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Supervised Conformance Checking using Recurrent Neural Network Classifiers

ML4PM

Jari Peeperkorn, Seppe vanden Broucke, Jochen De Weerdt

KU Leuven, LIRIS research group

jari.peeperkorn@kuleuven.be

Process mining – Conformance checking

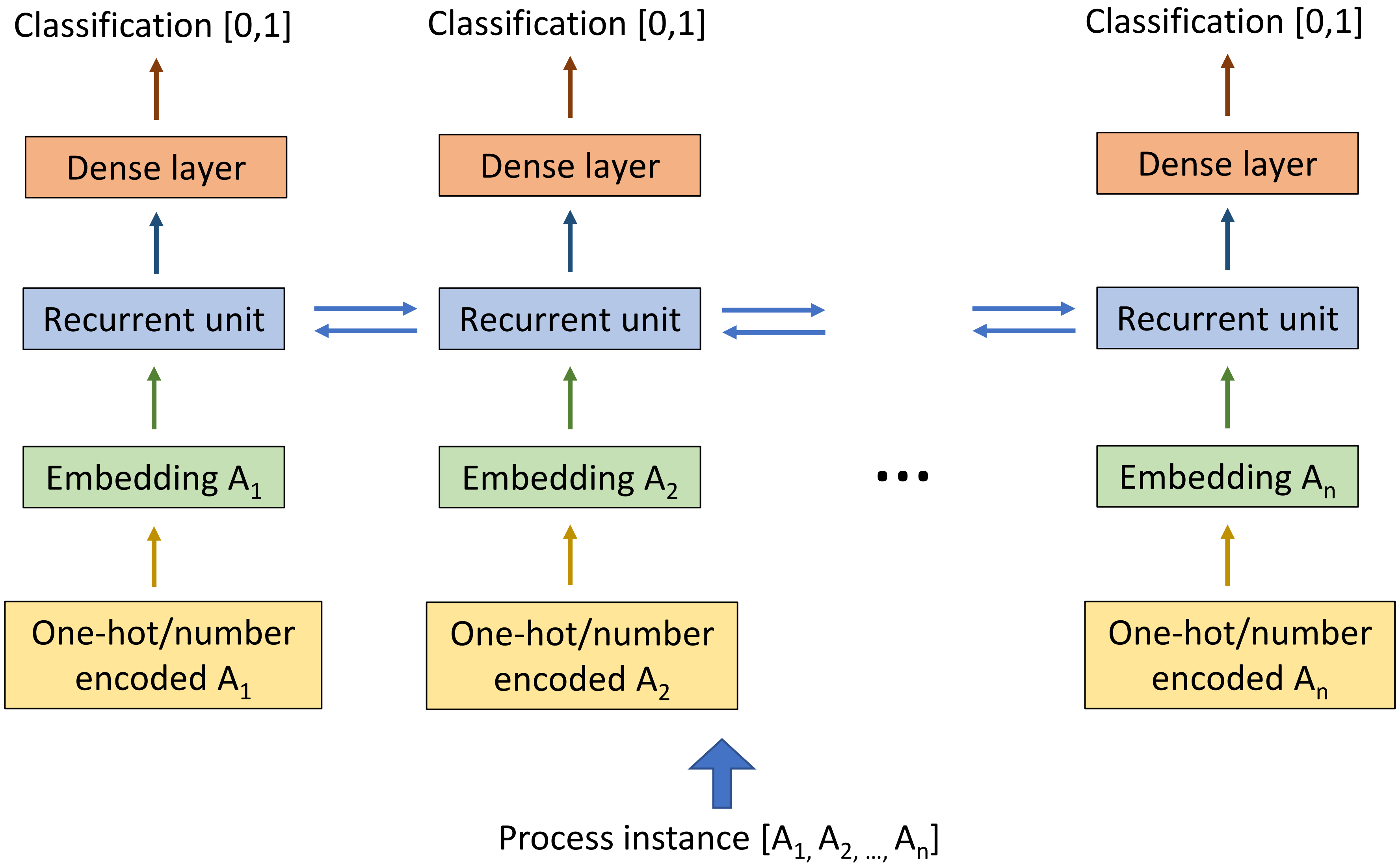
- How well does a certain model describe a certain log?
  - Global or local

- New conformance checking technique
  - Recall and Precision
  - Data driven
  - “Antilog“
  - Recurrent Neural Network

Recurrent Neural Network (RNN)

- Artificial neural network
- Sequential data
- Connected hidden layer
  - One- or bi-directional
- Simple RNN/LSTM/GRU

Local conformance?



Classification [0,1]

Dense layer

Recurrent unit

Embedding A_1

One-hot/number encoded A_1

Classification [0,1]

Dense layer

Recurrent unit

Embedding A_2

One-hot/number encoded A_2

…

Classification [0,1]

Dense layer

Recurrent unit

Embedding A_n

One-hot/number encoded A_n

Process instance $[A_1, A_2, \ldots, A_n]$

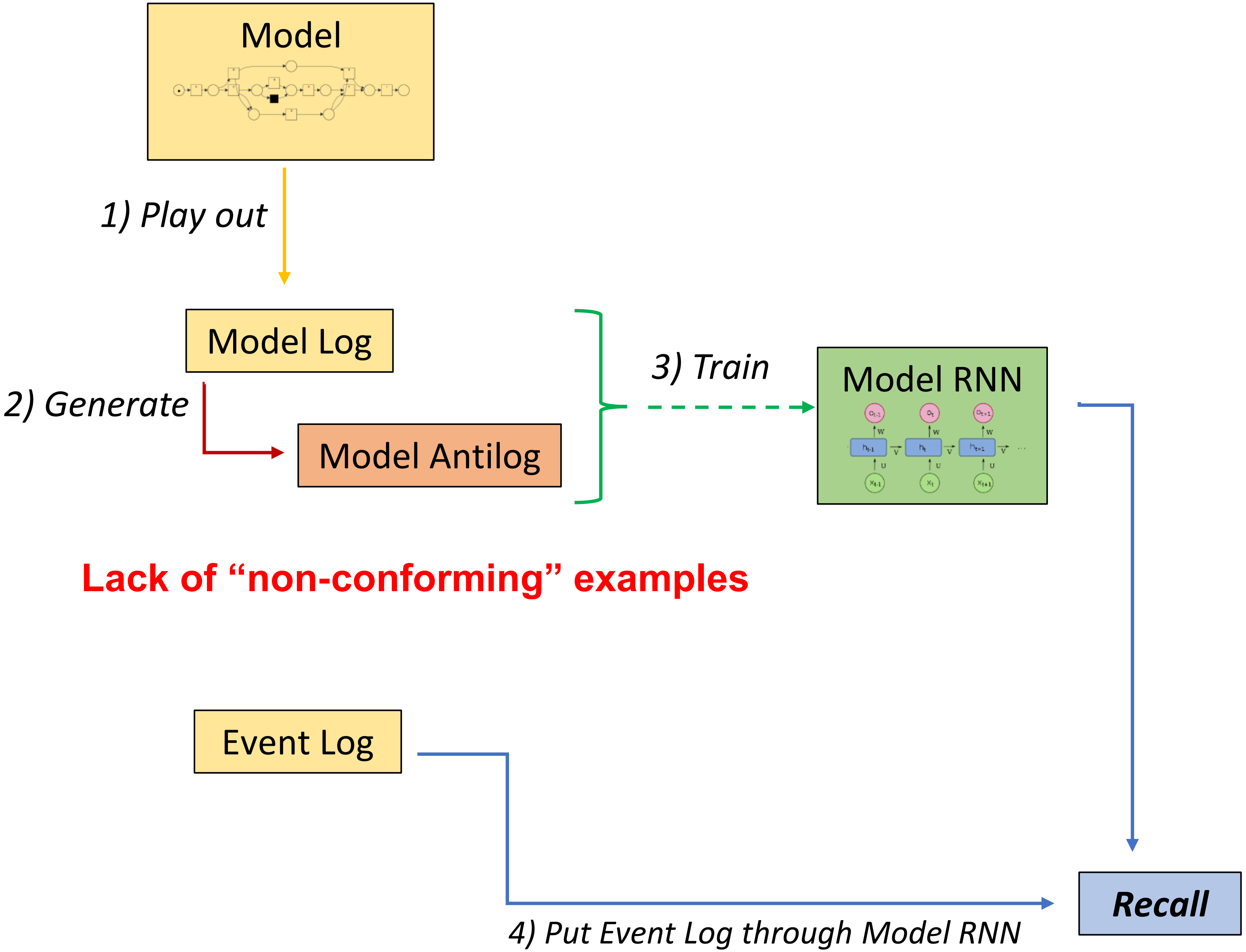
Our technique

- Depends on model simulation
    - Model log

- Antilog generation
    - Capture non-conforming behavior ≈ negative traces
    - Random
    - Other possibilities

- RNN
    - Train on either Real Event Log or Model Log
    - Use output of the other log

- Average output value over all instances (**Prob.**) or % of traces higher than threshold (**Count**)



Model

1) Play out

Model Log

2) Generate

Model Antilog

3) Train

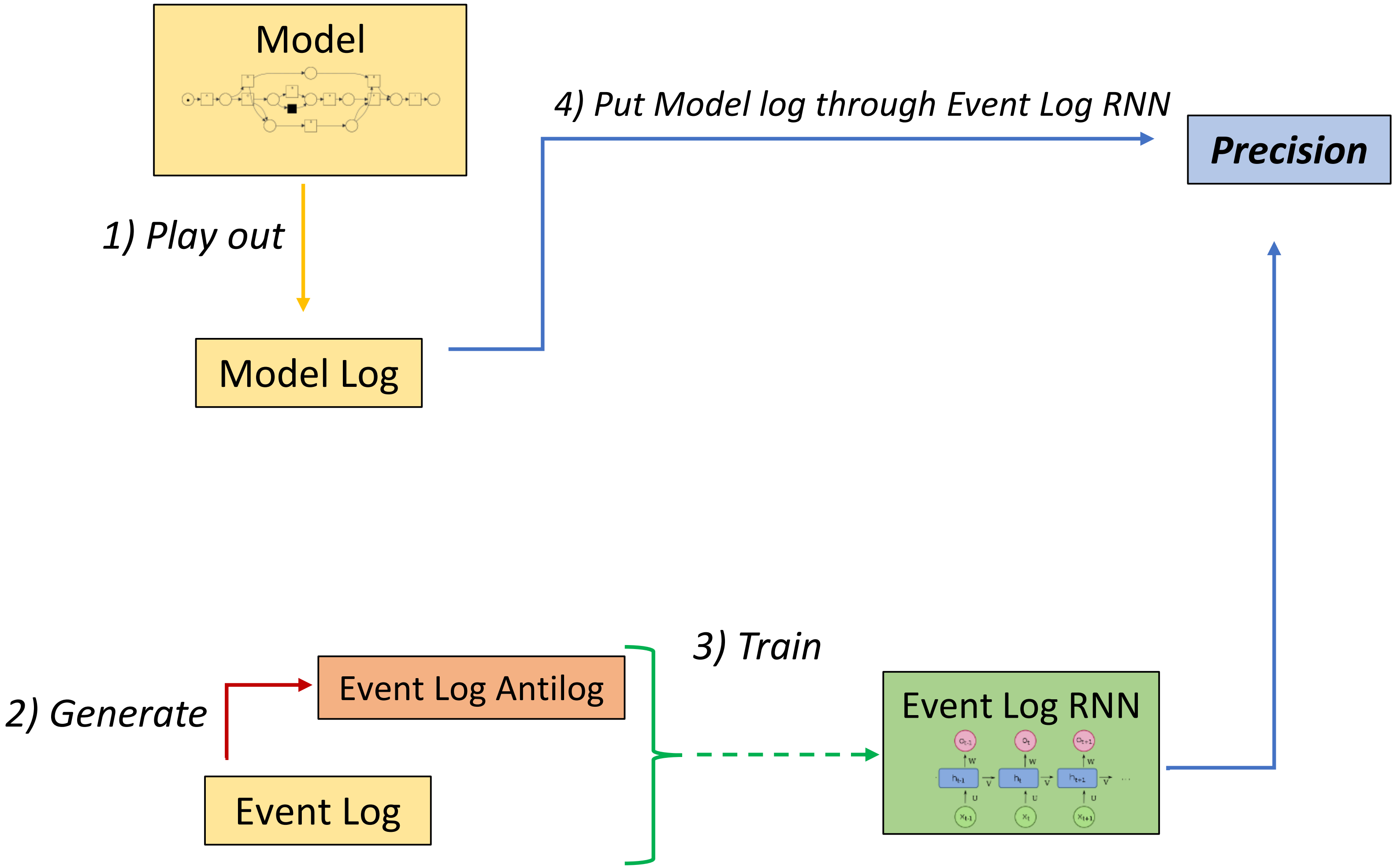
Model RNN

Lack of “non-conforming” examples

Event Log

4) Put Event Log through Model RNN

Recall



Model

1) *Play out*

Model Log

4) *Put Model log through Event Log RNN*

Precision

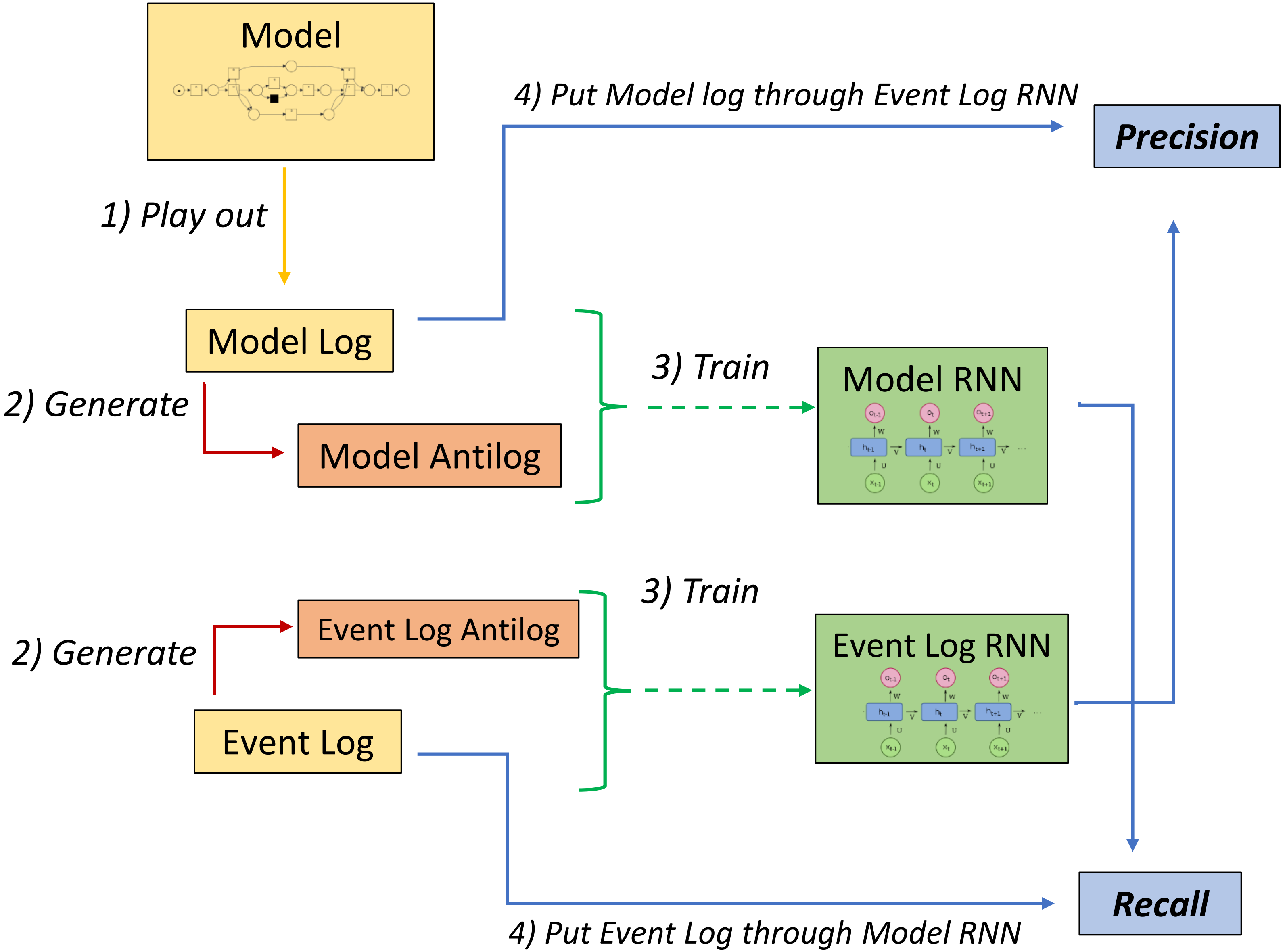
2) *Generate*

Event Log Antilog

Event Log

3) *Train*

Event Log RNN



Model

1) Play out

Model Log

2) Generate

Model Antilog

3) Train

Model RNN

4) Put Model log through Event Log RNN

Precision

Event Log Antilog

2) Generate

Event Log

3) Train

Event Log RNN

Recall

4) Put Event Log through Model RNN

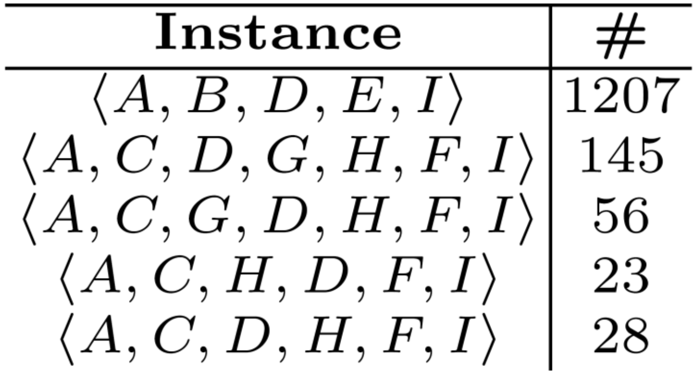
Testing

- Proof of concept global recall/precision

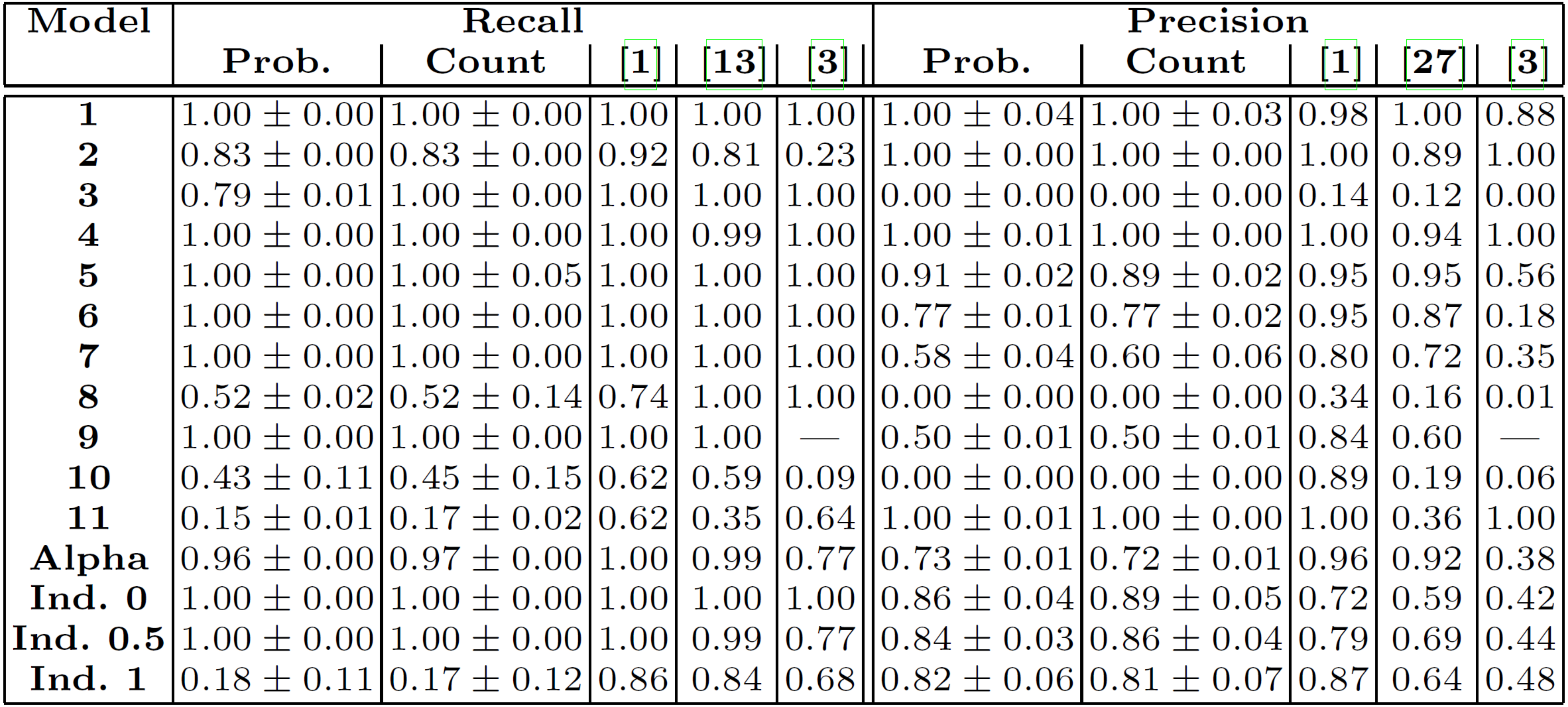
- Different models
  - With different recall/precision

- Discovered models

- Compared with literature (alignment based recall and precision, behavioral recall and precision and Markovian recall and precision)



Instance	#
$\langle A, B, D, E, I \rangle$	1207
$\langle A, C, D, G, H, F, I \rangle$	145
$\langle A, C, G, D, H, F, I \rangle$	56
$\langle A, C, H, D, F, I \rangle$	23
$\langle A, C, D, H, F, I \rangle$	28



Model	Recall					Precision				
	Prob.	Count	[1]	[13]	[3]	Prob.	Count	[1]	[27]	[3]
1	1.00 ± 0.00	1.00 ± 0.00	1.00	1.00	1.00	1.00 ± 0.04	1.00 ± 0.03	0.98	1.00	0.88
2	0.83 ± 0.00	0.83 ± 0.00	0.92	0.81	0.23	1.00 ± 0.00	1.00 ± 0.00	1.00	0.89	1.00
3	0.79 ± 0.01	1.00 ± 0.00	1.00	1.00	1.00	0.00 ± 0.00	0.00 ± 0.00	0.14	0.12	0.00
4	1.00 ± 0.00	1.00 ± 0.00	1.00	0.99	1.00	1.00 ± 0.01	1.00 ± 0.00	1.00	0.94	1.00
5	1.00 ± 0.00	1.00 ± 0.05	1.00	1.00	1.00	0.91 ± 0.02	0.89 ± 0.02	0.95	0.95	0.56
6	1.00 ± 0.00	1.00 ± 0.00	1.00	1.00	1.00	0.77 ± 0.01	0.77 ± 0.02	0.95	0.87	0.18
7	1.00 ± 0.00	1.00 ± 0.00	1.00	1.00	1.00	0.58 ± 0.04	0.60 ± 0.06	0.80	0.72	0.35
8	0.52 ± 0.02	0.52 ± 0.14	0.74	1.00	1.00	0.00 ± 0.00	0.00 ± 0.00	0.34	0.16	0.01
9	1.00 ± 0.00	1.00 ± 0.00	1.00	1.00	—	0.50 ± 0.01	0.50 ± 0.01	0.84	0.60	—
10	0.43 ± 0.11	0.45 ± 0.15	0.62	0.59	0.09	0.00 ± 0.00	0.00 ± 0.00	0.89	0.19	0.06
11	0.15 ± 0.01	0.17 ± 0.02	0.62	0.35	0.64	1.00 ± 0.01	1.00 ± 0.00	1.00	0.36	1.00
Alpha	0.96 ± 0.00	0.97 ± 0.00	1.00	0.99	0.77	0.73 ± 0.01	0.72 ± 0.01	0.96	0.92	0.38
Ind. 0	1.00 ± 0.00	1.00 ± 0.00	1.00	1.00	1.00	0.86 ± 0.04	0.89 ± 0.05	0.72	0.59	0.42
Ind. 0.5	1.00 ± 0.00	1.00 ± 0.00	1.00	0.99	0.77	0.84 ± 0.03	0.86 ± 0.04	0.79	0.69	0.44
Ind. 1	0.18 ± 0.11	0.17 ± 0.12	0.86	0.84	0.68	0.82 ± 0.06	0.81 ± 0.07	0.87	0.64	0.48

- Agrees with literature on most models

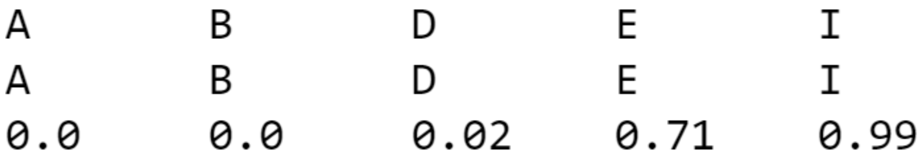
- Potential issues with overly general models (e.g. model 3 = flower)
  - Model simulation

- Other differences with literature
  - Our method puts more emphasis on most prevalent variant

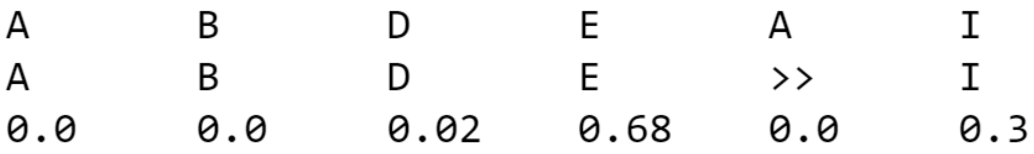
- Model log can be expanded
  - Antilog should be big enough

Other potential uses

- Using the output at each timestep to identify where the non-conforming behavior is detected.



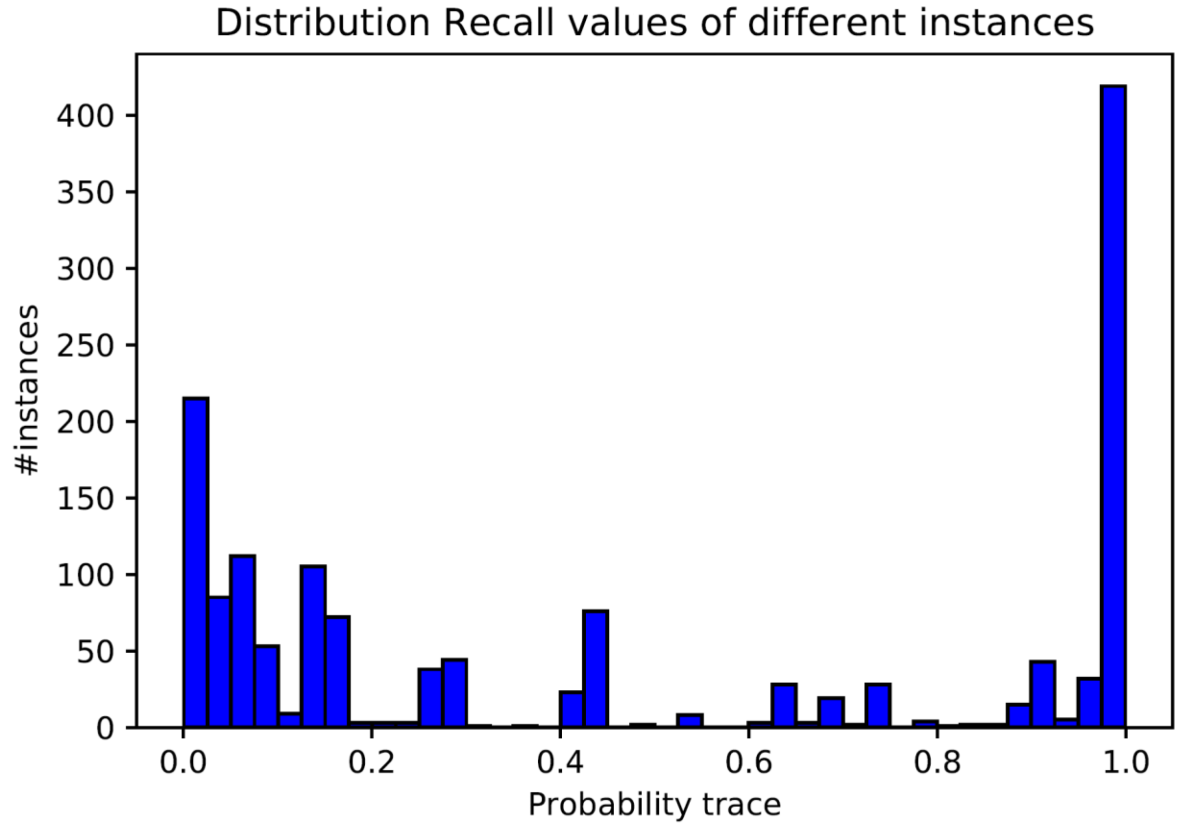
```
Trace       A      B      D      E      I
Alignment   A      B      D      E      I
Output      0.0    0.0    0.02   0.71   0.99
```



```
Trace       A      B      D      E      A      I
Alignment   A      B      D      E      >>     I
Output      0.0    0.0    0.02   0.68   0.0    0.3
```

Other potential uses

- Probability distribution
  - Individual probabilities for each instance

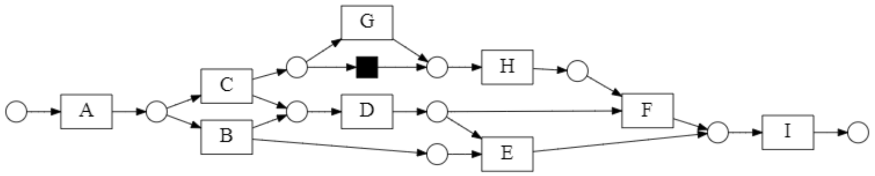


Conclusion

- New data-driven conformance checking technique
- Based on model simulation, random antilog generation and RNN’s
- Quick (once trained)
- Shows potential for global conformance analysis

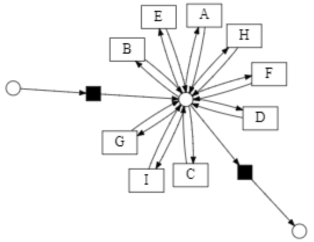
Future work

- Further local conformance possibilities
- Explore alternative antilogs
    - Negative events, noise…
- Include additional data attributes
- Directly rely on the given process model

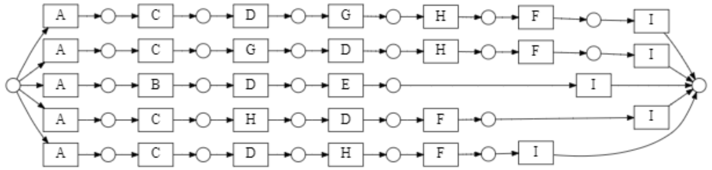


Model 1: fitting and good precision [1].

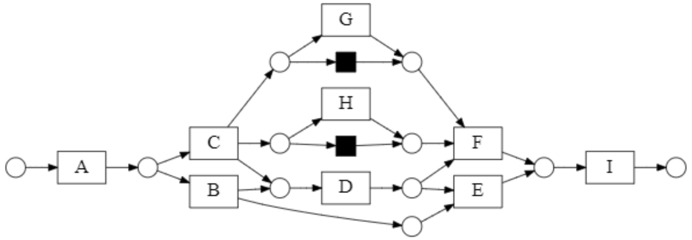
Model 2: single most frequent trace [1].



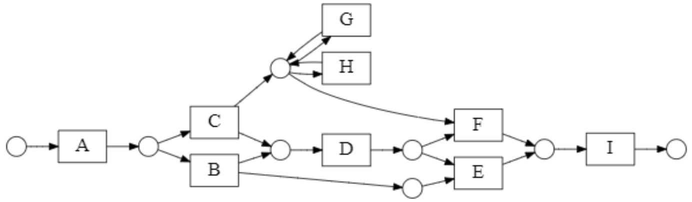
Model 3: flower model [1].



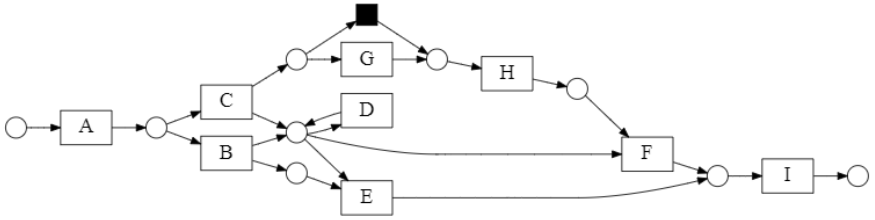
Model 4: all traces in parallel [1].



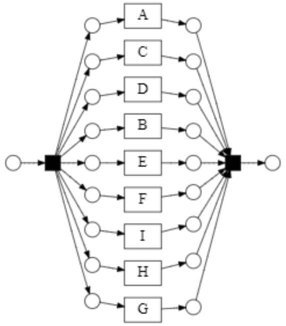
Model 5: G and H in parallel [1].



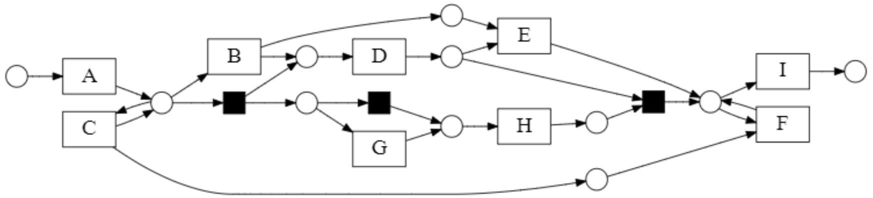
Model 6: G and H in self-loops [1].



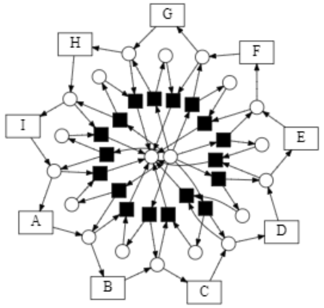
Model 7: D in a self-loop [1].



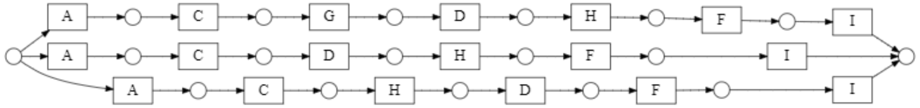
Model 8: all transitions in parallel [1].



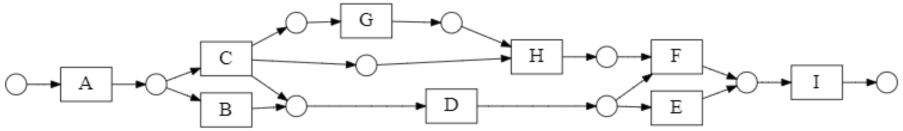
Model 9: C and F are in a loop and need to be executed the same amount to reach the final marking [1].



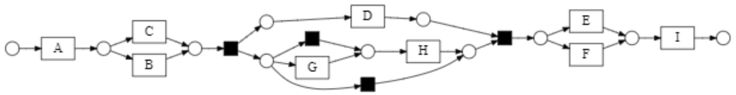
Model 10: Round-robin model [1].



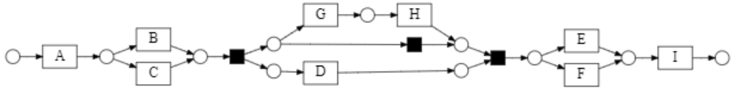
Model 11: 3 least common traces in parallel.



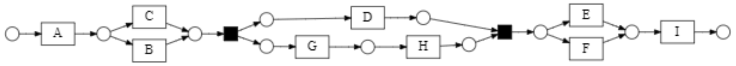
Model alpha: discovered by alpha miner [8] using the log in Table I.



Model Ind. 0: discovered by inductive miner with noise set to 0 [9] using the log in Table I.



Model Ind. 0.5: discovered by inductive miner with noise set to 0.5 [9] using the log in Table I.



Model Ind. 1: discovered by inductive miner with noise set to 1 [9] using the log in Table I.