



CSL model checking of biochemical networks with Interval Decision Diagrams

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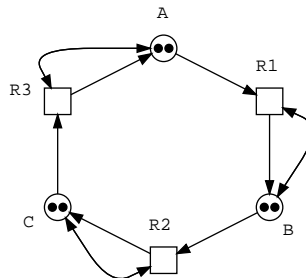
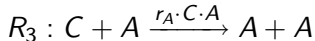
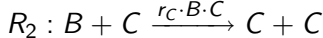
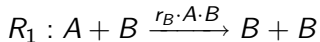
<http://www-dssz.informatik.tu-cottbus.de/software/mc.html>

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Stochastic Petri net (SPN)

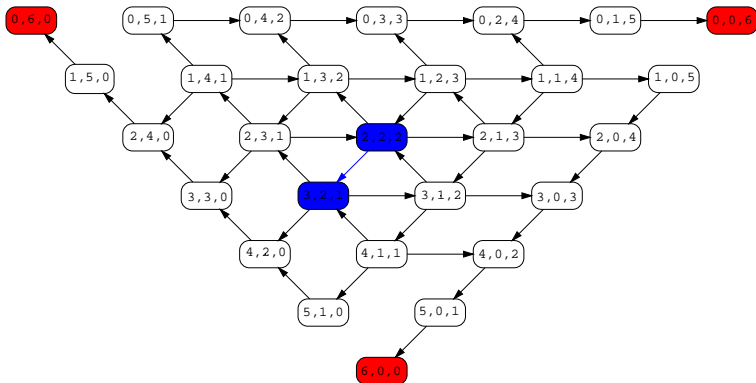


3way-oscillator model
[Ballarini2009]





Continuous Time Markov Chain (CTMC)



marking-dependent state transition rates: e.g. $(2, 2, 2) \xrightarrow{r_A \cdot 2 \cdot 2} (3, 2, 1)$



CTMC analysis



- ▶ Transient analysis
 - ▶ computation of $\underline{\pi}(\alpha, \tau)$
 - ▶ uniformisation method
- ▶ Steady state analysis
 - ▶ computation of $\underline{\pi}(\alpha)$
 - ▶ iterative methods (Jacobi, Gauss-Seidel)
- ▶ Model checking
 - ▶ Continuous Stochastic Logic (CSL)
 - ▶ can be reduced to transient and steady state analysis



CTMC analysis



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 - ▶ uniformisation method
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 - ▶ Continuous Stochastic Logic (CSL)
 - ▶ can be reduced to transient and steady state analysis

**In any case, basic operation:
multiplication of a matrix and a vector over real values.**



CTMC analysis



- ▶ Problem
 - ▶ possibly huge matrix and vector
 - ▶ explicit (**sparse**) matrix representation techniques fail
- ▶ Solutions
 - ▶ Kroneker algebra
 - ▶ Multi Terminal Binary Decision Diagrams (MTBDD)
 - ▶ matrix-free
 - ▶ sophisticated swapping (disc-based)



CTMC analysis



- ▶ Kronecker based techniques (SMART)
 - ▶ require regular models (partitioning of the place set)
- ▶ MTBDD based techniques (PRISM)
 - ▶ require prior knowledge of the boundedness degree
 - ▶ become inefficient when
 - ▶ high amount of variables \Rightarrow
must be doubled to encode a matrix
 - ▶ boundedness degree increases (binary encoding) \Rightarrow
#(BDD variables) increases
 - ▶ #(different matrix entries) increases \Rightarrow
#(terminal nodes) increases, destroys BDD compression effect

CTMC analysis



Biochemical network models

- ▶ often non-regular structure
- ▶ accurate analysis requires an high amount of tokens (molecules, concentration levels)
- ▶ many different real-valued matrix entries because of the marking-dependent rate functions

CTMC analysis



Biochemical network models

- ▶ often non-regular structure
- ▶ accurate analysis requires an high amount of tokens (molecules, concentration levels)
- ▶ many different real-valued matrix entries because of the marking-dependent rate functions

Our contribution:
a matrix-free technique based on Interval Decision Diagrams (IDD)

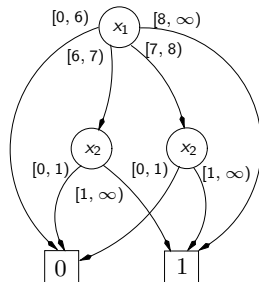


Interval Decision Diagrams



Characteristics

- ▶ $\#(\text{variables}) = \#(\text{places}) = \text{IDD height}$
- ▶ always two terminal nodes
- ▶ arcs are label with intervals over \mathbb{N}
- ▶ intervals of the outgoing arcs of a nonterminal node are a partitioning of \mathbb{N}





Matrix-free IDD-based approach



Basic ideas

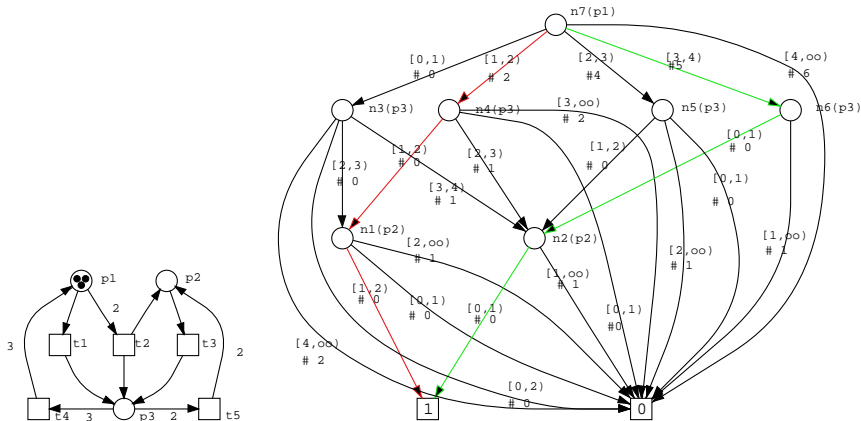
- ▶ no storage of the rate matrix
- ▶ the SPN and its state space (symbolically encoded by an IDD) represent the CTMC

CTMC = state space + net structure + rate functions

- ▶ for a state s all state transitions (s, s') and their rates are computed when needed
- ▶ defined by the firing of the transitions of the net
- ▶ forward (backward) firing means:
extracting the rows (columns) of the CTMC



Matrix-free IDD-based approach





IDD-CSL



Basics

- ▶ prototype implemented in C++
- ▶ command line tool

Features implemented so far

- ▶ subset of CSL (time bounded operators)
- ▶ Jacobi-based steady state analysis
- ▶ ordinary Place/Transition nets



Variable order

- ▶ variable order affects the size of decision diagrams
- ▶ finding an optimal order is NP complete
- ▶ solution: net structure based heuristics;
dependent places should be close together

$$W(p) := \frac{\sum_{t \in \bullet p} \frac{|\bullet t n Q|}{|\bullet t|} + \sum_{t \in p \bullet} \frac{|t \bullet n Q|}{|t \bullet|}}{|\bullet p \cup p \bullet|}$$

Q is the set of already used places

in each step select $p \in P \setminus Q$ such that $\forall p' \in P \setminus Q, p \neq p' : W(p) \geq W(p')$



Further techniques



- ▶ Caching (like PRISM)
 - ▶ no traversal of the whole IDD
 - ▶ introducing a cache layer
 - ▶ stopping traversal at the cache layer and processing the cached data (index pairs and rates)
 - ▶ problem: memory consumption for the cached data ⇒ finding the best layer
- ▶ Parallelisation
 - ▶ parallelised multiplication
 - ▶ partitioning of the state space
 - ▶ applying the traversal to the subsets



Benchmarks



- ▶ comparison with the probabilistic model checker PRISM
- ▶ 4× 2.8GHz Intel XEON, 4 GB RAM, 64bit Linux
- ▶ *only runtime*
- ▶ maximal runtime 24 h
- ▶ three biochemical networks
- ▶ different levels by multiplying the initial marking with a constant



PRISM vs. IDD-CSL



IDD-CSL is inspired by PRISM's [hybrid engine](#), there are several **Similarities**

- ▶ based on Decision Diagrams
- ▶ multiplication by DD traversal, state indices are computed using offsets during the traversal
- ▶ explicit storage of probability vectors and the diagonal entries
⇒ **for IDD-CSL the limiting factor**
- ▶ similar caching strategies

PRISM vs. IDD-CSL



Differences

PRISM

IDD-CSL



PRISM vs. IDD-CSL



Differences

	PRISM	IDD-CSL
state space	BDD	IDD

PRISM vs. IDD-CSL



Differences

	PRISM	IDD-CSL
state space	BDD	IDD
rate matrix	MTBDD	IDD + SPN



PRISM vs. IDD-CSL



Differences

	PRISM	IDD-CSL
state space	BDD	IDD
rate matrix	MTBDD	IDD + SPN
prior knowledge of the boundedness degree	yes	no



PRISM vs. IDD-CSL



Differences

	PRISM	IDD-CSL
state space	BDD	IDD
rate matrix	MTBDD	IDD + SPN
prior knowledge of the boundedness degree	yes	no
#(variables)	depends on the boundedness degree	#(places)

PRISM vs. IDD-CSL



Differences

	PRISM	IDD-CSL
state space	BDD	IDD
rate matrix	MTBDD	IDD + SPN
prior knowledge of the boundedness degree	yes	no
#(variables)	depends on the boundedness degree	#(places)
variable order	plain	heuristics



PRISM vs. IDD-CSL

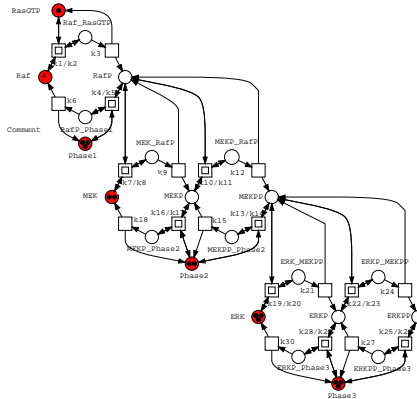


Differences

	PRISM	IDD-CSL
state space	BDD	IDD
rate matrix	MTBDD	IDD + SPN
prior knowledge of the boundedness degree	yes	no
#(variables)	depends on the boundedness degree	#(places)
variable order	plain	heuristics
rates		on-the-fly computation
	terminal nodes	



Mitogen Activated Protein Kinase [Levchenko2000]





CTMC size for different levels



levels	states	edges ^{a)}
4	24,065	206,007
8	6,110,643	78,948,888
12	315,647,600	4,958,809,056
16	6,920,337,880	122,381,517,819
20	88,125,763,956	1,689,018,298,500
24	769,371,342,640	15,635,976,824,982
28	5,084,605,436,988	108,065,356,604,208
32	27,124,071,792,125	597,236,499,605,178

^{a)} i.e., #(non-zero entries) in rate matrix;

For level 520 the MAPK model exhibits $3.40e+30$ states (IDD-CTL).



Influence of variable order



MTBDD size (PRISM) for different levels

levels	terminal nodes ^{a)}	time	original order nodes	time	good order nodes
4	30				
8	76				
12	140				
16	219				
20	320				
24	453				
28	697				
32	770				

^{a)} i.e., # (different entries) in the matrix;



Influence of variable order



MTBDD size (PRISM) for different levels

levels	terminal nodes ^{a)}	original order		good order	
		time	nodes	time	nodes
4	30	2.47	123,730		
8	76	401.68	3,881,914		
12	140	-	-		
16	219	-	-		
20	320	-	-		
24	453	-	-		
28	697	-	-		
32	770	-	-		

^{a)} i.e., # (different entries) in the matrix; - exceeds physical memory;



Influence of variable order



MTBDD size (PRISM) for different levels

levels	terminal nodes ^{a)}	original order		good order	
		time	nodes	time	nodes
4	30	2.47	123,730	0.12	8,672
8	76	401.68	3,881,914	1.56	60,452
12	140	-	-	22.99	199,496
16	219	-	-	71.25	542,339
20	320	-	-	296.87	953,146
24	453	-	-	635.92	2,029,598
28	697	-	-	928.45	3,771,617
32	770	-	-	1847.597	6,015,521

^{a)} i.e., # (different entries) in the matrix; - exceeds physical memory;



$\mathcal{P}_{>0.0}[\mathbf{F}_{[0,1]} \text{RafP} = 2]$, for 8 levels



cl ^{b)}	PRISM ^{a)}	
	total ^{c)}	iter ^{d)}
65	208.35	140.82
60	222.67	169.76
55	201.23	154.94
50	200.13	158.99
45	195.83	159.90
40	198.43	163.03
35	214.64	179.90
30	226.16	191.22
25	218.51	184.06
20	230.66	195.92
1	2318.86	2275.71

cl	IDD-CSL			
	1 thread		2 threads	
	total	iter	total	iter
3	440.23	170.06	432.77	157.08
5	158.65	110.02	158.71	99.75
7	93.84	79.48	72.71	55.01
9	84.62	75.61	62.57	50.55
10	84.49	75.04	60.81	49.17
11	90.65	81.73	64.08	52.18
13	100.40	91.39	67.47	55.97
15	127.72	118.09	81.40	69.71
17	253.60	243.05	147.85	134.09
19	692.84	676.05	387.62	368.08
21	1808.66	1771.00	957.26	917.07

^{a)} using a good variable order, determined by the network structure;

^{b)} cache layers; ^{c)} includes time for state space construction, initialisation, computation and determining the satisfying states; ^{d)} effective probability computation time;



$\mathcal{P}_{>0.0}[\mathbf{F}_{[1,1]} \text{RafP} = 2]$, for 8 levels



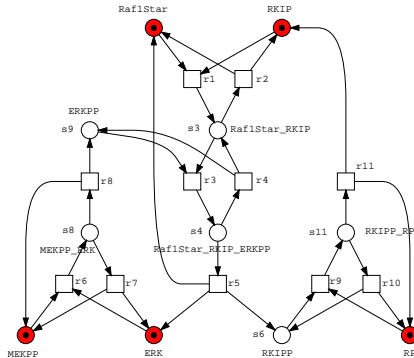
cl ^{b)}	PRISM ^{a)}	
	total ^{c)}	iter ^{d)}
65	242.80	163.05
60	231.65	170.69
55	275.53	219.89
50	222.23	173.32
45	210.13	167.48
40	209.91	168.83
35	212.23	171.38
30	211.43	170.39
25	221.78	181.28
20	231.90	192.46
1	2745.47	2691.70

cl	IDD-CSL			
	1 thread		2 threads	
	total	iter	total	iter
3	382.00	148.05	365.91	129.08
5	135.06	94.01	124.50	74.27
7	88.74	75.84	67.32	50.43
9	82.22	73.47	60.25	48.34
10	81.58	72.82	58.55	47.21
11	87.67	78.98	62.42	51.11
13	97.53	88.98	65.55	54.34
15	124.67	116.00	78.85	67.56
17	260.95	250.09	150.66	137.09
19	782.22	766.00	428.38	409.02
21	2128.20	2087.00	1150.41	1106.00

^{a)} using a good variable order, determined by the network structure;

^{b)} cache layers; ^{c)} includes time for state space construction, initialisation, computation and determining the satisfying states; ^{d)} effective probability computation time;

RKIP inhibited ERK pathway [Cho2003]





$$\mathcal{P}_{>0.0}[\mathbf{F}_{[1,1]} Raf1Star = 1]$$



level	CTMC size		PRISM ^{a)}		IDD-CSL	
	states	edges	hybrid	sparse	1 thread	2 threads
5	1,974	12,236				
10	47,047	372,372				
15	368,220	3,213,408				
20	1,696,618	15,609,594				
25	5,723,991	54,438,930				
30	15,721,464	152,964,146				

^{a)} using a good variable order, determined by the network structure;



$$\mathcal{P}_{>0.0}[\mathbf{F}_{[1,1]} Raf1Star = 1]$$



level	CTMC size		PRISM ^{a)}		IDD-CSL	
	states	edges	hybrid	sparse	1 thread	2 threads
5	1,974	12,236	0.73	0.65		
10	47,047	372,372	5.52	3.97		
15	368,220	3,213,408	†	†		
20	1,696,618	15,609,594	†	†		
25	5,723,991	54,438,930	†	†		
30	15,721,464	152,964,146	†	†		

^{a)} using a good variable order, determined by the network structure;

† time for initialisation exceeds 24 hours;



$$\mathcal{P}_{>0.0}[\mathbf{F}_{[1,1]} Raf1Star = 1]$$

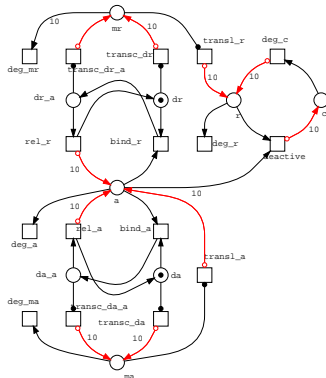


level	CTMC size		PRISM ^{a)}		IDD-CSL	
	states	edges	hybrid	sparse	1 thread	2 threads
5	1,974	12,236	0.73	0.65	0.20	0.17
10	47,047	372,372	5.52	3.97	1.27	1.05
15	368,220	3,213,408	†	†	20.73	16.67
20	1,696,618	15,609,594	†	†	148.92	118.59
25	5,723,991	54,438,930	†	†	740.28	581.39
30	15,721,464	152,964,146	†	†	3,005.62	2,455.57

^{a)} using a good variable order, determined by the network structure;

† time for initialisation exceeds 24 hours;

Circadian clock [Barkai2000]



For the experiments an ordinary SPN was used, the capacities being modelled by complementary places.

$$\mathcal{P}_{>0.0}[\mathbf{F}_{[1,1]}a = 1]$$



level	CTMC size		PRISM ^{a)}		IDD-CSL	
	states	edges	hybrid	sparse	1 thread	2 threads
5	31,104	290,160				
10	644,204	6,766,320				
15	4,194,304	45,972,480				
20	16,336,404	183,032,640				
25	47,525,504	539,650,800				
30	114,516,604	1,312,110,960				

^{a)} original model from the PRISM case study suite



$$\mathcal{P}_{>0.0}[\mathbf{F}_{[1,1]}a = 1]$$



level	CTMC size		PRISM ^{a)}		IDD-CSL	
	states	edges	hybrid	sparse	1 thread	2 threads
5	31,104	290,160	3.90	2.36		
10	644,204	6,766,320	122.55	64.94		
15	4,194,304	45,972,480	1,090.44	570.43		
20	16,336,404	183,032,640	5,569.65	2,835.89		
25	47,525,504	539,650,800	†	-		
30	114,516,604	1,312,110,960	†	-		

^{a)} original model from the PRISM case study suite

† time for initialisation exceeds 24 hours; - exceeds the physical memory;



$$\mathcal{P}_{>0.0}[\mathbf{F}_{[1,1]}a = 1]$$



level	CTMC size		PRISM ^{a)}		IDD-CSL	
	states	edges	hybrid	sparse	1 thread	2 threads
5	31,104	290,160	3.90	2.36	1.76	1.16
10	644,204	6,766,320	122.55	64.94	44.65	26.10
15	4,194,304	45,972,480	1,090.44	570.43	466.47	312.83
20	16,336,404	183,032,640	5,569.65	2,835.89	2,471.70	1,684.96
25	47,525,504	539,650,800	†	-	8,595.37	6,027.33
30	114,516,604	1,312,110,960	†	-	26,085.95	17,314.66

^{a)} original model from the PRISM case study suite

† time for initialisation exceeds 24 hours; – exceeds the physical memory;



Summary



- ▶ new symbolic matrix-free multiplication technique for the CTMC of an SPN and a probability vector
- ▶ very efficient prototype implementation of a CSL model checker
- ▶ efficiency is achieved by
 - ▶ IDD-based encoding of the state space
 - ▶ considering the Petri net structure
 - ⇒ variable order computation
 - ⇒ transition firing to extract matrix entries
 - ▶ parallelisation
- ▶ our variable order helps tuning PRISM



Outlook



- ▶ non-ordinary stochastic Petri nets with extended arcs
- ▶ steady states analysis based on Gauss-Seidel
- ▶ increasing performance
 - ▶ caching
 - ▶ parallelisation
 - ▶ controlled swapping
- ▶ porting to a cluster environment with distributed memory



Thanks for your attention.

Questions?
Demonstration?

<http://www-dssz.informatik.tu-cottbus.de/software/mc.html>