



Duration-Aware Alignment of Process Traces



National Institutes
of Health

Sen Yang

Moliang Zhou, Rachel Webman, JaeWon Yang, Aleksandra Sarcevic, Ivan Marsic and Randall S. Burd

Talk Overview

- ❑ Motivation of Research
- ❑ Duration-Aware Trace Alignment Algorithm
- ❑ Evaluation Criteria
- ❑ Case Studies

Previous Research: Expert Model

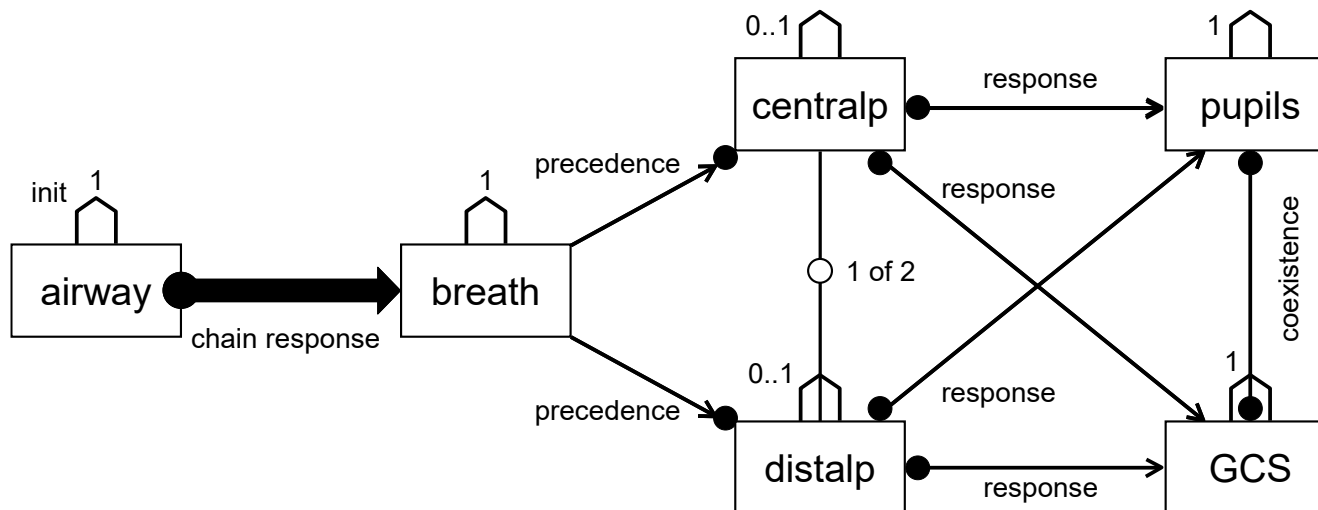


Figure: Expert-derived workflow model showing of essential activities by the bedside physician during the primary survey phase of ATLS (Advanced Trauma Life Support)

Previous Research: Trace Alignment

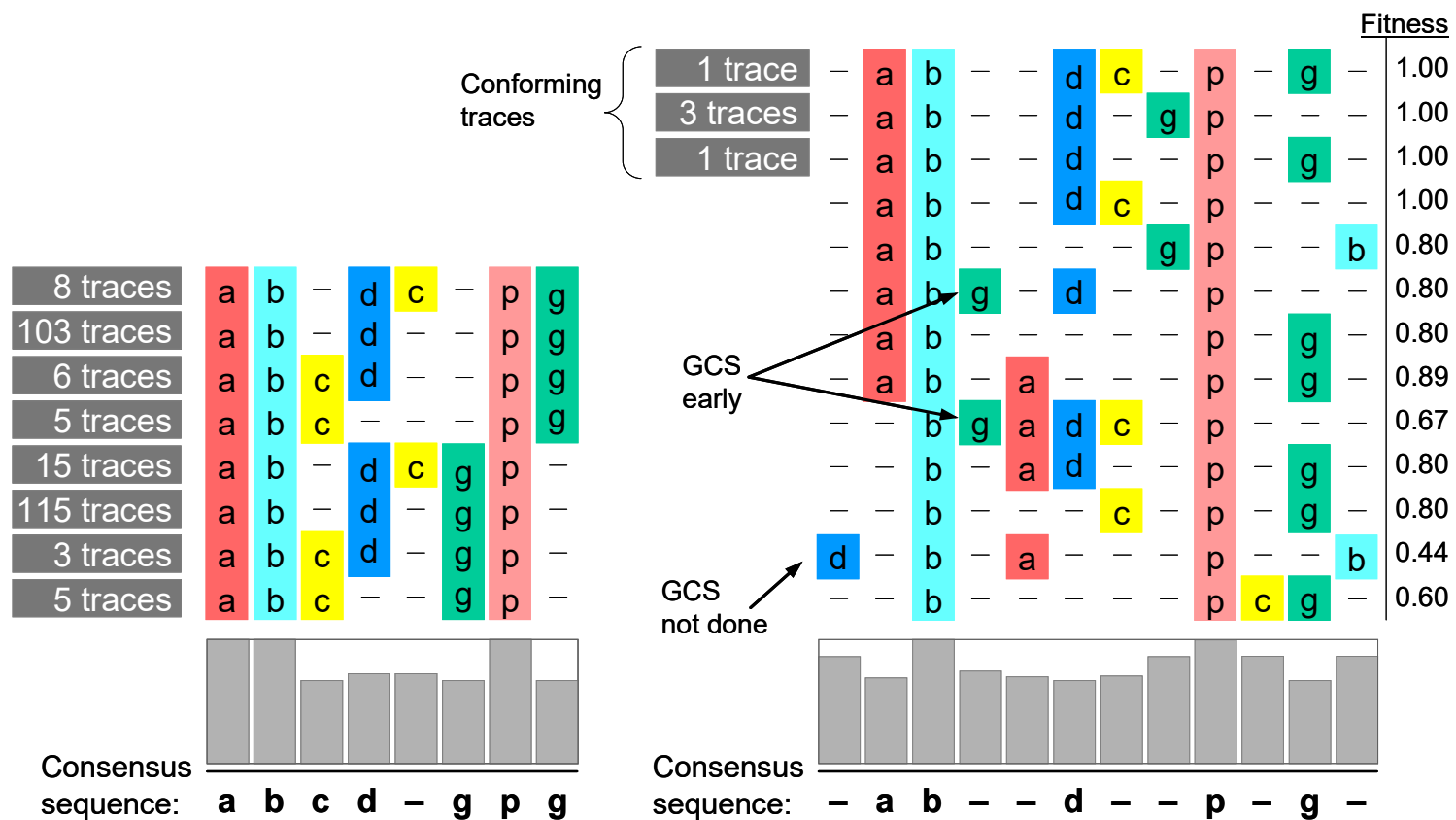


Figure: (left) Trace alignment of resuscitations conforming to the workflow model; (right) trace alignment of resuscitations in which evaluation of neurological status [GCS] was performed incorrectly.

Motivation of Duration-Aware Trace Alignment

Trace Alignment on medical processes:

- Helpful in visualizing the data
- Helpful in discovering **deviations**
 - similarities within a group of traces and to determine how a given trace differs from the well-established work practice
- Finding a sequential model
 - Consensus sequence can be seen as the backbone sequential model of the process

Limitation:

- Existing trace alignment approaches consider only the sequential order of activities and ignore activity duration.

Motivation of Duration-Aware Trace Alignment

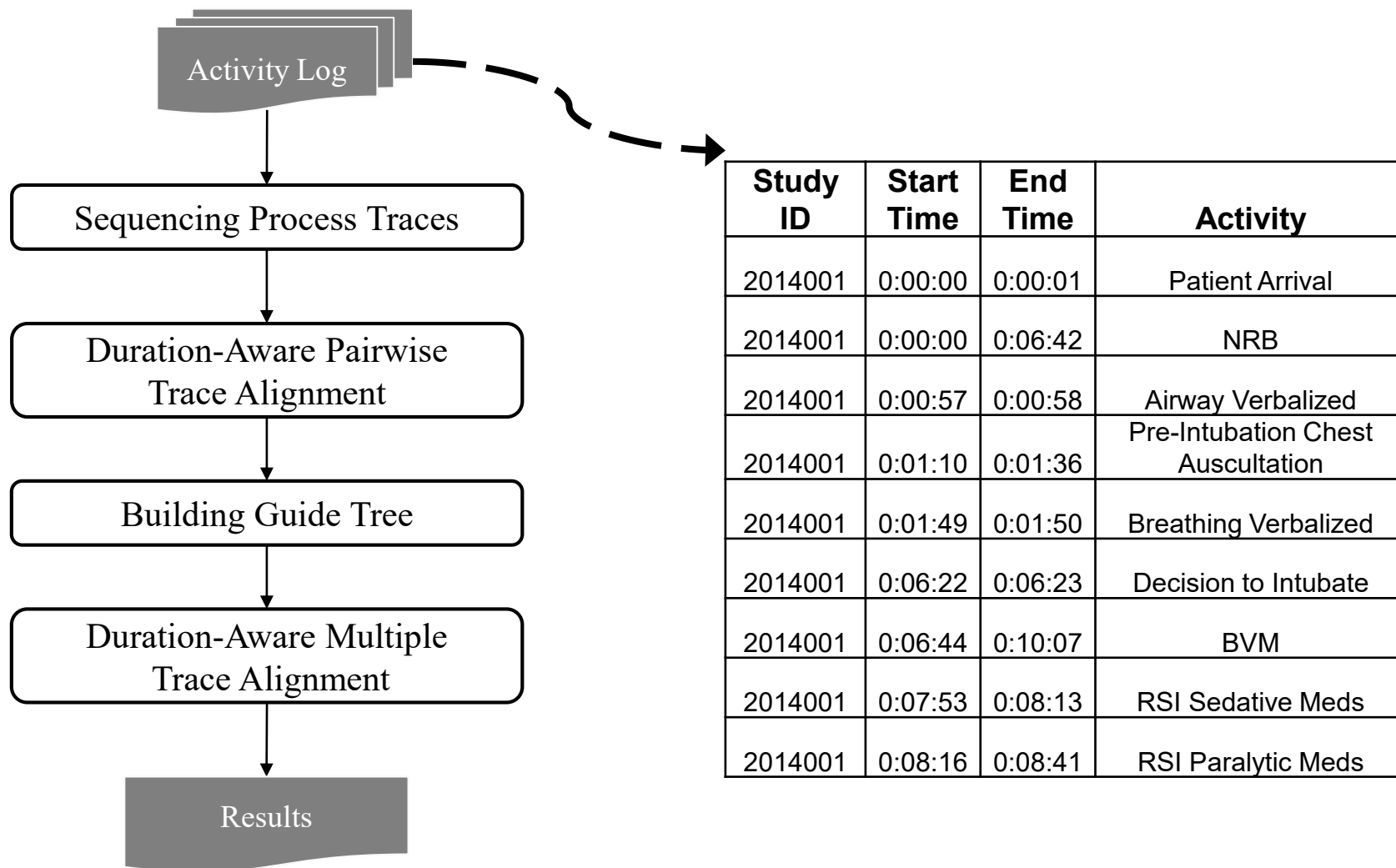
Activity duration is useful:

- Duration indicates activity similarity:
 - For example, consideration of duration helped understand that nurses routinely switch between tasks, spending less time on interrupted tasks that are later resumed
- Unusual durations indicate difficulties or atypical performance in the medical team operations

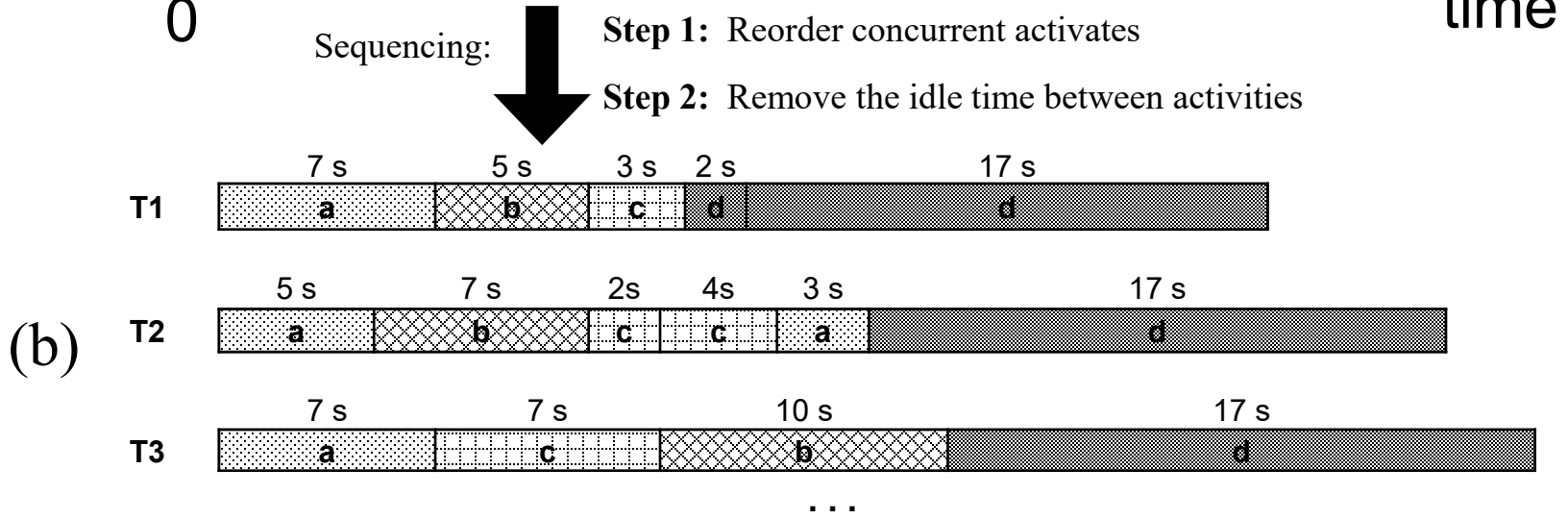
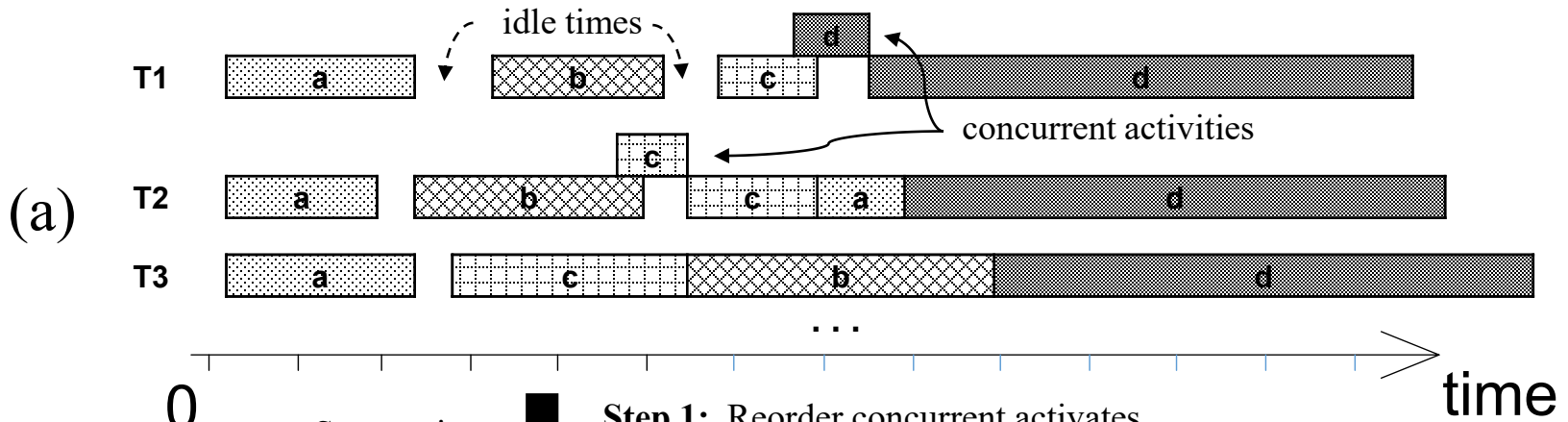
Question:

- How to include activity duration into consideration?
 - Dynamic Time Warping???

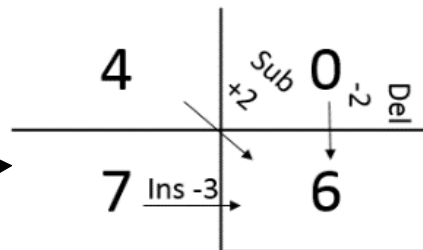
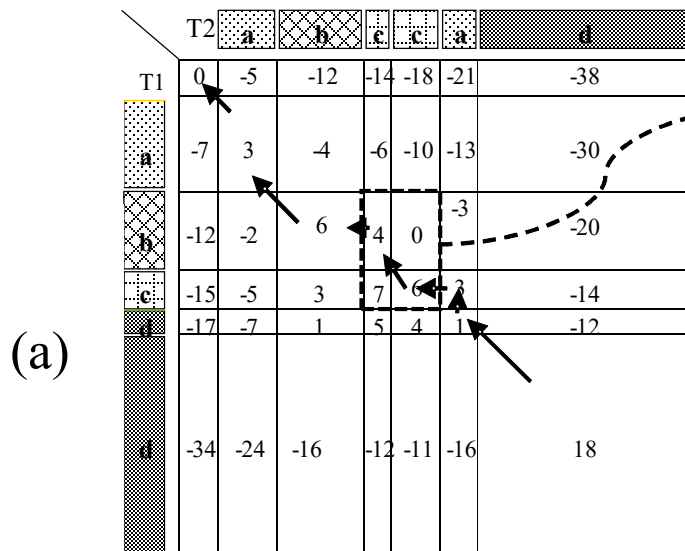
Duration-aware trace alignment flowchart



Sequencing of Process Traces

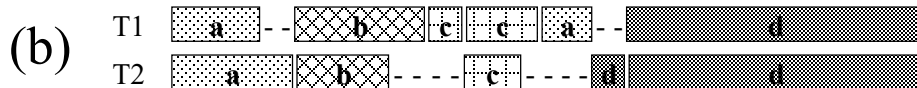


Pairwise Duration-Aware Trace Alignment



Scoring Scheme:

- $S(a,b) = 1$ Match
- $S(a,b) = -1$ Mismatch
- $g = -1$ Gap



$$F(i, j) = \max \begin{cases} F(i-1, j-1) + S(T_1(i), T_2(j)) * ddp(T_1(i), T_2(j)) & \text{Substitute} \\ F(i-1, j) + g * hdp(T_1(i)) & \text{Insert} \\ F(i, j-1) + g * vdp(T_2(j)) & \text{Delete} \end{cases}$$

Pairwise Duration-Aware Trace Alignment

Time Distortion Penalty Function:

$$hdp(T_1(i)) = \varphi(d(T_1(i)))$$

$$vdp(T_2(j)) = \varphi(d(T_2(j)))$$

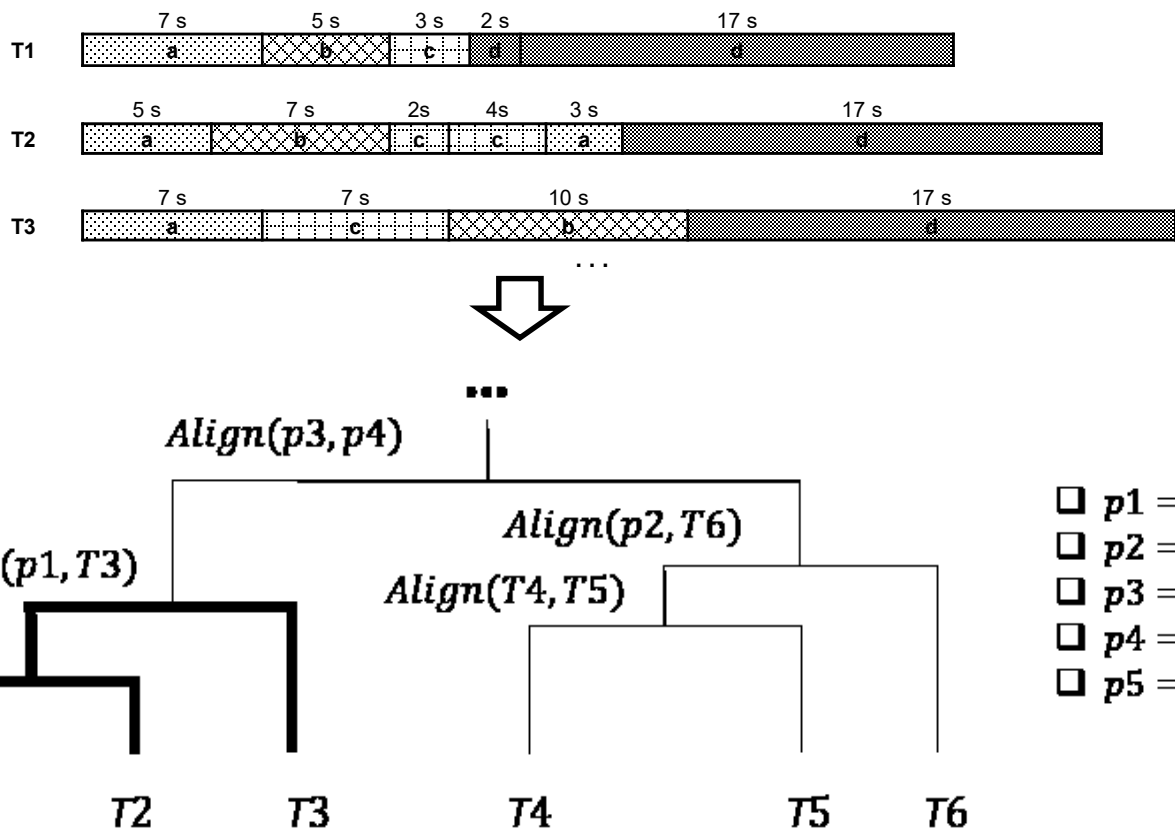
$$ddp(T_1(i), T_2(j))$$

$$= \begin{cases} \text{Min}(\varphi(d(T_1(i))), \varphi(d(T_2(j)))) - |\varphi(d(T_1(i))) - \varphi(d(T_2(j)))|, & S(T_1(i), T_2(j)) \geq 0 \\ \varphi(d(T_1(i))) + \varphi(d(T_2(j))), & S(T_1(i), T_2(j)) < 0 \end{cases}$$

Time Weighting Function:

$$\begin{cases} \varphi_{Linear}(d(event)) = c * d(event) & \longleftarrow \text{Linear weighting} \\ \varphi_{Log}(d(event)) = \log_b(d(event)) & \longleftarrow \text{Logarithmic weighting} \end{cases}$$

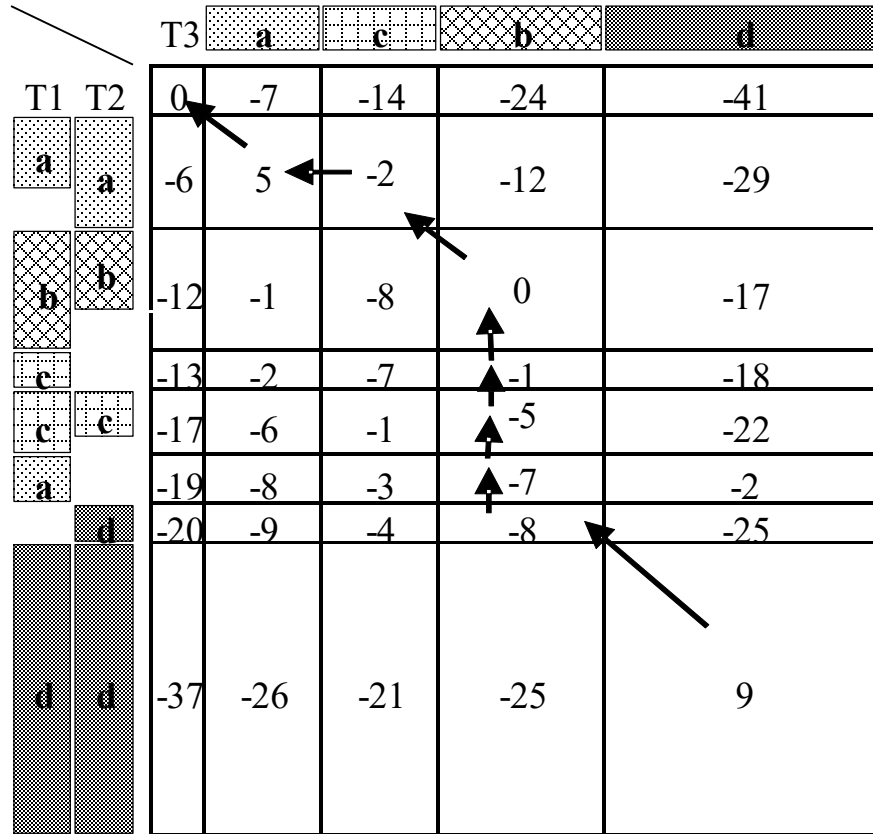
Guide Tree from Hierarchical Clustering



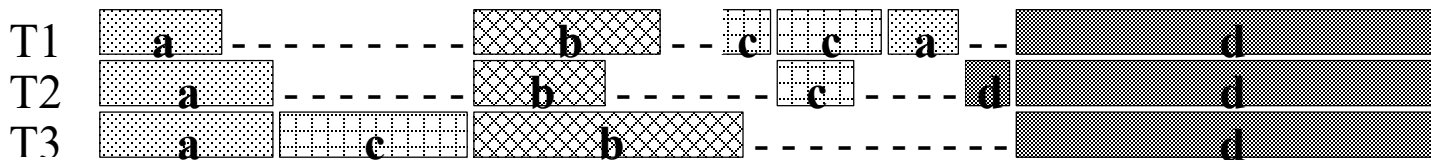
- Hierarchical tree grows based on Ward's method
- Similarity of process traces based on Edit Distance (a.k.a. Levenshtein Distance [11]) or Duration-Aware Edit Distance

Multiple Duration-Aware Trace Alignment

(a)



(b)



Evaluation Criteria

- *Sum-of-pairs Score (SPS)*
- *Average Information Score*
- *Consensus Sequence (CS)*
- *Alignment Matrix Length*
- *Deviation Detection Ability*



Quantitative

Qualitative

Evaluation Criteria

1. Sum-of-pairs Score (SPS)

$$SPS = n/N$$

n : # of correctly aligned residue (activity) pairs in the test alignment

N : total # of residue (activity) pairs in the reference alignment

Example:

Trace 1:

A	B
---	---

 -

Trace 2:

A	B
---	---

 -

Trace 3: -

B	A
---	---

Reference Alignment

Trace 1: -

A	B
---	---

Trace 2: -

A	B
---	---

Trace 3:

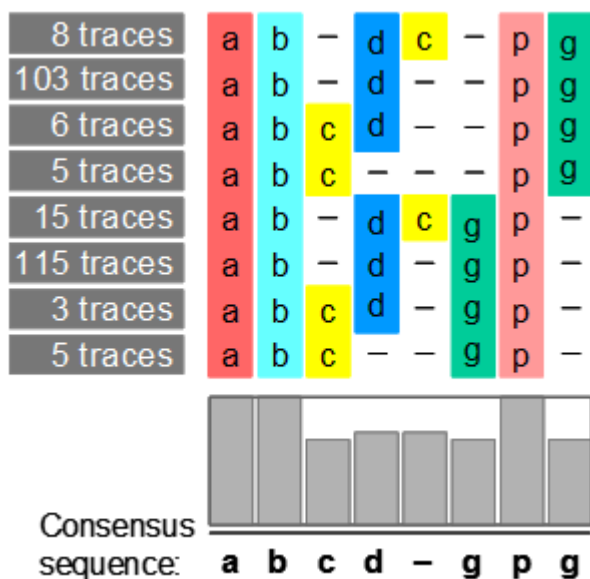
B	A
---	---

 -

Test Alignment

$$SPS = 2/8 = 0.25$$

Evaluation Criteria



2. Average Information Score (IS):

$$IS_i = \left(1 - \frac{E}{E_{max}}\right)$$

where $E_{max} = \log_2(|\mathbb{A}| + 1)$; $E = \sum_{a \in \mathbb{A} \cup \{-\}} -p_a \log_2(p_a)$

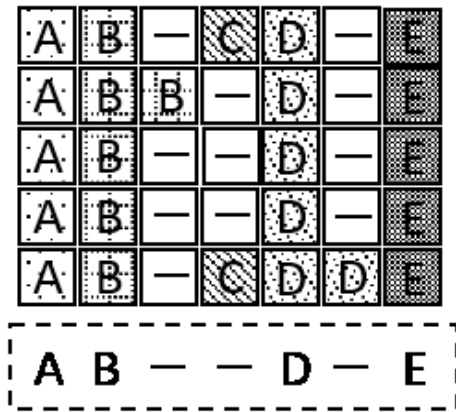
$$Avg. IS = \left(\sum IS_i\right) / L$$

L is alignment matrix length, i.e., # columns in alignment matrix

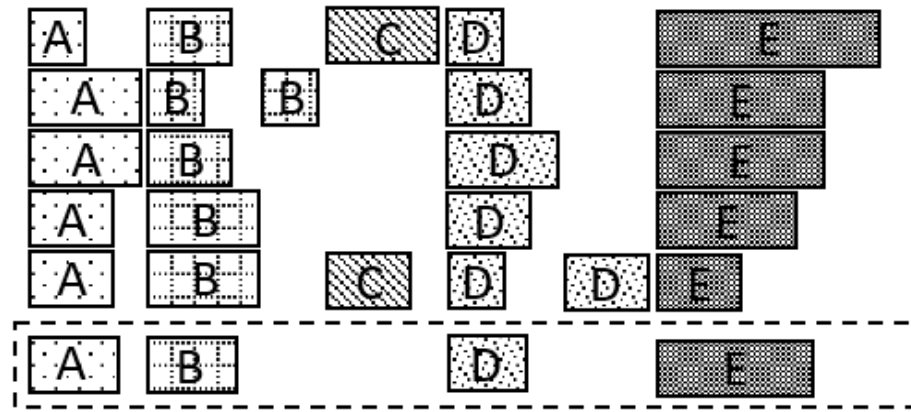
Evaluation Criteria

3. Consensus Sequence (CS):

The consensus sequence denotes a sequence of the most frequent activity found in each column of the alignment matrix.



(a)



(b)

Evaluation Criteria

4. *Alignment Matrix Length:*

Shorter matrix length is preferred. Longer alignment matrix may indicate that unnecessary gaps are included into the alignment.

Example:

Trace 1:

A	B	–
---	---	---

 Trace 2:

A	B	–
---	---	---

 Trace 3:

–	B	A
---	---	---

Dense Matrix

Trace 1:

–	A	B	–
---	---	---	---

 Trace 2:

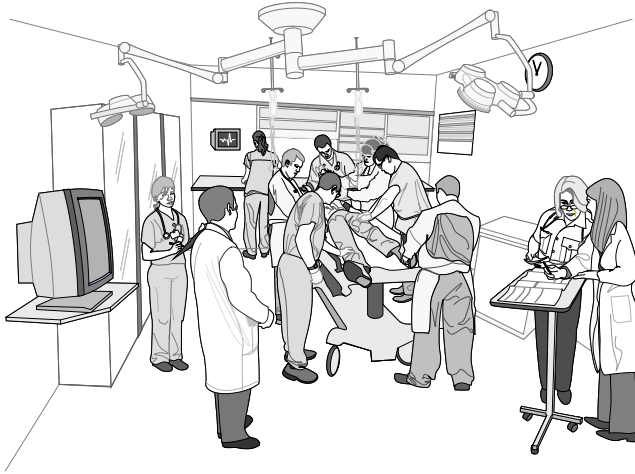
–	A	B	–
---	---	---	---

 Trace 3:

B	–	–	A
---	---	---	---

Sparse Matrix

Case Study 1: Trauma Resuscitation Process



- Data Coded based on the videos in CNMC
- 33 cases with a total 244 activities of 8 different types
(Question: small data?)

Metrics:	Algorithm:	Duration-Aware (linear)	Duration-Aware (logarithmic)	Context- based
Sum-of-pairs Score		0.617	0.807	0.731
Avg. Information Score		0.870	0.863	0.848
No. Non-gap Activities in CS		6	7	6
Alignment Matrix Length		49	39	36

Reference Alignment

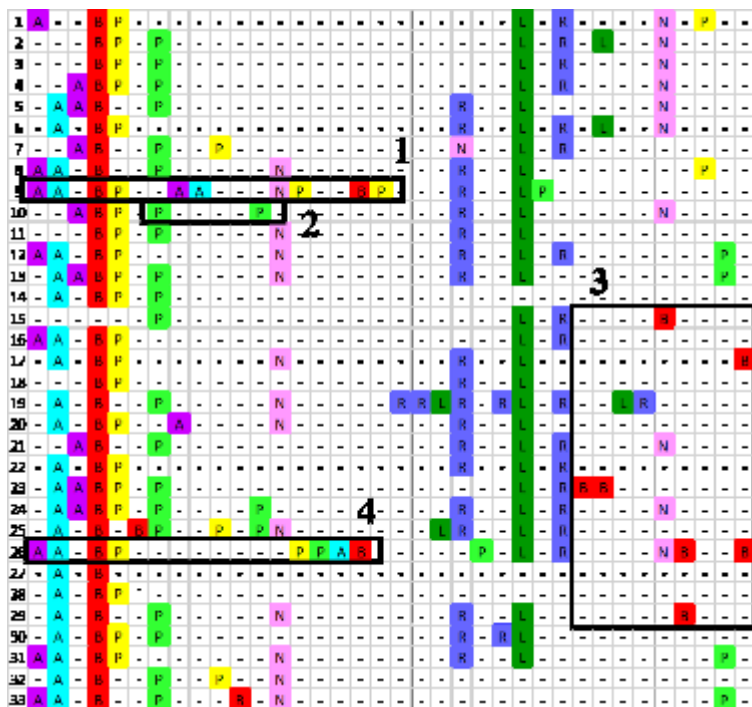
1	-	-	-	-	-	A	-	-	-	B	-	P	-	-	-	-	-	-	-	L	R	-	-	-	-	N	-	-	-	P	-	
2	-	-	-	-	-	-	-	-	-	B	-	P	-	P	-	-	-	-	-	-	L	R	-	L	-	-	N	-	-	-	-	
3	-	-	-	-	-	-	-	-	-	B	-	P	-	P	-	-	-	-	-	-	L	R	-	-	-	-	N	-	-	-	-	
4	-	-	-	-	-	A	-	-	-	B	-	P	-	P	-	-	-	-	-	-	L	R	-	-	-	-	N	-	-	-	-	
5	-	-	-	-	-	A	A	-	-	B	-	-	-	-	-	-	-	-	-	R	-	-	-	-	-	-	N	-	-	-	-	
6	-	-	-	-	-	A	-	-	-	B	-	P	-	-	-	-	-	-	-	R	L	R	-	L	-	-	N	-	-	-	-	
7	-	-	-	-	-	A	-	-	-	B	P	P	-	-	-	-	-	-	-	N	-	-	-	-	-	-	-	-	-	-	-	
8	-	-	-	-	-	A	A	-	-	B	-	-	-	P	-	-	-	-	-	N	R	-	L	-	-	-	-	-	-	-	P	
9	A	A	B	P	-	-	A	A	N	P	-	-	-	-	-	-	-	-	-	R	-	-	-	-	-	-	-	-	-	P	-	
10	-	-	-	-	-	-	-	-	-	B	-	P	-	P	P	-	-	-	-	-	R	-	-	-	-	-	N	-	-	-	-	
11	-	-	-	-	-	-	-	-	-	B	-	P	-	P	-	-	-	-	-	-	N	R	-	-	-	-	-	-	-	-	-	
12	-	-	-	-	-	A	A	-	-	B	-	P	-	-	-	-	-	-	-	-	N	R	-	-	-	-	-	-	-	P	-	
13	-	-	-	-	-	A	A	-	-	B	-	P	-	P	-	-	-	-	-	-	N	R	-	-	-	-	-	-	-	P	-	
14	-	-	-	-	-	A	-	-	-	B	-	P	-	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
15	-	-	-	-	-	-	-	-	-	-	-	-	-	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	B	
16	-	-	-	-	-	A	A	-	-	B	-	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
17	-	-	-	-	-	A	-	-	-	B	-	P	-	-	-	-	-	-	-	N	R	-	-	-	-	-	-	-	-	-	B	
18	-	-	-	-	-	-	-	-	-	B	-	P	-	-	-	-	-	-	-	-	R	-	-	-	-	-	-	-	-	-	-	
19	-	-	-	-	-	-	-	-	-	B	-	-	-	P	-	-	-	-	-	-	N	R	R	L	R	L	R	L	R	-	-	
20	-	-	-	-	-	-	-	-	-	B	-	P	-	-	-	-	-	-	-	-	N	R	-	-	-	-	-	-	-	-	-	
21	-	-	-	-	-	A	-	-	-	B	-	-	-	P	-	-	-	-	-	-	R	-	-	-	-	-	-	N	-	-	-	
22	-	-	-	-	-	-	-	-	-	B	-	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
23	-	-	-	-	-	A	A	-	-	B	-	P	-	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	B	B	
24	-	-	-	-	-	A	A	-	-	B	-	P	-	P	P	-	-	-	-	-	R	-	-	-	-	-	-	N	-	-	-	
25	-	-	-	-	-	A	-	-	-	B	B	P	-	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
26	A	A	B	P	P	P	-	-	-	B	-	-	-	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	B	B
27	-	-	-	-	-	-	-	-	-	B	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
28	-	-	-	-	-	-	-	-	-	B	-	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
29	-	-	-	-	-	-	-	-	-	B	-	-	-	P	-	-	-	-	-	-	N	R	-	L	-	-	-	-	-	-	B	
30	-	-	-	-	-	-	-	-	-	B	-	P	-	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
31	-	-	-	-	-	A	A	-	-	B	-	P	-	-	-	-	-	-	-	-	N	R	-	L	-	-	-	-	-	-	P	
32	-	-	-	-	-	-	-	-	-	B	P	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
33	-	-	-	-	-	A	A	-	-	B	-	-	-	P	-	-	-	-	-	-	B	N	-	-	-	-	-	-	-	-	P	

- ❑ The reference alignment functions as a ground truth.
- ❑ Created manually by medical experts.

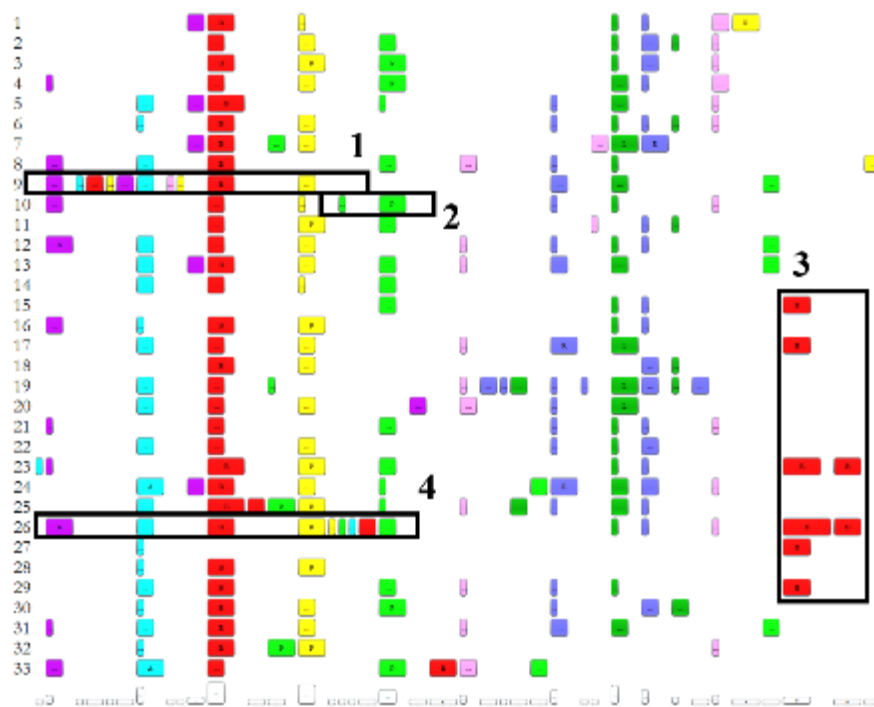
P Pulse Check - Upper Extremity	B Breath Sounds Check	P Pulse Check - Lower Extremity
L Left Pupil Check	R Right Pupil Check	N Neurologic assessment
A Airway Assessment Verbal	A Airway Assessment Visual	

Context-Aware vs. Duration-Aware Alignment

Context-Aware



Duration-Aware (Logarithmic Weighting)

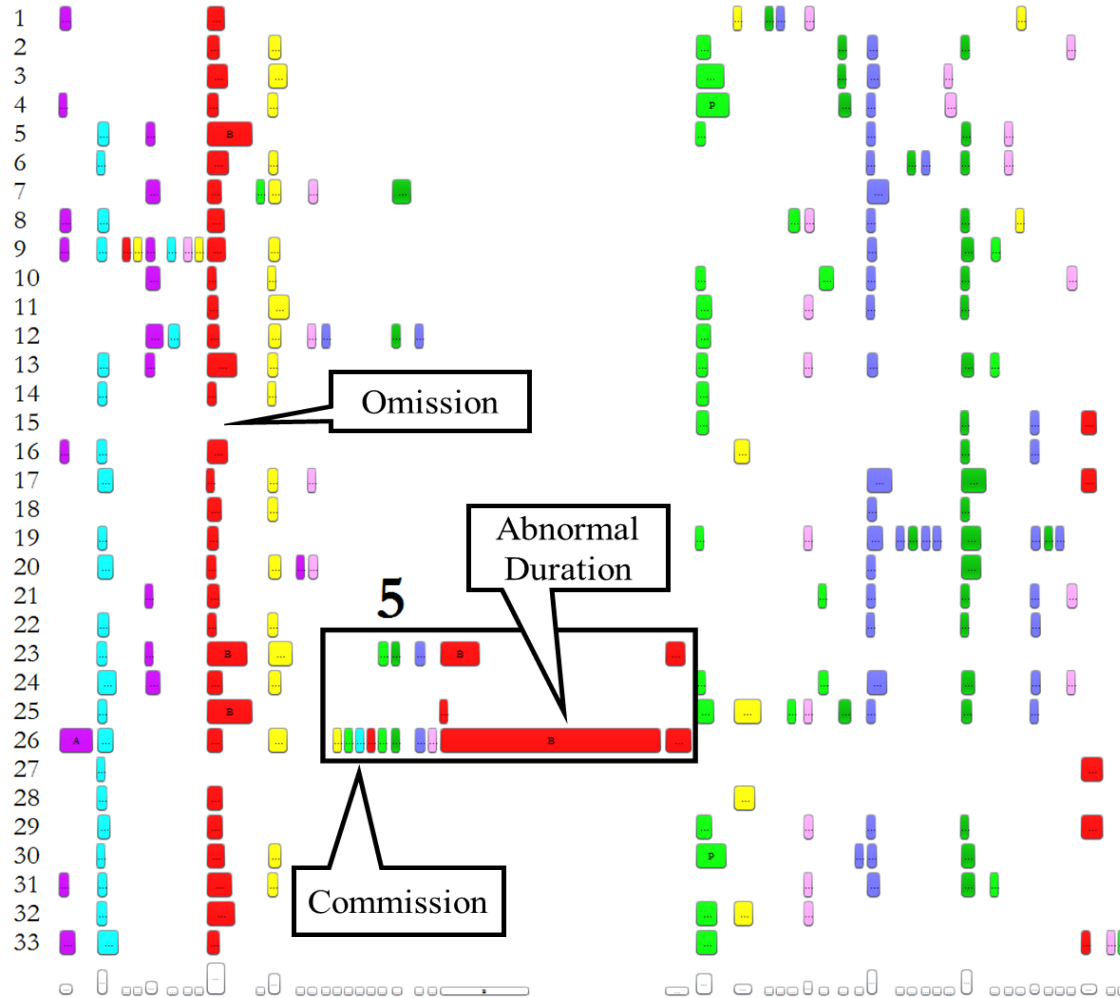


P Pulse Check - Upper Extremity
L Left Pupil Check
A Airway Assessment Verbal

B Breath Sounds Check
R Right Pupil Check
A Airway Assessment Visual

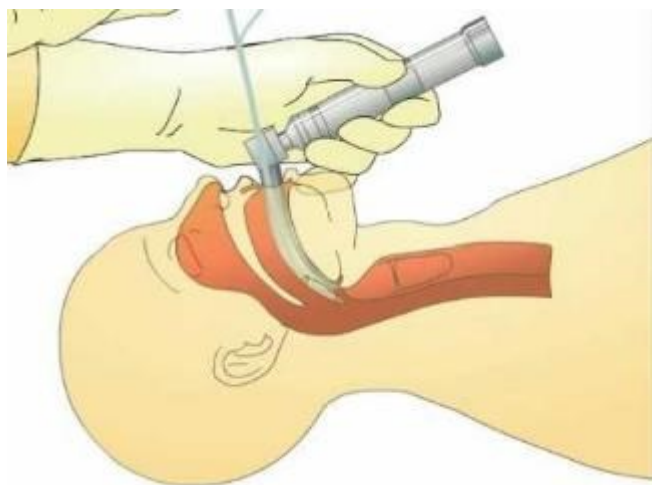
P Pulse Check - Lower Extremity
N Neurologic assessment

Duration-Aware (Linear Weighting)



- | | | | | | |
|----------|-------------------------------|----------|--------------------------|----------|-------------------------------|
| P | Pulse Check - Upper Extremity | B | Breath Sounds Check | P | Pulse Check - Lower Extremity |
| L | Left Pupil Check | R | Right Pupil Check | N | Neurologic assessment |
| A | Airway Assessment Verbal | A | Airway Assessment Visual | | |

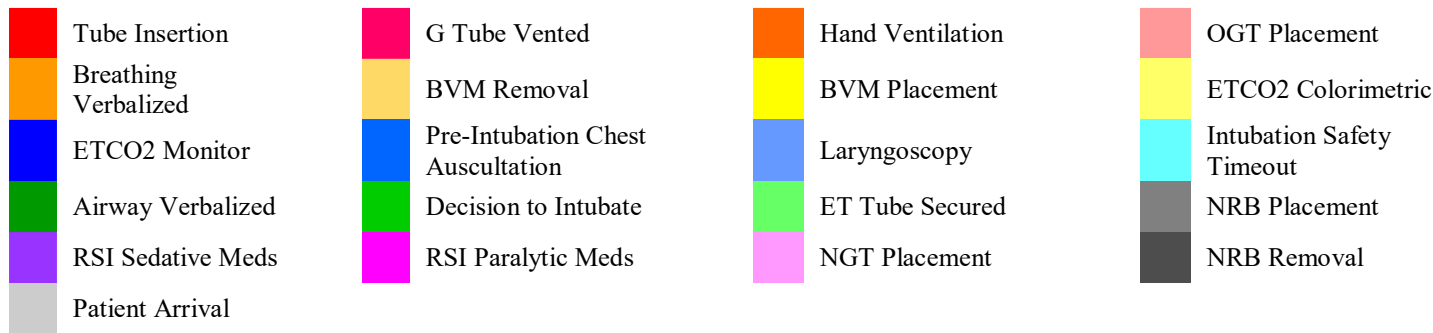
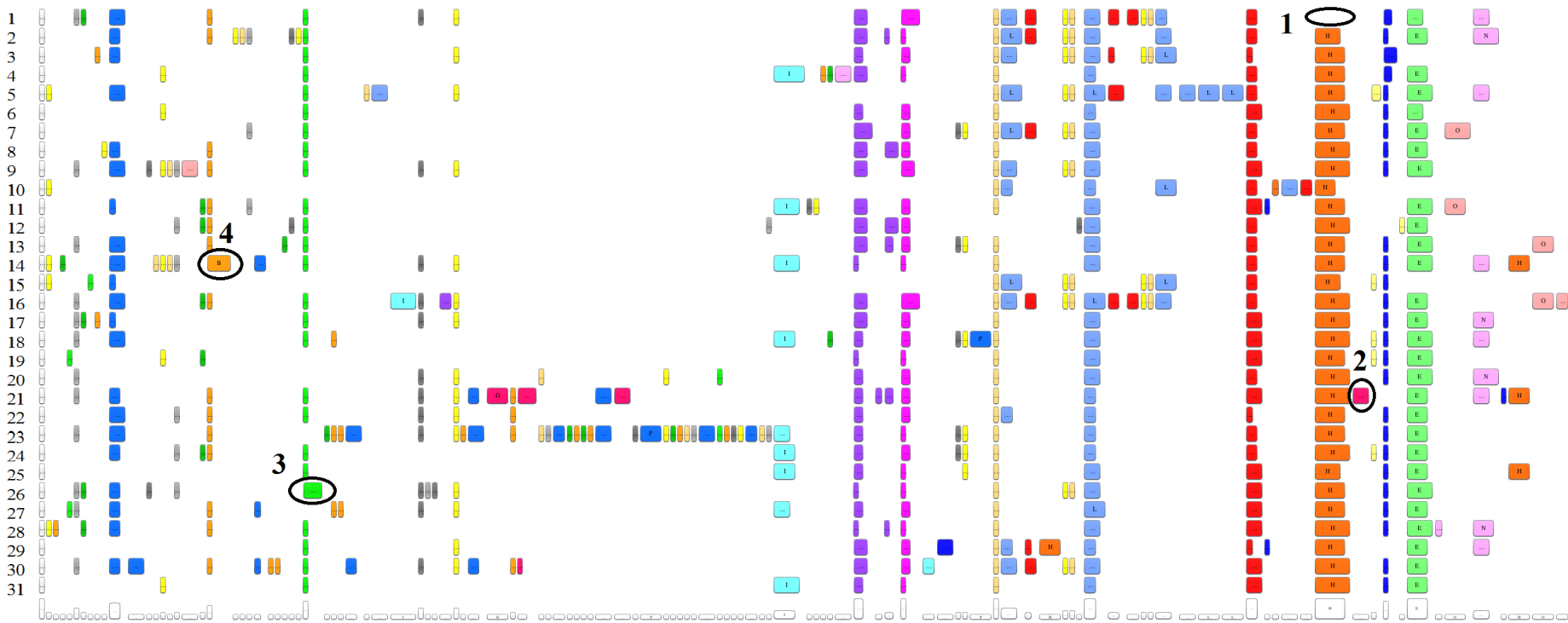
Case Study 2: Endotracheal Intubation Process



- Data Coded based on the videos in CNMC
- 31 cases with a total 602 activities of 21 different types

Metrics:	Algorithm:	Duration-Aware (linear)	Duration-Aware (logarithmic)	Context- based
Sum-of-pairs Score		0.731	0.843	0.721
Avg. Information Score		0.918	0.919	0.899
No. Non-gap Activities in CS		10	12	13
Alignment Matrix Length		134	119	115

Duration-Aware Alignment (Logarithmic)



Implementation

The screenshot displays the VIT-PLA software interface. The main window has a menu bar (File, Help) and a toolbar with tabs: Trace Visualization, Simplified Trace Visualization, Artificial Error Generator, Alignment Evaluation, and History. Below the toolbar are buttons for Clustering, Binomial Logistic Regression (One vs Rest), Align Cluster Prototypes, and Multinomial Logistic Regression (One vs. One). On the right, there are controls for Activity Filter, Color Map, Save Image, Export alignment, Zoom In/Out (slider from 0 to 20), and Linear Resizer (slider from 0 to 20).

The central area shows a grid of colored boxes representing clusters. A list on the left identifies clusters: Cluster 5 (14), Cluster 2 (85), Cluster 6 (22), Cluster 1 (31), Cluster 3 (10), Cluster 4 (9), and Percentage. Below this is a keyboard layout with keys labeled with letters A, B, C, G, P.

An inset window titled "Multinomial Logistic Regression" is open, showing the "p-Value" tab. The plot is titled "P-Value for Case Attributes" and shows p-values for various attributes: Daytime event, Weekend, <15, Discharged, Critical admission, Stat, Transfer, and Intercept. The x-axis is p-Value (0 to 1) and the y-axis is Attributes. A vertical line at p=0.05 is labeled $\alpha = 0.05$. A legend at the bottom identifies the markers: red square for Cluster 1, blue circle for Cluster 2, green triangle for Cluster 3, yellow diamond for Cluster 4, and pink square for Cluster 5. Below the legend is a field "Choose which cluster as the reference variable:" with a dropdown menu and "Finish" and "Close" buttons.

At the bottom left of the main window, a yellow box highlights "Level 10 Trace Number 171". Lines connect this box to "Level 7 Trace Number 50" and "Level 9 Trace Number 121" in the adjacent window.

Scalability

$O(n^2l^2 + n^3) \rightarrow$ Trace Clustering (i.e., Guide Tree)

$O(n^2L + nL^2) \rightarrow$ Trace Alignment

Where:

n : trace number

l : average trace length

L : average length of traces or profiles taken into alignment

Table. Computation Time. The notation $t \pm \delta$ denotes the computation time where t is the mean value over 20 difference runs and δ is the standard deviation

Log	No. traces	Total activities	Guide Tree (ms)	Progressive Alignment (ms)	Visualization (ms)
Intubation	31	605	15 ± 1	10 ± 1	4 ± 1
Trauma Resuscitation	33	4482	105 ± 5	242 ± 16	19 ± 2
Artificial Data	1000	52179	12493 ± 227	12353 ± 749	591 ± 51

Conclusion

- 1) A novel trace alignment algorithm that is duration-aware
- 2) A set of criteria to quantify trace alignment algorithm performance
- 3) Case studies showed our alignment algorithm achieved better alignment accuracy and provided more insights into deviations
- 4) Algorithm implemented into a JAVA APP

Limitations

- 1) Information lost in the “Process Trace Sequencing” step
- 2) Algorithm needs activity durations as input

Thank you

QUESTION?

Have workflow data that needs visualization and analysis?
Sen Yang sy358@scarletmail.rutgers.edu