

# Predicting Success of Motivational Interviews with Recurrent Neural Network and Probabilistic Model for Patient-Provider Communication Sequences

Mehedi Hasan, BS<sup>1\*</sup>, Alexander Kotov, PhD<sup>1\*</sup>, April Idalski Carcone, PhD<sup>2</sup>, Ming Dong, PhD<sup>1</sup>, Sylvie Naar, PhD<sup>2</sup>

<sup>1</sup>Department of Computer Science, <sup>2</sup>Department of Family Medicine and Public Health Sciences, School of Medicine, Wayne State University, Detroit, Michigan

**Abstract** *The problem of analyzing temporally ordered observation sequences to make predictions related to the outcome of the processes that generated these sequences arises in many domains of healthcare informatics. In this paper, we focus on patient-provider communication sequences in the context of clinical interviews and propose Recurrent Neural Network (RNN) with two baseline methods Markov chain and Hidden Markov Model (HMM), for predicting the likelihood of eliciting a particular type of patient behavioral response based on an observed sequence of patient-provider exchanges. Our method achieved 70.38%, 60.67%, 86.77% F1-score for under-sampled sequences and 77.75%, 75.20%, 83.81% F1-score for over-sampled sequences in predicting the outcome of motivational interviews with obese adolescents using Markov Chain, HMM, and RNN, respectively. The proposed method can be used to automatically identify the most effective communication strategies in motivational interviews, which significantly decreases the effort required to develop effective interventions to address many public health conditions.*

## Introduction

Data in the form of temporally ordered sequences of discrete or continuous observations (e.g., symbolic sequences such as notes in patient EHR, diagnostic codes, protein or DNA sequences or continuous time series, such as ECG measurements) arise in various domains of health informatics. The order of observations in a sequence is challenging to capture using features, which makes sequence classification a more challenging task than traditional classification. In general, sequence classification methods can be divided into three categories: feature-based, distance metric-based and model-based method. Feature-based classification methods transform a sequence into a feature vector and apply a standard supervised learning algorithm, such as support vector machine<sup>1</sup> or decision tree<sup>2</sup>. Shapelet<sup>3</sup> and pattern<sup>4,5</sup> based techniques as well as hierarchical approaches<sup>6</sup> have been proposed instead of standard classifiers as well. Distance-based methods measure the similarity between sequences to determine the quality of classification. The most commonly used distance function is Euclidian distance<sup>7</sup> with Dynamic Time Wrapping<sup>8</sup> used for more flexible matching in time series data. The third type of sequence classification methods, first creates a probabilistic model of a sequence, such as Markov Chain (MC) and Hidden Markov Model<sup>9</sup> (HMM).

However, Markov chain cannot handle long-term dependencies in sequences. Similarly, the hidden states of HMMs follow a first-order markov chain and can select only one hidden state at each time step. Therefore, Markov chain and HMMs are only capable of passing short-term dependency among sequence steps. On the other hand, Recurrent Neural Networks (RNNs) have no such limitations. RNNs are capable to capture long-term dependencies with their unlimited memory. It was shown that RNNs are very effective in sequence modeling with temporal data. Recently, two variant of RNNs is proposed: Long Short-Term Memory<sup>10</sup> (LSTM) and Gated Recurrent Unit<sup>11</sup> (GRU), which gave excellent performance in a wide range of sequence modeling problems<sup>12-14</sup>.

Sequence classification has a broad range of real word applications from genomics and health informatics to finance and anomaly detection. In genomics research, sequence classification is widely used to classify protein and text sequence data<sup>15</sup> and detect the function of new proteins<sup>16</sup>. In health informatics, ECG measurements are considered as multi-dimensional time series and are used to classify individuals as healthy or having a heart disease<sup>17</sup>. Sequence classification is also used for anomaly detection such as abnormal access to systems<sup>18</sup> and malware<sup>19</sup>.

In this paper, we direct our focus towards 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

---

\* Authors provided equal contribution.

indicate that approximately one third (31.8%) of US children age 2-19 years are overweight and 16.9% are obese<sup>20</sup>. Adolescents who are obese likely continue to be obese in adulthood and have a greater risk of heart disease, type 2 diabetes, stroke, cancer, and osteoarthritis<sup>21</sup>. One approach to effective obesity intervention is Motivational Interviewing, an evidence-based counseling technique to increase intrinsic motivation and self-efficacy for health-related behavior change. The goal of MI counseling session 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 CT), consistently predict actual behavior change that can be sustained for as long as 34 months 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 annotation and examination of transcripts is a very time-consuming process, tailoring of MI interventions 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 research addresses this problem from multiple angles. In our previous work<sup>22,23</sup>, we explored several machine learning methods for automatic annotation of clinical interview fragments with a specialized codebook containing a large number of patient and provider behavior codes<sup>24</sup>. In this work, we propose Recurrent Neural Networks with two baseline probabilistic methods to identify patient-provider communication sequences that are likely to elicit the desired patient behavioral response (i.e. change talk or commitment language) and to dynamically estimate the likelihood of observing this desired response at any point during a clinical interview based on all coded previous patient-provider communication exchanges in the same interview. While there have been some previous qualitative studies of patient-provider dialog in a clinical setting<sup>25</sup>, there have been no previous work on computational modeling of annotated patient-provider communication (PPC) exchanges and predicting the desired patient behavior in a context of motivational interviews.

## 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 a counselor-adolescent and a counselor-caregiver session. The utterances were annotated based on MYSCOPE codebook<sup>24</sup>, which are grouped into the adolescent and counselor code groups. Utterances were divided into successful and unsuccessful communication sequences. Successful communication sequences result in positive change talk and commitment language (a special class of change talk) statements by an adolescent, 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. For each of the probabilistic models (Markov chain and HMM), two models were trained, one model was trained using successful sequences and another one was trained using unsuccessful sequences. Statistics of the experimental dataset are presented in Table 1.

**Table 1:** Statistics of experimental dataset. Sequence length is the number of behavior codes in it.

Sequence Type	# of sequences	Ratio	Average length
Successful sequences	4225	82.15%	9.79
Unsuccessful sequences	918	17.85%	9.65

As can be seen from Table 1, our data set is imbalanced and predominately composed of successful sequences with only a small percentage (17.80%) of unsuccessful sequences. Usually, predictive accuracy misrepresents the performance of an employed algorithm for an imbalanced data. Because simply predict the majority class (successful) would provide a predictive accuracy 82.15%. Therefore, it is important to handle imbalance data properly. Many solutions are proposed to deal with the imbalanced data sets, which can be divided into two categories: data level and algorithmic level. In this study, we utilized under and over sampling methods at data processing level for balancing the adolescent obesity data set. Synthetic Minority Over-sampling (SMOTE) method is the most widely used

method for over-sampling an imbalanced data set, in which new synthetic examples were generated from minority class<sup>26</sup>. We generated synthetic examples along the borderline between minority examples and their selected nearest neighbors<sup>27</sup>. On the other hand, under sampling method under samples the majority class by replacing a cluster of majority samples by the cluster centroid of a K-Means algorithm. A fragment of an adolescent session transcript is presented in Table 2. Hence, annotation column shows the successful sequence of behavior codes from top to bottom, in particular, ( $SS \rightarrow OQO \rightarrow HUPO \rightarrow OQTBN \rightarrow CHT+$ ) is a successful behavior sequence, where counselor starts with a structured session and gets positive feedback at the end. It was noticed that same context “Yeah” and “Yes” represent different behavior codes CHT+ and HUPW, respectively. Because human brain can remember the past behaviors, and classify the current context into different behavior codes after considering their past behaviors. For this reason, we only consider those models that can capture the past events for the classification of behavior sequences.

**Table 2:** 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
OQTBN	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
CQTBN	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 is 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 classified each test sequence based on the maximum likelihood of generating that sequence from each model. Although HMM was originally developed for speech recognition<sup>9</sup>, it is one of the most widely used methods for sequence modeling<sup>28–30</sup>. However, the latest advances in deep learning technologies show that deep learning, in particular, RNNs provide better results than conventional machine learning methods for the task of sequence classification. Therefore, we employed two special variants of RNN models in our experiments: long short-term memory (LSTM) and gated recurrent unit (GRU).

**Markov Chain (MC)** is a probabilistic model that predicts the probability of next state based on its current state and not on its past states (Markov property). For the sequential analysis, we built two Markov models  $M$  and  $\bar{M}$  summarizing provider strategies and patient responses in case 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:

- $V = \{CML+, CHT+, CHT-, AMB-, LUP+, LUP-, HUPW, OQO, CQTBN, CQECHT+, \dots\}$  is a set of vertices, consisting of adolescent 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 using the following formula:

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

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

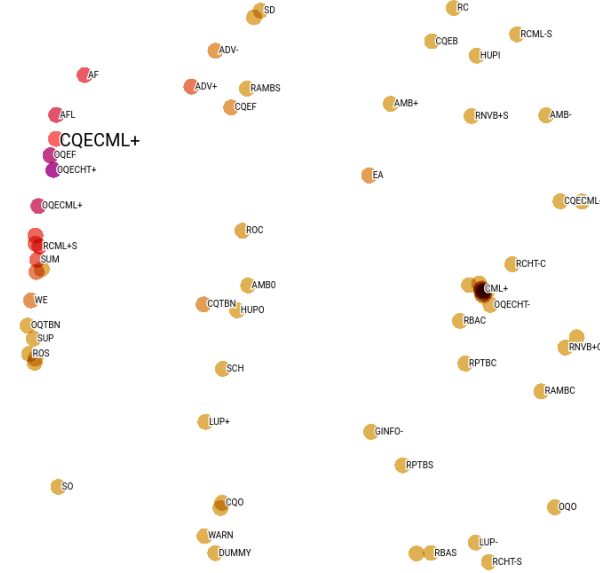
The above model also referred as first-order MC, since it only considers immediately preceding behavior code when computing the state transition probabilities. In our experiment, we also considered second-order Markov model that compute transition probabilities based on previous two states.

**Hidden Markov Model (HMM)** is another probabilistic model, which is 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:  $\lambda = (N, M, A, B, \pi)$

- $N$  is a number of hidden states in the model
- $M$  is a number of distinct observations symbols per state, i.e. the discrete vocabulary size
- $A$  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
- $\pi$  is the initial state distribution vector  $\pi = \{\pi_i\}$

HMM is also represented by a compact notation:  $\lambda = (A, B, \pi)$  after excluding the structure parameters  $M$  and  $N$ . 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 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.

**MYSCOPE code embedding:** We utilize word embedding technique in place of one-hot vectors for the representation of behavior code. Because one-hot vectors are high-dimensional and sparse. On the other hand, word embeddings have the ability to represent semantically similar words with similar vectors in a lower dimensional space by retaining their internal relations. Figure 1 illustrates the myscope code embedding in 44 dimensional vector space visualize with t-SNE, a sophisticated technique for visualizing high-dimensional data. It can be seen that similar behavior codes are placed close to each other in high dimensional vector space such as OQECHT+, OQECML+, AF, ADV+, RCML+S, etc. are nearest neighbors of CQECML+.



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

**Recurrent Neural Network (RNN)** is a type of Neural Network, which can send feedback from the current hidden state to the hidden state of the next time step. In this way, RNN can capture long-term dependencies for predicting the future events, which is the main advantage of RNN over feedforward Neural Network, MC, and HMM. The capability of remembering past event is very useful in motivational interviews where a behavior observed at some points in the interview is very informative for the future behaviors that will be observed. However, it was observed that RNN fails to capture long-term dependencies due to vanishing gradient problem<sup>31</sup>. In order to mitigate this problem, Hochreiter et al.<sup>32</sup> proposed a special kind of RNN called Long Short Term Memory networks or simply LSTM. Later, the model was enhanced by including forget gates and the tanh activation function<sup>10</sup>. There are several variants of LSTM model, where a dramatic variation on the LSTM is the Gated Recurrent Unit<sup>33</sup> or simply GRU. GRUs are simpler than LSTM units and experimentally outperform than other models in many cases. We reiterate the mathematical formulation of GRU defined by Chung et al.<sup>11</sup> as follows (Eq. 4 to 7):

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

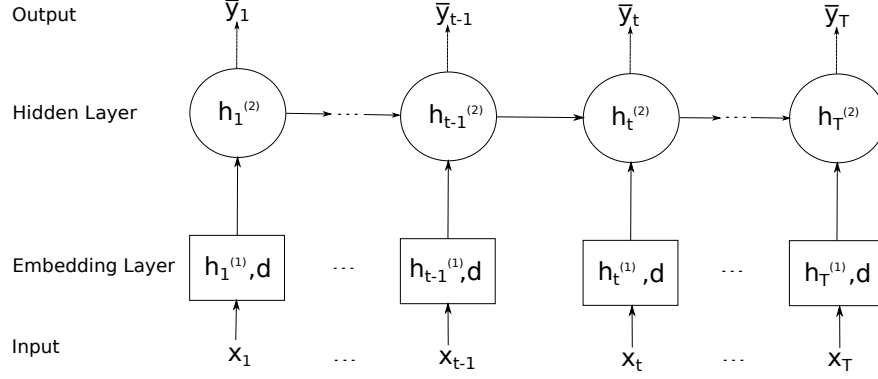
$$r_t = \sigma(W_r x_t + U_r h_{t-1} + b_r) \quad (5)$$

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

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

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

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 after embedding the given myscope codes from the input sequence. Then, we applied a softmax layer at each time step for predicting the target. This target replication (TR) strategy was used in several studies<sup>13,14</sup> after introduced by Lee et al.<sup>34</sup> in 2015 for convolutional neural networks. As it can be seen from equation (8), our loss is the combination of final loss and the mean of the losses over all sequence steps, where  $T$  is the total number of sequence step,  $\bar{y}$  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 by 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. A true positive (TP) was counted when the method correctly classified a sequence into its actual class; a false positive (FP) was counted for a class when the method incorrectly classified a sequence into that class; a false negative (FN) for an actual class of sequence was counted when the method incorrectly classified the sequence into other class. The Precision of a class was defined as the ratio of the numbers of correctly classified sequences and all sequences identified as belonging to that particular class by the classifier (i.e. Precision = TP / (TP + FP)). Recall of a class was defined as the ratio between the numbers of correctly classified sequences and all sequences of that particular class in the gold standard (i.e. Recall = TP / (TP + FN)). F-measure is computed as the harmonic mean of precision and recall (i.e.  $2 \times \text{Precision} \times \text{Recall} / (\text{Precision} + \text{Recall})$ ).

### **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 3.

#### **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 3. First, recurrent neural networks outperform over probabilistic models and achieved 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

**Table 3:** 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	Under-sampled dataset			Over-sampled dataset		
	Precision	Recall	F1-Score	Precision	Recall	F1-Score
Markov Chain 1 <sup>st</sup> Order	0.7060	0.7044	0.7038	0.7932	0.7799	0.7775
Markov Chain 2 <sup>nd</sup> 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	<b>0.8733</b>	<b>0.8681</b>	<b>0.8677</b>	<b>0.8424</b>	<b>0.8385</b>	<b>0.8381</b>
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

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 vanilla LSTM. Fourth, among probabilistic models, the MC-based method generally outperforms HMM across all metrics for under-sampled sequences. Fifth, it follows that second-order MC have 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 models.

#### *Predictive performance for over-sampled PPC code sequences*

Similar to the under-sampled dataset, early stopping strategy is also employed for the over-sampled dataset. For over-sampled data, RNN models are 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 although the performance of probabilistic models increases. We also observed that all models have the largest value in precision compared to other performance metrics.

**Table 4:** Most likely communication sequences in successful and unsuccessful motivational interviews.

Type	Most likely communication sequences
successful	GINFO+: General information, positive → LUP+: Low uptake, positive → OQTNB: 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 → CQTNB: Closed-ended question, target behavior neutral → OQECHT-: Open-ended question, elicit change talk negative → AMB-: Ambivalence negative

#### *Most likely communication sequences*

Table 4 provides examples of typical PPC sequences that frequently appear in successful and unsuccessful motivational interviews. It can be seen that most successful sequence starts with a summary of the discussion or structured statement. After that, if adolescents express positive change talk, the counselor immediately reflects on that to re-

inforce adolescent's intrinsic motivation about behavior change. On the other hand, asking open- or closed-ended questions with eliciting negative change talk can lead to negative change talk, even in the cases when adolescents were showing a positive tendency in their previous communication. This observation can be explained by adolescents quickly confused when reiterating negative information that undermines their motivation. Analyzing such cases will allow the counselors to determine the negative information that can be discussed during the interviews.

## **Discussion**

By analyzing the experimental results of different communication sequence outcome prediction schemes 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, RNN-based method achieves near-human accuracy for predicting the success of motivational interviews. This indicates that RNN are 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. In addition to that word embedding allows to reduce the dimensionality of codes in PPC sequences and consequently improve both precision and recall of the prediction method.

Second, computing loss with target replication at each time step results in better performance for all configurations of the proposed RNN method. 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 to achieve 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. Because the number of states in higher-order Markov models grows exponentially with their order. Therefore, 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 achieve 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 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 greater success rate of motivational interviews.

## **Conclusion**

In this paper, we proposed Recurrent Neural Networks with two baseline methods Markov Chain and Hidden Markov Model for 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 method 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. Our proposed method can also help to identify most likely sequences that are common to successful and unsuccessful motivational interviews, which can also directly inform clinical practice. This work also has broad implications for qualitative public health research by providing a formal theoretically-grounded computational mechanism to facilitate the development of effective behavioral interventions.



## Acknowledgments

This study was supported by an R21 grant DK108071 from the NIH. We would like to thank the student assistants in the Department of Family Medicine and Public Health Sciences at Wayne State University School of Medicine for their help with transcribing the recordings of motivational interviews.

## References

- [1] Leslie C, Kuang R. Fast string kernels using inexact matching for protein sequences. *Journal of Machine Learning Research*. 2004;5(Nov):1435–1455.
- [2] Chuzhanova NA, Jones AJ, Margetts S. Feature selection for genetic sequence classification. *Bioinformatics*. 1998;14(2):139–143.
- [3] Ye L, Keogh E. Time series shapelets: a new primitive for data mining. In: *Proceedings of the 15th ACM SIGKDD international conference on Knowledge discovery and data mining*. ACM; 2009. p. 947–956.
- [4] Kudenko D, Hirsh H. Feature generation for sequence categorization. In: *AAAI/IAAI*; 1998. p. 733–738.
- [5] Lesh N, Zaki MJ, Ogihara M. Mining features for sequence classification. In: *Proceedings of the fifth ACM SIGKDD international conference on Knowledge discovery and data mining*. ACM; 1999. p. 342–346.
- [6] Nallam K, et al. An Effective Implementation of Hierarchical Approach For Sequence Classification. *IJACTA*. 2016;3(2):143–146.
- [7] Keogh E, Kasetty S. On the need for time series data mining benchmarks: a survey and empirical demonstration. *Data Mining and knowledge discovery*. 2003;7(4):349–371.
- [8] Keogh EJ, Pazzani MJ. Scaling up dynamic time warping for datamining applications. In: *Proceedings of the sixth ACM SIGKDD international conference on Knowledge discovery and data mining*. ACM; 2000. p. 285–289.
- [9] Rabiner LR. A tutorial on hidden Markov models and selected applications in speech recognition. *Proceedings of the IEEE*. 1989;77(2):257–286.
- [10] Graves A, Mohamed Ar, Hinton G. Speech recognition with deep recurrent neural networks. In: *Acoustics, speech and signal processing (icassp), 2013 IEEE international conference on*. IEEE; 2013. p. 6645–6649.
- [11] Chung J, Gulcehre C, Cho K, Bengio Y. Empirical evaluation of gated recurrent neural networks on sequence modeling. *arXiv preprint arXiv:14123555*. 2014;.
- [12] Nion T, Menasri F, Louradour J, Sibade C, Retornaz T, Métaireau PY, et al. Handwritten information extraction from historical census documents. In: *Document Analysis and Recognition (ICDAR), 2013 12th International Conference on*. IEEE; 2013. p. 822–826.
- [13] Lipton ZC, Kale DC, Elkan C, Wetzell R. Learning to diagnose with LSTM recurrent neural networks. *arXiv preprint arXiv:151103677*. 2015;.
- [14] Choi E, Bahadori MT, Schuetz A, Stewart WF, Sun J. Doctor ai: Predicting clinical events via recurrent neural networks. In: *Machine Learning for Healthcare Conference*; 2016. p. 301–318.
- [15] Yakhnenko O, Silvescu A, Honavar V. Discriminatively trained markov model for sequence classification. In: *Data Mining, Fifth IEEE International Conference on*. IEEE; 2005. p. 8–pp.
- [16] Deshpande M, Karypis G. Evaluation of techniques for classifying biological sequences. In: *Pacific-Asia Conference on Knowledge Discovery and Data Mining*. Springer; 2002. p. 417–431.
- [17] Wei L, Keogh E. Semi-supervised time series classification. In: *Proceedings of the 12th ACM SIGKDD international conference on Knowledge discovery and data mining*. ACM; 2006. p. 748–753.

- [18] Lane T, Brodley CE. Temporal sequence learning and data reduction for anomaly detection. *ACM Transactions on Information and System Security (TISSEC)*. 1999;2(3):295–331.
- [19] Drew J, Hahsler M, Moore T. Polymorphic malware detection using sequence classification methods and ensembles. *EURASIP Journal on Information Security*. 2017;2017(1):2.
- [20] Ogden CL, Carroll MD, Kit BK, Flegal KM. Prevalence of obesity and trends in body mass index among US children and adolescents, 1999-2010. *Jama*. 2012;307(5):483–490.
- [21] General US. Surgeon Generals vision for a healthy and fit nation. Washington, DC: HHS. 2010;.
- [22] Kotov A, Hasan M, Carcone A, Dong M, Naar-King S, BroganHartlieb K. Interpretable probabilistic latent variable models for automatic annotation of clinical text. In: *AMIA Annual Symposium Proceedings*. vol. 2015. American Medical Informatics Association; 2015. p. 785.
- [23] Hasan M, Kotov A, Carcone AI, Dong M, Naar S, Hartlieb KB. A study of the effectiveness of machine learning methods for classification of clinical interview fragments into a large number of categories. *Journal of biomedical informatics*. 2016;62:21–31.
- [24] Carcone AI, Naar-King S, Brogan K, Albrecht T, Barton E, Foster T, et al. Provider communication behaviors that predict motivation to change in black adolescents with obesity. *Journal of developmental and behavioral pediatrics: JDBP*. 2013;34(8):599.
- [25] Eide H, Quera V, Graugaard P, Finset A. Physician–patient dialogue surrounding patients expression of concern: applying sequence analysis to RIAS. *Social Science & Medicine*. 2004;59(1):145–155.
- [26] Chawla NV, Bowyer KW, Hall LO, Kegelmeyer WP. SMOTE: synthetic minority over-sampling technique. *Journal of artificial intelligence research*. 2002;16:321–357.
- [27] Nguyen HM, Cooper EW, Kamei K. Borderline over-sampling for imbalanced data classification. *International Journal of Knowledge Engineering and Soft Data Paradigms*. 2011;3(1):4–21.
- [28] Mutsam N, Pernkopf F. Maximum margin hidden Markov models for sequence classification. *Pattern Recognition Letters*. 2016;77:14–20.
- [29] Won KJ, Prügél-Bennett A, Krogh A. Training HMM structure with genetic algorithm for biological sequence analysis. *Bioinformatics*. 2004;20(18):3613–3619.
- [30] Chai W, Vercoe B. Folk music classification using hidden Markov models. In: *Proceedings of International Conference on Artificial Intelligence*. vol. 6. sn; 2001. .
- [31] Bengio Y, Frasconi P, Simard P. The problem of learning long-term dependencies in recurrent networks. In: *Neural Networks, 1993., IEEE International Conference on*. IEEE; 1993. p. 1183–1188.
- [32] Hochreiter S, Schmidhuber J. Long short-term memory. *Neural computation*. 1997;9(8):1735–1780.
- [33] Cho K, Van Merriënboer B, Bahdanau D, Bengio Y. On the properties of neural machine translation: Encoder-decoder approaches. *arXiv preprint arXiv:1409.1259*. 2014;.
- [34] Lee CY, Xie S, Gallagher P, Zhang Z, Tu Z. Deeply-supervised nets. In: *Artificial Intelligence and Statistics*; 2015. p. 562–570.