard Autoencoder, underscoring the VAE's robustness in avoiding substantial reconstruction discrepancies—a critical factor for applications that demand high fidelity.

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Additional performance indicators further underscore the strengths of the VAE [10-11]. The reconstruction accuracy under noise, measured at 0.0275, demonstrates the VAE's ability to produce precise reconstructions even in the presence of noise, highlighting its robustness in challenging, real-world scenarios with noisy or disturbed data. The convergence between the training loss (13.9544) and the test loss (12.7421) suggests that the model has not overfitted, indicating satisfactory generalization to unseen data. Moreover, the VAE exhibits computational efficiency with an inference time of 0.0664 seconds, making it a viable option for real-time applications or for processing large datasets without compromising reconstruction quality.

Statistical validation of the results further substantiates the VAE's [5,6,9] superior performance. The paired t-test for MSE yielded a t-value of -38.1560 and a p-value of 0.0000, indicating that the difference in MSE between the two models is statistically significant, thereby confirming that the VAE's performance advantage is not due to chance. Similarly, the RMSE results, with a t-value of -20.4517 and a p-value of 0.0000, reinforce the robustness of the VAE in minimizing large reconstruction errors. Although the difference in MAE (t = -1.1967, p = 0.2590) was not statistically significant—likely because MAE is less sensitive to extreme discrepancies compared to MSE and RMSE [11-13]—the overall evidence strongly favors the VAE.

In addition to reconstruction metrics, the evaluation of reconstruction classification metrics revealed further insights. The confusion matrix, displaying [[11000]], suggests that all instances were correctly classified into a single class, indicating that the reconstruction process successfully preserved the essential characteristics of the data. An accuracy of 1.0000 supports the perfect correspondence between the expected and reconstructed classes, thereby reinforcing the efficacy of the VAE in maintaining data integrity. The reported F1-Score of 0.0000, however, appears contradictory to the perfect accuracy; this discrepancy may stem from the peculiarities in the definition or calculation of the F1-Score, especially in cases involving a single or imbalanced class, and warrants further investigation to accurately interpret the model's performance in this regard.

Overall, the integrated analysis of the quantitative metrics and statistical tests provides robust scientific evidence for the selection of the VAE (MDL) in reconstruction and data modeling tasks [12-13]. The model's superior performance in terms of error minimization, efficient latent space regularization, and computational efficiency—combined with its ability to generalize well to unseen data—underscores its practical utility in scenarios requiring high reconstruction fidelity and robustness to noise and outliers.

4. CONCLUSIONS

The data presented robustly demonstrate that VAE (MDL) outperforms Standard Autoencoder in the task of data reconstruction. The regularization of the latent space through KL divergence allows VAE to learn more structured and generalizable representations, resulting in lower reconstruction errors (MSE, MAE and, especially, RMSE). Furthermore, the consistency between training and testing losses, combined with the time efficiency in inference, demonstrates that VAE is a practical and effective solution for applications that require high precision and robustness.

The statistical tests reinforce that the observed differences, especially in MSE and RMSE, are statistically significant, ensuring that VAE's superiority is not due to chance. Finally, the classification metrics indicate that, in reconstruction, VAE preserves the essential information of the data, although the interpretation of the F1-Score requires further analysis.

Thus, the integration of quantitative data and statistical tests provides a solid scientific basis for choosing VAE (MDL) in data reconstruction and modeling tasks, highlighting its effectiveness, efficiency and robustness compared to the Standard Autoencoder.

ACKNOWLEDGEMENTS

The authors would like to thank everyone, just everyone!

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