Discovering Interpretable Medical Workflow Models

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I. PROBLEM STATEMENT AND METHOD

Medical workflow discovery and analysis can help teams better understand their practice and potentially improve patient outcomes. In the past, medical experts designed hand-made workflow models for this purpose. These models usually needed iterative revision for the experts to reach consensus. Actual practice, however, often deviates from a perceived ideal workflow model. Automatic workflow discovery algorithms [1] have recently been proposed to learn a workflow model from observed activity or event traces. These algorithms, however, can produce spaghetti-like graphical models, with many branches and loops. Although model interpretability is an initial requirement of medical process analysis, it is often difficult or impossible for medical experts to extract knowledge from these chaotic models. We present an algorithm for discovering interpretable medical workflow models that addresses these limitations. We show our preliminary results and evaluate our approach on a real-world medical process.

Our workflow discovery algorithm has two designs that make the discovered workflow model more interpretable. First, our algorithm finds a "backbone" sequential model to highlight in the final model. This design is inspired by the fact that a sequential structure is easier to understand when compared to a parallel structure. Second, our algorithm only produces left-to-right model structures, a property that
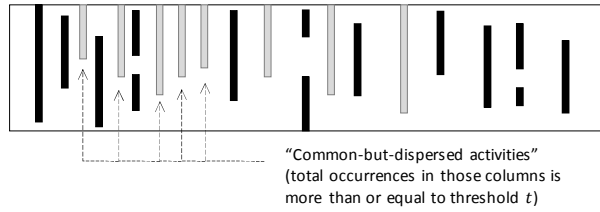

Figure 1. Trace alignment matrix. The black bars represent consensus activities; the gray bars represent non-consensus activities.

c_{a1}, c_{a2}, c_{a3} = consensus activities,
c_{d1}, c_{d2} = common-but-dispersed activities
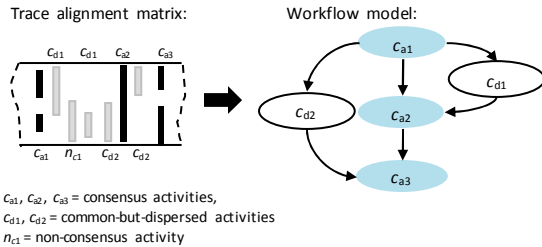n_{c1} = non-consensus activity

Figure 2. Proposed procedure for discovering the workflow model from an alignment matrix.

prohibits looping sequences, reduces the model implicitly and enhances model interpretability.

Our algorithm has two phases: discovering an alignment matrix, and then discovering a workflow model from the alignment. Given n activity traces $T = \{T_1, \dots, T_n\}$, where each T_i has a variable number of ordered treatment activities, $T_i = \{a_1, \dots, a_m\}$. The trace alignment algorithm [2] returns an alignment matrix M with the traces T as rows and activities of the same type as columns (Figure 1). For a given cell, if a matching activity cannot be found, a gap symbol (e.g., "-") is inserted. The columns with activity occurrence probability larger than a predefined threshold t are termed consensus columns and the corresponding activities in these columns are termed consensus activities. The sequence constructed from the consensus activities is termed the consensus sequence. The consensus sequence can be considered as the backbone workflow of the given medical process and represents a typical process execution. It records the most frequent activities in the trace and their sequential orders. The advantage of the consensus sequence is its interpretable sequential nature. The strict sequential property of the consensus sequence, however, does not allow parallel workflow branches. In addition, some of the non-consensus activities were found to be common-but-dispersed activities that appear in most traces. These types of non-consensus activities could not be aligned because they are interleaved with other consensus activities. If a non-consensus activity appears across a span of columns and the frequency of occurrences in those columns is more than or equal to t, it is defined to be a common-but-dispersed activity (Figure 1). The span is defined as the maximum number of consecutive consensus activities across which a common-but-dispersed activity can be spread. The consensus activities in this approach are used as location markers. The use of span can greatly reduce the model complexity in complex processes.

The 2nd phase of our algorithm (Alg. 1, Figure 2) aims to include the common-but-dispersed activities into the

| Algorithm 1. Workflow Model Discovery From Alignment Results	
Input: Alignment matrix M, Threshold t, Span s	
Output: Discovered Workflow model G	
Step 1.	Find the consensus activities C_a in M
Step 2.	Add the consensus activities C_a to a directed graph G, with each consensus activity as a vertex of the graph.
Step 3.	Find common-but-dispersed activities C_d in M
Step 4.	**for** each c_d in C_d:
Step 5.	Find nearest preceding consensus activity c_{pre}
Step 6.	Find nearest succeeding consensus activity c_{suc}
Step 7.	Add edges $c_{pre} \to c_d, c_d \to c_{pre}$ to G
Return G	
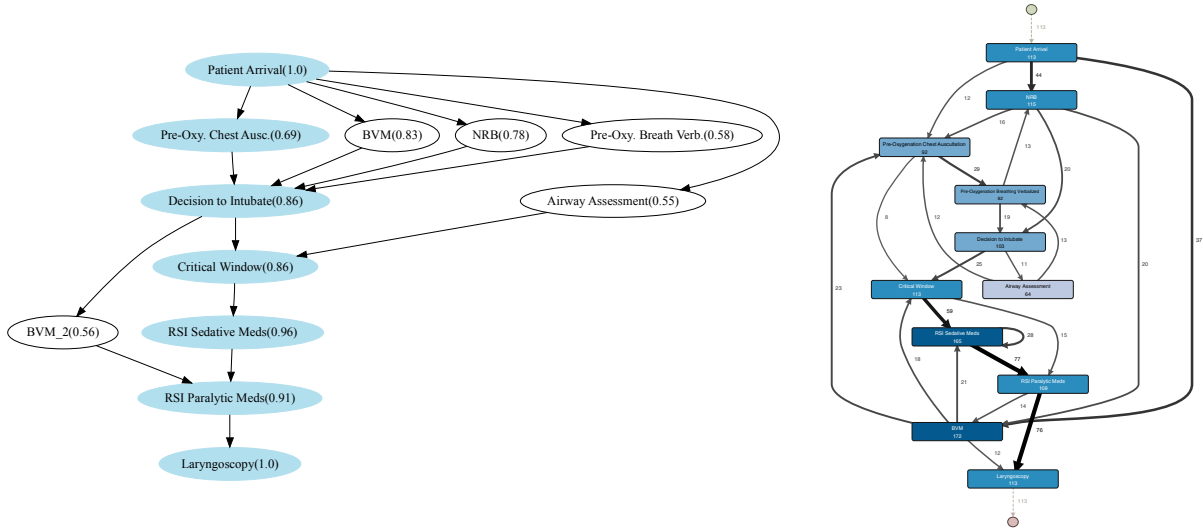
Figure 3. The workflow model generated by our method (left) and Disco (right). In our workflow model, the blue nodes are consensus activities and the white nodes are common-but-dispersed activities. The number within a brace is the frequency of the activity. Disco did better in visualization, the activities of higher occurrence were darker and the edges of higher occurrence were thicker.

workflow model as branches. The algorithm takes alignment matrix M, threshold t, and span s as inputs and outputs a workflow model (represented by a directed graph). In steps 1 and 2, we find the consensus activities and add them to the workflow model as the "backbone" of the graph. In the graph, each consensus activity transitions to the next consensus activity. In step 3, we iterate over non-consensus activities to find whether they are common-but-dispersed activities (denoted c_d). For each c_d, we find its nearest preceding and succeeding consensus activities, denoted as c_{pre} and c_{suc} respectively. Lastly, we include the common-but-dispersed activities into the model as new vertices and add edges from c_{pre} to c_d, and from c_d to c_{suc}.

II. EVALUATION AND PRELIMINARY RESULT

The use of the data was approved by the Institutional Review Board of Children's National Medical Center in Washington, DC. 113 endotracheal intubation (breathing tube insertion) records were manually coded using video review. This dataset includes 1394 treatment activities of 15 different types. The baseline method we used is Disco (https://fluxicon.com/disco/), a workflow discovery application based on the fuzzy mining algorithm [3].

For our experiments, we implemented the recently published PIMA [2] as our alignment algorithm. The threshold t was set to 0.5. The span s was set to the maximum

TABLE 1: THE STATISTICS OF THE WORKFLOW MODELS SHOWN IN FIGURE 3

Measures	Disco	Our Approach
Num. of Activities	11	12
Num. of Act. Types	11	11
Num. of Braches	14	5
Num. of Loops	16	0

number of consensus activities, leading to discovery of common-but-dispersed activities in the process. For Disco, we manually set the activity filter to 50% (preserving activities that occur in at least 50% cases) and path (vertices) filter to 20% (preserving the major paths) for a reasonable comparison. Although likely leading to a reasonable comparison, approaches for comparing parameters using different methods have not been established.

Seven consensus activities and six common-but-dispersed activities were discovered by our approach (Figure 3). In comparison, 11 consensus activities were discovered by Disco. Activity "BVM" was found to occur twice in our model. It represents the oxygen delivery method using a bag valve mask. This activity is often to be repeated to ensure sufficient oxygen is given during the intubation process. Disco does not support multiple nodes representing activities of the same type. For this reason, the multiple occurrences of "BVM" were reflected as loops in the model (e.g., BVM → RSI Sedative Meds → RSI Paralytic Meds → BVM in the Disco model). Sixteen loops (Table 1) were found in the Disco model. These loops compromised model interpretability. Another way to reduce the model interpretability is to reduce the number of branches. A branch is defined as a path that connects to but is not part of the main path (e.g., the consensus sequence). The Disco model has 14 branches, while our model only has six.

III. CONCLUSION

In this poster, we present a novel discovery algorithm that can produce more interpretable workflow model compared to baseline method. We present initial preliminary results using this approach. More comprehensive evaluation and numerical experiments will be needed to validate the value of this approach, including applying carefully defined metrics for assessing interpretability.

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