FIT: a Fast and Accurate Framework for Solving Medical Inquiring and Diagnosing Tasks

Weijie He*, 1 Xiaohao Mao*, 1 Chao Ma, 2 José Miguel Hernández-Lobato, 2, 3 Ting Chen1

1 Department of Computer Science & Institute of Artificial Intelligence & BRNist, Tsinghua University, Beijing, China 100084
2 Department of Engineering, University of Cambridge
3 Microsoft Research Cambridge

{hwj19,mxh19}@mails.tsinghua.edu.cn, {cm905,jmh233}@cam.ac.uk, tingchen@tsinghua.edu.cn

Abstract

Automatic self-diagnosis provides low-cost and accessible healthcare via an agent that queries the patient and makes predictions about possible diseases. From a machine learning perspective, symptom-based self-diagnosis can be viewed as a sequential feature selection and classification problem. Reinforcement learning methods have shown good performance in this task but often suffer from large search spaces and costly training. To address these problems, we propose a competitive framework, called FIT, which uses an information-theoretic reward to determine what data to collect next. FIT improves over previous information-based approaches by using a multimodal variational autoencoder (MV AE) model and a two-step sampling strategy for disease prediction. Furthermore, we propose novel methods to substantially reduce the computational cost of FIT to a level that is acceptable for practical online self-diagnosis. Our results in two simulated datasets show that FIT can effectively deal with large search space problems, outperforming existing baselines. Moreover, using two medical datasets, we show that FIT is a competitive alternative in real-world settings.

Introduction

In healthcare, self-diagnosis through online services is a promising approach for reducing costs and still maintaining wide accessibility. However, online search-based services for self-diagnosis often return irrelevant information and sometimes absurd results. With the explosive development of mobile internet and big data techniques, the need for online self-diagnosis in the healthcare domain has increased. A growing number of adults first attempt to self-diagnose their illness or diseases through online search services instead of walking into a hospital. According to a 2012 survey (Semigran et al. 2015), 35% of U.S. adults regularly use the internet to self-diagnose.

As described by Ledley and Lusted (1959), a disease-diagnosis process includes three sequential steps: (i) a patient presents an initial symptom, (ii) a doctor inquires a patient with a series of reasonable questions, (iii) a final diagnosis for a disease is given by the doctor. In the case of online self-diagnosis, the above process is referred to as symptom checking and it is an agent who implements inquiry and diagnosis instead of the doctor. Figure 1 presents the logical components of symptom checking.

From the healthcare perspective, high disease-prediction accuracy is the primary aim of symptom checking. High accuracy requires a long list of possible symptoms. For example, most existing questionnaire systems acquire a large number of symptom values from the patient through exhaustive questions (Shim, Hwang, and Yang 2018; Lewenberg et al. 2017). This is inefficient and time consuming for both the patient and the expert. Therefore, the other design goal of symptom checking is efficiency; in other words, the number of inquiries should be as low as possible.

From the machine learning perspective, symptom checking can be viewed as a sequential feature selection and classification problem. Reinforcement learning (RL) methods have shown good performance in this task (Tang et al. 2016; Kao, Tang, and Chang 2018; Peng et al. 2018; Xia et al. 2020). However, they often suffer from large search spaces and struggle during training. An alternative is given by EDDI, a framework for instance-based active feature acquisition (Ma et al. 2019), which chooses the next feature to observe by maximizing a defined information reward over all features. EDDI uses a Partial VAE to handle data with missing values. Such a model can deal with the situation where an agent just knows part of the information from patients while inquiring. Although promising, the EDDI framework is limited by its high computational cost when the number of symptoms is very high.

To address these problems, we propose FIT, a competitive
framework to automate symptom-based self-diagnosis based on EDDI. The contributions of this paper are:

- A novel and practical framework for symptom checking. FIT has two main advantages over previous RL methods. First, FIT can make predictions at any step of the self-diagnosis process and achieve high performance, while the previous RL methods only return the disease prediction at the end of inquiry. Second, FIT is more suitable for real-life diagnosis since it can handle large disease spaces better than RL baselines, which typically struggle in those settings.

- Improvements on model. Instead of VAEs (Kingma and Welling 2013), we use a multi-modal variational autoencoder (MVAE) (Wu and Goodman) as a probabilistic model for dealing with partially observed data. The main difference of MVAE over the original VAE (Kingma and Welling 2013) is that it uses a product of experts (PoE) encoder. Furthermore, to make better predictions, we adopt a two-step sampling strategy. Both MVAE and our two-step sampling strategy significantly improve the accuracy of disease diagnosis.

- Significant speed-up of computations. We accelerate the inquiry steps so that they take less than one second on average, making our framework practical in real-life settings. At any inquiry step, we first ignore irrelevant symptoms that are unlikely to co-occur with the ones currently observed and second, when computing the information reward, we ignore the contribution of symptoms whenever they are predicted to be not present given the current context. Both modifications can reduce the time cost of our self-diagnosis framework by three orders of magnitude.

### Background

#### Problem Formulation

In this paper, we consider the following feature acquisition problem: given a data point $x$, we are interested in predicting the target variables of interest $x_o \subset x_i$ given corresponding observed features $x_O$ ($x_o \cap x_O = \emptyset$), where $x_O$ is the set of observed variables, and $x_i$ are the unobserved ones. More specifically, we consider which variable $x_i \in x_i \setminus x_o$ to observe next, so that our belief regarding $x_o$ can be optimally improved.

#### Variational AutoEncoder (VAE)

A variational autoencoder (VAE) (Kingma and Welling 2013) defines a generative model of the form $p(x|z) = \prod_i p_i(x_i|z)p(z)$ in which the data $x$ is generated from latent variables $z$, $p(z)$ is a prior, e.g., spherical Gaussian. $p_i(x_i|z)$ is given by a neural network decoder with parameters $\theta$, which specify a simple likelihood, e.g., Bernoulli. A VAE uses another neural network with parameters $\Phi$ as an encoder to produce a variational approximation of the posterior, that is, $q_\phi(z|x)$. A VAE is trained by maximizing an evidence lower bound (ELBO):

$$E_{q_\phi(z|x)}[\log p_\theta(x|z)] - \beta \cdot D_{KL}[q_\phi(z|x) \parallel p(z)], \quad (1)$$

where $\beta$ is the weight to balance the two terms in the expression. The ELBO is usually optimized by stochastic gradient descent using the reparameterization trick (Kingma and Welling 2013).

#### EDDI Framework Formulation

EDDI is a recently proposed solution (Ma et al. 2019) that is designed to solve the formulated feature acquisition problem efficiently using a VAE. EDDI chooses the next feature $x_i$ to observe by maximizing over $i$ the information reward

$$R(i, x_O) = E_{x_i \sim p(x_i|x_O)} D_{KL} [p(x_o|x_i, x_O) \parallel p(x_o|x_O)], \quad (2)$$

where $D_{KL}$ is the Kullback-Leibler divergence between two distributions. The conditionals $p(x_i|x_O)$, $p(x_o|x_O, x_i)$, and $p(x_o|x_O)$ are described by a VAE. Unfortunately, estimating the values of these quantities in Eqn. (2) is too expensive in practice. To avoid this problem, Ma et al. (2019) show that Eqn. (2) can be estimated efficiently by using VAE encoding distributions:

$$\hat{R}(i, x_O) = E_{x_i \sim p(x_i|x_O)} D_{KL} [q(z|x_i, x_O) \parallel q(z|x_O)] - E_{x_o, x_i \sim p(x_o, x_i|x_O)} D_{KL} [q(z|x_o, x_i, x_O) \parallel q(z|x_o, x_O)], \quad (3)$$

where $q(\cdot)$ is the encoder function of the underlying VAE model. The encoder is parameterized by a permutation invariant set function (detailed in the next section), so that it is able to produce a Gaussian approximation of the posterior of $z$ conditioned on any set of observed variables. The first term of Eqn. (3) quantifies how much information $x_i$ provides about $z$, and the second term quantifies how much information $x_i$ provides about $z$ in addition to $x_o$. A feature $x_i$ will be penalized by the second term, if it is informative about $z$ but not about $x_o$. All quantities in the KL divergences above can be computed analytically thanks to the Gaussian approximations. The expectations in Eqn. (3) can be approximated by Monte Carlo, by averaging over samples $x_o, x_i \sim p(x_o, x_i|x_O)$ that can be shared between the two terms in Eqn. (3). The number of samples is denoted as $M$.

### Methodology

In this section, we first introduce our improvements on the model and sampling scheme of the EDDI framework, and then elaborate on how to accelerate computations in the case of disease diagnosis. A summary of our FIT framework is presented at the end.

#### Model

During active variable selection, the inference network of the VAE should be capable to handle arbitrary partial observations of feature variables. The EDDI framework (Ma et al. 2019) proposed a permutation invariant set function, given by

$$c(x_O) := g(h(s_1), h(s_2), ..., h(s_{|O|})), \quad (4)$$

where $|O|$ is the number of observed variables and $s_i$ is obtained from the product of the feature value $x_i$ and an embedding vector $e_i$ describing the $i$-th feature. The value of
the embedding vector is optimized during training together with the recognition network. \( h(\cdot) \) is a neural network and \( g(\cdot) \) is summation or max-pooling operation.

**Product of Experts (PoE) Encoder** The Multimodal Variational Autoencoder (MVVAE) was proposed by Wu and Goodman (2018) to capture a joint distribution across data modalities and uses a PoE encoder with the recognition network. The MV AE assumes conditional independence among data modalities and flexibly support missing multimodal data. Goodman (2018) to capture a joint distribution across data.

The MVVAE encodes and decodes the input data, and the PoE encoder is designed to handle missing data. In our implementation of the PoE encoder, we first, construct \( s_i \) by concatenation: \( s_i = [x_i, e_i] \), which is widely used in the computer vision domain (Qi et al. 2017). Then we use an MLP with 4 hidden layers as \( h(\cdot) \) to map the input \( s_i \) to a factorized Gaussian distribution in latent space with mean vector \( \mu_i \) and marginal standard deviation \( \sigma_i \). Because a product of Gaussian experts is itself Gaussian (Cao and Fleet 2014), when \( p(z) \) and \( q(z|x_i) \) are Gaussian, we can compute the mean and covariance parameters for the distribution in Eqn.\([5]\) easily:

\[
\mu = \left( \sum_{t=1}^{O} \mu_t T_i \right) \left( \sum_{t=1}^{O} V_t^{-1} \right)^{-1}, \quad \Sigma = \left( \sum_{t=1}^{O} V_t^{-1} \right)^{-1},
\]

where \( \mu \) and \( \Sigma \) are the mean vector and covariance matrix, respectively. The structure of our PoE encoder is illustrated in Figure\([2]\) The decoder, \( p(x|z) \), is given by a product of Bernoulli distributions whose probabilities are specified by a 4-layer MLP that receives as input \( z \).

Given a dataset with no missing variables, if we trained the PoE encoder on all the available data, its performance would then be poor when the input presents missing entries since the PoE encoder never dealt with such situation.

**Algorithm 1 Overview of FIT framework.**

**Require:** Training dataset \( X \); Test dataset \( X^* \) with no observations; Indices \( \phi \) of target variables(diseases).

1: Train VAE with PoE encoder and classifier \( C(\cdot) \) on \( X \)
2: Actively acquire symptom \( x_i \) to estimate \( x_i^o \) by \( C(\cdot) \)

for each test point:

for each test point do

\( x_O \leftarrow \{x_y\} \) (initial symptom)

\( S \leftarrow S_y \)

repeat

for every symptom \( x_i \) in \( S \) do

\( m \leftarrow 0 \)

repeat

// Two-step sampling

\( \hat{z} \sim q(z|x_O) \)

\( x_i \sim \tilde{p}(x_i|z) \)

\( \hat{R}_{ts} \leftarrow 0 \)

if \( x_i \) is positive then

\( x_O \sim C(x_i,x_O) \)

\( \hat{R}_{ts} \leftarrow E\text{qn.}[3] \)

end if

\( m \leftarrow m + 1 \)

until \( m = M \)

\( \hat{R}_t \leftarrow \frac{\sum_{i\in S} \hat{R}_{ts}}{M} \) // Positive attention reward

end for

choose symptom \( x_i \) with maximum reward \( \hat{R}_t \)

\( x_O \leftarrow x_i \cup x_O \)

if \( x_i \) is positive then

\( S \leftarrow S_i \cap S \) // Filtering irrelevant symptoms

end if

until reaching maximum steps \( T \) or \( \hat{R}_t < \epsilon \)

end for

at training time. To address this, we follow Wu and Goodman (2018) and drop a random fraction of the fully observed variables for each data point during training. Later, we report experiments on active variable selection that show that this encoder out-performs the original EDDI encoder described in Eqn.\([4]\).

Note that we may want to make predictions for possible diseases at any step of the feature collection process. This is something that RL methods are sub-optimal at since they use a classifier that is trained to make predictions once the RL agent stops collecting data and not at any stage of the data collection process. FIT does not have this problem. In particular, in FIT, we denote by \( C(\cdot) \) the function returning the disease prediction probabilities \( p(x_\phi|x_i,x_O) \). We use an MLP classifier with 4 hidden layers as the \( C(\cdot) \). In contrast to the training of VAE, we train \( C(\cdot) \) on the complete data. Therefore, to make predictions, the missing variables of input are imputed by zero when fed into \( C(\cdot) \). Our experiments show that the imputation would not affect the accuracy of disease-prediction.

**Two-step Sampling Strategy** To estimate the information reward, we approximate expectations by Monte Carlo. In
particular, we average over samples \( \hat{x}_\phi, \hat{x}_i \sim p(x_\phi, x_i | x_O) \).
This can be implemented by first sampling \( \hat{z} \sim q(z|x_i) \), and then
\( x_\phi, \hat{x}_i \sim \tilde{p}(x_\phi, x_i | \hat{z}) \), where \( \tilde{p}(x_\phi, x_i | \hat{z}) \) is the decoder
network in the EDDI VAE. However, we propose a better
sampling method for FIT, which samples \( \hat{x}_i \) and \( x_\phi \) in two
steps. Note that
\[
p(x_\phi, x_i | x_O) = p(x_\phi | x_i, x_O) \cdot p(x_i | x_O).
\] (7)
Therefore, we propose to sample \( \hat{x}_i \) from the VAE by sampling
\( \hat{z} \sim q(z|x_O) \), and then \( \hat{x}_i \sim \tilde{p}(x_i | \hat{z}) \). Next we sample
\( x_\phi \) from \( C(\hat{x}_i, x_O) \). In this way we are actually using two
networks (the VAE decoder and \( C(\cdot) \)) to decompose the
approximation of the joint posterior. By combining the generative
model and the classification model we can help improve
the performance of entire framework. Our experiments (Table 2)
show that this two-step sampling process provides better
than the original approach.

**Speedup**
The computational cost of the EDDI framework [Ma et al. 2019] is \( O(T \cdot N \cdot M) \), where \( T \) is the number of maximum
inquiry steps, \( N \) is the number of total features, and \( M \) is the
number of samples used in the Monte Carlo approximation.
In practice, this is too high for an online service. In what
follows, we show how we can reduce the cost by a large
amount by taking advantage of feature sparsity.

**Filtering Irrelevant Symptoms** At each step, the EDDI
framework chooses variable \( x_i \) from \( U \setminus \phi \) to maximize the
information reward. Under the setting of inquiry for symptoms,
we can filter irrelevant symptoms to reduce the number
of variables that need to be queried. For example, if a
patient comes to visit a doctor with a broken leg, the first
question from the doctor shall not be "Do you cough a lot?".

For every symptom \( i \), we calculate the set \( S_i \) of additional
symptoms which may appear together with symptom \( i \) in one patient with high probability, according to training
data statistics. More specifically, a symptom \( j \in S_i \) if
\( p_{data}(x_j = 1 | x_i = 1) \) is larger than a given threshold \( p \).
We simply set \( p \) to 0 in experiments. The set of candidate
symptoms is initialized to \( S_i \) when symptom \( i \) is present at
the beginning of the inquiry. Every time the framework
selects an additional positive symptom \( j \), we update the set of
candidate symptoms to be the intersection of the current set
and \( S_j \) (see Algorithm 1).

**Attention on Positive Symptoms** The number of symp-
toms that a patient of a certain disease suffers from is much
smaller than the number of possible symptoms for the dis-
ease. With such a sparse feature space, the inquiry process
should acquire positive symptoms, otherwise there is not
enough evidence for the diagnosis component to perform ac-
curate predictions [Peng et al. 2018]. Motivated by this, we
encourage FIT to discover positive symptoms, which drasti-
cally reduces computational cost without degrading predic-
tion accuracy.

We implement the previous approach when evaluating the
information reward of symptom \( i \). For this, we first obtain
\( M \) samples \( \hat{x}_i \) from \( x_i \sim p(x_i | x_O) \). Then, for each \( \hat{x}_i \)
that is positive, we sample a corresponding \( x_\phi \), and evaluate
\( \hat{R}(i, x_O) \) according to Eqn. 3 with expectations replaced
by evaluations on \( \hat{x}_i \) and \( x_\phi \). By contrast, \( \hat{R}(i, x_O) \) is zero
for each negative \( \hat{x}_i \). The information reward is then
\[
\hat{R}_i = \frac{\sum_{m : \hat{x}_{im} = 1} \hat{R}_{im}}{M}
\] (8)
and, unlike in EDDI, we do not average across all samples.

The two previous techniques result in a speed-up of 1000x
experimentally.

**Overview of the FIT Framework**
Algorithm 1 illustrates how the FIT framework is imple-
mented in practice by combining the previous techniques,
where \( \epsilon \) is a small threshold that determines when to stop
and that we set to \( 10^{-4} \).

**Related Work**

**Bayesian Inference and Tree-Based Methods** There is
a significant amount of previous work dealing with self-
diagnosing. One large family of models applies Bayesian
inference and tree-based methods [Kononenko 1995, 2001
Xu et al. 2013, Kohavi 1996], which use entropy functions
to pick symptoms on the basis of the theory of informa-
tion gain. For instance, Nan, Wang, and Saligrama [2013
2016] and Zakim et al. [2008] proposed to address the cost
of feature acquisition by using decision tree and random for-
est methods. In addition to this, [Hayashi 1991] attempted
to extract rule-based representations from medical data and
human knowledge with the goal of performing disease diag-
nosis. Since the global maximization of the information gain
RL Based Method  Recently Janisch, Pevny, and Lisy (2019) show that reinforcement learning (RL) methods outperform tree-based methods in the task of sequential feature acquisition with a given cost function. In particular, Tang et al. (2016) first formulated the inquiry and diagnosis process as a Markov decision process and used RL to perform symptom checking based on a simulated environment and data. More recently, Peng et al. (2018), Kao, Tang, and Chang (2018) and work first with simulated medical data. For this, we use the SymCAT symptom-disease database (AHEAD Research Inc, 2017), which consists of 801 diseases and 474 symptoms in total. For each disease in SymCAT, you have information about its symptoms including the symptom marginal probabilities. The simulation process first samples a disease and its related symptoms from the set of all diseases. Then, symptoms are generated by performing a Bernoulli trial on each extracted symptom according to its corresponding probability. For instance, if the disease “abscess of nose” is first sampled, and the probabilities of “cough” and “fever” under “abscess of nose” are 73% and 62% respectively, we obtain one data instance by sampling Bernoulli random variables according to these probabilities.

As in the experiments by Peng et al. (2018), we sample $10^4$, $10^5$ and $10^6$ data points for training, validation and testing. We use Adam (Kingma and Ba, 2014) as optimizer. The initial learning rate is $10^{-4}$ and the batch size is 128.

To evaluate the performance of FIT, we follow Peng et al. (2018) and form three different disease diagnosis tasks, which contain respectively 200, 300 and 400 diseases to discriminate among. The number of possible symptoms is more than 300 while the average number of positive symptoms per patient is about 3. More properties of the dataset are listed in Table ?? in the Appendix. Typically, it is very hard to identify positive symptoms. Hence, besides predictive accuracy, we also report the average number of inquired positive symptoms, which we abbreviate as AIPS. At the beginning of the inquiring process, one positive symptom is chosen uniformly at random among the positive symptoms for that patient in particular, as a patient self-report. Therefore, the maximum AIPS is about 2. The experiments shown below are implemented by applying the speedup techniques mentioned in the previous section.

Figure ?? shows how accuracy and AIPS change as the number of inquiry steps increases on 1000 simulated patients. $M$ is selected to be 200. It can be found that, when the number of inquiry steps is less than 15, the four curves

Table 1: Performance of REFUEL (Peng et al. 2018) and FIT framework on synthetic SymCAT dataset. The results of FIT framework are shown in percentage with a 95% confidence interval.

| #Diseases | Method        | Top1     | Top3     | Top5     | AIPS     | #Steps |
|-----------|---------------|----------|----------|----------|----------|-------|
| 200       | EDDI          | 56.21 ± 0.18 | 81.66 ± 0.13 | 89.67 ± 0.13 | 2.00 ± 0.00 | 13.67 ± 0.00 |
| 300       | EDDI          | 47.86 ± 0.22 | 73.51 ± 0.18 | 83.68 ± 0.17 | 1.85 ± 0.00 | 13.83 ± 0.00 |
| 400       | EDDI          | 44.50 ± 0.17 | 68.78 ± 0.11 | 79.16 ± 0.15 | 1.78 ± 0.00 | 14.86 ± 0.00 |

Table 2: Ablation study of the PoE encoder and two-step sampling scheme, on the SymCat dataset. The results are shown in percentage with a 95% confidence interval.

| #Diseases | Method                      | Top1     | Top3     | Top5     | AIPS     | #Steps |
|-----------|-----------------------------|----------|----------|----------|----------|-------|
| 300       | EDDI                        | 33.6 ± 0.6 | 56.9 ± 0.9 | 71.3 ± 0.8 | 1.06 ± 0.01 | 9.25 ± 0.03 |
|           | EDDI + two-step sampling    | 34.6 ± 0.4 | 57.8 ± 0.6 | 72.5 ± 0.8 | 1.13 ± 0.02 | 9.52 ± 0.04 |
|           | EDDI + PoE                  | 47.7 ± 0.6 | 71.5 ± 0.4 | 82.6 ± 0.4 | 1.88 ± 0.01 | 13.85 ± 0.01 |
|           | EDDI + two-step sampling + PoE| 48.3 ± 0.4 | 72.0 ± 0.4 | 82.7 ± 0.5 | 1.91 ± 0.01 | 13.85 ± 0.01 |
| #Diseases | FIT (without speedup) | FIT (with FIS) | FIT (with FIS and APS) |
|-----------|-----------------------|---------------|-----------------------|
| 200       | 4,815,368 × 200 (1.0) | 766,573 × 200 (6.3) | 1,048,605 (918.4)   |
| 300       | 5,168,341 × 200 (1.0) | 994,136 × 200 (5.2) | 1,097,482 (941.9)   |
| 400       | 5,634,915 × 200 (1.0) | 1,317,205 × 200 (4.3) | 1,246,399 (904.2)   |

Table 3: Ablation study of the proposed speedup scheme on SymCat. "FIS" refers to "Filtering Irrelevant Symptoms" and "APS" is the abbreviation of "Attention on Positive Symptoms".

Figure 4: Distribution of information reward among several symptoms in first three inquiry steps. The symptoms with maximum reward are marked with star in every step. The initial symptom is "Nasal Congestion". "SAP" means "sharp abdominal pain". "SB" means "shortness of breath". "CO" means "cough". "FV" means "fever". "ST" means "sore throat". "EP" means "ear pain". "HA" means "headache". "WZ" means "wheezing". "PE" means "pain in eye". "IE" means "itchiness of eye".

in the figure all show the tendency of fast rising. And when the number of inquiry steps exceeds 15, the four curves still increase, but with less speed. When it gets to 30, all positive symptoms are almost inquired since AIPS reaches around 2. According to this, to perform as few steps as possible, we set the number of maximum inquiry steps to 14, 14 and 15 respectively for the tasks with 200, 300 and 400 diseases on 10,000 test patients, and report results in Table [1] where is selected to be 200. We choose REFUEL (Peng et al. 2018), a SOTA reinforcement learning method on the synthetic SymCAT dataset, as a baseline. We can see that FIT outperforms REFUEL in every metric. In particular, the Top3 and Top5 accuracies are increased by at least 8 percent units. It is worth noting that the number of inquiry steps cannot be fixed, especially increased, in the RL-based method, which makes it unsuitable for some applications.

We study changes in accuracy and AIPS in FIT as the number of Monte Carlo samples is increased. Figure ?? with these results can be found in the Appendix. The figure shows that it is reasonable to choose values of M that range from 200 to 400.

We performed an ablation study to investigate the effects of the PoE encoder and the two-step sampling strategy on the task with 300 diseases. We generated 1000 test patients and set M as 200. The number of maximum inquiry steps is selected as 14. The EDDI framework tends to stop early. At the same time, the PoE encoder seems to provide a narrower confidence interval, i.e. a more stable result. Finally, Table 2 shows that the two-step sampling strategy produces improvements in accuracy and AIPS in both tasks, especially in Top1 and AIPS, although in this case the gains are smaller.

Note that FIT could be easily extended to handle comorbidity, i.e. suffering from multiple diseases. In this case the different disease variables are considered to be independent. For the extension, all we need to change is to train a multi-label classifier instead of a multi-class one. Since we have not sought out appropriate data, we did not experiment with this possibility.

Speedup Ratio We performed another ablation study to show the acceleration given by the different elements within the proposed speedup scheme (filtering irrelevant symptoms and attention on positive symptoms). We generated 1000 simulated patients from SymCAT and set M as 200. The number of maximum inquiry steps is selected as 14. The results are presented in Table [2] Each entry in the table contains the number of samples used to calculate the information reward, which is the most time-demanding operation. The numbers in parenthesis are speed-up ratios as compared with the numbers in the first column. For instance, in the task with 200 diseases, without speedup, the EDDI framework checks over 4,815,368 symptoms totally, each requiring to draw 200 Monte Carlo samples to estimate the information reward. After filtering irrelevant symptoms, the sum of checked symptoms drops to 766,573 with 6.3 times less cost. If we only focus on the positive samples, the number of Monte Carlo samples that are used to calculate the reward for each candidate symptom is much lower than 200. The total number of samples is 1,048,605, which translates
in 918.4 times less computational cost than the EDDI framework. This large reduction in cost allows each inquiry step to take less than one second on average.

We also performed a case study to show that Attention on Positive Symptoms makes little difference on the computed information reward values and on the actual symptoms queried by the framework. Figure 4 shows the partial distribution of information reward among different symptoms in the first three inquiry steps. The test data point is from the SymCAT task with 200 diseases and corresponds to a patient that suffers from Common Cold. The number of maximum steps was fixed to 14 and M was set to 200. A comparison for all inquiry steps is listed in Table ?? in the Appendix.

**Rare Diseases**

The Human Phenotype Ontology (HPO) provides a standardized vocabulary of phenotypic abnormalities for human disease. So far, HPO includes over 13,000 terms and 156,000 expert annotations to human hereditary diseases, obtained from multiple sources (the medical literature, Orphanet, DECIPHER, and OMIM). We downloaded diseases and related symptoms from the public rare disease dictionary, which includes 11,441 diseases and 13,032 annotated symptoms. We considered two different diagnosis tasks, each containing 500 and 1000 diseases to discriminate among. Our goal is to evaluate FIT in settings in which the number of symptoms is higher and closer to real-life applications: the number of symptoms is now 6 times larger than in SymCAT. More properties of the dataset are listed in Table 5.

For these experiments, we generated 10,000 patients and set the maximum inquiry steps to 10 and 15 for the tasks with 500 and 1000 diseases, respectively. M was fixed to 100. While training REFUEL, the numbers of maximum inquiry steps are set to 14 and 18 respectively. We show results for FIT and REFUEL in Table 4. In this case, FIT outperforms REFUEL by a larger magnitude than before, with FIT’s accuracy being at least 10 percent units larger and the number of steps not increasing much when compared to REFUEL.

**Two Real-life Dialogue Datasets**

Wei et al. (2018) constructed the MuZhi Medical Dialogue dataset, which uses collected dialogue data from the pediatric department of a Chinese online healthcare website[2] MuZhi includes four diagnosed diseases: children’s bronchitis, children functional dyspepsia, infantile diarrhea infection and upper respiratory infection. There are 710 conversational data points, each representing a different patient, and 66 symptoms in total.

The Dxy Dialogue Medical dataset (Xu et al. 2019) contains data from a prevalent Chinese online healthcare website[3] where people often inquire experts for professional medical advice. This dataset contains 527 dialogue data points, each one representing a different patient, five diagnosed diseases and 41 specific symptoms.

Table 6 shows results for GAMP (Xia et al. 2020), which uses GAN to implement an RL agent, and FIT on Dxy and MuZhi. FIT was implemented by setting M to 100 and the average inquiry steps to 16 and 11 for MuZhi and Dxy, respectively. These results show that FIT has competitive performance on these two real-life datasets, with slightly better accuracy when compared to GAMP.

**Conclusion**

We have proposed FIT, an information-based framework for fast and accurate disease self-diagnosis, which shows better performance than prior methods (Tang et al. 2016; Peng et al. 2018; Ma et al. 2019; Xia et al. 2020). We adopt a PoE Encoder to efficiently handle missing data and design a two-step sampling strategy to improve the quality of the generated samples. Both contributions result in higher disease diagnosis accuracy. We slightly modify previous calculations of the information reward to significantly speed up inference to a level that is practical in real-life settings while maintaining good disease-prediction accuracy. As the experiments show, our results in two simulated datasets, SymCAT and HPO, outperform existing baselines, and reveal that FIT can effectively deal with large search space problems at a

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[2]https://muzhi.baidu.com
[3]https://dxy.com/
small cost of time. Furthermore, we evaluate FIT on two real-life datasets and achieve a competitive performance.

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