CS 4072 - Topics in CS Process Mining

Lecture # 24

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Spring 2022

FAST - NUCES, CFD Campus

Dr. Rabia Maqsood

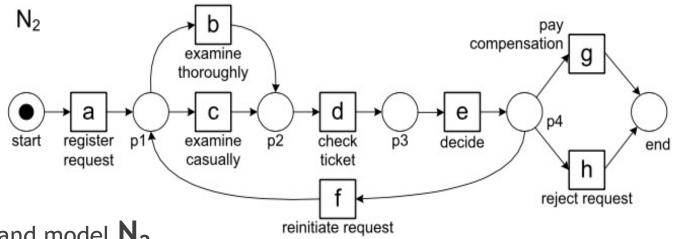
rabia.maqsood@nu.edu.pk

Today's Topics

- Conformance Checking
 - Sequence Alignment (continued)

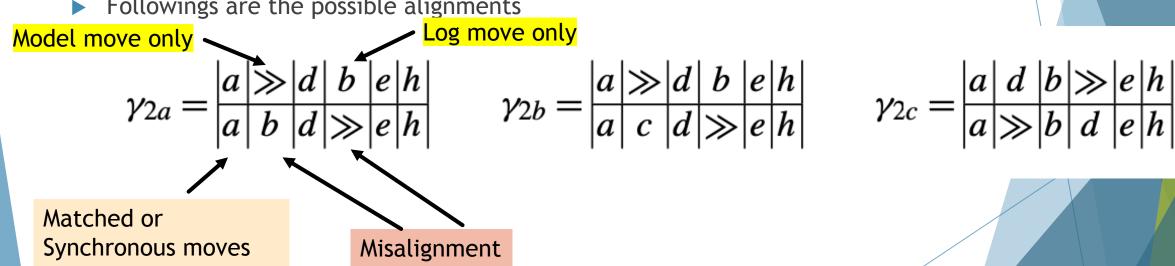
Alignments were introduced to overcome the limitations of token-based replay.

▶ The objective is to find the *optimal* sequence alignment between two traces.



► Consider a trace: $\sigma = \langle a, d, b, e, h \rangle$ and model N_2

Followings are the possible alignments

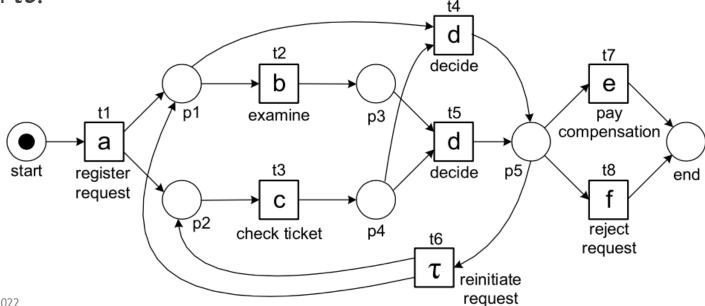


Top row: projection on top row (excluding "no moves" or >>) corresponds to trace in an event log Bottom row: projection on bottom row (excluding "no moves" or >>) corresponds to a run of a model

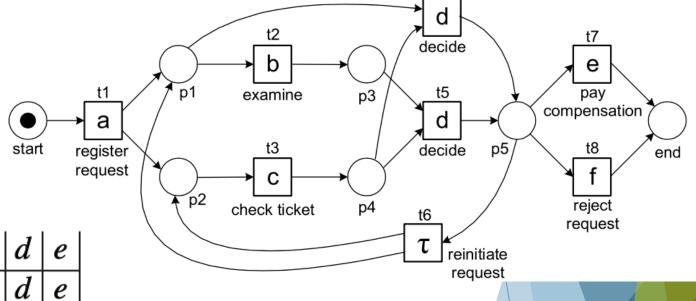
Alignments can be defined for any process notation, including Petri nets having duplicate and silent activities.

Consider the model N5 with duplicate transition d (t4 & t5) and a silent

transition *t6*.



► Consider $\sigma_1 = \langle a, c, d, e \rangle$ and N_5



A possible alignment is: $\gamma_{5,1} = \begin{vmatrix} a & c & d & e \\ a & c & d & e \\ t1 & t3 & t4 & t7 \end{vmatrix}$

A move will be defined by a pair (x,(y,t))

First element refers to the log

Second element refers to the model

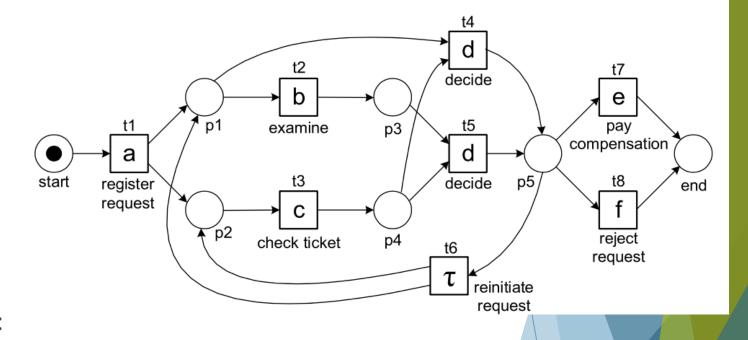
Examples:

 $(a,(a,t_1)) \rightarrow both log & model make "a" move using t_1$

 $(\gg,(c,t_3)) \rightarrow$ "c" using t_3 is not mimicked by log

 $(f, \gg) \rightarrow log makes "f" move not followed by model$

► Consider $\sigma_2 = \langle a,b,d,f \rangle$ and N_5

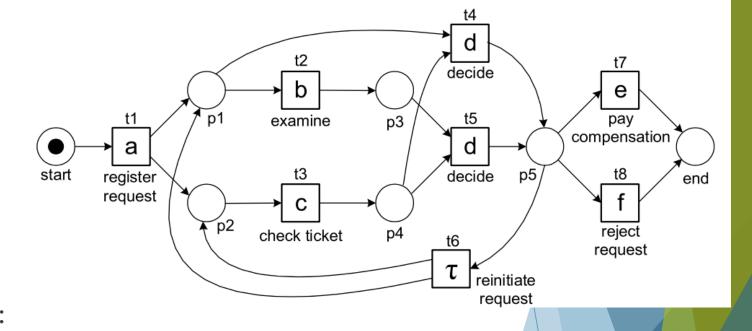


Following are the possible alignments:

$$\gamma_{5,2a} = \begin{vmatrix} a & b & \gg |d| & f \\ a & b & c & d & f \\ t1 & t2 & t3 & t5 & t8 \end{vmatrix}$$

$$\gamma_{5,2b} = \begin{vmatrix} a & \gg & b & d & f \\ a & c & b & d & f \\ t1 & t3 & t2 & t5 & t8 \end{vmatrix}$$

► Consider $\sigma_3 = \langle a, c, d, e, f \rangle$ and N_5



Following are the possible alignments:

$$\gamma_{5,3a} = \begin{vmatrix} a & c & d & e & f \\ a & c & d & e & \gg \\ t1 & t3 & t4 & t7 \end{vmatrix}$$

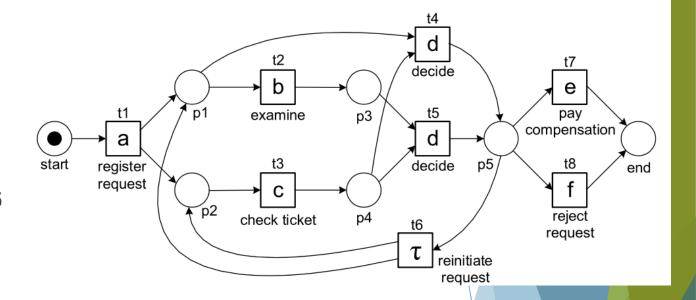
$$\gamma_{5,3b} = \begin{vmatrix} a & c & d & e & f \\ a & c & d \gg f \\ t1 & t3 & t4 & t8 \end{vmatrix}$$

NOTE: silent transition leaves no trail in the event log

Alignments

Consider

$$\sigma_4 = \langle a,c,d,b,c,d,c,d,c,b,d,f \rangle$$
 and N_5

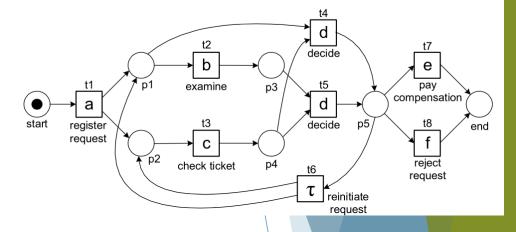


Following are the possible alignments:

$$\gamma_{5,4} = \begin{vmatrix} a & c & d & \gg & b & c & d & \gg & c & d & \gg & c & b & d & f \\ a & c & d & \tau & b & c & d & \tau & c & d & \tau & c & b & d & f \\ t1 & t3 & t4 & t6 & t2 & t3 & t5 & t6 & t3 & t4 & t6 & t3 & t2 & t5 & t8 \end{vmatrix}$$

- \triangleright (x,(y,t)) is a *legal move* if one of the following four cases holds:
 - x = y and y is the visible label of transition t (synchronous move)
 - $x = \infty$ and y is the visible label of transition t (visible model move)
 - $x = \infty$, $y = \tau$ and transition t is silent (*invisible model move*)
 - \rightarrow x/= \gg and (y,t) = \gg (log move)
- ▶ Other moves such as (\gg, \gg) and (x, (y, t)) with $x \not= y$ are illegal moves.

- Given a log trace and a process model, there may be many (if not infinitely many) alignments.
- The objective of sequence alignment is to find an optimal matching sequences.
- How to find the optimal alignment?
- ▶ What about the *worst* alignment?



For $\sigma_2 = \langle a,b,d,f \rangle$ and N_5 other possible alignments are:

$$\gamma_{5,2c} = \begin{vmatrix} a & b & d & f & \gg \gg \gg \gg \\ \gg \gg \gg \gg \gg a & b & c & d & f \\ & & t1 & t2 & t3 & t5 & t8 \end{vmatrix}$$

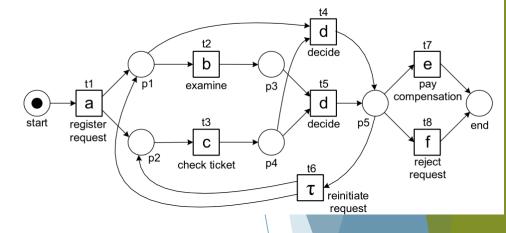
$$\gamma_{5,2c} = \begin{vmatrix} a & b & d & f & \gg \gg \gg \\ a & \gg \gg \approx c & d & e \\ t1 & & & t3 & t4 & t7 \end{vmatrix}$$

$$\gamma_{5,2d} = \begin{vmatrix} a & b & d & f \gg \gg \gg \\ a & \gg \gg c & d & e \\ t1 & & t3 & t4 & t7 \end{vmatrix}$$

Previously identified alignments were:

$$\gamma_{5,2a} = \begin{vmatrix} a & b & \gg |d| & f \\ a & b & c & d & f \\ t1 & t2 & t3 & t5 & t8 \end{vmatrix}$$

$$\gamma_{5,2a} = \begin{vmatrix} a & b & \gg & d & f \\ a & b & c & d & f \\ t1 & t2 & t3 & t5 & t8 \end{vmatrix} \qquad \gamma_{5,2b} = \begin{vmatrix} a & \gg & b & d & f \\ a & c & b & d & f \\ t1 & t3 & t2 & t5 & t8 \end{vmatrix}$$



For $\sigma_2 = \langle a,b,d,f \rangle$ and N_5 other possible alignments are:

$$\gamma_{5,2d} = \begin{vmatrix} a & b & d & f \gg \gg \gg \\ a & \gg \gg c & d & e \\ t1 & & t3 & t4 & t7 \end{vmatrix}$$

9 misalignments

6 misalignments

Previously identified alignments were:

There can be multiple optimal alignments with same cost.

$$\gamma_{5,2a} = \begin{vmatrix} a & b & \gg & d & f \\ a & b & c & d & f \\ t1 & t2 & t3 & t5 & t8 \end{vmatrix}$$

$$\gamma_{5,2a} = \begin{vmatrix} a & b & \gg & d & f \\ a & b & c & d & f \\ t1 & t2 & t3 & t5 & t8 \end{vmatrix} \qquad \gamma_{5,2b} = \begin{vmatrix} a & \gg & b & d & f \\ a & c & b & d & f \\ t1 & t3 & t2 & t5 & t8 \end{vmatrix}$$

1 misalignment

1 misalignment 14

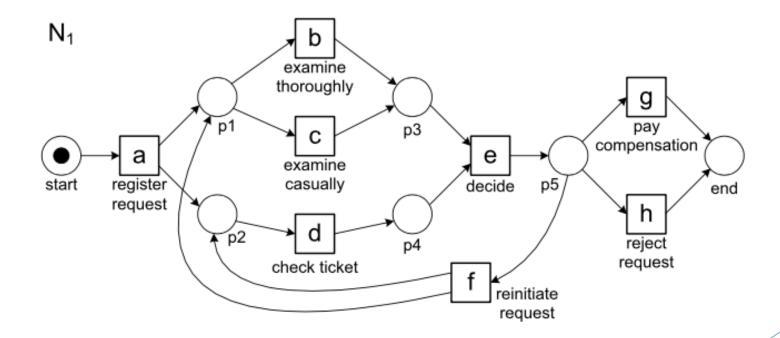
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The count of misalignments can be taken as cost of aligning a log and a model.

- ► To select the most appropriate alignment, we associate *costs* to undesirable moves and select an alignment with the lowest total costs.
- Generic cost function:
 - \triangleright Cost function δ assigns costs to **legal moves**.
 - Moves where log and model agree have no costs, i.e., $\delta(x,(y,t)) = 0$ for synchronous moves (with x = y).
 - Moves in model only have no costs if the transition is invisible, i.e., $\delta(\gg,(\tau,t)) = 0$ for invisible model moves.
 - ▶ $\delta(\gg,(y,t)) > 0$ is the cost when the model makes a "y move" without a corresponding move of the log (visible model move).
 - ▶ δ (x , ≫) > 0 is the cost for an "x move" in just the log (*log move*).

Question

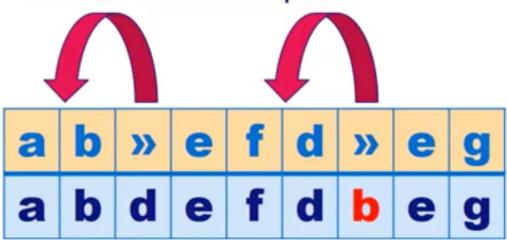
▶ Given N_1 , how many optimal alignments are there for a,b,e,f,d,e,g?

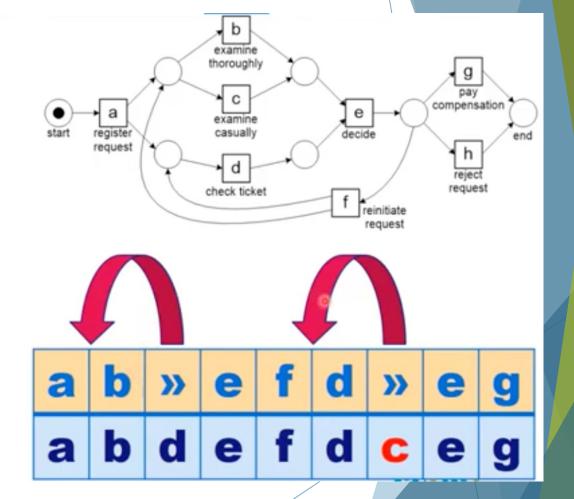


Answer



move in model can be reordered in concurrent part





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1 + 2x2 + 2x2 = 9 optimal alignments with cost = 2

Reading Material

► Chapter 8: Aalst