Exploration on Generating Traditional Chinese Medicine Prescription from Symptoms with an End-to-End method

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Abstract

Traditional Chinese Medicine (TCM) is an influential form of medical treatment in China and surrounding areas. In this paper, we propose a TCM prescription generation task that aims to automatically generate a herbal medicine prescription based on textual symptom descriptions. Sequence-to-sequence (seq2seq) model has been successful in dealing with conditional sequence generation tasks like dialogue generation. We explore a potential end-to-end solution to the TCM prescription generation task using seq2seq models. However, experiments show that directly applying seq2seq model leads to unfruitful results due to the severe repetition problem. To solve the problem, we propose a novel architecture for the decoder with masking and coverage mechanism. The experimental results demonstrate that the proposed method is effective in diversifying the outputs, which significantly improves the F1 score by nearly 10 points (8.34 on test set 1 and 10.23 on test set 2).

1 Introduction

Traditional Chinese Medicine (TCM) is one of the most important forms of medical therapy in China and the surrounding areas. TCM has accumulated a large amount of documentation and therapy records in the long process of development. Prescription consisting of herbal medication is the most important form of TCM treatment. TCM practitioners write prescriptions corresponding to the patients’ symptoms which are mainly observed and analyzed by the practitioners themselves instead of armariums. The patients take the decoction made from the herbal medication in the prescription. A complete prescription includes the composition of herbs, the preprocessing method and doses of herbs. We only focus on the composition part now for simplicity.

During the long history of TCM, there has been a lot of therapy records or treatment guidance in the TCM classics composed by outstanding TCM researchers and practitioners. There are many descriptions of symptoms and the corresponding prescription in the records. In the real life, TCM doctors often take these classical records for reference when prescribing medicine for the patient, which inspires us to design a deep learning model that can automatically generating prescriptions by learning from these classics. We hope this may one day help the practitioners generating a prescription, since deep learning is good at utilizing large scale data.

An example of TCM prescription is shown in Table 1. The herbs in the prescription are organized in a weak order. Superficially, the herbs are not in strict order like words in natural language, while in fact, the herbs are connected to each other, and herbs of the most importance are usually listed first. Another thing that should be noted is that there is no duplicate herb in a prescription.

Due to the lack of digitalization and formalization, TCM has not attracted enough attention in the Artificial Intelligence (NLP included) community. To facilitate the studies on automatically generating TCM prescriptions, we collected a large number of prescriptions as well as their corresponding symptom descriptions from the Internet. Inspired by the great success of natural language generation tasks like neural machine translation (NMT) (Bahdanau et al., 2014; Cho et al., 2014; Sutskever et al., 2014), abstractive summarization (See et al., 2017; Ma and Sun, 2017; Ma et al., 2017), generative question answering (Yin et al., 2015) and neural dialogue response generation (Li et al., 2017, 2016), we propose to use the end-to-end learning methods, mainly the sequence to sequence model to tackle the task of generating TCM prescriptions based on textual symptom de-
Table 1: An example of TCM prescriptions. The prescription and its corresponding symptoms are both given. We roughly translate them into English.

| Symptoms | Translation |
|----------|-------------|
| 外感风寒表实证。恶寒发热，头身疼痛，无汗自喘，舌苔薄白，脉浮紧。 | Affection of exogenous wind-cold; aversion to cold, fever; headache and body pain; adiaphoresis and pant; thin and white tongue coating, floating and tense pulse |
| 麻黄、桂枝、杏仁、甘草 | Mahuang (ephrada), Guizhi (cassia twig), Xingren (almond), Gancao (glycyrrhiza) |

The prescription generation task is similar to generative question answering problem or a single round dialogue response generation. In such task settings, the encoder part of the model takes in the question or the history message, and encodes the sequence of tokens into a set of hidden states, which embodies the information of the message or the question. The decoder part then iteratively generates tokens based on the information encoded in the hidden states of the encoder. The model would learn how to generate response after training on the corresponding (question-answer) or (message-response) pairs.

In the TCM prescription generation task, the textual symptom descriptions can be seen as the question and the aim of the task is to produce a set of TCM herbs that form a prescription as the answer to the question. However, the herbs are very different from the usual answers to a question in the Question Answering task. An obvious difference between a herbal prescription and a natural language sentence is that there will not be any duplication of herbs, while there is no such restriction in natural language.

When directly applying a seq2seq model to the TCM prescription generation task, the basic seq2seq model often produces some herb tokens repeatedly. The phenomenon of token repetition severely hurts the performance of recall rate even after we apply a post-process to prune repetitions. Because in a limited length of prescription, the model would produce the same token over and over again, rather than novel ones.

In this paper, we explore how to automatically generate TCM prescriptions based on textual symptoms. We propose a Diversified seq2seq model with masking and a coverage mechanism that are designed for diversifying the generation of herb tokens. In the experiment results, we observe a large increase in both recall rate and F value compared with the basic seq2seq model.

The main contributions of this paper lie in the following three folds:

- We propose a TCM prescription generation task and collect a big amount of TCM prescription data with symptom descriptions. As far as we know, this is the first time that the task of TCM prescription generation has been considered. The task may make a profound impact on health care in real life.
- We propose to apply end-to-end learning methods to deal with the TCM prescription generation problem. In the experiments we observe that directly applying seq2seq model would result in low recall rate.
- We propose to enhance the basic seq2seq model with masking and cover mechanism, which can diversify the predicted herb tokens, thus increasing the recall rate. In our experiments, our final model can increase the F value and recall rate by a big margin compared with the basic seq2seq model.

2 Related Work

2.1 Computational TCM Methods

There has not been much work concerning on computational TCM. Zhou et al. (2010) attempted to build a TCM clinical data warehouse to make use of TCM knowledge. This is a typical way of collecting big data, since the number of prescriptions given by the doctors in the clinics is very large. However, in reality, most of the TCM doctors don’t use these digital systems. And the quality of the inputed data tends to be poor. Therefore, we choose prescriptions in the classics (books or documentations) of TCM. Although this may suffer from lower data magnitude, it guarantees the quality of the prescriptions.

Wang et al. (2004) attempted to construct a self-learning expert system with several simple classifiers to facilitate the TCM diagnosis procedure,
Wang (2013) proposed to use deep learning and CRF based multi-labeling learning methods to model TCM inquiry process, but their systems are too simple to be actually effective in the real life TCM diagnosis. These methods either utilize traditional data mining methods or are highly involved with expert crafted systems.

2.2 Deep Learning for Medical Treatment

Many previous work that tries to adapt deep learning into biomedical research uses deep reinforcement learning to deal with some certain medicine or certain disease, as reinforcement learning is good at optimizing therapy policy. Nemati et al. (2016) used deep reinforcement learning to optimize the medication (heparin in their paper) dose based on retrospective data. Weng et al. (2017) proposed to learn personalized optimal glycemic trajectories for severely ill septic patients with sparse autoencoder and reinforcement learning. Raghu et al. (2017) also applied deep reinforcement learning to optimize treatment policies for septic patients. Prasad et al. (2017) proposed to use off-policy reinforcement learning algorithm to determine the best action at a given patient state from sub-optimal historical ICU data. These methods are concerned about optimizing treatment policy based on historical data.

Yousefi et al. (2017) proposed to predict the clinical outcomes based on the vast data generated by genomic platforms with Bayesian optimized deep survival models. Ciresan et al. (2013) proposed a deep max-pooling convolutional neural network to detect mitosis in breast histology images. These studies apply simple deep learning models to do classification problem.

Our task is more general that focuses on a wider field of diseases instead of a certain one. The data input of our task is the textual symptom descriptions given by TCM practitioners rather than images or inspection result. Apart from that, our output is simpler, which does not include time sequence or dose of medicine. We only concern about the herbal formation of the prescription for now.

2.3 Coverage Mechanism

Seq2seq model which consists of an Encoder and a decoder was first introduced by Cho et al. (2014) and Sutskever et al. (2014). This framework is suitable for natural language generation tasks like machine translation. Given one source sequence of variable length, the model is able to produce an respective target sequence that is close to the gold target sequence in a certain sense. However, the decoder may repeatedly pay attention to the same parts of the source, especially when these parts of the source are dominant compared with other parts. This phenomenon would lead to producing the same content over and over again, or over-stressing some part of the source while completely omit other parts.

Tu et al. (2016) proposed a coverage mechanism to try to control the attention process by introducing a fertility vector which indicates how much one part of the source has been paid attention to. Nema et al. (2017) stated that this repetition problem is even more damaging in the summarization task. They proposed a diversity based attention model that tries to make the current context vector derived from attention mechanism orthogonal to the last context vector.

The previous attempts to alleviate repetition are inspiring to us. However, their approaches can not be directly adapted to this task. The alignment between the herb and symptom is not very clear. Different herb tokens are often related to the same symptom of the disease. Based on this observation, we propose to incorporate a coverage vector that indicates which herbs have been generated to help decide what the next token is.

3 Data Construction

When constructing our TCM herbal therapy dataset, we first considered the TCM medical records (中医医案) in the history, which contain a lot of very good resource. The medical records are widely referenced by the doctors in the treatment, however, they have not been well digitalized, which makes it hard to extract the prescriptions out of the descriptive natural language from the records. Another way to get large scale prescriptions is from TCM clinics, the problem is that most of this kind of valuable data is not publicly available. Therefore, we turn to Internet resources, which contain large scale digitalized prescription data.

We crawl the data from TCM Prescription Knowledge Base (中医方剂知识库) \(^1\). This knowledge base includes quite comprehensive TCM documentations in the history. The database includes 710 TCM historical books or document-

\(^1\)http://www.hhjfs1.com/fang/
lations as well as some modern ones, consisting of 85,166 prescriptions in total. Each item in the database provides the name, origin, composition, effect, contraindications and preparation methods. We clean and formalize the database and get 82,044 usable symptoms-prescription pairs.

In the process of normalization, we temporarily omit the dose information and the preparation method description, which we may use in the future. Word segmentation is typically the first step to Chinese text processing (Xu and Sun, 2016; Zhao et al., 2010; Sun et al., 2014, 2012, 2009). Word segmentation is used to pre-process the text into word based sequences. In addition to the traditional word segmentation techniques, we use more heuristics to assist the segmentation process because this domain has specific features. We also write some heuristic rules to project some rarely seen herbs to their similar form that is normally referred to. For example, if the herb appears less than 5 times and all the characters of the herb name is a substring of another more popular herb, then the herb would be mapped to the other one. This simple projection procedure can partly solve the data sparsity problem.

4 Diversified Seq2seq Model

Neural sequence to sequence model has proven to be very effective in a wide range of natural language generation tasks, including Neural Machine Translation and abstractive summarization, which are related to our task. In this section, we first describe the definition of the TCM prescription generation task, then we introduce how to apply seq2seq model in the prescription composition task, at last we show how to encourage the model to generate more diverse herbs in the specific setting of this task by introducing masking and coverage mechanism. An overview of the complete model is shown in Figure 1.

4.1 Task Definition

Given a TCM herbal therapy dataset that consists of \( N \) data samples, the i-th data sample \((x^{(i)}, p^{(i)})\) contains one source text \(x^{(i)}\) that describes the symptoms, and \( M_i \) TCM herbs \( p_1^{(i)}, p_2^{(i)}, \ldots, p_{M_i}^{(i)} \) that make up the herb prescription \( p^{(i)} \).

We see the symptoms as a sequence of characters \(x^{(i)} = x_1^{(i)}, x_2^{(i)}, \ldots, x_T^{(i)}\) as they are mostly in traditional Chinese which are hard to segment. The herbs \( p_1^{(i)}, p_2^{(i)}, \ldots, p_{M_i}^{(i)} \) are all different from each other.

4.2 Basic Encoder-Decoder Model

Sequence-to-sequence model was first proposed to solve machine translation problem. The model consists of two parts, an Encoder and a Decoder. The Encoder is bound to take in the source sequence and compresses the sequence into hidden states. Decoder is used to produce a sequence of target tokens based on the information embodied in the hidden states given by the Encoder. Both Encoder and Decoder are implemented with Recurrent neural network (RNN) in the classical framework.

In our TCM prescription generation task, the encoder RNN converts the variable-length symptoms in character sequence \( x = x_1, x_2, \ldots, x_T \) into a set of hidden representation \( h = (h_1, h_2, \ldots, h_T) \), by iterating the following equations along time \( t \):

\[
h_t = f(x_t, h_{t-1})
\]

where \( f \) is a RNN family function. In our implementation, we choose Gated Recurrent Unit (GRU) as the \( f \), as the gating mechanism is expected to be better able to model long distance dependency. Furthermore, we choose bidirectional recurrent networks as the encoder to solve the problem of back bias. We concatenate both the \( h_t \) in the forward and backward pass and get \( \hat{h}_t \) as the final representation of the hidden state at time step \( t \):

\[
\hat{h}_t = [h_t^{forward}; h_t^{backward}]
\]

We get the context vector \( c \) acting as the representation of the whole source \( x \) through a non-linear function \( q \):

\[
c = q(\hat{h}_1, \hat{h}_2, ..., \hat{h}_T)
\]

The decoder is another RNN; it generates a variable-length sequence \( y = (y_1, y_2, ..., y_T) \) token by token (herb), through a conditional language model:

\[
s_t = f(s_{t-1}, c_t)
\]

\[
p(y_t | y_1, ..., t, x) = g(s_t)
\]

where \( s_t \) is the hidden state of the decoder RNN at time step \( t \). \( f \) is also a Gated Recurrent Unit. The non-linear function \( g \) is a \textit{softmax} classifier,
which outputs the probabilities of all the herbs in the herb vocabulary.

Note that in our model, we don’t feed the vector of the predicted previous word to the GRU, because unlike machine translate or other natural language generation tasks, the target sequence of the herbs are not in strict order. The very last generated herb token is not directly related to the current one.

In the decoder, the context vector $c_t$ is calculated based on the hidden state of the decoder at time step $t$ and all the hidden states in the encoder, which is also known as the attention mechanism. The attention mechanism is expected to supplement the information from source sequence that is more connected to the current hidden state of the decoder instead of only depending on a fixed vector produced by the encoder.

$$c_t = \sum_{j=1}^{T'} \alpha_{tj} h_j \quad (6)$$

$$\alpha_{tj} = \frac{\exp(a(s_{t-1}, h_j))}{\sum_{k=1}^{T} \exp(a(s_{t-1}, h_k))} \quad (7)$$

The context vector $c_t$ is calculated as a weighted sum of hidden representation produced by the encoder $h = (h_1, ..., h_T)$. $a(s_{t-1}, h_j)$ is a soft alignment function that measures the relevance between $s_{t-1}$ and $h_j$. To put it more clearly, function $a$ is expected to measure to which degree the decoder needs to extract information from $j$-th time step in the encoder.

The encoder and decoder networks are trained jointly to maximize the conditional probability of the target sequence.

### 4.3 How to Diversify Generated Herb Tokens

Different from the usual language tasks, there is no duplicate token (herb) in the TCM prescription generation task. When directly applying seq2seq model to this task, the decoder tends to generate some frequently appeared herbs over and over again. Although we can prune the repeated herbs through post-processing by turning the outputs into a set, it still greatly hurts the recall performance as the maximum length of a prescription is limited. This situation holds when we use a $<EOS>$ label to guide the decoder when to stop the generation procedure.

To encourage the decoder to generate more diverse and sensible herb tokens, we propose two methods, masking and coverage mechanism.

**Masking**

The first one is to mask the probability of generated words to zero when producing a new token in the inference stage. That is to say, at time step $t$ of decoding, the probability of words that have been already in the generated sequence would be manually degraded.

$$p_i = 0 \quad \text{for } i \in D_t \quad (8)$$

where $i$ is the index of the herb, $D_t$ is the set of words that have already been generated until the time step $t$.

We only use masking in the inference part, as it may influence the normal training process by reducing the punishment of repeated tokens.
Coverage Mechanism

Coverage mechanism was first proposed to help the decoder focus on the part that has not been shed much attention by feeding a fertility vector to the attention calculation.

In our model, we do not use fertility vector to tune the attention weights, as it is explained in the Introduction section that the symptoms are related to others and altogether describe the whole disease. However, inspired by its motivation, we adapt the coverage mechanism to the decoder where a coverage vector is fed to the GRU cell together with the context vector. Equation 4 is then replaced by the following equation.

\[ a_t = \text{tanh}(WD_t + b) \]  
\[ s_t = f(s_{t-1}, c_t, a_t) \]  

where \( a_t \) is the coverage vector at the \( t-th \) time step in decoding. \( D_t \) is the one-hot representation of the generated tokens until the \( t-th \) time step. \( W \in (V \times H) \) is a learnable matrix, where \( V \) is the size of the herb vocabulary and \( H \) is the size of the hidden state. By feeding the cover vector to the GRU cell, which is also a sketch of the generated herbs, our model can softly switch more probability to the herbs that have not been predicted. This way, the model is encouraged to produce novel herbs rather than repeatedly predict the frequently observed ones, thus increasing the recall rate.

5 Experiment

5.1 Experiment Data

To make the experiment result more robust, we conduct our experiment on two separate test datasets. The first one is a subset of the data described in section 3. We randomly split the whole data into three parts, the training data (90%), the development data (5%) and the test data (5%). The second one is a set of symptom-prescription pairs we manually extracted from the text book of the course Formulaology of TCM (中医方剂学) that is popularly adopted by many TCM colleges in China.

There are more cases in the first sampled test dataset (4102), but it suffers from the low quality problem, as this dataset was parsed with simple rules, which may encounter exceptions. The second test dataset has been human proofed and the prescriptions are all most classical and influential ones in the history. So the quality is much better than the first one. However, the number of cases is limited, there are only 141 symptoms-prescription pairs in the second dataset. Thus we use two test sets to do evaluation to take the advantages of both data magnitude and quality.

5.2 Experiment Settings

In our experiments, we implement our models with pytorch toolkit. We set the embedding size of both Chinese characters in the symptoms and the herb tokens to 100. We set the hidden state size to 300, and set the batch size to 20. We set the maximum length of the herb sequence to 20. Unless specifically stated, we use bidirectional gated recurrent neural networks (BiGRNN) to encode the symptoms. The negative log-likelihood loss is applied as the objective function. Adam (Kingma and Ba, 2014) is adopted to optimize the parameters. We tune all the parameters on the development set, and use the model parameters that have generated the best F score on the development set.

We use Precision, Recall rate and F value to evaluate the results, because the internal order between the herbs does not matter when we don’t consider the generating order.

5.3 Proposed Baseline

In this sub-section, we present the Multi-label baseline we apply. In this model, we use a BiGRNN as the encoder, which encodes symptoms in the same way as it is described in Section 4. Because the position of the herbs does not matter in decoding, for the generation part, we implement a multi-label classification method to predict the herbs. We use the multi-label max-margin loss (MultiLabelMarginLoss in pytorch) as the optimization objective. The way to calculate probability is shown below.

\[ p(i) = \sigma(W_o h_T) \]  

where \( \sigma \) indicates the non-linear function sigmoid, \( W_o \in (H \times V) \), \( H \) is the size of the hidden state produced by the encoder and \( V \) is the size of the herb vocabulary. \( h_T \) is the last hidden state produced by the encoder.

During evaluation, we choose herbs satisfying two conditions.

1. The predicted probability of the herb is within top \( k \) among all the herbs, where \( k \) is a
Table 2: Results of different models on the two test datasets. Test set 1 is the subset of the large dataset collected from the Internet, which is homogeneous to the training set. Test set 2 is the test set extracted from the TCM textbook.

| Model               | Test set 1    | Test set 2    |
|---------------------|---------------|---------------|
|                     | Precision     | Recall        | F value  | Precision | Recall | F Value |
| Multi-label         | 10.78         | 28.21         | 15.60    | 14.56     | 41.45  | 21.55   |
| Basic seq2seq       | 28.70         | 8.49          | 13.10    | 37.02     | 15.30  | 21.65   |
| + mask              | 28.39         | 15.06         | 19.68    | 29.59     | 26.57  | 28.00   |
| + coverage          | 30.48         | 11.14         | 16.31    | 40.73     | 20.30  | 27.09   |
| + mask & coverage   | 25.82         | **18.33**     | **21.44**| 32.42     | **31.35**| **31.88**|

hyper-parameter. We set $k$ to be the same as the maximum length of seq2seq based models.

2. The predicted probability is above 0.5 (related to the max-margin).

5.4 Experiment Results

In Table 2 we show the results of our proposed models as well as the baseline models. One thing that should be noted is that since the data in Test set 2 (extracted from text book) has much better quality than Test set 1, the performance on Test set 2 is much higher than it is on Test set 1, which is consistent with our instinct.

From the experiment results in Table 2 we can see that the baseline Multi-label model has high recall rate 28.21,41.45. However, its low precision drags the F value down to 15.60 and 21.55. This means that the model generates too many tokens than there actually needs.

For the performance of the basic seq2seq model, it even achieves lower F value because of the unacceptable low recall rate. This problem is mainly caused by the repetition problem, the basic seq2seq model often predicts some high frequent tokens instead of more meaningful ones. We have tried to add a simple extra loss to penalize producing repetitive terms, but it would lead to the consequence of producing nothing but $<EOS>$. We think the reason of this drawback is that the embeddings of the herbs are similar, directly penalizing existed herbs would discourage the tendency of producing the right tokens too.

After adding a mask to the probability outputs layer, the recall rate gains a large improvement ($8.49 \rightarrow 15.06$, $15.30 \rightarrow 26.57$), although the precision may decrease. Still, this is a cost worth taking, as the F value is largely improved on both of the two test sets ($13.10 \rightarrow 19.68$, $21.65 \rightarrow 28.00$).

For the coverage mechanism, the performance also gains consistent improvement on both test sets (F value $13.10 \rightarrow 16.31$, $15.30 \rightarrow 26.57$). Different from adding a mask, which is simpler and more direct, the coverage vector implicitly indicates what tokens have been generated. This model lets the network (the GRU part) itself determine how to make use of this information. An improvement of precision is also observed compared with the basic seq2seq model on both test sets. This may be because the coverage vector not only tells what tokens have been generated, but also provides a sketch of the generated prescription.

By utilizing both the masking and coverage mechanism, we get the best F value on both test sets ($21.44$, $31.88$), which is much higher than the basic seq2seq model and the multi-label model.

![Figure 2: An illustration of the distribution of length of the generated results and the length of the reference](image)

We can analyze the effect of adding masking and coverage mechanism from another aspect — the length of the generated sequence length. Intuitively, the longer the generated sequence is,
Table 3: Actual predictions made by various models in test set 2. Multi-label model generates too many herb tokens, so we do not list all of them here. Reference is the standard answer prescription given by the text book.

| Reference          | 大黄、厚朴、积实、芒硝 |
|--------------------|------------------------|
| Candidate - Multi-label | 朱砂、知母、陈皮、槟榔、朴硝、滑石、甘草、栀子 etc. |
| Candidate - Basic seq2seq | 大黄、芒硝×9 \langle EOS \rangle |
| Candidate - seq2seq + mask    | 大黄、芒硝、栀子、积实 \langle EOS \rangle |
| Candidate - seq2seq + coverage | 大黄×4、积实、黄芩、当归、大黄×2、甘草 \langle EOS \rangle |
| Candidate - Multi-label + mask & coverage | 大黄、芒硝、积实、当归、积壳 \langle EOS \rangle |

the more diverse the output is, and hopefully the higher recall rate one may achieve. In Figure 2, we show the length of the generated sequence, which are guaranteed to have no repetitive tokens with post-processing and the token \langle EOS \rangle is excluded.

From Figure 2 we can see, the length of the longest sequence of reference (gold sequence) is much higher than the results from all our models (16), which means even with masking and coverage mechanism our model may still not be aggressive enough. However, the length of our final model has a similar average length with the reference (6.5’6.7), which means our final model has a close expressing ability with the gold (human practitioner). Furthermore, adding masking and coverage mechanism can all consistently increase both the average and maximum length of the generated sequence compared with the basic seq2seq model, which verifies the ability of masking and coverage mechanism work correspondingly with our expectation.

5.5 Case Study

In this sub-section, we show an example generated by various models in the Table 3 in test set 2 because the quality of test set 2 is much more satisfactory. \langle EOS \rangle is used to determine when to stop the generation process, which is not included when calculating statistical evaluations (precision, etc.). The multi-label model produces too many herbs that lowers the precision.

For the basic seq2seq model, it produces two herb tokens which are right. However, it heavily suffers from the repetition problem. The model doesn’t stop until producing 芒硝 (Mirabilite) for nine times. We assume that this repetition problem restricts the model from producing more herb tokens which are be as probable as the first two tokens, but are still sensible.

The masking adds a strict restriction to forbid repeatedly generating same herb tokens, this can be reflected from the results produced by the seq2seq + mask model shown in Table 3. The last two herbs 栀子 (Cape Jasmine Fruit)、积壳 (Fructus Aurantii) are actually related to the symptoms and this variant of the original prescription can be used to deal with other similar disease.

The coverage mechanism seems to make the model more aggressive. It produces five different herb tokens. The token 积实 (Fructus Aurantii Immaturus) is properly included in the prescription. However, this model still produces a lot of repetitive tokens like 大黄 (Rhubarb). This herb can actually be seen as the most important component to cure the disease, which is consistent to the fact that most models predict the herb 大黄 (Rhubarb).

The results from our final model are the closest combination to the gold prescription, which properly generates 大黄 (Rhubarb)、芒硝 (Mirabilite)、积实 (Fructus Aurantii Immaturus), but leaves out 厚朴 (Magnolia officinalis). Actually, all of the models fail to produce this herb, maybe this is because that this way of combining herbs is rare, or the symptoms are rarely connected with this herb in the training data.

6 Conclusion

In this paper, we propose a TCM prescription generation task that is designed to predict the herbs in a prescription corresponding to symptoms descriptions. To our knowledge, this is the first time that this critical and practicable task has been concerned.

Directly applying seq2seq model would lead to severe repetition problem which lowers the recall rate. We propose to use seq2seq framework en-
hanced with masking and coverage mechanism to solve this problem. From the experimental results we can see that this method can alleviate the repetition problem while improving recall rate. We hope this work can lay a foundation and encourage more researchers to pay attention to automatic TCM treatment.

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