

# Towards Examining Learner Behaviors in a Medical Intelligent Tutoring System: A Hidden Markov Model Approach

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**Abstract**— In BioWorld, a medical intelligent tutoring system, novice physicians are tasked with diagnosing virtual patient cases. Although we are often interested in considering whether learners diagnosed the case correctly or not, we cannot discount the actions that learners take to arrive at a final diagnosis. Thus, the consideration of the sequence of actions becomes important. In this preliminary study, we propose a line of research to investigate learner actions involved in diagnosing virtual patient cases using Hidden Markov Models.

**Keywords**—*learner modeling, intelligent tutoring systems, hidden markov models*

## I. INTRODUCTION

Although much research has been conducted on clinical reasoning, most studies tend to focus on whether learners diagnosed the disease correctly or not. While it is important to consider diagnosis correctness, these studies do not take into account how the learners arrived at the diagnosis. The learning trajectory, i.e., actions that learners take, holds considerable information that can be useful for learner modeling and for improving learning systems. Biswas et al. [1] recommend that shifting focus from the frequency and relevance of learner activities to considering the internal states and related learning strategies, can be useful in illuminating additional information for examining learning in learning systems. A sizable body of research has investigated clinical reasoning, but heretofore, no studies have proposed the use of modeling techniques like Hidden Markov Models (HMMs) for evaluating the clinical reasoning process of learners. Recent research in computer-supported education has leveraged data mining techniques for examining varied problems [2]. One method that has proven useful in investigating a range of problems is HMMs [3]. A survey of the literature reveals examples of the use of HMM in educational contexts with success; Beal et al. [4] applied HMM for determining the level of engagement in a tutoring system for high school mathematics to predict the subsequent action. Similarly, Jeong et al. [5] employed HMM in predicting transitions between learner activities in a teachable agent environment and demonstrated the efficacy of HMMs in ascertaining learners' pattern of activities. Employing HMM analysis may facilitate considerable progression and

improvements in learner modeling by providing an alternate understanding of learner activities.

## II. LEARNING ENVIRONMENT: BIOWORLD

Gaining clinical reasoning skills is crucial for medical students. Clinical reasoning is a complex and ill-defined task, thus requiring training and practice. BioWorld (figure 1) is a medical intelligent tutoring system designed to support medical students by affording them an opportunity to practice their diagnostic skills with virtual patients [6]. BioWorld comprises four major spaces (Problem, Chart, Library, and Consult). In the 'Problem' space, the learner is provided a case history, which describes the patient symptoms and other relevant details. In solving the patient case, the learner reviews the patient summary, gathers evidence by highlighting relevant symptoms, and formulates a differential diagnosis (using the Hypothesis Manager Tool), along with updating their level of confidence in the diagnosis (via the Belief Meter). In the 'Chart' space, learners can review patient's vital signs and order lab-tests (results of lab tests are recorded in the Evidence Table). Learners can seek help, if necessary, via the 'Library' and 'Consult' tools. The final step involves submitting a final diagnosis, prioritizing evidence, and writing a case summary.

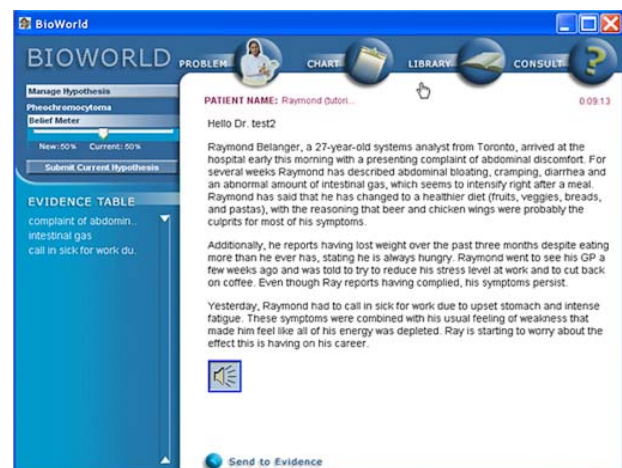


Fig. 1. BioWorld Interface

### III. METHODS

#### A. Participant Profile

Participants for this study were recruited via advertisements and newsletters. The convenience sample included nineteen women (63%) and eleven men (37%), with an average age of twenty-three) volunteer undergraduate students, who completed a two-hour study session. The participants, twenty-eight Medical students and two dental students, were registered in the same classes at a large Northeastern Canadian University.

#### B. Procedure

Participants initially completed a training case, which allowed them to learn how to navigate and use the BioWorld system. Following the training case, students solved the three endocrinology cases in a 2-hour session. The order of the cases was counterbalanced to mitigate practice effects. Upon completion of each case, participants completed a retrospective outcome achievement emotions questionnaire.

#### C. Measures

The BioWorld system records user-system interactions in the log-files, which comprise three types of performance metrics: *efficiency* (e.g., time taken to solve a case), *efficacy* (e.g., count of matches with experts), and *affect* (e.g., confidence). The log file records specific parameters such as: the attempt identifier (e.g., user ID), a timestamp, the space (e.g., chart), the specific action taken (e.g., add test), and action specifics (e.g., 3HbA1C Result: 12.5%). The log-file records of learner actions logged while solving the three cases were used in this present study.

### IV. HIDDEN MARKOV MODELS

A Hidden Markov Model (HMM) is a double scholastic process with an underlying stochastic process that is unseen, but can only be seen through another set of visible stochastic processes that generate the observation sequence [7]. HMMs are formal foundation for making probabilistic models of linear sequence ‘labeling’ problems [3, 7]. A formal definition and additional details on HMMs can be found in [7]. HMMs have been applied to a range of applications including protein sequence modeling, profile searches, speech recognition, multiple sequence alignment, and regulatory site identification.

A state diagram is used to visually represent the HMM model (figure 2). The rectangles (labeled 1 and 2) denote the possible states of a process, while the arrows denote shifts between states. The arrow labels denote the probability of state shifts. At each step of the process, the model may generate an emission depending on which state it is in and then make a shift to another state. In this model, the subsequent state depends only on the current state and not on the history of shift that lead to the current state. As the observed sequence is the only given sequence, this underlying state path is hidden – these are the residue labels that needed to be inferred.

The present study has been conducted to ascertain the feasibility and efficacy of employing HMMs to usage data from computer based learning environments.

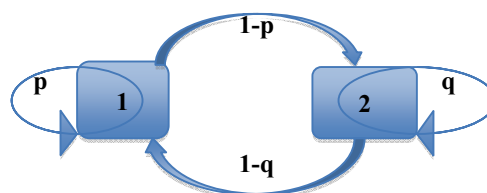


Fig. 2. HMM Example

### V. EXPERIMENTAL SETUP AND RESULTS

One major affordance of intelligent tutoring systems is that learner interactions are captured. Such fine-grained user-system data can be beneficial in learner modeling. When solving a case in BioWorld, the system logs learners’ actions during problem solving while interacting with several tools, such as the library, chart, consult, etc. The learner actions are time stamped and categorized according to both superordinate (e.g., Action: add lab-test) and subordinate categories (e.g., Evidence: 3HbA1C Result: 12.5%). From the log files, a line of diagnostic reasoning (i.e., sequence data) can be extracted. We extracted the sequence data for each of the endocrinology cases (Amy, Cynthia, and Susan Taylor) using a parser [8]. For the present study, we only analyzed the sequences for one case—the Amy case. Once we had the sequence data (input), the HMM for this data was generated. The HMM generation tool [1] for modeling generative sequences was used to calculate and generate the HMMs. The tool generates the action emission probabilities for each state and also a visualization to illustrate the major connections between states. The set of actions captured by BioWorld: AE=‘add evidence’; AH=‘add hypothesis’; CHC=‘change hypothesis conviction’; LE=‘link evidence’; SEH=‘select hypothesis’; AT=‘add test’; SH=‘submit hypothesis’; P=‘prioritize’; EM=‘expert match’; FP=‘final priority’; LL=‘library load’; C=‘categorize’; RP=‘reprioritize’; SU=‘submit summary’; UL=‘unlink evidence’; DH=‘delete hypothesis’; SLC=‘select library category’; ASH=‘abort submit hypothesis’; SL=‘search library’; U=‘unprioritize’; RC=‘recategorize’.

We provide the results of applying HMM on the sequence data for 1 case (Amy). The learned HMM structure for the Amy case is given in figure 5. The HMM output illustrates the transition probabilities among states. In the visualizations, the arrows indicate the possible transitions between and within states, and the percentage attached to each arrow indicates the transition probabilities. The generated structure has ten hidden states. For the purpose of this analysis, we focus on the state transition with the highest probability: the transition from S6 to S10 (16%). To understand the transition from S6 to S10, we consider the emission probabilities in each state (figures 3 & 4 respectively). For S6, the emission probabilities included: Add Hypothesis (0.73) and Change Hypothesis Conviction (0.16). For S10, the emission probabilities included: Change Hypothesis Conviction (0.60) and Submit Hypothesis (0.29). Thus, the transition from S6 (Diagnosis Formulation) to S10 (Evaluation) represents learners’ transition from *diagnosis formulation* to *evaluation*.

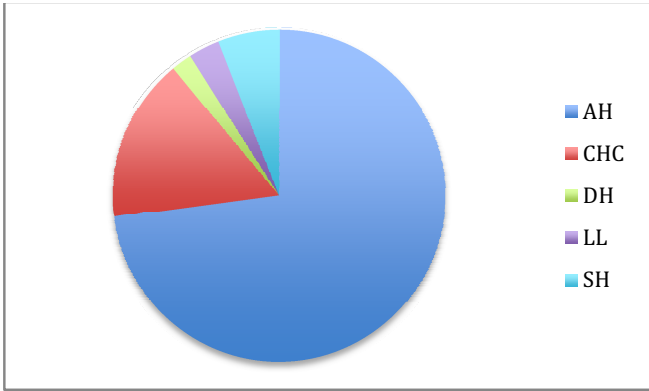


Fig. 3. State 6 –Emission Probabilities

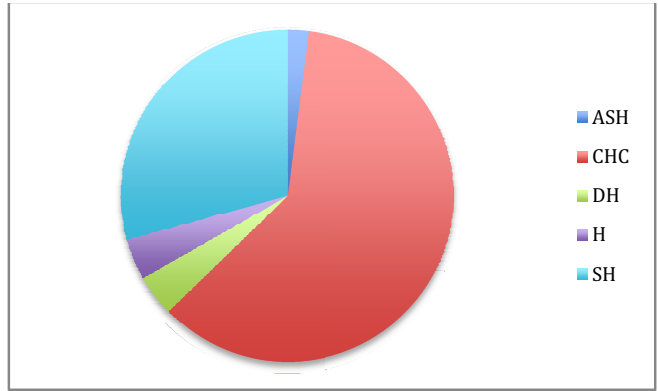


Fig. 4. State 10 –Emission Probabilities

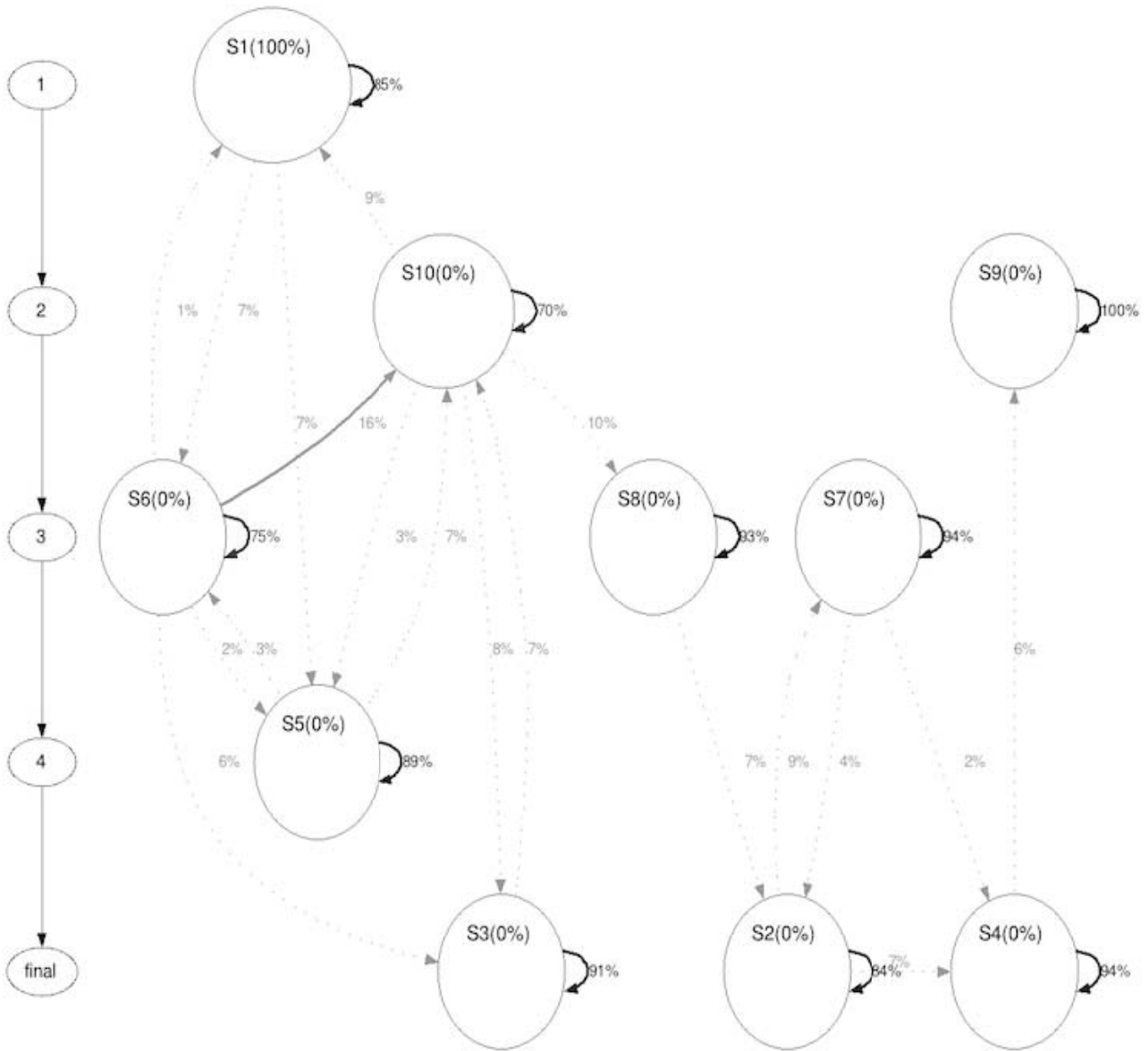


Fig. 5. HMM Structure (Output) for the Amy Case

## VI. CONCLUSION

Learner modeling is an increasingly important problem in computer-supported education. The overarching goal of this study is to model learner actions involved in diagnosing virtual patient cases. In our previous investigations, we considered specific learner actions, namely, help seeking & preliminary hypotheses selection [9, 10]. In this current work, we have extended our focus to span the entire set of learner actions in problem solving. Preliminary results from the present study indicate that HMM is an effective method to process and analyze user-system interaction data. The results provide an understanding of how learners approach problem solving. The HMM analysis on the clinical reasoning data from BioWorld represents an effort towards revealing rich information about learner behaviors that can be valuable from both an instructional design and technology perspective. The findings show that the HMM model did capture a pattern in the lines of diagnostic reasoning. In particular, for the Amy case, the learners engaged in a pattern of formulating a hypothesis, and then re-evaluating their final diagnosis.

Learner modeling is widely acknowledged to be crucial in the process of adapting instruction in computer-based learning environments. The current study could prove useful in the refinement of adaptive functionalities in the learning system. For future work, a natural extension is to consider other cases; we intend on applying HMM analysis to other cases to ascertain differences, if any, in learner behaviors across cases. Additionally, we plan to examine other state transitions for each of the cases to understand other differences, if any, in behavior patterns.

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