

Predicting the Outcome of Patient-Provider Communication Sequences using Recurrent Neural Networks and Probabilistic Models

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Abstract *The problem of analyzing temporally ordered observation sequences generated by a physiological, genomic or psychological process to make predictions about the outcome of that process arises in many domains of clinical informatics. In this paper, we focus on the problem of predicting the outcome of patient-provider communication sequences in the context of clinical interviewing. Specifically, we formulate the problem of predicting the success of a motivational interview (i.e. eliciting a particular type of patient behavioral response) based on an observed sequence of coded patient-provider communication exchanges as binary sequence classification. We propose two methods that are based on deep learning, such as Recurrent Neural Networks (RNNs), and probabilistic models, such as Markov Chain (MC) and Hidden Markov Model (HMM), and compare the accuracy of these methods using communication sequences annotated with behavior codes from real-life motivational interviews. Our experiments indicate that the deep learning-based method is significantly more accurate than the methods based on probabilistic models in predicting the success of motivational interviews (0.8677 versus 0.7038 and 0.6067 F1-score by RNN, MC and HMM, respectively, when using under-sampling to correct for class imbalance, and 0.8381 versus 0.7775 and 0.7520 F1-score by RNN, MC and HMM, respectively, when using over-sampling). These results indicate that the proposed method can be used for real-time monitoring of the progression of clinical interviews and identification of the most effective communication strategies, which significantly decreases the effort required to develop psychological interventions and increases their effectiveness.*

Introduction

Temporally ordered sequences of discrete or continuous observations generated by genomic, psychological or psychological processes arise in many different domains of clinical informatics (e.g., DNA sequences, gene activations, ECG measurements, laboratory results, diagnostic codes, utterances during clinical interviews). Classification (or categorization) is a type of analysis of those sequences that has a broad range of important practical applications, from protein classification¹ and function prediction² to detecting individuals with a heart disease³. Taking into account both the entire set of observations in a sequence, as well as their temporal order, makes sequence classification a more challenging task than traditional classification. Predicting the outcome of those sequences (e.g. physiological or behavior response) can also be formulated as sequence classification.

In general, sequence classification methods fall into one of the three major categories: feature-based, distance-based and model-based. Feature-based methods transform a sequence into a feature vector and apply a standard supervised learning methods, such as Support Vector Machine⁴ or Decision Tree⁵ to arrive at a classification decision. Feature-based methods for sequence classification have had limited success, since traditional bag-of-words feature representation methods cannot easily account for the order of observations in a sequence. Distance-based methods classify a sequence by finding the most similar sequences with known classes based on a distance metric. The most commonly used distance metric is Euclidean distance with Dynamic Time Wrapping⁶. However, distance metrics are primarily designed for time series data, in which the observations are discretized by time points. The third type of sequence classification methods first creates a probabilistic model, such as Markov Chain (MC) or Hidden Markov Model⁷ (HMM), for sequences in each class using the training data and then classifies new sequences by applying the constructed models. MC and HMM explicitly capture short-term temporal dependencies (e.g. first- and second-order MC and HMM⁸) between adjacent observations in a sequence. By encoding sequences into low-dimensional representations, Recurrent Neural Networks (RNNs) are able to capture both short- and long-term dependencies and were shown to be effective for modeling different types of sequential data. Long Short-Term Memory (LSTM)⁹ is a variant

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of RNNs, which successfully addresses the vanishing gradient problem¹⁰ of traditional RNN. LSTM demonstrated excellent performance in different domains, from speech¹¹ and handwriting¹² recognition to health informatics^{13,14}. Specifically, LSTM was used as part of a multi-label classification method to recognize patterns in multivariate time series of clinical measurements, such as body temperature, heart rate and blood pressure¹³. LSTM was also effectively used for predicting the diagnosis and medication codes, given a sequence of codes from previous patient visits¹⁴. A further simplification and improvement of LSTM model, called the Gated Recurrent Unit¹⁵ (GRU), was later proposed. LSTM and GRU demonstrated markedly better performance among all other RNN variants for a variety of tasks in different domains.

In this paper, we address the problem of predicting the outcome of patient-provider communication sequences in the context of clinical interviews. Specifically, we focus on the transcripts of Motivational Interviews (MI) with obese adolescents and their caregivers. Childhood obesity is a serious public health concern in the United States and worldwide. Recent estimates indicate that approximately one-third (31.8%) of US children 2-19 years of age are overweight and 16.9% are obese¹⁶. Adolescents, who are obese, are likely to be obese in adulthood and have a greater risk of heart disease, type 2 diabetes, stroke, cancer, and osteoarthritis¹⁷. One approach to effective obesity intervention is Motivational Interviewing (MI), an evidence-based counseling technique to increase intrinsic motivation and self-efficacy for health-related behavior change. The goal of MI is to encourage patients to explore their own desires, ability, reasons, need for and commitment to the targeted behavior change. These statements, referred to as “change talk” or CHT, consistently predict actual behavior change¹⁸ that can be sustained for as long as 34 months¹⁹ after an interview. However, the ability of counselors to consistently elicit this type of patient communication requires knowledge of effective communication strategies for a variety of patients, which can only be obtained through analysis of a large number of annotated interviews. Since manual examination and sequential pattern analysis of transcripts is a very time-consuming process, designing effective MI interventions and tailoring them to particular populations can take years. Therefore, there is a need for informatics-based methods to facilitate the development of effective MI-based interventions, in general, and theoretically-grounded computational models to explore the mechanisms of MI’s efficacy, in particular.

Our goal is to test the applicability of probabilistic models, such as MC and HMM, and deep learning methods, such as LSTM and GRU, for predicting the success of clinical interviews (i.e. eliciting a particular type of patient behavioral response, such as CHT) and dynamically estimate the likelihood of observing this desired response at any point during a clinical interview based on a sequence of coded previous patient-provider communication exchanges in the same interview. This study is a continuation of our previous work^{20,21}, in which we explored several machine learning methods for automatic annotation of clinical interview fragments with a large number of patient and provider behavior codes from a specialized codebook²². While there have been some previous qualitative studies of patient-provider dialog in a clinical setting²³, no previous work explored applicability of state-of-the-art methods for sequence modeling to analysis of patient-provider communication (PPC) exchanges, in general, and predicting the desired patient behavior in a context of motivational interviews, in particular.

Methods

Data collection

The experimental dataset for this work was constructed from the transcripts of 129 motivational interviews, which include a total of 50,239 segmented and annotated utterances. Each transcript consists of an MI interview session involving counselor, adolescent, and caregiver. The utterances were annotated based on MYSCOPE codebook²², in which the codes are grouped into patient (adolescent and caregiver) codes and counselor codes. Utterances were divided into successful and unsuccessful communication sequences. Successful communication sequences result in positive change talk and commitment language statements by an adolescent or caregiver, while unsuccessful sequences are the ones that result in negative change talk or commitment language and the sequences, in which no change talk or commitment language statements occur. Out of 5143 observed sequences, 4225 were positive and 918 were negative. Successful sequences had an average length of 9.79 utterances, while unsuccessful sequences had on average 9.65 utterances. For each of the probabilistic models (MC and HMM), two models were trained, one model was trained using successful sequences and another one was trained using unsuccessful sequences.

Our dataset is imbalanced and predominately composed of successful sequences with only a small percentage (17.85%) of unsuccessful sequences. Usually, predictive accuracy misrepresents the performance of an employed algorithm for an imbalanced data, since simply predicting the majority class (successful) would provide a predictive accuracy 82.15%. Therefore, it is important to handle class imbalance properly. Many solutions have been proposed to deal with the imbalanced datasets, which can be divided into two categories: data level and algorithmic level. In this study, we utilized under-sampling and over-sampling for balancing the samples in different classes in our dataset. Synthetic Minority Over Sampling Technique (SMOTE) is the most widely used method for oversampling an imbalanced dataset, in which new synthetic examples were generated from minority class²⁴. We generated synthetic examples along the borderline between minority examples and their selected nearest neighbors²⁵. On the other hand, the under-sampling method reduces the number of samples in majority class by replacing the clusters of samples by the cluster centroid in a k -means clustering algorithm.

A fragment of an adolescent session transcript is presented in Table 1. Annotation column shows successful sequences of behavior codes from top to bottom. For example, ($SS \rightarrow OQO \rightarrow HUPO \rightarrow OQTCN \rightarrow CHT+$) is a successful behavior sequence, where counselor starts with a structured session and gets positive change talk at the end. As can be seen, similar utterances, such as “Yeah” and “Yes”, can have different behavior codes (CHT+ and HUPW, respectively) depending on the context.

Table 1: Fragment of the annotated transcript of a dialogue between a counselor and an adolescent.

Annotation	Behavior	Speaker	Text
SS	Structure Session	Counselor	Okay. Can I meet with Xxxx alone for a few minutes?
OQO	Open-ended question, other	Counselor	So, Xxxx, how you doing?
HUPO	High uptake, other	Adolescent	Fine
OQTCN	Open-ended question, target behavior neutral	Counselor	That’s good. So, tell me how do you feel about your weight?
CHT+	Change talk positive	Adolescent	It’s not the best.
CQECHT+	Closed question, elicit change talk positive	Counselor	It’s not the best?
CHT+	Change talk positive	Adolescent	Yeah
CQTCN	Closed question, target behavior neutral	Counselor	Okay, so have you tried to lose weight before?
HUPW	High uptake, weight	Adolescent	Yes

Prediction method

Generally, a sequence can be viewed as a temporally ordered set of events. In this study, an event is a behavior code that also has a symbolic representation, such as $LUP+$ (low uptake, positive), $OQECHT+$ (open-ended question, elicit change talk positive), etc. Given a sequence of behavior codes $S_i = \{c_1, c_2, \dots, c_n\}$ representing patient-provider communication exchanges during some part of a motivational interview, the task of predicting interview success can be viewed as sequence classification. Given a set of class labels $L = \{l_1, l_2, \dots, l_m\}$ (in our case, the labels are “successful” and “unsuccessful” motivational interview), a sequence classifier C learns a function $S_i \rightarrow l_i, l_i \in L$ that maps a sequence S_i into a class label $l_i \in L$.

Our proposed baseline prediction method consists of two steps. In the first step, we model successful and unsuccessful patient-provider interactions using first and second-order Markov Chain and Hidden Markov Model, which are popular probabilistic models for discrete observation sequences with finite vocabulary. In the second step, we classify each test sequence based on the maximum likelihood of generating that sequence from each model. Although HMM was originally developed for speech recognition⁷, it is one of the most widely used methods for sequence modeling^{26,27}. However, the latest advances in deep learning indicate that RNNs provide better results than conventional machine learning methods for the task of sequence classification. Therefore, we employed two special variants of RNN in our

experiments: Long Short-Term Memory (LSTM)⁹ and Gated Recurrent Unit (GRU)¹⁵.

Markov Chain (MC) is a probabilistic model that predicts the probability of next state based on its current state but not on its past states (Markov property). For the sequential analysis, we built two Markov models M and \bar{M} , summarizing counselor strategies and patient responses, in the cases of successful (M) and unsuccessful (\bar{M}) motivational interviews. A Markov model M can be represented as a weighted directed graph $G = (V, E, p)$, in which:

- $V = \{CML+, CHT+, CHT-, AMB-, LUP+, LUP-, HUPW, OQO, CQTCN, CQECHT+, \dots\}$ is a set of vertices, consisting of adolescent, caregiver and counselor MI behavior codes;
- $E \subseteq V \times V$ is a set of edges corresponding to possible transitions from one MI behavior code to the other in a sequence;
- $p_M : E \rightarrow [0..1]$ is a function that assigns probability $p(c_i|c_j)$ to an edge between the MI behavior codes c_i and c_j based on maximum likelihood estimator:

$$P_M(c_j|c_i) = \frac{n_{c_i, c_j}}{n_{c_i}} \quad (1)$$

where n_{c_i, c_j} and n_{c_i} are the number of times a transition between the MI behavior codes c_i and c_j and the code c_i has been observed in the training data. Given a Markov model M (such that $S \subseteq V$), the probability that a sequence of MI behavior codes $S = \{C_1, \dots, C_N\}$ has been generated from a Markov model M is:

$$P_M(S) = \prod_{i=2}^N p_M(c_i|c_1, \dots, c_{i-1}) = \prod_{i=2}^N p_M(c_i|c_{i-1}) \quad (2)$$

In the second step, we quantify the likelihood of success of a given motivational interview at a certain time point given a sequence of MI behavior codes S observed prior to that point as:

$$p(S \rightarrow \text{successful}) = \log \left(\frac{P_M(S)}{P_{\bar{M}}(S)} \right) = \sum_{i=2}^N \log p_M(c_i|c_{i-1}) - \sum_{i=2}^N \log p_{\bar{M}}(c_i|c_{i-1}) \quad (3)$$

If $p(S \rightarrow \text{successful}) > 0$, a communication sequence is predicted to result in positive change talk or commitment language. Otherwise, it would be classified as a negative change talk or commitment language.

The above model also referred as first-order MC, since it only considers immediately preceding behavior code, when computing the state transition probabilities. In our experiment, we also considered second-order Markov model that computes transition probabilities based on previous two states.

Hidden Markov Model (HMM) is another probabilistic model used for modeling processes varying in time. HMMs are widely used for sequence analysis because of their ability to incorporate dependencies among elements in sequence. Mathematically, HMM can be defined as the following: $\lambda = (A, B, \pi)$.

- A is an $N \times N$ state transition probability distribution matrix $A = \{a_{ij}\}$
- B is an $N \times M$ matrix $B = \{b_j(k)\}$ with observation symbol probability distribution for each state
- π is the initial state distribution vector $\pi = \{\pi_i\}$

Hence, N is a number of hidden states in the model and M is a number of distinct observations symbols per state, i.e. the discrete vocabulary size. The key difference between HMM and MC is that HMM requires specifying the number of hidden states as a model parameter and then the model deduces a sequence of hidden states that best explains the observations along with state transition probabilities and distributions of observation symbols (emission probabilities) for each state. The Baum-Welch algorithm was used to estimate the parameters of HMMs for successful

and unsuccessful interviews using the corresponding training set, while the Viterbi algorithm was used to determine the most likely sequence of hidden states for a given sequence of observations. After assignment of hidden states, the log-likelihood of successful outcome can be estimated using Eq. 3.

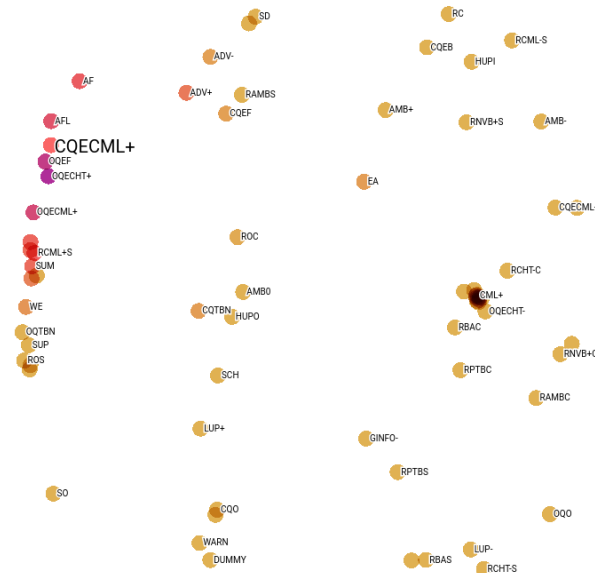


Figure 1: T-SNE diagram of behavior codes drawn after 4000 steps with perplexity 30.

$$z_t = \sigma(W_z x_t + U_z h_{t-1} + b_z) \quad (4)$$

$$\tilde{h}_t = \tanh(W_h x_t + r_t \odot U_h h_{t-1} + b_h) \quad (6)$$

$$h_t = z_t \odot h_{t-1} + (1 - z_t) \odot \tilde{h}_t \quad (7)$$

As these equations, σ stands for an element-wise application of the sigmoid function and \odot is an element-wise product. The update gate z_t and reset gate r_t at time step t are computed by the Eq. (4) and (5), where W and U represent weights and b represents biases. The activation h_t of the GRU at time t is a linear combination of previous activation h_{t-1} and the candidate activation \tilde{h}_t , which is represented by Eq. (7) and (6).

$$total\ loss = \alpha \cdot \frac{1}{T} \sum_{t=1}^T loss(\bar{y}^{(t)}, y^{(t)}) + (1 - \alpha) \cdot loss(\bar{y}^{(T)}, y^{(T)}) \quad (8)$$

The architecture of the proposed Recurrent Neural Network is shown in Figure 2. We used one hidden layer of 15

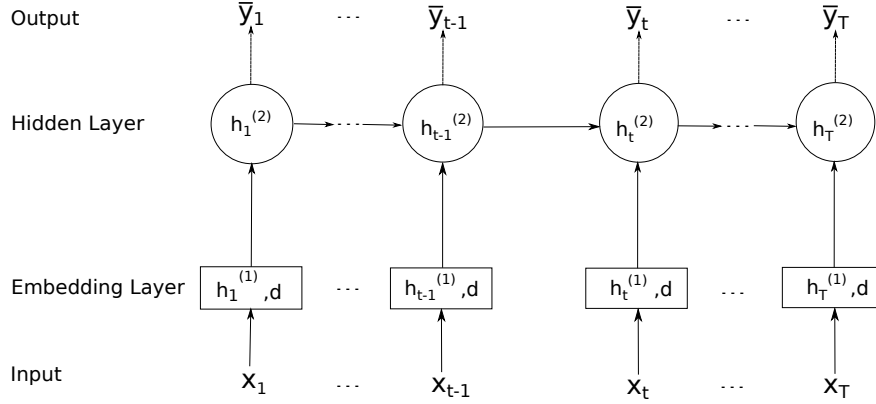


Figure 2: Proposed RNN model with target replication (TR).

LSTM or GRU nodes and embedding of MYSCOPE codes in an observed sequence of communication behaviors as input. Then, we applied a softmax layer at each time-step for predicting the target which is the predicted label of the sequence. As can be seen from Eq. 8, the total loss of our prediction models is the combination of final loss and the mean of the losses over all sequence steps, where T is the total number of elements in a sequence, $\bar{y}^{(t)}$ is the output at step t , and $\alpha \in [0, 1]$ is a hyperparameter that determines the relative importance of intermediate outputs. Experimentally, it was determined that best performance achieved when we use $\alpha = 0.5$. Our model also contains several other hyperparameters such as embedding dimension, number of hidden units, learning rate, batch size, etc., which were determined on the validation set. We implemented our models in Tensorflow with Adam optimizer and early stopping based on the validation loss. Experimentally, we observed that our model converges to optimal after 100 epoch and have no effect of dropout and regularization. The code for all models is publicly available at <https://github.com/teanalab/myscope-sequential-analysis>.

Evaluation metrics

Performance of the proposed method was evaluated in terms of precision, recall, and F-measure using 10 folds cross-validation and weighted macro-averaging of these metrics over the folds. However, LSTM and GRU are trained on 80% of the data and validated on 10%. The remaining 10% of the data is used as a test set for reporting the performance of the model.

Results

Experimental evaluation of the proposed method is conducted on both under and over-sampled sequences. Predictive performance summary of the proposed methods on under and over-sampled sequences is presented in Table 2.

Table 2: Performance of MC, HMM, and RNN for predicting the success of under and over-sampled patient-provider communication sequences. The highest value for each performance metric is highlighted in bold.

Method	Undersampling			Oversampling		
	Precision	Recall	F1-Score	Precision	Recall	F1-Score
Markov Chain 1 st Order	0.7060	0.7044	0.7038	0.7932	0.7799	0.7775
Markov Chain 2 nd Order	0.6395	0.6385	0.6379	0.7111	0.7029	0.7000
Hidden Markov Model	0.6244	0.6143	0.6067	0.7775	0.7567	0.7520
LSTM RNN	0.8672	0.8626	0.8622	0.8411	0.8372	0.8368
LSTM RNN - TR	0.8733	0.8681	0.8677	0.8424	0.8385	0.8381
GRU RNN	0.8674	0.8648	0.8646	0.8379	0.8342	0.8337
GRU RNN - TR	0.8705	0.8676	0.8673	0.8412	0.8377	0.8373

Predictive performance for under-sampled PPC code sequences

We applied small learning rate (0.00005) and batch size (8) with early stopping strategy for training deep learning models when the under-sampled dataset is used. Five major conclusions can be drawn from the results in Table 2. First, recurrent neural networks outperform probabilistic models and achieve 16.39%-26.1% higher F1-score. Second, LSTM with target replication has the best performance over all other RNN methods, and achieved F1-score 0.8677 with precision 0.8733 and recall 0.8681. Third, target replication strategy improves the performance of GRU and LSTM, while conventional GRU shows better performance than traditional LSTM. Fourth, among probabilistic models, the MC-based method generally outperforms HMM across all metrics for under-sampled sequences. Fifth, second-order MC has lower precision, recall, and F-measure than first-order MC. In particular, precision, recall and F-measure decrease by 9.42%, 9.36% and 9.36%, when going from first to second-order MC model.

Predictive performance for over-sampled PPC code sequences

Similar to the under-sampled dataset, early stopping strategy was also employed for the over-sampled dataset. For over-sampled data, RNN models were trained with learning rate 0.00010 and batch size 55. Experimental results indicate that HMM had better performance than second-order MC, achieving 9.34%, 7.65%, and 7.43% higher precision, recall, and F-measure, while HMM still has 1.98%, 2.97%, and 3.28% lower precision, recall, and F-measure than first-order Markov chain. Similar to under-sampled sequences, target replication improves the performance of RNN models, and LSTM with target replication has the highest F1-score among all models. However, the predictive performance of recurrent neural networks decreases in over-sampled sequences, while the performance of probabilistic models increases. We also observed that all models have the largest value in precision compared to other performance metrics.

Table 3: Most likely communication sequences in successful and unsuccessful motivational interviews.

Type	Most likely communication sequences
successful	GINFO+: General information, positive → LUP+: Low uptake, positive → OQTBN: Open-ended question, target behavior neutral
successful	SS: Structure session → GINFO+: General information, positive → CQECHT+: Closed-ended question, elicit change talk positive
successful	SO: Statement, other → LUP+: Low uptake, positive → AF: Affirm → HUPW: High uptake, weight → OQECML+: Open-ended question, elicit commitment language positive.
unsuccessful	ADV+: Advise, positive → AMB-: Ambivalence negative → OQECHT-: Open-ended question, elicit change talk negative
unsuccessful	CQECHT+: Open-ended question, elicit change talk positive → RCHT-S: Reflect, change talk negative → OQECHT-: Open-ended question, elicit change talk negative
unsuccessful	SUP: Support → AF: Affirm → CQTBN: Closed-ended question, target behavior neutral → OQECHT-: Open-ended question, elicit change talk negative → AMB-: Ambivalence negative

Most likely communication sequences

Table 3 provides examples of typical patient-provider communication sequences that frequently appear in successful and unsuccessful motivational interviews. In successful sequences, we observed that information is frequently provided using patient-centered communication (GINFO+) and structure session, when the counselor either explains the therapeutic agenda or attempts to transition to a new topic or session content (SS). Sometimes, counselor acknowledges the clients' communication or an off topic comment (SO). We also observed that the affirm and OQECML+ are consistent with MI theory, which claims their strong effect for eliciting positive change talk or commitment language. For unsuccessful sequences, it can be seen that providing advice using non-patient centered strategies (ADV-) leads to the ambivalence that is weighted against change (AMB-), which is heading in the wrong direction therapeutically. Questions phased to elicit negative change talk or commitment language leads to CHT- or CML-, which is consistent with the manual coding approach or analysis, or AMB-.

Discussion

By analyzing the experimental results of different communication sequence outcome prediction methods proposed in this paper, we arrived at the following conclusions. First, the overall predictive performance of RNN models is substantially better than probabilistic models. In particular, the RNN-based method achieves near-human accuracy for predicting the label of motivational interviews. This indicates that RNN is able to capture the structure of discourse in motivational interviews by preserving long-term dependencies among the behavior codes, which reflect the overall progression of the interviews. This provides evidence that the RNN is able to successfully replicate human cognitive processes to integrate previous information when formulating higher level thinking. In addition to that, embeddings allow to reduce the dimensionality of codes in PPC sequences and consequently improve both precision and recall of the prediction method.

Second, using target replication to compute the loss at each time step results in better performance for all configurations of the proposed RNN-based methods. This indicates that mean of the losses over all steps emphasize the dependencies between the pairs of patient and provider codes, which results in more accurate estimates of the model parameters. Better estimates of parameters in RNN models of motivational interviews are propagated to the next step based on the relative importance of intermediate output, where they are aggregated into predictions for the entire sequence. This allows achieving an improvement in the prediction accuracy of the method.

Third, using first-order Markov model results in better prediction accuracy compared to higher-order Markov models, which we attribute to the fact that the number of states in higher-order Markov models grows exponentially with their order. As a result, accurate estimation of transition probabilities requires much larger training set. Using smaller datasets such as under-sampled dataset will result in a sparsity problem, when many transitions are either not observed in the training set at all or observed only a few times, leading to missing or potentially inaccurate probability estimates. Obtaining large training sets cannot be easily accomplished in many domains, including motivational interviewing. In this study, we found out that using first-order Markov models is a reasonable trade-off between efficiency and accuracy.

Fourth, similar to traditional Markov model, HMM achieves a dramatic improvement in the prediction accuracy when larger training set is used. This indicates that sufficient training data is required to estimate optimal hyperparameters such as a number of hidden states, initial state distribution, transition probabilities, and emission probabilities.

Fifth, the proposed method can be used to identify the most effective communication strategies at eliciting a particular type of behavioral response. Awareness of these strategies by researchers can significantly decrease the time and effort required to develop effective interventions to address many public health conditions, such as childhood obesity, and tailor these interventions to particular patient cohorts. Awareness of these strategies by the counselors can lead to a greater success rate of motivational interviews.

Conclusion

In this paper, we compared the accuracy of Recurrent Neural Networks with Markov Chain and Hidden Markov Model for the task of predicting the success of motivational interviews. We found out that individual patient-provider communication exchanges are highly indicative of the overall progression and future trajectory of clinical interviews and

can be used to predict their overall success. Our proposed methods can facilitate motivational interviewing researchers in establishing causal relationships between different communication strategies and the desired behavioral outcomes during the interviews without resource-intensive manual qualitative analysis of interview transcripts, which can significantly decrease the time and effort required to develop behavioral interventions. Our proposed methods can also help to identify most likely sequences that are common to successful and unsuccessful motivational interviews, which can directly inform clinical practice and increase the effectiveness of behavioral interventions. Our experimental results indicate that the proposed methods can also be used for real-time monitoring of the progression of clinical interviews. This work also has broad implications for public health research by providing a formal theoretically-grounded computational mechanism for qualitative data analysis.

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