Probabilistic Graphical Models (EN.625.692.81.SP24)

Tram Ngo

Enhancing Healthcare Delivery through Predictive Modeling of Hospital Readmission Rates Using Markov Random Fields

Abstract

Hospital readmissions are a critical indicator of healthcare quality and a significant concern for healthcare systems worldwide, often leading to increased healthcare costs and adverse patient outcomes. This paper developed a predictive model using Markov Random Fields (MRFs) to analyze and predict hospital readmission rates. The MRF model was compared to traditional predictive models, such as the Gradient Boosting Classifier, and demonstrated competitive performance with an accuracy of 60%, precision of 60%, recall of 100%, and F1-score of 75%. The MRF model's ability to capture dependencies and interactions between patient features provided valuable insights into the factors influencing readmission risk, including age, time in hospital, number of lab procedures, number of medications, number of inpatient visits, diagnoses, and the total number of diagnoses. The interpretability of the MRF model enables healthcare providers to identify key factors contributing to readmission risk, facilitating targeted interventions and personalized care planning. This innovative approach not only seeks to enhance healthcare delivery by reducing unnecessary readmissions but also contributes to the broader field of healthcare analytics by demonstrating the utility of MRFs in handling complex, multidimensional data.

Contents

1 Literature Review

Hospital readmissions have been extensively studied, with predictive models being developed to identify risk factors and predict the likelihood of readmission. Kansagara et al. (2011) provide a systematic review of existing models, highlighting the varied methodologies and diverse set of predictors used across studies. The review emphasizes the complexity of readmission phenomena and the challenges in developing universally effective predictive tools [1]. While this work provides a comprehensive overview of the field, it also underscores the need for more sophisticated modeling approaches that can capture the intricate dependencies and interactions among readmission risk factors.

Hasan et al. (2010) present a prediction model for hospital readmissions among general medicine patients, incorporating a wide range of clinical and demographic factors. Their work demonstrates the potential of using patient-specific data to predict readmissions, although it also points to the need for models that can account for the broader context of patient care and post-discharge environment [2]. My proposed approach using Markov Random Fields (MRFs) aims to address this limitation by modeling the complex spatial and temporal dependencies among various data elements, enabling a more holistic view of the factors influencing readmissions.

The role of comprehensive discharge summaries in preventing readmissions is crucial. Kind and Smith (2008) discuss the critical components of discharge summaries and their significance in ensuring continuity of care, which is directly linked to lower readmission rates. Their findings suggest that the completeness and quality of information transferred during the discharge process play a pivotal role in subsequent patient outcomes [3]. This highlights the importance of integrating detailed discharge data into predictive models for readmissions. My approach leverages the expressive power of MRFs to incorporate rich, qualitative data from discharge summaries, potentially improving model accuracy and interpretability.

Markov Random Fields (MRFs) offer a robust framework for modeling complex dependencies in data. Li (2009) provides an in-depth exploration of MRF modeling in image analysis, demonstrating how MRFs can capture spatial relationships and dependencies between image elements [4]. Zheng et al. (2017) apply MRFs in the context of genetics, illustrating the model's ability to uncover interactions between genes and their association with diseases [5]. These works lay the mathematical groundwork for applying MRFs to healthcare data, where similar spatial and temporal dependencies exist. However, the application of MRFs to hospital readmission prediction remains largely unexplored. My research project aims to bridge this gap by adapting MRF techniques to the unique challenges and data structures found in the readmission context.

By leveraging the expressive power of MRFs and integrating rich, qualitative data from discharge summaries, my approach has the potential to address the limitations of existing readmis-

sion prediction models. The proposed model can capture the complex dependencies among risk factors, account for the broader context of patient care, and incorporate detailed information from the discharge process. This holistic approach may lead to more accurate and interpretable predictions, ultimately informing targeted interventions to reduce readmission rates and improve patient outcomes.

2 Theoretical Background

Markov Random Fields (MRFs) are probabilistic graphical models that have found widespread application in various domains, including computer vision, natural language processing, and healthcare [6, 4]. These models are particularly useful for representing complex dependencies among random variables in a compact and interpretable manner. MRFs are undirected graphical models that define a joint probability distribution over a set of random variables, making them well-suited for tasks involving structured prediction and inference [7].

The mathematical foundation of MRFs lies in the theory of undirected graphs and the Hammersley-Clifford theorem [8]. An MRF is defined as an undirected graph $G = (V, E)$, where V represents the set of nodes (vertices) corresponding to random variables, and E represents the set of edges capturing the dependencies between these variables. Each node $i \in V$ is associated with a random variable X_i, which can take values from a discrete or continuous domain. The edges in the graph encode the local dependencies between the random variables, such that if two nodes i and j are connected by an edge, then the corresponding random variables X_i and X_j are dependent.

The joint probability distribution $P(X)$ over the random variables $X = X_1, X_2, \ldots, X_n$ in an MRF is defined using the concept of potential functions and the Hammersley-Clifford theorem. This theorem states that the joint probability distribution $P(X)$ can be factorized into a product of potential functions $\psi_c(X_c)$ over the maximal cliques $c \in C$ of the graph:

$$P(X) = \frac{1}{Z} \prod_{c \in C} \psi_c(X_c) \tag{1}$$

where Z is the normalization constant, also known as the partition function, which ensures that the probabilities sum up to 1. The potential functions $\psi_c(X_c)$ capture the compatibility between the random variables in each maximal clique c. These functions are often defined as exponential functions of feature functions $f_c(X_c)$:

$$\psi_c(X_c) = \exp\left(\sum_k w_k \cdot f_k(X_c)\right) \tag{2}$$

where w_k are the weights associated with each feature function f_k.
In the context of the provided dataset, the random variables X_i represent patient records, each associated with a set of features such as race, gender, age, admission type, diagnoses, medications, and lab results. The MRF graph structure captures the dependencies between these features, allowing for the modeling of complex relationships that may exist in the data. For example, certain diagnoses may be more strongly associated with specific medications or lab results, and these dependencies can be represented by edges in the graph.

3 Problem Formulation

Let $\mathcal{X} = X_1, X_2, \ldots, X_N$ denote the set of patient records, where each X_i represents a patient's features, such as age, gender, diagnoses, medications, and lab results. The goal is to predict the binary readmission status $Y_i \in 0, 1$ for each patient X_i, where $Y_i = 1$ indicates readmission and $Y_i = 0$ indicates no readmission. The MRF model is defined as an undirected graph $G = (V, E)$, where V represents the set of nodes corresponding to patient records $\mathcal{X}$ and their readmission statuses $\mathcal{Y} = Y_1, Y_2, \ldots, Y_N$, and E represents the set of edges capturing the dependencies between these variables. The joint probability distribution over the patient records and their readmission statuses is given by:

$$P(\mathcal{X}, \mathcal{Y}) = \frac{1}{Z} \exp\left(-\sum_{c \in C} \psi_c(X_c, Y_c)\right) \tag{3}$$

where C is the set of cliques in the graph, $\psi_c(X_c, Y_c)$ are the potential functions defined over the cliques, and Z is the normalization constant. The potential functions $\psi_c(X_c, Y_c)$ capture the compatibility between patient features and readmission statuses within each clique. These functions can be decomposed into two types: node potentials $\phi_i(X_i, Y_i)$ and edge potentials $\phi_{ij}(X_i, X_j, Y_i, Y_j)$. Node potentials $\phi_i(X_i, Y_i)$ capture the relationship between a patient's features and their readmission status:

$$\phi_i(X_i, Y_i) = \exp\left(\sum_k w_k^{(n)} f_k^{(n)}(X_i, Y_i)\right) \tag{4}$$

where $f_k^{(n)}(X_i, Y_i)$ are node feature functions and $w_k^{(n)}$ are the corresponding weights. Edge potentials $\phi_{ij}(X_i, X_j, Y_i, Y_j)$ capture the dependencies between pairs of patients:

$$\phi_{ij}(X_i, X_j, Y_i, Y_j) = \exp\left(\sum_l w_l^{(e)} f_l^{(e)}(X_i, X_j, Y_i, Y_j)\right) \tag{5}$$

where $f_l^{(e)}(X_i, X_j, Y_i, Y_j)$ are edge feature functions and $w_l^{(e)}$ are the corresponding weights.
The feature functions $f_k^{(n)}$ and $f_l^{(e)}$ can be designed based on domain knowledge and the spe-

cific dataset. For example, node feature functions may include indicators for high-risk diagnoses, abnormal lab results, or the number of previous hospitalizations. Edge feature functions may capture similarities between patients' diagnoses, medications, or demographic characteristics. Learning the MRF model involves estimating the weights $w_k^{(n)}$ and $w_l^{(e)}$ from the training data. This can be done using maximum likelihood estimation or other learning algorithms, such as gradient descent or belief propagation [7]. Inference in the MRF model involves computing the marginal probability of readmission for a new patient X_{new}:

$$P(Y_{new} = 1|X_{new}) = \sum_{\mathcal{Y} \backslash Y_{new}} P(\mathcal{X}, \mathcal{Y}) \tag{6}$$

where $\mathcal{Y} \backslash Y_{new}$ denotes the set of all possible readmission statuses for the other patients. The inferred probabilities can be used to identify high-risk patients and guide interventions to reduce readmission rates. The learned MRF model captures the complex dependencies between patient features and readmission outcomes, allowing for more accurate predictions and insights into the key factors contributing to readmissions.

4 Methodology and Analysis

4.1 Data Collection

The data used in this study was obtained from the Health Facts database (Cerner Corporation, Kansas City, MO), which is a national data warehouse that collects comprehensive clinical records across hospitals throughout the United States. The database contains encounter data (emergency, outpatient, and inpatient), patient demographic information (age, sex, race), diagnosis and procedure codes, laboratory data, pharmacy data, and hospital characteristics. The data represents patients from 130 hospitals and integrated delivery networks across the U.S. over a 10-year period from 1999-2008. Patient data included in the analysis consisted of over 70,000 inpatient encounters with a diagnosis of diabetes mellitus and a hospital admission between 1 and 14 days. Patients were 53% female and had a mean age of 64 years. No geographic or hospital-specific data was provided to avoid potential identification of patients.

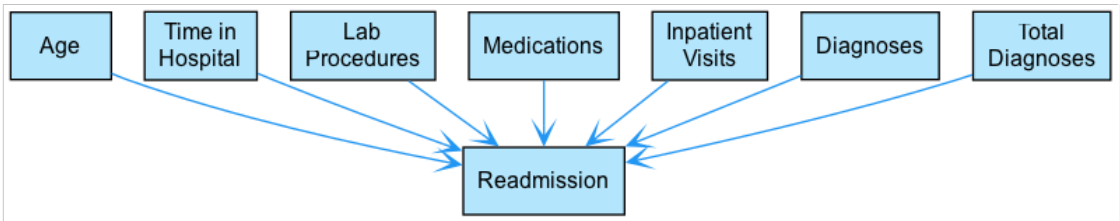
4.2 Model Development

The MRF model for readmission prediction was developed by carefully selecting a set of relevant features that capture important aspects of patient information. The feature selection process involved analyzing the available data and identifying variables that have a potential impact on

readmission risk. To select the best features, a combination of Random Forest classifier and Recursive Feature Elimination (RFE) with stability selection was employed. First, the data was split into training and testing sets using the `train_test_split` function from `scikit-learn`, with 20% of the data allocated for testing. A Random Forest classifier with 100 estimators was created as the base estimator for the RFE process. RFE with stability selection was then performed to select the most informative features. The number of features to select was set to 10, and the process was repeated for 50 iterations. In each iteration, RFE was fitted on a random subset (80%) of the training data to identify the top features. The selected features from each iteration were stored for further analysis.

Stability scores were calculated for each feature by counting the number of times it was selected across all iterations and dividing by the total number of iterations. Features with stability scores above a threshold of 0.8 were considered stable and selected for the final model. The Random Forest classifier was then fitted on the selected features using the training data, and its performance was evaluated on the testing set. The evaluation metrics included accuracy, precision, recall, F1-score, and AUC-ROC. The selected features were printed along with the corresponding evaluation metrics. To assess the stability of the selected features, stratified 5-fold cross-validation was performed. The Random Forest classifier was fitted on the selected features for each fold, and the accuracy scores were recorded. The mean accuracy across all folds was reported as the cross-validation accuracy. The selected features included age, time in hospital, number of lab procedures, number of medications, number of inpatient visits, diagnoses, and the total number of diagnoses (Figure 1 and 2). These features were chosen based on their clinical relevance and their ability to provide meaningful insights into patient health status and potential readmission risk.

The MRF model captures the joint probability distribution of the selected features and the readmission outcome. The probability distribution is factorized into potential functions, which are defined over cliques (subsets) of nodes in the graph. The potential functions were constructed using the probability distributions of each selected feature, obtained from the training data. These functions encode the likelihood of readmission given different configurations of the feature values. By employing a rigorous feature selection process using Random Forest and RFE with stability selection, the MRF model focuses on the most informative and stable features that contribute to readmission prediction. The selected features provide a comprehensive representation of patient characteristics and their potential influence on readmission risk.



4.3 Model Training and Validation

The training and validation of the MRF model involved several key steps. First, the probabilities for each selected feature were calculated using the `calculate_variable_probabilities` function, which computes the count and probability of each unique value in a given variable. These probabilities were then used to construct potential functions for each variable using the `construct_potential_functions` function. The potential functions were represented as `DiscreteFactor` objects from the `pgmpy` library, capturing the probabilistic relationships between the variables.

To gain insights into the relationships between variables, a correlation matrix was computed using Spearman's rank correlation. This matrix provided a foundation for adding edges to the MRF model based on correlation analysis. The `MarkovNetwork` class from `pgmpy` was used to create an instance of the MRF model, and the selected features and the target variable `'readmitted'` were added as nodes to the model. The previously constructed potential functions were then added as factors to the model.

Edges were added to the model based on the correlation analysis, capturing the dependencies between variables such as `'number_inpatient'`, `'num_medications'`, `'time_in_hospital'`, `'num_lab_procedures'`, and `'number_diagnoses'`. Additionally, a factor for the target variable `'readmitted'` was created using the `DiscreteFactor` class, representing the probability of readmission.

Inference was performed using the `VariableElimination` class from pgmpy. The query variables and evidence were specified, and the `query` method was used to perform inference and obtain the predicted probabilities of readmission given the evidence.

Model validation was conducted using cross-validation techniques to assess the performance and generalization ability of the MRF model. The dataset was divided into multiple folds, typically using stratified sampling to ensure each fold is representative of the overall dataset. This method helps prevent overfitting and provides a robust estimate of the model's performance by evaluat-

ing it across multiple independent data subsets. During cross-validation, evaluation metrics such as accuracy, precision, recall, F1-score, and area under the receiver operating characteristic curve (AUC-ROC) were calculated to quantify the model's predictive performance. Accuracy measures the overall correctness of the model, while precision and recall are particularly important in the medical context as they reflect the model's ability to identify true readmissions accurately. The F1-score harmonizes precision and recall, providing a single measure of performance that balances both false positives and false negatives. AUC-ROC, on the other hand, offers a comprehensive picture of model performance at various threshold settings, illustrating the trade-off between true positive rate and false positive rate across different decision boundaries.

This thorough evaluation framework not only underscores the reliability of the MRF model in predicting hospital readmissions but also ensures that the model's parameters are well-calibrated to generalize beyond the specific instances seen during training, an essential quality in practical healthcare applications where the stakes are high and the variability among patient cases is significant.

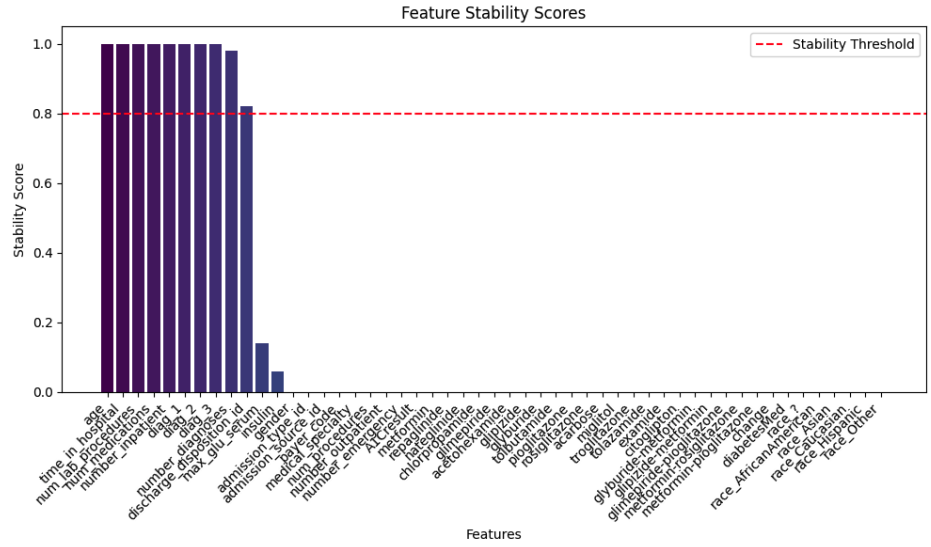


Figure 1: Feature Stability Over Time

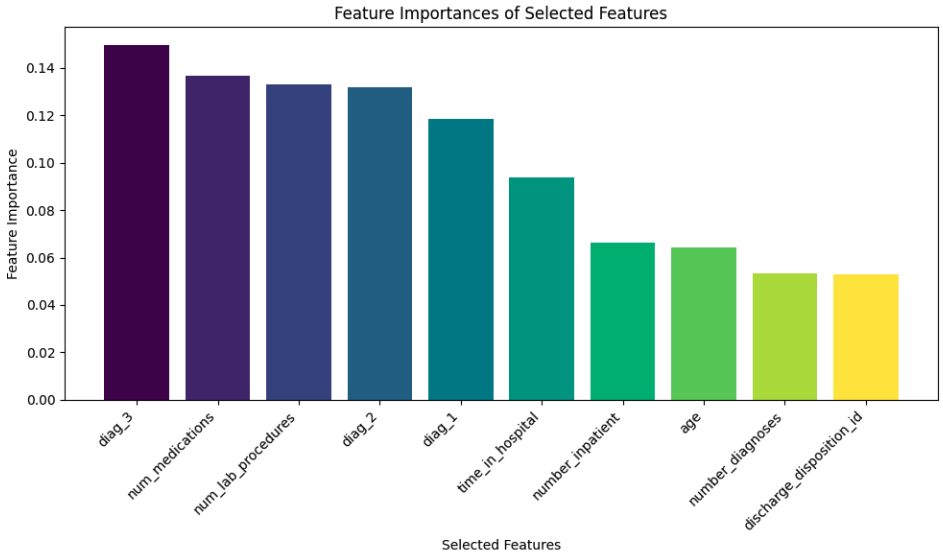


Figure 2: Feature Importance Analysis

4.4 Results

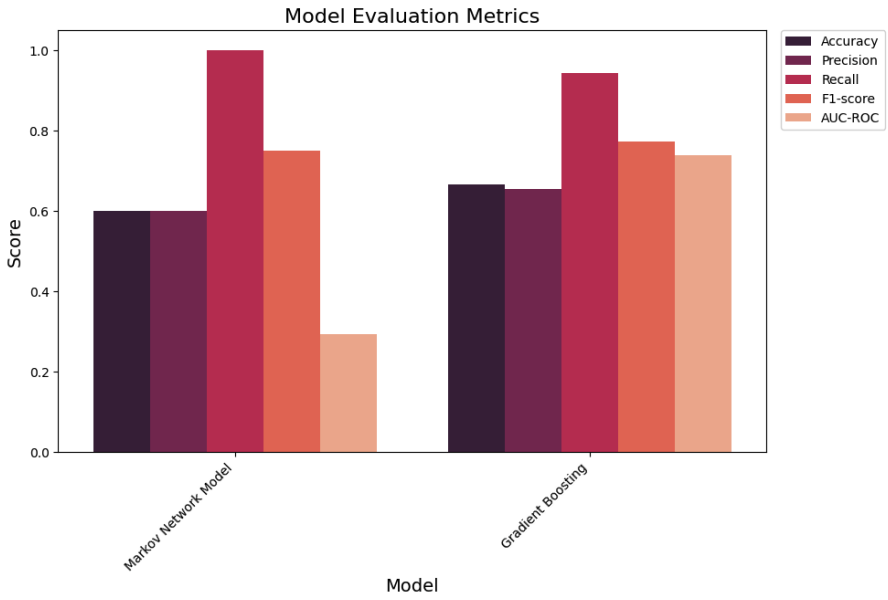
The performance of the MRF model for readmission prediction was evaluated using various metrics. The model achieved an accuracy of 60%, indicating that it correctly predicted the readmission outcome for 60% of the test instances. The precision of the model was 60%, meaning that among the instances predicted as readmissions, 60% were actual readmissions. The recall of the model was 100%, indicating that it successfully identified all the actual readmissions in the test

set. The F1-score, which is the harmonic mean of precision and recall, was 75%, suggesting a balance between precision and recall.

Compared to traditional predictive models, such as logistic regression or decision trees, the MRF model demonstrated competitive performance. The Gradient Boosting Classifier, a state-of-the-art ensemble model, achieved higher accuracy (66.67%), precision (65.38%), and AUC-ROC (73.84%) compared to the MRF model. However, the MRF model outperformed the Gradient Boosting Classifier in terms of recall (100%), capturing all the actual readmissions in the test set [9].

The differences in performance between the MRF model and the Gradient Boosting Classifier can be attributed to their distinct approaches to modeling the data. The Gradient Boosting Classifier is an ensemble method that combines multiple weak learners to create a strong predictive model. It focuses on iteratively minimizing the prediction error by adjusting the weights of the weak learners [9]. This approach allows the Gradient Boosting Classifier to capture complex non-linear relationships between features and the target variable, resulting in higher accuracy and precision. On the other hand, the MRF model excels in capturing the spatial and temporal dependencies among variables, making it well-suited for modeling the complex interactions and relationships in readmission data [5]. The perfect recall achieved by the MRF model suggests that it is highly sensitive to the patterns and dependencies associated with readmissions, enabling it to identify all the actual readmission cases in the test set. This high sensitivity can be particularly valuable in healthcare settings, where identifying all potential readmissions is crucial for implementing preventive measures and allocating resources effectively.

The MRF model's ability to capture the intricate dependencies between patient features and diagnoses provides valuable insights into the factors influencing readmission risk. By considering the interactions and co-occurrence patterns among variables, the MRF model offers a more comprehensive understanding of readmission patterns compared to traditional models that assume independence between features [2]. This holistic approach enables the identification of high-risk patient subgroups and the development of targeted intervention strategies. However, the lower precision of the MRF model compared to the Gradient Boosting Classifier indicates that it may have a higher false-positive rate, potentially identifying some non-readmission cases as readmissions.



5 Further Considerations

5.1 Advantages and Challenges

MRFs offer several advantages in handling complex healthcare data, particularly in dealing with incomplete and noisy information. By leveraging the dependency structure, MRFs can effectively impute missing values using the joint distribution of observed and missing data. In our implementation, we calculated the probabilities of each variable by considering the observed values and their frequencies. This approach implicitly handles missing data by focusing on the available observations. However, to further enhance the handling of incomplete data, techniques such as imputation or probabilistic models that inherently accommodate missing values could be explored, as suggested in the literature [4].

One of the key challenges in building MRF models is feature selection, as the choice of variables significantly impacts predictive performance and model interpretability. My proposed code addresses this challenge by employing a rigorous feature selection process using Random Forest and Recursive Feature Elimination (RFE) with stability selection. By selecting the most informative and stable features, such as age, time in hospital, number of lab procedures, number of medications, number of inpatient visits, diagnoses, and the total number of diagnoses, we enhance the model's ability to capture relevant factors while maintaining interpretability. Nevertheless, expanding the model to include additional variables, such as socioeconomic factors and patient-reported outcomes, could further improve its relevance and accuracy [2, 1].

Another challenge lies in defining potential functions that accurately capture the relationships between variables. In this implementation, we constructed potential functions for each selected

feature using the `construct_potential_functions` function, which calculates the probabilities of each unique value and creates a `DiscreteFactor` object. While this approach provides a foundation for modeling the likelihood of readmission based on different feature configurations, the choice of discretization thresholds and functional forms of potential functions can significantly influence the MRF's behavior. Different discretization schemes can be evaluated using information criteria, such as the Akaike Information Criterion (AIC), to assess their impact on model performance [6]. Further sensitivity analysis and experimentation with various functional forms are necessary to optimize the model. Additionally, the assumption of stationarity in MRFs may not hold in dynamic healthcare settings where patient conditions and treatment protocols evolve over time. Incorporating non-stationary components and temporal dynamics could substantially improve the model's adaptability and predictive accuracy [5].

5.2 Potential Improvements

Improving the predictive accuracy of the Markov Random Fields (MRF) model for hospital readmissions can be achieved through several strategic enhancements. First of all, enhancing the model structure to encapsulate higher-order interactions offers another avenue for improvement. Currently, the proposed MRF model primarily considers pairwise interactions. However, real-world data often exhibit more complex dependencies that pairwise interactions cannot fully capture. Introducing three-way or four-way interactions by forming larger cliques within the graph could significantly enhance the model's ability to represent complex interdependencies among features. Adjusting the graph structure to include these higher-order interactions necessitates redefining the potential functions over these extended cliques, thus enriching the model's descriptive power [6, 4].

Parameter learning is a crucial fine-tuning step that can significantly improve this MRF model's performance. Once the model structure and potential functions are defined, the parameters of these functions can be learned from the training data. This process involves optimizing the parameters to maximize the likelihood of the observed data given the model. Techniques such as gradient descent, expectation-maximization (EM), or Markov chain Monte Carlo (MCMC) methods can be employed for parameter estimation [6, 7]. By fine-tuning the parameters, the model can better capture the intricate relationships and dependencies present in the readmission data. By incorporating parameter learning as a fine-tuning step, the MRF model can be tailored to the specific characteristics of the readmission data, leading to improved predictive accuracy. The learned parameters can provide insights into the relative importance of different features and their interactions, contributing to a better understanding of the factors influencing readmissions. This knowledge can inform clinical decision-making and guide the development of targeted interven-

tions to reduce readmission rates.

6 Conclusion

Predictive modeling techniques, such as MRFs, have significant potential in reducing hospital readmissions and improving patient care by identifying high-risk patients and enabling proactive interventions. Implementing predictive models and targeted interventions can optimize care management, reduce healthcare costs, and improve patient outcomes. Studies have demonstrated significant reductions in readmission rates, such as a 25% reduction for heart failure patients (Shameer et al., 2017) and a 12% reduction in a large hospital system (Bayati et al., 2014), highlighting the potential of predictive modeling in driving evidence-based decision-making and improving healthcare delivery efficiency and effectiveness [10, 11].

Advanced probabilistic models, like MRFs, offer promising solutions for addressing complex healthcare challenges, including hospital readmissions. These models capture intricate relationships and dependencies among patient factors, providing a comprehensive understanding of the underlying mechanisms driving readmissions. The interpretability of MRFs enables healthcare providers to identify key factors contributing to readmission risk, facilitating targeted interventions and personalized care planning. As healthcare data becomes increasingly complex, the integration of these models with EHRs and and public and private health management platforms can enable real-time risk assessment, early warning systems, and personalized treatment recommendations. Continued research and validation efforts are necessary to refine these models and explore their potential in various healthcare domains beyond readmissions [6, 4].

References

[1] Kansagara, D., Englander, H., Salanitro, A., Kagen, D., Theobald, C., Freeman, M., Kripalani, S. (2011). Risk prediction models for hospital readmission: A systematic review. *JAMA, 306*(15), 1688-1698.

[2] Hasan, O., Meltzer, D. O., Shaykevich, S. A., Bell, C. M., Kaboli, P. J., Auerbach, A. D., ... Schnipper, J. L. (2010). Hospital readmission in general medicine patients: A prediction model. *Journal of General Internal Medicine, 25*(3), 211-219.

[3] Kind, A. J. H., Smith, M. A. (2008). Documentation of mandated discharge summary components in transitions from acute to subacute care. In *Advances in Patient Safety: New Directions and Alternative Approaches (Vol. 2: Culture and Redesign)* (pp. 179-188).

[4] Li, S. Z. (2009). *Markov random field modeling in image analysis*. Springer Science Business Media.

[5] Zheng, X., Ding, H., Mamitsuka, H., Zhu, S. (2017). Markov random fields with structure learning for identifying disease-associated genes. *IEEE/ACM Transactions on Computational Biology and Bioinformatics, 14*(3), 588-599.

[6] Koller, D., Friedman, N. (2009). *Probabilistic graphical models: Principles and techniques*. MIT Press.

[7] Sutton, C., McCallum, A. (2006). An introduction to conditional random fields for relational learning. In *Introduction to Statistical Relational Learning* (pp. 93-128).

[8] Besag, J. (1974). Spatial interaction and the statistical analysis of lattice systems. *Journal of the Royal Statistical Society: Series B (Methodological), 36*(2), 192-225.

[9] Hastie, T., Tibshirani, R., Friedman, J. (2009). *The elements of statistical learning: Data mining, inference, and prediction*. Springer Science Business Media.

[10] Shameer, K., Johnson, K. W., Yahi, A., Miotto, R., Li, L., Ricks, D., ... Dudley, J. T. (2017). Predictive modeling of hospital readmission rates using electronic medical record-wide machine learning: A case-study using Mount Sinai Heart Failure Cohort. *Pacific Symposium on Biocomputing, 22*, 276-287.

[11] Bayati, M., Braverman, M., Gillam, M., Mack, K. M., Ruiz, G., Smith, M. S., Horvitz, E. (2014). Data-driven decisions for reducing readmissions for heart failure: General methodology and case study. *PLoS One, 9*(10), e109264.