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A Framework for Personalized Drug Prescriptions Decision Support System using Hybrid Techniques

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Abstract

The increased complexities in healthcare data require the need to have intelligent systems that can be used to provide accurate as well as a personalized prescription of drugs. This research proposes a novel framework for a Personalized Drug Prescription Decision Support System (PDSS) based on improved approaches that will combine the Viterbi algorithm, neural networks, and Beam Search. The framework will take advantage of the Viterbi algorithm's modeling strength of sequence and follow the most likely course of treatment for a patient's history. As such, to overcome these limitations inherent to a Viterbi algorithm, such as local optimality and a high requirement of memory consumption, a neural network layer will be integrated into dynamically estimated transition and emission probabilities, boosting generalization and the ability to deal with various patient profiles. Additionally, Beam search will be employed to cut the computational overhead and enable exploration of multiple high-probability treatment paths, improving both efficiency and decision robustness. The proposed improved model will use 70% of the data to train and the remaining 30% to test, utilizing the Saliva-Derived SNP Datasets. The main performance indicators will be related to prescription accuracy, the time taken to make a computation, and memory efficiency. A comparison will be made and an analysis performed between the performance of the standard Viterbi algorithm as compared to the enhanced Viterbi algorithm. Early findings will verify the hypothesis that an improved system will be more successful than a traditional single-model system with its ability to apply more precise and resource-saving drug recommendations in accordance with the profiles of individual patients. This framework will present an appealing progress in clinical decision support that advocates a safer and more fruitful delivery of personalized drug prescription.

Keywords: Personalized Prescription, Decision Support System, Viterbi Algorithm, Neural Networks, Beam Search

1. Introduction

Digitalization of the healthcare sector has resulted in the exponential development of electronic health records (EHRs), drug administration records, diagnostic records as well as patient-monitoring systems. Well-utilized, these big-data have the potential to dramatically transform the process of clinical decision, especially with regards to personalized prescription of drugs. The historical method of prescribing drugs has been highly dependent on inert clinical guidelines and the subjective experience of clinician which has led to less than optimal outcomes due to variation in patients [1] [2]. In the past 10 years, personalized medicine with the focus on providing medical care in accordance with specific features of a patient has received growing attention. It takes into account the variety of factors, genetic profiles, comorbidities, treatment history, allergies, and even social-economic conditions to prescribe the exact therapeutic measures to be undertaken. Nevertheless, the intricacy and heterogeneity of data regarding patients may often limit the ability to produce a high-quality and flexible

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drug recommendation using rule-driven or linear models [3].

To limit this gap, scientists have resorted to the technique of machine learning (ML) and sequencing modeling of the drug prescription Decision Support Systems (DP-DSS). The Viterbi algorithm is a widely used dynamic programming algorithm, which was invented to decode the most probable path of hidden states on Hidden Markov Models (HMMs). It has been looked into in medical ways regarding disease progression monitoring, treatment regimes and medical pathway foretelling [4][5]. The capacity of the algorithm to calculate the most likely treatment course of action, according to past observations, renders it appropriate to make patient-specific recommendations on drugs.

Nevertheless, in spite of the success in modeling the sequences, the normal Viterbi algorithm has significant shortcomings. To begin with, it is likely to get trapped at local optima, without paying attention to the other alternative (although near-optimal) treatment paths that are clinically feasible. Secondly, its fully complete state transition examination uses considerable computational and memory overhead, specifically in cases of large-dimensional medical information [6]. It does not scale well and adapt to the real world clinic environment due to these restrictions.

To overcome these drawbacks, this study suggests an enhanced algorithm based on Viterbi, which will use neural networks (NNs) and Beam Search to complement the Viterbi algorithm. Neural networks and deep learning in particular, including Recurrent Neural Networks (RNNs), LSTM, and Transformer models have been shown to be successful in learning complex temporal data in longitudinal medical records [7][8]. In the outlined framework, a neural network can be used to dynamically estimate the transition and emission probabilities used in the Viterbi decoder, and the system allows for adaptation to different patient conditions and data distributions.

In addition, the Beam Search, which is a heuristic search technique that has found much application in natural language processing and recommendation systems, is presented in optimization of path selection without the need to explore the full state space. Beam Search achieves a great saving of computation costs and memory access by only storing the k most likely sequences at each step, and still maintaining a goodness of prediction [9][10].

The improved paradigm tries to find a stable compromise amid accuracy, efficiency, and flexibility when recommending custom drug prescriptions. The combination of learning-based probability estimation and optimized path decoding is likely to enhance the accuracy of prescriptions, decrease the error rate and increase the interpretability of treatment choices. Since access to utilize the Saliva-Derived SNP Dataset, such as the UniProt and those that have their tertiary structures solved, has been rising in recent years, the proposed system could be trained and validated on the actual clinical data, making sure that it was robust enough and relevant in clinical practice.

2. Related Works

Ren *et al.* [11] used the Viterbi algorithm in modeling the progression of chronic diseases through Hidden Markov Models (HMMs). With the help of sequences of patient health records, they could infer the most likely disease state transitions, which is of utmost importance in providing recommendations about the courses of treatment. The research, however also showed flaws in the assumption of static probabilities, which normally makes it less able to adjust to the individual differences in patients. This is what illustrates the necessity towards dynamic modeling improvements like neural networks.

Le et al. [13] proposed a Dual Control Memory Augmented Neural Network (DC-MANN) to recommend a form of treatment. The past history of patients is stored in the external memory, and a certain chain to inform the next drug is retrieved. The method enhanced tremendously the quality of therapy sequencing and enabled it to become possible in intensive care conditions as well.

Shang *et al.* [15] reported GAMENet, a new architecture, which integrates drug-drug interaction knowledge graphs into attention-mapped memory networks. The model allows creation of safe and effective combination of medications by reaching into an organized memory bank of clinical information. On experiments over MIMIC-III, GAMENet strongly outperformed traditional ML models of both precision and safety of prescription of drugs, particularly polypharmacy.

Kumar *et al.* [16] came up with a hybrid decision support system that combines a rule-based logic system and neural network models in drug repurposing. With the use of genomic information as well as electronic health records, the system will be able to prescribe off-label drug use based on individual patient profile. They tested their system on datasets representing rare diseases showing that incorporating machine learning into structured domain rules gave more reliable and clinically interpretable results compared to only one method.

Ghassemi *et al.* [17] have emphasised the importance of interpretability of machine learning models used to interpret the healthcare system. The article overviewed numerous clinical use cases of AI and revealed that trust, transparency, and description of model behaviour are keys to successful adoption of such a prototype into the working environment of the physician. They also found the technical and ethical risks of the opaque process of decision-making, particularly when it comes to prescribing medication.

A very Comprehensive review of decision support systems that use machine learning in a clinical setting was conducted by Awaysheh *et al.* [18]. Their discoveries indicate that even with the significant gains that were recorded in performance predictive, there still exist difficulties in real-time implementation, data quality, clinician uptake as well as ethical regulation. The authors suggested adaptation of the construction of DSS future design into adaptive learning and modularity.

Huehn *et al.* [19] created an oncology-oriented clinical DSS based on a Bayesian Network used in the treatment planning process. The system was very accurate in its recommendations which were personal by modeling the probabilistic dependencies between treatments, outcomes and patient characteristics. They found that probabilistic graphical models had superior explainability and confidence scores of probabilistic graphical methods than black-box neural ones.

Singh *et al.* [15] elaborated on highly valuable obstacles of AI collection in the clinical environment but considered ethical clarity, bias of models, restrictions on data transfer services, and explainability. The authors highlighted the necessity of AI models to promote system interoperability and be capable of adhering to medical ethic provisions. Such issues are still the important considerations in the design and implementation of next-generation customised DSSs.

3. Expected Methodology

3.1 Data Collection

The history of drug taking of the patients and the treatment record will be available to be used and an Electropherogram Deoxyribonucleic Acid (DNA) base sequence could be collected by visiting the Molecular and Genetic Laboratory of Fountain University. Such databases possess valuable clinical data, such as diagnoses, prescription of medication, and results of treatment. A few preprocessing will be carried out in order to ready the data to be used to train the model. These involve normalization to get values on features to a standard, time to maintain the chronological order of medical events, and conversion into a structured form of sequel.

The format of each patient-record will be set in such a way that a consistent flow (diagnosis, medication, outcome) will be reflected, thus allowing adequate modeling of treatment-pathways that may be utilized to effect adequate prescription-recommendation of personalized medications. Figure 1 shows the architectural design to be adopted in the proposed research model.

Model Components

Viterbi Algorithm: Will Emulate the successive decision-making procedure in drugs prescription through the determination of the most likely treatment course.

Neural Network: A recurrent model (e.g. LSTM or GRU) will be then trained to estimate dynamic transition and emission probabilities against patient data.

Beam Search: will be used in the decoding phase of NIST RNN-SE, this method keeps the k most likely treatment sequences to increase the computational efficiency and prevent premature selection of a suboptimal path.

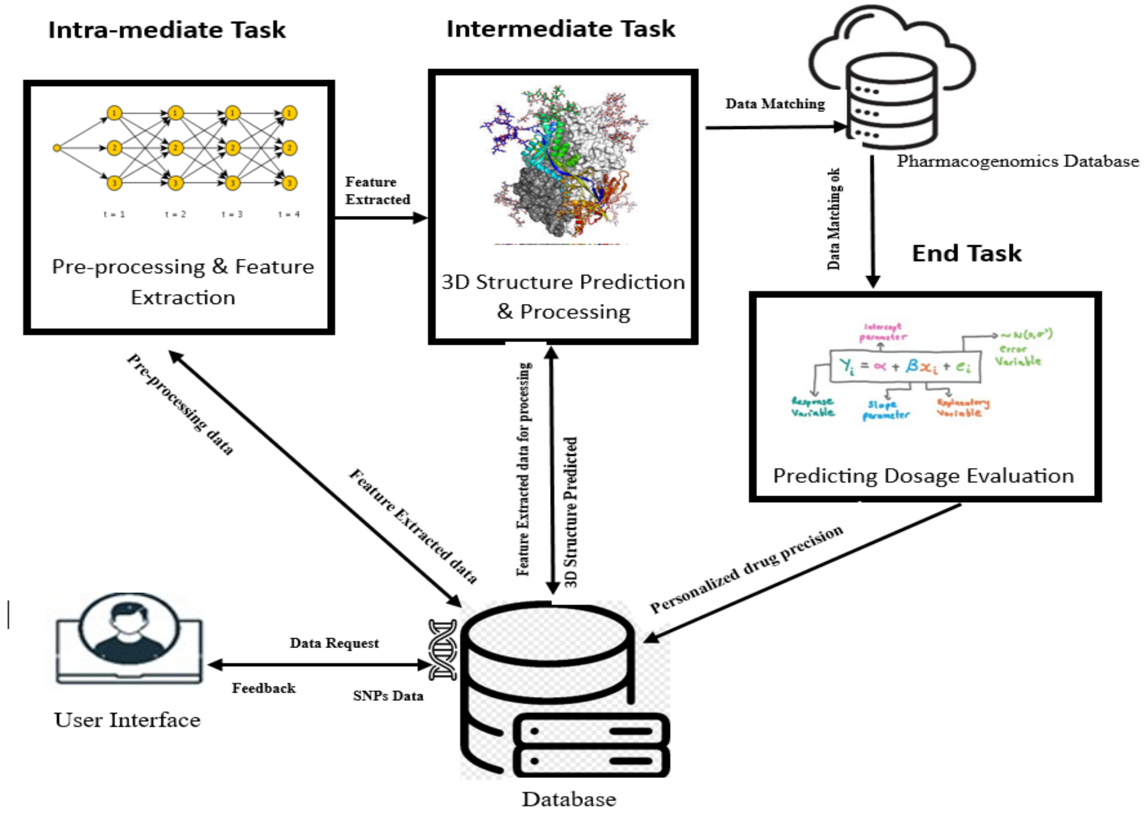

Figure 1: Architectural Framework

3.3 System design

The purpose of the proposed system is to propose a chain of drug prescriptions using neural network, Viterbi algorithm and Beam search. Initiating the system, the input of the system is a clinical profile of a patient and a list of his/her diagnosis. An element of a neural network is used to dynamically estimate the probabilities of transitions and emissions using an input data. The Viterbi algorithm then uses these probabilities in decoding the most likely treatment pathway. To increase the robustness of decision and minimize chances of suboptimal paths, the use of a Beam Search maintains the k highest probability paths. The last output is a prioritized list of drug recommendations based on the health history of the particular patient.

3.4 Evaluation Metrics

In order to gauge the performance and efficiency of the proposed hybrid Decision Support System, an exhaustive list of evaluation measures will be used. These metrics are devised in terms of capturing the predictive accuracy as well as the computational performance of the system.

First, the effect of the capability of the system to produce accurate drug recommendations as compared to the ground truth prescriptions in the dataset will be measured using the measure Prescription Accuracy. This measure offers a direct picture of clinical importance and usefulness.

Then F-1 Score and the Area Under the Receiver Operating Characteristic Curve (AUC) will be calculated to have a balanced evaluation of both the precision and recall of the model especially with regards to dealing with imbalanced data in the medical field. F1-Score is a composite of false positives and false negatives whereas AUC indicates the ability of the model to differentiate between the successful and ineffective treatment methods.

Whilst in the respect of computational performance Execution Time will serve as a metric used to measure the time performance of generating a recommendation, since it is essential in the capacity of time-efficient clinical decision support in a real-time or near real-time environment. Moreover, Memory Usage will also be checked in order to evaluate the scale and efficiency of the resources used by a particular system, which is particularly significant when working with patient data (probably lots of it).

Finally, the standard Viterbi algorithm and the proposed improved model using Neural Networks and Beam Search will be compared. It will be pointed out in this comparison that the hybrid approach introduces accuracy improvements, robustness, and computational performance. The outcomes of this assessment will also give us information on the actual feasibility of the system to be implemented in a real setting of healthcare.

4. Expected Results

The developed improved model which combines Neural Networks, the algorithm Viterbi, and Beam Search will also drastically outperform the traditional Viterbi algorithm in a number of performance aspects. Particularly, it is expected that the model will outperform due to its capacity to increase the accuracy of prescriptions that can be confirmed by the capacity of the neural net to generalize on a broad and sophisticated basis of patients. Such an improvement in generalization is vital to personalizing drug suggestions to the overall treatment history.

Also, it is likely that the implementation of the Beam Search will opt to minimize the use of memory by optimally pruning the search space and retaining only k most high-probability treatment paths. The change can lead to the enhancement of the computational scalability of the model and thus it could be more applicable in the clinical real-time practice.

It is also anticipated that the hybrid model will have a higher degree of flexibility to deal with new profiles of patients and changing trends of treatments that have often been cited as the disadvantages of the traditional models. By thorough assessment, the experiment should be able to prove the strength of integrating the components of deep learning with classical methods of sequence modeling in circumstances of intelligent decisioning assistance. These expected results will highlight the practical significance of improved architectures towards the progress of real-life, data-driven, and individualized healthcare remedies.

5. Expected Conclusion

This study will show that by integrating the Viterbi algorithm, neural networks, and Beam Search the predictive capacity and efficiency of drug prescription decision support systems can be grossly improved. The improved model will deliver the individualized, explainable, and computationally effective drug suggestions. This framework will add to delivery of intelligent healthcare solutions that assist in personalized treatment planning and raise the outcome of patients.

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