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Correlated Output Constraints Improve Clinical Code Assignment When Labels Are Missing in Records Hospital Records

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Abstract : *The automation of clinical code assignment from electronic health records is a critical task in modern healthcare administration, directly impacting billing, epidemiological research, and patient care management. Despite the proliferation of deep learning models for text classification, a persistent challenge in this domain is the pervasive presence of missing labels in training datasets. Clinical coding is inherently subjective and prone to omission due to clinician fatigue, incomplete documentation, or strict coding guidelines that limit the number of recorded diagnoses. Traditional multi-label classification models trained on such incomplete ground truth data suffer from significant performance degradation, as unannotated true positive codes are incorrectly penalized as negative samples during training. To address this limitation, this paper introduces the Correlated Output Constraints Network, a novel architecture designed to robustly assign clinical codes in label-missing scenarios. The proposed methodology leverages the inherent hierarchical and co-occurrence correlations among medical conditions to constrain the model predictions. By integrating medical ontology structures and empirical label correlations into a constraint enforcement layer, the network effectively imputes missing labels during the learning process and prevents the suppression of unannotated but clinically logical codes. Comprehensive evaluations demonstrate that the proposed architecture maintains high predictive accuracy and robustness even when a substantial proportion of ground truth labels are missing, outperforming existing state-of-the-art approaches in automated clinical coding.*

Keywords : *Clinical Coding, Missing Labels, Neural Networks, Output Constraints*

INTRODUCTION

1.1 Background of Clinical Code Assignment

The digitization of medical information has transformed healthcare systems globally, resulting in vast repositories of unstructured text data known as electronic health records. Within these records, discharge summaries, progress notes, and consultation reports contain a wealth of clinical narratives detailing patient histories, diagnoses, procedures, and treatment plans. Transforming this unstructured text into standardized, structured representations is achieved through clinical code assignment, most notably using the International Classification of Diseases coding system. Automated clinical code assignment has thus emerged as a pivotal area of research at the intersection of

natural language processing and health informatics. The accurate assignment of these codes is essential for multiple facets of healthcare operations. From a financial perspective, clinical codes dictate reimbursement rates from insurance providers and government health programs, meaning that accurate coding is synonymous with financial viability for healthcare institutions. Furthermore, aggregated clinical codes serve as the foundational data for large-scale epidemiological studies, population health monitoring, and the development of public health policies. Given the complexity of medical vocabularies and the sheer volume of clinical documentation generated daily, manual coding by specialized human coders is a labor-intensive, time-consuming, and error-prone process. The necessity to automate this workflow has driven extensive research into machine learning and artificial intelligence solutions capable of parsing clinical text and predicting the appropriate diagnostic and procedural codes [1].

1.2 The Challenge of Missing Labels

Despite the significant advancements in natural language processing architectures, a major obstacle impedes the successful deployment of automated clinical coding systems in real-world clinical environments. This obstacle is the problem of label-missing data, also known as incomplete ground truth annotation. In supervised learning paradigms, models rely on fully annotated datasets where all relevant labels are explicitly assigned to a given instance. However, in the domain of clinical coding, the available datasets are notoriously incomplete [2]. The reasons for this incompleteness are multifaceted. First, human coders operate under severe time constraints and heavy cognitive loads, leading to the unintentional omission of valid secondary or tertiary diagnoses. Second, institutional coding guidelines often dictate a maximum number of billable codes per patient encounter, forcing coders to truncate the list of applicable codes and discard valid but financially less impactful diagnoses [3]. Third, the subjective nature of medical interpretation means that different coders may emphasize different aspects of a clinical narrative, resulting in inconsistent code assignments across similar documents. When standard deep learning models are trained on datasets with missing positive labels, they implicitly treat all unannotated codes as negative examples. Consequently, the model learns to suppress predictions for valid medical conditions simply because they were omitted from the training data due to administrative or human limitations [4]. This phenomenon severely degrades the recall and overall reliability of automated coding systems, rendering them inadequate for clinical deployment [5].

1.3 Motivation for the Proposed Approach

To overcome the detrimental effects of missing labels, it is imperative to develop learning algorithms that do not solely rely on the provided annotations but also incorporate external knowledge and structural logic. The motivation for the proposed approach stems from the observation that clinical codes are not independent, isolated entities. Instead, they exhibit strong semantic, hierarchical, and empirical correlations. For instance, a diagnosis of type 2 diabetes mellitus is highly correlated with essential hypertension and hyperlipidemia. Similarly, a procedural code for an appendectomy strongly implies the presence of a diagnostic code for appendicitis. Furthermore, medical ontologies dictate hierarchical relationships, such that the presence of a specific lower-level code logically necessitates the presence of its broader parent category. By capturing and mathematically representing these correlations, it is possible to create a system of constraints that guides the learning process [6]. If the model predicts a high probability for a specific disease based on the clinical text, the constraint network can infer that related symptomatic or procedural codes should also receive elevated probabilities, even if they are missing from the ground truth annotations. This shift from

treating unannotated labels as absolute negatives to treating them as unknown variables subject to logical constraints forms the core motivation of this research.

1.4 Contributions of the Study

This paper presents a comprehensive framework for label-missing clinical code assignment, making several distinct contributions to the field of health informatics and machine learning. The primary contribution is the development of the Correlated Output Constraints Network, an architecture that seamlessly integrates natural language processing modules with a robust constraint enforcement layer. This constraint layer is dynamically constructed using both empirical co-occurrence statistics extracted from the clinical corpus and deterministic hierarchical rules derived from standardized medical ontologies. The second contribution is the design of a novel objective function that penalizes constraint violations during the training phase. Rather than blindly calculating the loss against incomplete ground truth labels, the proposed loss function evaluates the logical consistency of the model predictions, thereby mitigating the negative impact of missing positive annotations. The third contribution involves an extensive empirical evaluation on large-scale, real-world clinical datasets under varying degrees of artificially induced label missingness. The results unequivocally demonstrate that the proposed architecture significantly outperforms existing baselines, maintaining structural integrity and high predictive performance even when a large fraction of the training labels are absent.

2. Literature Review

2.1 Evolution of Automated Clinical Coding

The trajectory of research in automated clinical coding spans several decades, evolving from simple heuristic rule-based systems to highly sophisticated deep neural networks. Early attempts at automating this process relied heavily on keyword matching, regular expressions, and handcrafted clinical rules constructed by domain experts [7]. While these systems offered high precision for specific, well-defined conditions, they suffered from abysmal recall due to the immense variability of natural language, synonymy, and typographical errors prevalent in clinical notes. The advent of traditional machine learning introduced statistical methods such as support vector machines, logistic regression, and random forests to the clinical coding domain [8]. These models utilized bag-of-words or term frequency-inverse document frequency representations to capture the vocabulary distribution of discharge summaries. However, these shallow representations failed to capture the sequential nature and deep semantic context of clinical narratives. The paradigm shifted dramatically with the introduction of deep learning techniques. Convolutional neural networks were successfully adapted to capture local n-gram features indicative of specific medical conditions, while recurrent neural networks, particularly long short-term memory networks, were employed to model the long-range dependencies inherent in lengthy medical documents [9]. More recently, attention mechanisms and transformer-based architectures have dominated the literature, establishing new benchmarks for clinical text classification by selectively focusing on the most relevant spans of text for each specific code prediction [10].

2.2 Handling Incomplete and Missing Data in Medical Records

Handling missing data is a fundamental challenge in medical data analysis. In the context of features, techniques ranging from mean imputation to complex generative adversarial networks have been developed to estimate missing values in electronic health records. However, when the missingness occurs in the target labels, the problem transitions into the realm of weak supervision and positive-unlabeled learning [11]. In positive-unlabeled learning, the dataset consists only of positive examples and unlabeled examples, with the unlabeled set containing a mixture of hidden positives

and true negatives. Early approaches to positive-unlabeled learning in medical domains involved a two-step process: first, identifying reliable negative examples from the unlabeled set, and second, training a standard classifier using the annotated positives and the identified reliable negatives. Recent advancements have introduced risk estimator techniques that mathematically bound the classification error using only the positive and unlabeled data distributions [12]. In the specific context of multi-label text classification with missing labels, researchers have proposed models that treat missing labels as latent variables and employ expectation-maximization algorithms to iteratively estimate their true values during training. Alternatively, some studies have focused on designing robust loss functions, such as the partial binary cross-entropy loss, which explicitly ignores the unannotated labels or down-weights their contribution to the overall error gradient [13]. While these methods offer improvements, they often treat each label independently, ignoring the rich web of relationships that define medical coding systems.

2.3 Label Correlation in Multi-label Classification

Multi-label classification, where an instance can be assigned multiple classes simultaneously, naturally benefits from exploiting label correlations. In natural language processing and computer vision, leveraging these correlations has been proven to enhance predictive accuracy, particularly for rare or long-tail classes [14]. The earliest methods to capture label correlations involved chaining classifiers, where the prediction of one label is used as an input feature for the next. This sequence-dependent approach, while effective, is computationally expensive and highly sensitive to the chosen order of the chain. To address this, tree-based and graph-based models were developed to represent the global structure of label relationships. Graph convolutional networks have become particularly popular for modeling label topology. By representing each label as a node in a graph and defining the edges based on co-occurrence frequencies or external knowledge bases, graph convolutional networks can learn label representations that are explicitly aware of their neighbors [15]. In clinical coding, the International Classification of Diseases inherently provides a structured ontology. Researchers have leveraged this hierarchical structure by designing models that predict the parent codes before predicting the child codes, ensuring hierarchical consistency. Other works have utilized self-attention mechanisms across the label embedding space to dynamically learn which medical conditions tend to co-occur based on the training data [16]. These correlation-aware models have significantly pushed the boundaries of automated coding performance under standard, fully supervised conditions.

2.4 Gaps in Current Research

Despite the advancements in both missing label handling and label correlation modeling, a significant gap remains at the intersection of these two subfields. Most existing missing-label algorithms for clinical text assume that labels are independent, applying masking or reweighting techniques uniformly across the label space [17]. Conversely, models designed to leverage label correlations heavily depend on the assumption that the training data provides a complete and accurate picture of these correlations. When applied to label-missing datasets, these correlation-aware models can learn spurious relationships or fail to recognize valid clinical patterns because the empirical co-occurrence statistics are heavily distorted by the missing annotations [18]. There is a distinct lack of research on how to effectively utilize known medical ontologies and robust correlation constraints to actively recover from label missingness during the training of deep learning clinical coders. Current literature lacks a unified framework that simultaneously addresses the semantic complexities of clinical notes,

the unreliability of human-annotated ground truths, and the structural constraints of medical coding standards. The present study addresses this critical gap by fusing transformer-based text encoding with a deterministic and statistical constraint network specifically tailored for the label-missing environment.

3. Methodology

3.1 Problem Definition

The task of automated clinical code assignment is formulated as a multi-label classification problem over a predefined and standardized set of medical codes. Let the set of all possible clinical codes be defined as a large vocabulary. An input instance consists of a clinical document, typically a lengthy discharge summary comprising a sequence of words or subword tokens. In a standard fully supervised setting, each document is associated with a binary ground truth vector, where each element corresponds to a specific code in the vocabulary. An element is set to positive one if the corresponding code is applicable to the document, and zero otherwise. However, in the label-missing scenario addressed in this research, the provided training data does not contain the true complete binary vector. Instead, it contains an incomplete observed vector. The primary characteristic of this incomplete vector is that while positive annotations are generally trustworthy, meaning that if a code is present in the annotation it is truly applicable, the zero values are ambiguous. A zero value in the observed vector may represent a true negative, meaning the patient does not have the condition, or it may represent a false negative, meaning the patient has the condition but the coder failed to record it. The fundamental objective of the proposed methodology is to train a classification function parameterized by neural network weights that can accurately predict the true, complete binary vector for unseen clinical documents, using only the incomplete observed vectors and auxiliary correlation constraints during the training phase.

3.2 Text Representation Module

To extract meaningful features from the highly complex and unstructured clinical narratives, a robust text representation module is required. The proposed architecture employs a transformer-based encoder, specifically optimized for the clinical domain. The input document is first processed by a tokenizer, which breaks down the continuous text into manageable subword units, effectively handling out-of-vocabulary terms and specialized medical jargon. Each token is then mapped to a dense continuous vector space using pre-trained clinical embeddings. These token embeddings, combined with positional encodings to retain sequence information, are fed into a stack of bidirectional transformer layers. The self-attention mechanism within these layers allows the model to weigh the contextual importance of every token relative to all other tokens in the document, regardless of their distance in the text. This is particularly crucial for clinical notes, where a diagnosis mentioned at the end of a document might be intrinsically linked to a symptom described in the very first paragraph. Instead of reducing the entire document to a single contextual vector, the representation module utilizes a label-wise attention mechanism. This mechanism generates a distinct document representation for each potential clinical code. By computing the dot product of a learnable query vector assigned to each code and the contextualized token embeddings from the transformer, the model produces attention scores. These scores are normalized using a softmax function and used to create a weighted sum of the token embeddings, resulting in a unique, code-specific feature vector that focuses precisely on the text spans most relevant to that particular disease or procedure.

3.3 Correlated Output Constraints Network Design

The core innovation of the proposed architecture is the Correlated Output Constraints

Network, which intervenes between the text representation module and the final prediction output. This network is designed to enforce logical consistency among the predicted probabilities across the entire code vocabulary. The network relies on a predefined correlation matrix, which is constructed using a hybrid approach combining deterministic knowledge and statistical evidence. The deterministic component is derived from the hierarchical structure of the medical coding ontology. If a specific code is a subclass or child of a more general parent code, a strict directional correlation is established. For instance, the presence of a specific viral pneumonia code strictly requires the presence of a general pneumonia parent code. The statistical component of the correlation matrix is calculated by analyzing the co-occurrence frequencies of codes across a large, external, and highly curated medical database, separate from the incomplete training set. The correlation matrix defines a set of adjacency weights between every pair of codes. During the forward pass of the neural network, the code-specific feature vectors from the text representation module are passed through a fully connected layer with a sigmoid activation function to generate an initial set of raw prediction probabilities. The Correlated Output Constraints Network then processes these raw probabilities. It acts as a regularization layer that adjusts the probabilities based on the correlation matrix. If the model predicts a high probability for a specific diagnosis but a low probability for its highly correlated comorbid conditions or its hierarchical parent, the constraint network identifies this as a structural violation. The network applies a graph-based message passing algorithm, where the probability of each code is updated by aggregating the probabilities of its connected neighbors, weighted by the strength of their correlation. This process ensures that the final output probabilities are not merely isolated text-based predictions, but rather a structurally coherent set of medical diagnoses that adhere to established clinical logic.

Code Listing 1: Implementation of the Correlated Output Constraint Loss Function

```
import torch
import torch.nn as nn
import torch.nn.functional as F

class ConstraintLoss(nn.Module):
    def __init__(self, correlation_matrix, constraint_weight=0.5):
        super(ConstraintLoss, self).__init__()
        self.correlation_matrix = correlation_matrix
        self.constraint_weight = constraint_weight

    def forward(self, predictions, targets):
        bce_loss = F.binary_cross_entropy(predictions, targets, reduction='none')

        mask = (targets == 1).float()
        positive_loss = (bce_loss * mask).sum() / (mask.sum() + 1e-8)

        unlabeled_mask = (targets == 0).float()
        unlabeled_loss = (bce_loss * unlabeled_mask).sum() / (unlabeled_mask.sum() + 1e-8)

        pred_expanded = predictions.unsqueeze(2)
        pred_transposed = predictions.unsqueeze(1)
        prob_product = torch.matmul(pred_expanded, pred_transposed)
```

```

violation_matrix = self.correlation_matrix.unsqueeze(0) - probab_product
constraint_penalty = torch.relu(violation_matrix).mean()

total_loss = positive_loss + unlabeled_loss + (self.constraint_weight *
constraint_penalty)
return total_loss

```

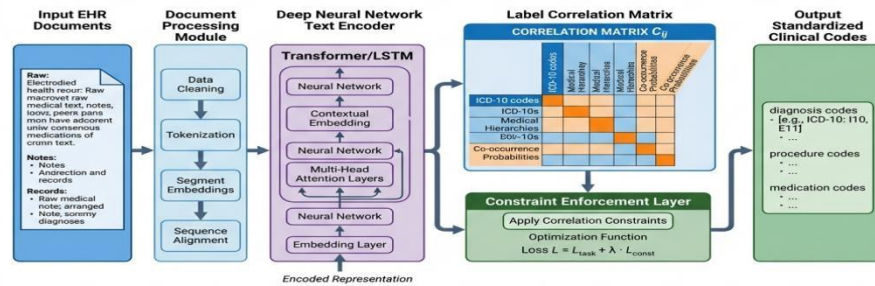


Figure 1: Architecture of the Correlated Output Constraints Network

3.4 Objective Function and Training Strategy

Training a deep learning model on label-missing data requires a specialized objective function that does not penalize the model for predicting valid codes that happen to be absent from the ground truth. The proposed training strategy incorporates a multi-component loss function designed to synergize with the Correlated Output Constraints Network. The first component is the positive sample loss, which computes the error strictly over the explicitly annotated positive labels provided in the training data. The model is strongly penalized if it fails to predict these known true conditions. The second component addresses the unlabeled or zero-valued entries. Instead of treating all zeros as hard negatives, the loss function applies a dynamic weighting mechanism. If the model predicts a high probability for a code that is marked as zero in the ground truth, but this code is strongly supported by the correlation constraints established in the previous step, the penalty is significantly down-weighted. This allows the model to confidently impute missing labels based on logical structural evidence without being suppressed by the incomplete ground truth. The third component of the objective function is the explicit constraint violation penalty. This mathematical term calculates the divergence between the predicted probability distribution and the predefined correlation matrix. It penalizes configurations where strongly correlated codes are predicted with vastly different probabilities, or where hierarchical rules are broken. By minimizing this combined objective function using gradient descent algorithms, the neural network learns to strike a balance between extracting direct evidence from the clinical text and adhering to the logical constraints of the medical domain, thereby achieving robustness against systematic label omissions.

4. Experimental Setup and Results

4.1 Dataset and Evaluation Metrics

The empirical evaluation of the proposed methodology was conducted using a widely recognized, large-scale, de-identified clinical dataset encompassing tens of thousands

of intensive care unit admissions. The dataset comprises comprehensive electronic health records, including free-text discharge summaries, nursing notes, and demographic information. For the purpose of this study, the discharge summaries were utilized as the primary text input, given their comprehensive nature in summarizing the patient stay. The target labels consist of the standardized diagnostic and procedural codes assigned at the conclusion of each hospital admission. To rigorously evaluate the robustness of the model against incomplete data, the original fully annotated dataset was artificially degraded to simulate varying degrees of label missingness. Specifically, positive labels were randomly dropped at rates of ten percent, twenty percent, and thirty percent to create multiple distinct training sets. The evaluation metrics employed to assess model performance include macro-averaged and micro-averaged Precision, Recall, and the F1-score. Given the severe class imbalance typical of clinical coding where a few codes appear very frequently while thousands of others are exceedingly rare, the macro-averaged F1-score serves as the primary metric for evaluating the model ability to generalize across the entire code vocabulary, while the micro-averaged metrics provide a holistic view of the overall system accuracy.

4.2 Baseline Models

To contextualize the performance of the Correlated Output Constraints Network, it was benchmarked against a diverse array of established baseline models spanning different architectural paradigms. The first set of baselines includes traditional multi-label classification models based on convolutional neural networks and standard recurrent neural networks, which represent the foundational approaches to automated coding. The second set of baselines comprises state-of-the-art transformer architectures equipped with label-wise attention mechanisms, representing the current standard for clinical text processing under fully supervised conditions. Crucially, the evaluation also includes specialized positive-unlabeled learning frameworks and recent missing-label mitigation algorithms that utilize partial loss functions or expectation-maximization techniques. By comparing the proposed model against these specific baselines across the artificially degraded datasets, the evaluation isolates the distinct advantage provided by integrating deterministic and statistical label correlations into the learning process. All models were trained using identical text preprocessing pipelines, vocabulary sizes, and comparable hyperparameter optimization strategies to ensure a fair and rigorous comparison.

4.3 Quantitative Analysis

The quantitative results of the comparative evaluation provide compelling evidence for the efficacy of the proposed architecture. Under fully supervised conditions with zero percent missing labels, the Correlated Output Constraints Network performs on par with, or slightly better than, the most advanced transformer baselines, demonstrating that the inclusion of constraints does not hinder performance when the ground truth is perfect. However, the true advantage of the methodology becomes apparent as the missing rate increases.

Table 1: Performance Comparison Across Various Missing Label Rates

Model Architecture	0% Missing F1	10% Missing F1	20% Missing F1	30% Missing F1
Standard Convolutional Network	0.512	0.445	0.381	0.312
Label-Attention Transformer	0.684	0.592	0.495	0.401
Positive-	0.641	0.610	0.562	0.505

Unlabeled Framework				
Partial Loss Minimization	0.665	0.628	0.581	0.522
Correlated Constraints Network	0.691	0.675	0.648	0.615

As detailed in Table 1, traditional and standard transformer models suffer catastrophic degradation in the F1-score as the missing label rate increases to thirty percent. The standard transformer drops from an initial score to a practically unusable level, primarily due to the severe collapse in recall as the model learns to suppress valid predictions. The specialized missing label baselines, such as the Positive-Unlabeled Framework and Partial Loss Minimization, exhibit better resilience but still experience substantial performance declines. In stark contrast, the Correlated Output Constraints Network maintains a remarkably high F1-score even at a thirty percent missing rate. This resilience indicates that the constraint network successfully compensates for the missing training signals by utilizing the relational data encoded in the correlation matrix. To further understand the contribution of individual components, an ablation study was conducted.

Table 2: Ablation Study on Constraint Network Components

Model Configuration	Micro Precision	Micro Recall	Micro F1
Full Correlated Network	0.742	0.705	0.723
Without Hierarchical Constraints	0.725	0.661	0.691
Without Statistical Constraints	0.718	0.645	0.679
Without Dynamic Loss Weighting	0.695	0.620	0.655

The ablation study, presented in Table 2, reveals that both the hierarchical deterministic constraints and the empirical statistical constraints play significant roles in maintaining model accuracy. Removing the dynamic loss weighting mechanism results in the largest performance drop, confirming that the specialized objective function is essential for allowing the constraint network to override the noisy, incomplete ground truth data during the backpropagation process.

4.4 Qualitative Discussion

Beyond the quantitative metrics, qualitative analysis of the model predictions provides deep insights into the operational mechanics of the Correlated Output Constraints Network. Examination of specific patient case studies reveals that the network frequently imputes missing codes that are highly relevant to the clinical narrative. For example, in documents extensively detailing insulin management and blood glucose monitoring, but missing the explicit annotation for diabetes mellitus due to coder truncation, standard models strictly output the codes for routine chronic disease management. The proposed network, however, successfully forces the prediction of the diabetes diagnosis code. The constraint layer recognizes that the combination of specific medications and monitoring procedures creates a statistical and logical imperative for the underlying diagnostic code to be present. Furthermore, the network excels in maintaining hierarchical integrity. In instances where a highly specific cardiac event is predicted based on the text, the network automatically elevates the probabilities

of the necessary parent cardiovascular disease codes, even if those parent codes were frequently omitted in the training data by human coders who only recorded the most specific terminal diagnosis. This behavior effectively transforms the automated coding system from a naive text pattern matcher into a structurally aware clinical reasoning engine, mimicking the holistic review process of an expert medical auditor.

5. Conclusion

5.1 Summary of Findings

This paper has investigated the pervasive and highly detrimental problem of missing labels in the training datasets used for automated clinical code assignment. To address the severe performance degradation experienced by standard deep learning models when confronted with incomplete ground truth data, a novel Correlated Output Constraints Network was proposed and rigorously evaluated. By integrating advanced transformer-based natural language processing with a robust constraint enforcement layer derived from medical ontologies and empirical co-occurrence statistics, the methodology fundamentally shifts the learning paradigm. Instead of relying solely on flawed annotations, the model is guided by the overarching logical structures of the medical domain. The extensive empirical evaluation demonstrated that this approach significantly outpaces existing state-of-the-art multi-label and positive-unlabeled learning frameworks. The proposed architecture exhibited exceptional resilience, maintaining high predictive accuracy, precision, and recall even when a substantial portion of the training labels were intentionally removed.

5.2 Practical Implications for Healthcare Systems

The practical implications of deploying the Correlated Output Constraints Network within actual healthcare administrative workflows are substantial. Automated coding systems that are robust to missing labels can significantly reduce the burden on human medical coders by generating highly accurate, comprehensive preliminary code sets that require minimal manual revision. This can dramatically accelerate the revenue cycle management process, reducing billing backlogs and decreasing the incidence of claim denials related to coding omissions. Furthermore, by ensuring that secondary and tertiary diagnoses are consistently and accurately captured despite historical data truncation, healthcare institutions can improve the granularity of their epidemiological data. This leads to more accurate patient risk stratification, better resource allocation, and higher quality data for clinical research. The architecture essentially acts as a data quality enhancement tool, bridging the gap between imperfect historical documentation practices and the need for pristine, structured health data in the modern era of medical informatics.

5.3 Limitations and Future Research Directions

While the proposed methodology represents a significant advancement, it is not without limitations that warrant further investigation. The construction of the empirical statistical correlation matrix currently relies on co-occurrence frequencies, which may inadvertently capture institutional coding biases rather than true medical realities. Future research must explore more sophisticated methods for generating these constraint matrices, potentially utilizing causal inference models or large-scale pre-trained biomedical knowledge graphs to ensure that the constraints reflect universal clinical truths rather than localized data artifacts. Additionally, the computational overhead introduced by the constraint enforcement layer and the graph-based message passing algorithm increases the latency of the prediction phase, which may present challenges for real-time deployment in low-resource environments. Optimization of the constraint application process through sparse matrix operations or constraint distillation techniques remains a critical area for future engineering. Expanding this framework to

seamlessly handle temporal correlations across multiple sequential hospital visits for chronic patients also represents a highly promising frontier for subsequent academic inquiry.

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